```
BLASTP 2.16.0+


Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A.
Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J.
Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of
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Reference for composition-based statistics: Alejandro A. Schaffer,
L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri
I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001),
"Improving the accuracy of PSI-BLAST protein database searches with
composition-based statistics and other refinements", Nucleic Acids
Res. 29:2994-3005.



Database: uniprotkb_refprotswissprot
           142,881,524 sequences; 55,731,415,880 total letters



Query= tr|Q3J125|Q3J125_CERS4 Cellulose synthase catalytic subunit
[UDP-forming] OS=Cereibacter sphaeroides (strain ATCC 17023 / DSM
158 / JCM 6121 / CCUG 31486 / LMG 2827 / NBRC 12203 / NCIMB 8253 /
ATH 2.4.1.) OX=272943 PE=1 SV=1

Length=788
                                                                         Score     E
Sequences producing significant alignments:                             (Bits)  Value

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  TR:S3HPC9 S3HPC9_9HYPH Cellulose synthase catalytic subunit [UDP-f...  565     0.0
  TR:A0A5D4GQK2 A0A5D4GQK2_9HYPH Cellulose synthase catalytic subuni...  565     0.0
  TR:A0ABW4M9L3 A0ABW4M9L3_9HYPH Cellulose synthase catalytic subuni...  565     0.0
  TR:A0A125Q599 A0A125Q599_9HYPH Cellulose synthase catalytic subuni...  565     0.0
  TR:A0ABU7TZN9 A0ABU7TZN9_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A9X3KGF6 A0A9X3KGF6_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A1I5KM00 A0A1I5KM00_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A7L5BLW1 A0A7L5BLW1_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0AA37H9T5 A0AA37H9T5_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0ABT0CTE6 A0ABT0CTE6_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A9W5B551 A0A9W5B551_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0ABY9KA08 A0ABY9KA08_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0AA44IYU6 A0AA44IYU6_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0ABY8RR92 A0ABY8RR92_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A1S7U1W9 A0A1S7U1W9_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A2U8W9W9 A0A2U8W9W9_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0A6N6MVW7 A0A6N6MVW7_9HYPH Cellulose synthase catalytic subuni...  564     0.0
  TR:A0ABQ4SLE8 A0ABQ4SLE8_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0ABV2NCP4 A0ABV2NCP4_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:W6RJE0 W6RJE0_9HYPH Cellulose synthase catalytic subunit [UDP-f...  563     0.0
  TR:A0A0B4XAZ2 A0A0B4XAZ2_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0A068T187 A0A068T187_NEOGA Cellulose synthase catalytic subuni...  563     0.0
  TR:A0ABU0MCJ3 A0ABU0MCJ3_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0A6L3T0K5 A0A6L3T0K5_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0ABQ4TDV6 A0ABQ4TDV6_METOR Cellulose synthase catalytic subuni...  563     0.0
  TR:A0A561QSG9 A0A561QSG9_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0A7W7YUP6 A0A7W7YUP6_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0ABD5LD58 A0ABD5LD58_AGRRD Cellulose synthase catalytic subuni...  563     0.0
  TR:A0A0J6TFL2 A0A0J6TFL2_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0ABZ2BLE2 A0ABZ2BLE2_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0AA50H747 A0AA50H747_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0A9X3QZK9 A0A9X3QZK9_9HYPH Cellulose synthase catalytic subuni...  563     0.0
  TR:A0ABN0HLS1 A0ABN0HLS1_RHILU Cellulose synthase catalytic subuni...  562     0.0
  TR:A0A549THQ6 A0A549THQ6_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0ABP2BN87 A0ABP2BN87_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0A6N8SBI2 A0A6N8SBI2_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0ABV3X165 A0ABV3X165_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0ABS4EPM3 A0ABS4EPM3_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0ABS7HGD6 A0ABS7HGD6_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0A6M1S6N4 A0A6M1S6N4_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0ABS7GT74 A0ABS7GT74_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0ABT8X7H5 A0ABT8X7H5_9HYPH Cellulose synthase catalytic subuni...  562     0.0
  TR:A0A8J6Q509 A0A8J6Q509_9HYPH Cellulose synthase catalytic subuni...  562     0.0
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TR:A0ABV2QYT9 A0ABV2QYT9_9HYPH Cellulose synthase catalytic subuni...  562     0.0
TR:A0A1C3WWX6 A0A1C3WWX6_9HYPH Cellulose synthase catalytic subuni...  562     0.0
TR:A0ABU1MD03 A0ABU1MD03_9HYPH Cellulose synthase catalytic subuni...  562     0.0
TR:A0A9Q8YF04 A0A9Q8YF04_ENSAD Cellulose synthase catalytic subuni...  562     0.0
TR:A0AA37WTB9 A0AA37WTB9_9HYPH Cellulose synthase catalytic subuni...  561     0.0
TR:A0A2U8W6R4 A0A2U8W6R4_9HYPH Cellulose synthase catalytic subuni...  561     0.0


>TR:Q3J125 Q3J125_CERS4 Cellulose synthase catalytic subunit [UDP-forming]
OS=Cereibacter sphaeroides (strain ATCC 17023 / DSM 158 /
JCM 6121 / CCUG 31486 / LMG 2827 / NBRC 12203 / NCIMB 8253
/ ATH 2.4.1.) OX=272943 GN=RSP_0333 PE=1 SV=1
Length=788

 Score = 1563 bits (4048),  Expect = 0.0
 Identities = 788/788 (100%), Positives = 788/788 (100%), Gaps = 0/788 (0%)

Query  1    MTVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA  60
            MTVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA
Sbjct  1    MTVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA  60

Query  61   DKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGF  120
            DKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGF
Sbjct  61   DKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGF  120

Query  121  LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD  180
            LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD
Sbjct  121  LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD  180

Query  181  GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE  240
            GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE
Sbjct  181  GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE  240

Query  241  LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM  300
            LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM
Sbjct  241  LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM  300

Query  301  FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI  360
            FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI
Sbjct  301  FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI  360

Query  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP  420
            DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP
Sbjct  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP  420

Query  421  LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE  480
            LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE
Sbjct  421  LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE  480

Query  481  VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLV  540
            VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLV
Sbjct  481  VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLV  540

Query  541  RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN  600
            RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN
Sbjct  541  RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN  600

Query  601  RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA  660
            RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA
Sbjct  601  RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA  660

Query  661  RREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            RREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA
Sbjct  661  RREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720

Query  721  AASLPKTARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP  780
            AASLPKTARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP
Sbjct  721  AASLPKTARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP  780
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Query  781  NTVAWGSN  788
            NTVAWGSN
Sbjct  781  NTVAWGSN  788


>TR:A0ABX5JAV1 A0ABX5JAV1_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Cereibacter johrii OX=445629 GN=C8J29_102663 PE=4
SV=1
Length=788

 Score = 1549 bits (4011),  Expect = 0.0
 Identities = 780/788 (99%), Positives = 782/788 (99%), Gaps = 0/788 (0%)

Query  1    MTVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA  60
            MTVRAKARSP+RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA
Sbjct  1    MTVRAKARSPIRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA  60

Query  61   DKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGF  120
            D+MVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLF VETFSISIFFLNGF
Sbjct  61   DRMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFTVETFSISIFFLNGF  120

Query  121  LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD  180
            LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD
Sbjct  121  LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD  180

Query  181  GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE  240
            GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE
Sbjct  181  GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE  240

Query  241  LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM  300
            LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM
Sbjct  241  LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM  300

Query  301  FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI  360
            FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI
Sbjct  301  FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI  360

Query  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP  420
            DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP
Sbjct  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP  420

Query  421  LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE  480
            LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE
Sbjct  421  LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE  480

Query  481  VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLV  540
            VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGV A LV
Sbjct  481  VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVFAALV  540

Query  541  RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN  600
            RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN
Sbjct  541  RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN  600

Query  601  RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA  660
            RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA
Sbjct  601  RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA  660

Query  661  RREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            RREGGTVMVGVIFEAGQP AVRETVAYLIFGESAHWRTMREAT RPIGLLHGMARILWMA
Sbjct  661  RREGGTVMVGVIFEAGQPTAVRETVAYLIFGESAHWRTMREATTRPIGLLHGMARILWMA  720

Query  721  AASLPKTARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP  780
            AASLPKTARDFMDEPARRRRR EEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP
Sbjct  721  AASLPKTARDFMDEPARRRRRQEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP  780

Query  781  NTVAWGSN  788
            NTVAWGSN
Sbjct  781  NTVAWGSN  788
```

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>TR:A0A2T5K0D2 A0A2T5K0D2_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Cereibacter azotoformans OX=43057 GN=C8J28_11321 PE=4
SV=1
Length=788

 Score = 1394 bits (3609),  Expect = 0.0
 Identities = 686/788 (87%), Positives = 736/788 (93%), Gaps = 0/788 (0%)

Query  1    MTVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA  60
            MT R  AR+  RV+P+ LFL+W ALLVPF LLAAAPVAPSAQGLIALSAV+LVA+LKPFA
Sbjct  1    MTDRTAARARSRVLPLFLFLMWAALLVPFALLAAAPVAPSAQGLIALSAVLLVAVLKPFA  60

Query  61   DKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGF  120
              MVPRFLLLSAASMLVMRYWFWRLFETLPPPALD SF+FA+LLFAVETFSI IFFLNGF
Sbjct  61   SHMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDPSFVFAMLLFAVETFSIGIFFLNGF  120

Query  121  LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD  180
            LSADPTDRPFP  +QPE+LPTVDILVPSYNEPADMLSVTL+AAKNMIYP+RLRTVVLCDD
Sbjct  121  LSADPTDRPFPPQVQPEDLPTVDILVPSYNEPADMLSVTLSAAKNMIYPSRLRTVVLCDD  180

Query  181  GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE  240
            GGTDQRC+SPDPE+A++AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKG+
Sbjct  181  GGTDQRCLSPDPEIARQAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGD  240

Query  241  LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM  300
            LVVVFDADHVPSRDFLARTVGYFVEDP LFLVQTPHFFINPDPIQRNLALGD CPPENEM
Sbjct  241  LVVVFDADHVPSRDFLARTVGYFVEDPKLFLVQTPHFFINPDPIQRNLALGDDCPPENEM  300

Query  301  FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI  360
            FY KIHRGLDRWGGAFFCGSAAVLRRRALD+ GGFAGETITEDAETALEIH+RGWKSLYI
Sbjct  301  FYAKIHRGLDRWGGAFFCGSAAVLRRRALDDVGGFAGETITEDAETALEIHARGWKSLYI  360

Query  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP  420
            DRAMIAGLQPETFASFIQQRGRWATGMMQML LKNPLFR GLGIAQRLCYLNSMSFWFFP
Sbjct  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLRLKNPLFRPGLGIAQRLCYLNSMSFWFFP  420

Query  421  LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE  480
            LVRM FL+APLIYLFFG+++FVATFEEVLAYMPGYLAVSFLVQNALF+RQRWPLVSEVYE
Sbjct  421  LVRMTFLIAPLIYLFFGVQVFVATFEEVLAYMPGYLAVSFLVQNALFSRQRWPLVSEVYE  480

Query  481  VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLV  540
            VAQAPYL+RA++ TLLRPR ARFAVTAKDETLSENYISPIYRPLL TFLLC +GV A+LV
Sbjct  481  VAQAPYLSRAVIGTLLRPRGARFAVTAKDETLSENYISPIYRPLLLTFLLCAAGVAASLV  540

Query  541  RWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN  600
            RWVAFPGDRSVLLVVGGWA+ N +LVGFALRAVAEKQQRR APRV MEVPAEAQ+PAFGN
Sbjct  541  RWVAFPGDRSVLLVVGGWALFNFVLVGFALRAVAEKQQRRTAPRVHMEVPAEAQLPAFGN  600

Query  601  RSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA  660
            R L ATVLDAST GVRLL+RLPG GDP PA+E GG+IQFQPKFPDAPQLERMVRGRIRSA
Sbjct  601  RPLAATVLDASTRGVRLLLRLPGSGDPRPAIEPGGMIQFQPKFPDAPQLERMVRGRIRSA  660

Query  661  RREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            RR+GGTVM+G++FEA QPIAVRETVAYLIFGESAHWRTMREAT +P+GLL G+ RILW A
Sbjct  661  RRDGGTVMIGMVFEADQPIAVRETVAYLIFGESAHWRTMREATSQPMGLLRGLGRILWKA  720

Query  721  AASLPKTARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARP  780
             ASLP TA DF+ EPARR+RR EEP E+QAHLLAFGTDF+TE DW  +LLDPT+QV+ RP
Sbjct  721  VASLPSTAGDFLAEPARRKRRREEPVERQAHLLAFGTDFATEADWQDDLLDPTSQVAPRP  780

Query  781  NTVAWGSN  788
             TVAWG+N
Sbjct  781  GTVAWGAN  788


>TR:A0A2T4JQ26 A0A2T4JQ26_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Cereibacter changlensis JA139 OX=1188249 GN=bcsA PE=4
SV=1
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Length=787

 Score = 1096 bits (2834),  Expect = 0.0
 Identities = 538/772 (70%), Positives = 633/772 (82%), Gaps = 1/772 (0%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+  LWV LLVP  LLA+ P + +AQ ++A++ VV+VA+LKPFA+ +  RF L++ AS+
Sbjct  15   LILALWVLLLVPVALLASVPTSTTAQAMLAIATVVVVAVLKPFAEHIGVRFFLIATASVS  74

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            VMRYW WRL ETLPP  L  SF+   +LFA+ET+SI +FFLNGFL+ADPT+RPFP  +
Sbjct  75   VMRYWSWRLHETLPPVGLTPSFIIGAILFAIETYSILVFFLNGFLTADPTERPFPPKVAT  134

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E+LP VDILVPSYNEP +MLSVTL+AAKNMIYPARLRTVVLCDDGGTDQRC S DPELAQ
Sbjct  135  EDLPRVDILVPSYNEPTEMLSVTLSAAKNMIYPARLRTVVLCDDGGTDQRCQSDDPELAQ  194

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            K+Q RRRELQQLCR+LGV YSTR RNE+AKAGNMSAALE+L G+LVVVFDADHVPSRDFL
Sbjct  195  KSQARRRELQQLCRDLGVTYSTRARNENAKAGNMSAALEKLNGDLVVVFDADHVPSRDFL  254

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            ARTVGYFVEDP LFLVQTPHFFIN DPIQRNL L + CPPENEMFY  IHRGLDRWGGAF
Sbjct  255  ARTVGYFVEDPKLFLVQTPHFFINKDPIQRNLGLSEECPPENEMFYSFIHRGLDRWGGAF  314

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR+ALD  GGFAGETITEDAETALEIH+ GWKSLYI+RAMIAGLQPETFASF
Sbjct  315  FCGSAAVLRRKALDSVGGFAGETITEDAETALEIHASGWKSLYINRAMIAGLQPETFASF  374

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWA GMMQML+LKNPLFRRGLG  QRLCY+NSMSFW FP+VRM+FL+APL+YLFF
Sbjct  375  IQQRGRWAAGMMQMLMLKNPLFRRGLGATQRLCYINSMSFWLFPIVRMVFLLAPLVYLFF  434

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            GI+IFV+TFEEVLAY  GYLA+SF+VQNALFAR RWPL+SE+YEVAQAPYLA+A++ TL+
Sbjct  435  GIQIFVSTFEEVLAYALGYLAISFMVQNALFARHRWPLISEIYEVAQAPYLAKAVIGTLI  494

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            +PR A+F VTAKDETLSE+YISPIY+PLL  FLL L+GV+A ++RW+AFPGDRSVL VVG
Sbjct  495  KPRGAKFNVTAKDETLSEDYISPIYKPLLAVFLLMLAGVVALVIRWIAFPGDRSVLAVVG  554

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GWA+ N LL+  ALRAVAEKQQRR+APRV M+  AE +  + G+ ++ A VLDAST G R
Sbjct  555  GWAIFNFLLMSLALRAVAEKQQRRSAPRVLMQTTAEVRASSLGDLAMPAMVLDASTGGAR  614

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            + +RLP   +   ++E G  + F+P FPDAP LER VR R+R   REG TV VG++F+A
Sbjct  615  VTLRLPPSTEGRVSIEPGETLHFKPSFPDAPHLERPVRARVRMVTREGATVTVGLLFDAD  674

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPA  736
            Q   VRETVAYLIFGES +W  MR++T R  G+L GM  +LW+A AS+P+T RDF+ EPA
Sbjct  675  QSFEVRETVAYLIFGESENWLRMRQSTSRRKGMLAGMGYVLWLAIASIPRTLRDFLREPA  734

Query  737  RRRRRH-EEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARPNTVAWGS  787
            RR R   E+P+ K AHLLAFG DFS E D     +   A V A  + +  G+
Sbjct  735  RRSRLDVEQPRSKPAHLLAFGADFSRETDTPAPAVPVVAVVDAPVSPILRGA  786


>TR:A0ABW4S7K5 A0ABW4S7K5_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Halodurantibacterium flavum OX=1382802 GN=bcsA PE=4
SV=1
Length=786

 Score = 1011 bits (2615),  Expect = 0.0
 Identities = 502/750 (67%), Positives = 593/750 (79%), Gaps = 4/750 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+ LLW+ +LVP  ++  AP +   QGL+ ++AV++VALLKP ++    RFLL++ AS++
Sbjct  14   LMLLLWLVMLVPIMVMVMAPTSTFTQGLLGVTAVIIVALLKPLSELRPVRFLLMATASVI  73
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Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RYWFWRL  TLPPP L   F+FA+ LF VET++I +FFLN  L+ADPT+RP P  + P
Sbjct  74   VLRYWFWRLTTTLPPPGLTPDFIFAVALFVVETYAIMVFFLNALLTADPTERPMPPQVAP  133

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            ++LPTVD+LVPSYNEP +MLSVTL+AAKNMIYP   RTVVLCDDGGTDQRCMS +PELA+
Sbjct  134  DDLPTVDVLVPSYNEPIEMLSVTLSAAKNMIYPTHKRTVVLCDDGGTDQRCMSDNPELAK  193

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             AQERRR+LQ LC ELGV YSTRERN HAKAGNMSAALERL G+LVVVFDADHVPSRDFL
Sbjct  194  AAQERRRDLQALCAELGVTYSTRERNVHAKAGNMSAALERLNGDLVVVFDADHVPSRDFL  253

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            ARTVGYFV+DP LFLVQTPHFFIN DPIQRNL L  RCPPENEMFY  IHRGLDRWGGAF
Sbjct  254  ARTVGYFVDDPKLFLVQTPHFFINKDPIQRNLDLSPRCPPENEMFYSFIHRGLDRWGGAF  313

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR ALD  GGF+GETITEDAETAL+IHSRGWKSLYI+RAMI GLQPETFASF
Sbjct  314  FCGSAAVLRREALDSVGGFSGETITEDAETALDIHSRGWKSLYINRAMIGGLQPETFASF  373

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWA+GMMQML+LKNPLFRRGLG+ QRLCYLNSMSFWFFPLVR+ FL+APLIYLFF
Sbjct  374  IQQRGRWASGMMQMLMLKNPLFRRGLGLTQRLCYLNSMSFWFFPLVRLTFLLAPLIYLFF  433

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            GIEIFV+TF+EV  Y+  Y+A+SF+VQNALFAR RWPL+SE+YEVAQAPYLA AI  T+ 
Sbjct  434  GIEIFVSTFDEVAVYVFTYMAISFMVQNALFARYRWPLISEIYEVAQAPYLATAIFRTIW  493

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            +PR+A+FAVTAKDETL+ENYISPIY PLL  FLL  +G++A  +RWVAFPGDR+VL+VVG
Sbjct  494  KPRAAKFAVTAKDETLAENYISPIYWPLLTLFLLTFAGLVALGIRWVAFPGDRAVLMVVG  553

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GWA+ N LLV  ALR+VAEKQQRRAAPR    VP+   +    +     TVLDASTSG +
Sbjct  554  GWAIFNFLLVSLALRSVAEKQQRRAAPRTDTNVPSTVWLDGAPDEVFDGTVLDASTSGAK  613

Query  617  LLVRLP---GVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIF  673
            LLV  P      D       G +I F+PK P+AP +E+ VR  IRSA       ++G+ F
Sbjct  614  LLVARPRRFDSADQQRRFAPGDVIVFRPKLPEAPHIEQPVRATIRSAGSNPEGAVLGLSF  673

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
               Q +AV+  VAYLIFG+S +W  +R+ + R  G+L GM  + W+A  S+PKT  DF  
Sbjct  674  LPNQSVAVQGAVAYLIFGDSENWVRVRQFSQRRKGMLAGMGYVFWLALRSIPKTFMDFAR  733

Query  734  EPARRRR-RHEEPKEKQAHLLAFGTDFSTE  762
            EPARR+R      + + AHLLAFG DF  E
Sbjct  734  EPARRKRVATAGTRRRGAHLLAFGADFVEE  763


>TR:A0A844HM69 A0A844HM69_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus litorisediminis OX=2006130 GN=bcsA PE=4
SV=1
Length=773

 Score = 982 bits (2538),  Expect = 0.0
 Identities = 495/756 (65%), Positives = 591/756 (78%), Gaps = 8/756 (1%)

Query  10   PLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLL  69
            PLR+V   L  LWVA L+P  +L++APV+  AQG++ + AV++V LLKPF   +V R   
Sbjct  2    PLRIV---LLALWVATLIPVFILSSAPVSNMAQGMLGIVAVLMVMLLKPFTSNIVARTAF  58

Query  70   LSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRP  129
            ++ AS++V+RYWFWR+  TLP P L+ASF+FA+LL  VET+SI +FFL GF++ADP +R 
Sbjct  59   VAVASVVVLRYWFWRVTATLPEPGLNASFVFAVLLLIVETYSILVFFLGGFITADPLERG  118

Query  130  FPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMS  189
             P  ++ ++LPTVDILVPSYNEP +MLS+TL+AAKNM+YPA  R VVLCDDGGTDQRC S
Sbjct  119  LPPKVELDQLPTVDILVPSYNEPTEMLSITLSAAKNMVYPASRRRVVLCDDGGTDQRCNS  178
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Query  190  PDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADH  249
            PDPELA +++ RR ELQ LC ELGV+YSTR RNEHAKAGNMSAALERL G+LVVVFDADH
Sbjct  179  PDPELAARSRARRAELQALCAELGVIYSTRARNEHAKAGNMSAALERLDGDLVVVFDADH  238

Query  250  VPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGL  309
            VPSRDFLARTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGL
Sbjct  239  VPSRDFLARTVGYFAQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGL  296

Query  310  DRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQ  369
            DRWGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALEIHSRGW+SLYIDRAMIAGLQ
Sbjct  297  DRWGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSRGWRSLYIDRAMIAGLQ  356

Query  370  PETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVA  429
            PETF SFIQQRGRWA+GM+QML+LKNPLFR GL   QRLCY+NSMSFWFFPL+R+++++A
Sbjct  357  PETFVSFIQQRGRWASGMVQMLMLKNPLFRPGLKPLQRLCYINSMSFWFFPLIRLVYIIA  416

Query  430  PLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLAR  489
            PL YLFFG+EI V TF+E +AY+  Y+AV  +VQN +FAR RWPL+SE+YEVAQAPYLA
Sbjct  417  PLTYLFFGVEIVVTTFQEAMAYVLSYMAVVLMVQNGIFARYRWPLISEIYEVAQAPYLAT  476

Query  490  AIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDR  549
            +I  T+LRPR+A+F VTAKDETL+ENYISPIY+PLL  F L L+GV+A +VRW+AFPGDR
Sbjct  477  SIFRTILRPRAAKFNVTAKDETLAENYISPIYKPLLGLFGLTLAGVIALVVRWIAFPGDR  536

Query  550  SVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLD  609
            SVL VVG WAV+N+LLV  +LRAV+EKQQRRAAPRV ++VPA       G   L ATVLD
Sbjct  537  SVLSVVGVWAVINLLLVSLSLRAVSEKQQRRAAPRVAIDVPATISWANSGPFPLKATVLD  596

Query  610  ASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTV-M  668
             STSG +L V  P  G     +  G  I F+P+F +AP LE+ VR  +   +       +
Sbjct  597  VSTSGAQLRVDQPPSGKDARMVRVGDEISFRPRFDNAPHLEQNVRAVVLGIKNGANNANL  656

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            +GV F   QPI VRE VA LIFG S  W   REA     GLL G+A I+ +   S+PKT
Sbjct  657  LGVRFLPDQPIVVREVVAQLIFGNSETWLMQREANREGKGLLAGLAYIIGLMVTSIPKTI  716

Query  729  RDFMDEPARRRR--RHEEPKEKQAHLLAFGTDFSTE  762
             DFM EPARRRR  R +   +K AHL+AFG DF T+
Sbjct  717  SDFMREPARRRRNARMQHQGQKPAHLMAFGADFDTD  752


>TR:A0A6L6JEM8 A0A6L6JEM8_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus aestuariivivens OX=1820333 GN=bcsA PE=4
SV=1
Length=777

 Score = 969 bits (2505),  Expect = 0.0
 Identities = 486/750 (65%), Positives = 585/750 (78%), Gaps = 9/750 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            +L  LW+  L+P  +L+A PV+ +AQ ++ L+AV LV LLKPF+   + R  L++ +S++
Sbjct  10   ILTTLWIVTLIPVIVLSAIPVSNAAQAMLGLAAVALVVLLKPFSSNTIARTALVAVSSIV  69

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RYWFWR+  TLP P L+ASF+FA+LL  VET+SI +FFL GF++ADP DR  P  ++
Sbjct  70   VLRYWFWRVTATLPEPGLNASFIFAILLLLVETYSILVFFLGGFITADPLDRGLPPKVEL  129

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E+LPTVDILVPSYNEP +MLS+TL+AAKNM+YPA  R VVLCDDGGTDQRC SPDPELA
Sbjct  130  EDLPTVDILVPSYNEPIEMLSITLSAAKNMVYPASRRRVVLCDDGGTDQRCNSPDPELAA  189

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ LC ELG++YSTR RNEHAKAGNMSAALERL G+LVVVFDADHVPSRDFL
Sbjct  190  RARARRAELQALCAELGIIYSTRARNEHAKAGNMSAALERLDGDLVVVFDADHVPSRDFL  249

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            ARTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGLDRWGGAF
Sbjct  250  ARTVGYFAQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGLDRWGGAF  307
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Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR+ALD  GGFAGETITEDAETALEIH+RGW+SLY+DRAMIAGLQPETF SF
Sbjct  308  FCGSAAVLRRKALDSVGGFAGETITEDAETALEIHARGWRSLYLDRAMIAGLQPETFVSF  367

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWA+GM+QML+LKNPLFR GL   QRLCY+NSMSFWFFPLVR+++++APL YLFF
Sbjct  368  IQQRGRWASGMVQMLMLKNPLFRPGLKPLQRLCYINSMSFWFFPLVRLVYILAPLTYLFF  427

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+EI V TF+E +AY+  Y+AV  LVQNA+FAR RWPL+SE+YEVAQAPYLA +I  T+
Sbjct  428  GVEIVVTTFQEAMAYVLSYMAVVLLVQNAIFARYRWPLISEIYEVAQAPYLASSIFRTIF  487

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            RPR A+F VTAKDETL+E+Y SPI+ PLL  F L ++GV+A L RW+AFPGDRSVL VVG
Sbjct  488  RPRGAKFNVTAKDETLAEDYTSPIFGPLLGLFGLTVAGVVALLARWIAFPGDRSVLSVVG  547

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             WAV+N+LLV  +LR+V+EKQQRRA+PRV +  PA A     G+  L AT++D STSG +
Sbjct  548  VWAVINLLLVSLSLRSVSEKQQRRASPRVTINAPAVASWAGSGSVPLKATIIDVSTSGAQ  607

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRS---ARREGGTVMVGVIF  673
            + V      +    +  G  I F+P F DAP LE+ V   + S   + ++G T   GV F
Sbjct  608  IRVDQANRAESTRPIRQGDEISFRPLFSDAPHLEQDVHATVLSVLNSAKQGTT--FGVRF  665

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
             A QP+ VRETVA +IFG S  WR  REAT    GL+ G+  I+W+   S+PKT RDFM
Sbjct  666  IADQPLRVRETVAQMIFGSSEVWRMQREATRGRKGLIAGLFYIIWLMITSIPKTFRDFMR  725

Query  734  EPARRRRRH--EEPKEKQAHLLAFGTDFST  761
            EPARRRR        EK AHL+AFGTDF T
Sbjct  726  EPARRRRNALVSTQSEKPAHLMAFGTDFDT  755


>TR:A0ABW7LG88 A0ABW7LG88_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus broussonetiae subsp. drimophilus OX=3373869
GN=bcsA PE=4 SV=1
Length=771

 Score = 965 bits (2495),  Expect = 0.0
 Identities = 487/750 (65%), Positives = 580/750 (77%), Gaps = 7/750 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            LL  LWV  LVP  +L+AAPV+  AQ ++ + AV+LV +LKPF   +  R  L+  AS++
Sbjct  4    LLMSLWVLALVPVFILSAAPVSNMAQAMLGVVAVLLVMILKPFTTNIAARMALVGVASVV  63

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RYWFWR+  TLP P L ASF+FA+LL  VET+SI +FFL GF++ADP +R  P  ++
Sbjct  64   VLRYWFWRVTATLPEPELSASFVFAVLLLVVETYSILVFFLGGFITADPLERGLPPKVEL  123

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LPTVDILVPSYNEP +MLS+TL+AAKNM+YPA  R VVLCDDGGTDQRC S DPELA
Sbjct  124  ENLPTVDILVPSYNEPVEMLSITLSAAKNMVYPASRRRVVLCDDGGTDQRCNSSDPELAA  183

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ+LC EL V+YSTR +NEHAKAGNMSAALERL G+LVVVFDADHVPSRDFL
Sbjct  184  RARARRAELQKLCEELNVIYSTRAKNEHAKAGNMSAALERLDGDLVVVFDADHVPSRDFL  243

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            ARTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGLDRWGGAF
Sbjct  244  ARTVGYFAQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGLDRWGGAF  301

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR+ALD  GGFAGETITEDAETALEIHSRGW+SLYIDRAMIAGLQPETF SF
Sbjct  302  FCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSRGWRSLYIDRAMIAGLQPETFVSF  361

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWA+GM+QML+LKNPLFRRGL   QRLCY+NSMSFWFFPL+R+++++APL YLFF
Sbjct  362  IQQRGRWASGMVQMLMLKNPLFRRGLKPLQRLCYINSMSFWFFPLIRLVYIIAPLTYLFF  421
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Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+EI V TF+E + Y+  Y+AV  LVQN +FAR RWPL+SE+YE+AQAPYLA AI  T+L
Sbjct  422  GVEIVVTTFQEAMTYVLSYMAVVLLVQNGIFARYRWPLISEIYEIAQAPYLATAIFRTIL  481

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            RPR+A+FAVTAKDETL+ENYISPIY+PLL  F L L+GV+A + RW+AFPGDRSVL VVG
Sbjct  482  RPRAAKFAVTAKDETLAENYISPIYKPLLGLFALTLAGVIALVARWIAFPGDRSVLSVVG  541

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             WAV+N+LLV  +LRAV+EKQQRR+APR+ + VP      + G   L  TVLD STSG
Sbjct  542  VWAVINLLLVSLSLRAVSEKQQRRSAPRIAISVPTTISWASCGPFPLKGTVLDVSTSGAH  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARR--EGGTVMVGVIFE  674
            L +     G     +  G  I F+P+F +A  LE+ VR  + + +   + GT + GV F
Sbjct  602  LRLDQTPQGKDARMIRQGDEISFRPRFENATHLEQNVRAVVLALQNSAQNGTTL-GVRFL  660

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDE  734
              QP+AVRE VA LIFG S  W   REAT    GL  G+  I+ +   S+PKT  DFM E
Sbjct  661  PDQPMAVREVVAQLIFGSSETWLAQREATREGKGLTAGLLYIVGLMLTSIPKTISDFMRE  720

Query  735  PARRRR--RHEEPKEKQAHLLAFGTDFSTE  762
            PARRRR  R ++  +K AHL+AFG DF TE
Sbjct  721  PARRRRNARAQQMDQKPAHLMAFGADFDTE  750


>TR:A0ABV6I940 A0ABV6I940_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus niistensis OX=632935 GN=bcsA PE=4 SV=1
Length=783

 Score = 965 bits (2494),  Expect = 0.0
 Identities = 489/763 (64%), Positives = 590/763 (77%), Gaps = 13/763 (2%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPR  66
            A+S  ++   +LF +W   L+P  +LA+ PV+ +AQG+  L+AV+LV LLKPF+  M  R
Sbjct  6    AKSRRKLSRAVLFPIWGLALIPVLVLASVPVSNTAQGMFGLAAVLLVILLKPFSASMPVR  65

Query  67   FLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPT  126
              LL+ AS++V+RYW WR+  TLP P + ASF+FA +L  VET+SI +FFLN F++ADP
Sbjct  66   VTLLAIASVIVLRYWLWRVTATLPDPGMSASFIFATILLLVETYSIFVFFLNAFITADPV  125

Query  127  DRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQR  186
            +R  P  ++ E+LPTVDILVPSYNE  +MLSVTL+AAKNMIYPA+LR VVLCDDGGTDQR
Sbjct  126  ERGLPPKVELEDLPTVDILVPSYNEAVEMLSVTLSAAKNMIYPAKLRRVVLCDDGGTDQR  185

Query  187  CMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFD  246
            C SPDPELA  A+ RR ELQ LCRELGV+YSTR RNE AKAGNMSAALERL G+LVV+FD
Sbjct  186  CNSPDPELAAAARHRRAELQALCRELGVIYSTRARNEQAKAGNMSAALERLDGDLVVIFD  245

Query  247  ADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIH  306
            ADHVPSRDFLARTVGYFV+DP LFLVQTPH+FIN DPI+RNL L  + PPE+EMFYG IH
Sbjct  246  ADHVPSRDFLARTVGYFVQDPKLFLVQTPHYFINRDPIERNLNL--KSPPESEMFYGMIH  303

Query  307  RGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIA  366
            RGLDRWGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALEIHS GW+S+Y++RAMIA
Sbjct  304  RGLDRWGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSCGWRSIYLNRAMIA  363

Query  367  GLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMF  426
            GLQPETFASFIQQRGRWA+GMMQML+LKNPLFR GL   QRLCYLNSMSFWFFP++RM +
Sbjct  364  GLQPETFASFIQQRGRWASGMMQMLMLKNPLFRPGLSFMQRLCYLNSMSFWFFPIIRMAY  423

Query  427  LVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPY  486
            L+APL YLFFG+EIFV TF E +AY+  Y+AV  LVQN  FA  RWPL+SE+YE+AQ PY
Sbjct  424  LLAPLAYLFFGVEIFVTTFGEAVAYVLSYMAVVLLVQNTSFASYRWPLISEIYEIAQTPY  483

Query  487  LARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFP  546
            L  AI  T+LRPR+ARF VTAKDETL+E+YISP+YRPL+F FLL  +GV+A + RWVAFP
Sbjct  484  LVSAIFRTVLRPRNARFNVTAKDETLAEDYISPVYRPLMFLFLLTFAGVVALVARWVAFP  543
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Query  547  GDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTAT  606
            GDR+VL VVG WAVLN LLV  +LRAV+EKQQRR +PRV+M+ P   Q    G ++L+
Sbjct  544  GDRNVLAVVGVWAVLNFLLVSLSLRAVSEKQQRRTSPRVEMQAPGVIQWVGSGQKTLSVE  603

Query  607  VLDASTSGVRL-LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGG  665
            + D STSGVRL L+ +P  G+    +E G  + F+P F   P LER VR  +RS R   G
Sbjct  604  IFDGSTSGVRLKLIGMP-QGEGARMVEKGDEVVFRPVFKQCPHLERDVRAVVRSVR---G  659

Query  666  T----VMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
            T     ++G+ F A Q + VRE VA L+FG S +W   RE T +  GL+ G+  ILW+
Sbjct  660  TPHDGFVLGLQFIAEQSMDVREAVAQLVFGSSENWALQREQTCKSKGLVAGLGYILWLMI  719

Query  722  ASLPKTARDFMDEPARRRRR--HEEPKEKQAHLLAFGTDFSTE  762
             S+P+T RDF+ EPARRRR    E    K AHL+AFG DF +E
Sbjct  720  VSIPRTFRDFLREPARRRRAALSERQSRKPAHLVAFGADFDSE  762


>TR:A0ABT4JCG6 A0ABT4JCG6_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus benzoatiresistens OX=2997341 GN=bcsA PE=4
SV=1
Length=783

 Score = 964 bits (2491),  Expect = 0.0
 Identities = 491/785 (63%), Positives = 598/785 (76%), Gaps = 18/785 (2%)

Query  4    RAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM  63
            R   +S  +V   +L  LW   L+P  ++A+ PV+ +AQ +  L+AV++V LLKPFA KM
Sbjct  3    REPGKSRRKVFRAMLLPLWAMALLPVLVIASVPVSNTAQSVFGLAAVLVVVLLKPFAFKM  62

Query  64   VPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSA  123
              R +L++ AS++V+RYW WR+  T+P P   ASF+ A +L  VET+SI +FFLN F++A
Sbjct  63   PVRVVLMAIASVIVLRYWLWRVTATMPDPGFTASFILATILLLVETYSILVFFLNAFITA  122

Query  124  DPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGT  183
            DP DR  P  ++  ELPTVDILVPSYNE  +MLS+TL+AAKNMIYPA+LR VVLCDDGGT
Sbjct  123  DPVDRGLPPKVELAELPTVDILVPSYNEAIEMLSITLSAAKNMIYPAKLRRVVLCDDGGT  182

Query  184  DQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVV  243
            DQRC S DPELA  A+ RR ELQ LCRELGV+YSTR RNE+AKAGNMSAALERL G+LVV
Sbjct  183  DQRCNSSDPELAAAARRRRAELQALCRELGVIYSTRARNENAKAGNMSAALERLDGDLVV  242

Query  244  VFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYG  303
            +FDADHVPSRDFLARTVGYFV+DP LFLVQTPH FINPDPI+RNL L  + PPENEMFYG
Sbjct  243  IFDADHVPSRDFLARTVGYFVQDPKLFLVQTPHHFINPDPIERNLNL--KAPPENEMFYG  300

Query  304  KIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRA  363
             IHRGLDRWGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALEIHSRGW+S+Y++RA
Sbjct  301  MIHRGLDRWGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSRGWRSMYLNRA  360

Query  364  MIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVR  423
            MIAGLQPETFASFIQQRGRWA+GMMQMLLLKNPLFR GL   QRLCY+NSMSFWFFP++R
Sbjct  361  MIAGLQPETFASFIQQRGRWASGMMQMLLLKNPLFRPGLSFMQRLCYINSMSFWFFPVIR  420

Query  424  MMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQ  483
            M++L+APL YLFFG+EIFV TF E +AY+  Y+AV  LVQNA+FA  RWPL+SE+YEVAQ
Sbjct  421  MVYLLAPLAYLFFGVEIFVTTFGEAVAYVLSYMAVVLLVQNAVFASYRWPLISEIYEVAQ  480

Query  484  APYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWV  543
            APYL  AI  T+LRPR+ARF VTAKDETL+E+YISPIYRPL+F FLL  +G++A ++RW+
Sbjct  481  APYLVSAIFRTVLRPRNARFNVTAKDETLAEDYISPIYRPLMFVFLLMFAGLIALVIRWI  540

Query  544  AFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSL  603
            AFPGDR+VL VVG WAVLN LLV  +LRAV+EKQQRR++PRV+M  P   +    G   L
Sbjct  541  AFPGDRNVLAVVGVWAVLNFLLVSLSLRAVSEKQQRRSSPRVEMRAPGVIRWKNSGLEPL  600

Query  604  TATVLDASTSGVRL-LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRS---  659
            +  + D STSG RL L+ +P  G+    +E G  + F+P+F  +P LER VR  +R+
Sbjct  601  SVEIFDGSTSGARLRLIGMP-QGEGARMVEKGEEVVFRPRFDQSPHLERDVRAVVRAVFG  659
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Query  660  ARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWM  719
              REG  +M+GV F A Q + VRE +A+L+FG S +W   RE + +  GLL G+  ILW+
Sbjct  660  TPREG--IMLGVQFVAQQNMDVREAIAHLVFGSSENWAAQREQSCKRKGLLAGLVYILWL  717

Query  720  AAASLPKTARDFMDEPARRRRR--HEEPKEKQAHLLAFGTDFSTE-------PDWAGELL  770
             A S+PKT  DF  EP RRR+    E    K AHL+AFG DF  E       P   G  +
Sbjct  718  MATSIPKTMGDFWREPGRRRQAALSERQMRKPAHLVAFGADFDQEEHRQVAAPSPFGAWI  777

Query  771  DPTAQ  775
            +P A+
Sbjct  778  EPEAR  782


>TR:A0A1N7PX55 A0A1N7PX55_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Gemmobacter megaterium OX=1086013 GN=SAMN05421774_106222
PE=4 SV=1
Length=775

 Score = 962 bits (2487),  Expect = 0.0
 Identities = 485/751 (65%), Positives = 589/751 (78%), Gaps = 8/751 (1%)

Query  15   PVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAAS  74
            PV+   LW+ +LVP  +L++AP + +AQ +++L+A+V++AL+KPFA  +V R +LL  AS
Sbjct  8    PVMFVGLWLVMLVPIVVLSSAPASNAAQVVLSLAALVIIALMKPFARHIVARSVLLGVAS  67

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
            ++V+RYWFWRL  TLP   L+ASF+FA+LLF VET+SI +FFLN  +SADP DR  P  +
Sbjct  68   VIVLRYWFWRLTATLPDAGLNASFIFAVLLFVVETYSILVFFLNTVISADPVDRGLPPRV  127

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
            + ++LPTVDILVPSYNEP +MLS+TL+AAKNMIYPA+LRTVVLCDDGGTDQRC SP+ EL
Sbjct  128  ELDQLPTVDILVPSYNEPVEMLSITLSAAKNMIYPAKLRTVVLCDDGGTDQRCNSPNEEL  187

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A+ ++ERR +LQ LC+ELGVVYSTR RNEHAKAGNMSAALERL GELVVVFDADHVPSRD
Sbjct  188  ARASRERRAQLQALCQELGVVYSTRARNEHAKAGNMSAALERLNGELVVVFDADHVPSRD  247

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FLARTVGYFV+DP LFLVQTPHFFIN DPI+RNL L   CPPENEMFYG IHRGLDRWGG
Sbjct  248  FLARTVGYFVQDPQLFLVQTPHFFINQDPIERNLGLA--CPPENEMFYGMIHRGLDRWGG  305

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR+ALD  GGF+GETITEDAETAL+IHS+GW+S+Y++RAMIAGLQPETFA
Sbjct  306  AFFCGSAAVLRRKALDSVGGFSGETITEDAETALDIHSKGWRSIYLNRAMIAGLQPETFA  365

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFIQQRGRWA GMMQM +LKNPLFR GL   QRLCYLNSMSFWFFPL+R++FL+APL YL
Sbjct  366  SFIQQRGRWAAGMMQMFMLKNPLFRPGLKPLQRLCYLNSMSFWFFPLIRLIFLLAPLTYL  425

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FFG+EIFV T ++ +AY  GY+AVS +VQNA+F + RWPL+SE+YE AQAPYL  AI+ T
Sbjct  426  FFGVEIFVTTIQDAMAYTLGYMAVSLMVQNAIFGKYRWPLISEIYETAQAPYLGMAIIRT  485

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +LRPR A+F VTAKDETL  +YISPI+ PL   FLL L GV+    RW+AFPGDRSVL V
Sbjct  486  VLRPRGAKFNVTAKDETLEADYISPIFMPLFVLFLLMLLGVVVLGARWLAFPGDRSVLSV  545

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VG WA++N LLV  +LRAV+EKQQRR +PR++M  PA          +L A VLDASTSG
Sbjct  546  VGVWAIINFLLVSLSLRAVSEKQQRRTSPRIEMREPALVGWSGL-EGTLDAEVLDASTSG  604

Query  615  VRL-LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGT-VMVGVI  672
             R+ L+  P + D     E G  I  +P+FPDAP LER VR  +R      G   ++G++
Sbjct  605  ARVRLLDSPRLRDLQGVRE-GDEIVVRPRFPDAPHLERDVRAVVRGKMTTSGEGNVLGLM  663

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
            F A QP+ VRE VAYLIFG S +W  +R+  +R  GL+ G+  +LW+  AS PKT  D +
Sbjct  664  FVADQPMDVREAVAYLIFGSSENWLAVRQRGLRGKGLVAGLLYVLWLVLASFPKTIADLL  723
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Query  733  DEPARRRRR--HEEPKEKQAHLLAFGTDFST  761
             EP RRR+    E  + K AHL+AFG DF T
Sbjct  724  REPGRRRQAAVTERLERKPAHLVAFGADFDT  754


>TR:A0ABU3EDG1 A0ABU3EDG1_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus broussonetiae OX=3075834 GN=bcsA PE=4 SV=1
Length=771

 Score = 962 bits (2487),  Expect = 0.0
 Identities = 486/750 (65%), Positives = 579/750 (77%), Gaps = 7/750 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            LL  LWV  LVP  +L+AAPV+  AQ ++ + AV+LV +LKPF   +  R  L+  AS++
Sbjct  4    LLMSLWVLALVPVFILSAAPVSNMAQAMLGVVAVLLVMILKPFTTNIAARMALVGVASVV  63

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RYWFWR+  TLP P L ASF+FA+LL  VET+SI +FFL GF++ADP +R  P  ++
Sbjct  64   VLRYWFWRVTATLPEPELSASFVFAVLLLVVETYSILVFFLGGFITADPLERGLPPKVEL  123

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LPTVDILVPSYNEP +MLS+TL+AAKNM+YPA  R VVLCDDGGTDQRC S DPELA
Sbjct  124  ENLPTVDILVPSYNEPVEMLSITLSAAKNMVYPASRRRVVLCDDGGTDQRCNSSDPELAA  183

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ+LC+EL V+YSTR +NEHAKAGNMSAALERL G+LVVVFDADHVPSRDFL
Sbjct  184  RARARRAELQKLCQELNVIYSTRAKNEHAKAGNMSAALERLDGDLVVVFDADHVPSRDFL  243

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            ARTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGLDRWGGAF
Sbjct  244  ARTVGYFAQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGLDRWGGAF  301

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR+ALD  GGFAGETITEDAETALEIHSRGW+SLYIDRAMIAGLQPETF  F
Sbjct  302  FCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSRGWRSLYIDRAMIAGLQPETFVFF  361

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWA+GM+QML+LKNPLFRRGL   QRLCY+NSMSFWFFPL+R+++++APL YLFF
Sbjct  362  IQQRGRWASGMVQMLMLKNPLFRRGLKPLQRLCYINSMSFWFFPLIRLVYIIAPLTYLFF  421

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+EI V TF+E + Y+  Y+AV  LVQN +FAR RWPL+SE+YE+AQAPYLA AI  T+L
Sbjct  422  GVEIVVTTFQEAMTYVLSYMAVVLLVQNGIFARYRWPLISEIYEIAQAPYLATAIFRTIL  481

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            RPR+A+FAVTAKDETL+ENYISPIY+PLL  F L L+GV+A + RW+AFPGDRSVL VVG
Sbjct  482  RPRAAKFAVTAKDETLAENYISPIYKPLLGLFALTLAGVIALVARWIAFPGDRSVLSVVG  541

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             WAV+N+LLV  +LRAV+EKQQRR+APR+ + VP        G   L  TVLD STSG
Sbjct  542  VWAVINLLLVSLSLRAVSEKQQRRSAPRIAISVPTTISWANCGPFPLKGTVLDVSTSGAH  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARR--EGGTVMVGVIFE  674
            L +     G     +  G  I F+P+F +A  LE+ VR  + + +   + GT + GV F
Sbjct  602  LRLDQTPQGKDARMIRQGDEISFRPRFENATHLEQNVRAVVLALQNSAQNGTTL-GVRFL  660

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDE  734
              QP+AVRE VA LIFG S  W   REAT    GL  G+  I+ +   S+PKT  DFM E
Sbjct  661  PDQPMAVREVVAQLIFGSSETWLAQREATREGKGLTAGLLYIVGLMLTSIPKTISDFMRE  720

Query  735  PARRRR--RHEEPKEKQAHLLAFGTDFSTE  762
            PARRRR  R ++  +K AHL+AFG DF TE
Sbjct  721  PARRRRNARAQQMDQKPAHLMAFGADFDTE  750


>TR:A0A3P3DV53 A0A3P3DV53_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Falsigemmobacter faecalis OX=2488730 GN=bcsA PE=4
SV=1
Length=779
```

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 Score = 957 bits (2474),  Expect = 0.0
 Identities = 482/756 (64%), Positives = 585/756 (77%), Gaps = 7/756 (1%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            R++  L   LW+ LLVP  LL   PV+ +AQ ++  SAV+LV  LKPF   M  R  L+
Sbjct  5    RLIGSLAIPLWICLLVPVVLLCILPVSNAAQAMLGASAVLLVMCLKPFVHHMAGRLALMG  64

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS++V+RYW WR+  TLP P L+ASF+ AL L  VET+SI +FFLN F++ADP DR  P
Sbjct  65   TASVVVLRYWSWRITSTLPDPGLNASFILALALLLVETYSILVFFLNAFITADPVDRGLP  124

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
              L+ +++PTVDILVPSYNEP +MLS+TL+AAKNM+YPARLRTVVLCDDGGTDQRC S D
Sbjct  125  PKLELDQMPTVDILVPSYNEPVEMLSITLSAAKNMVYPARLRTVVLCDDGGTDQRCNSSD  184

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            P+LA KA+ RR ELQ LCR+LGVVYSTR +NEHAKAGNMSAAL +L G+LVVVFDADHVP
Sbjct  185  PDLAAKARARRAELQALCRDLGVVYSTRAKNEHAKAGNMSAALAKLDGDLVVVFDADHVP  244

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTVGYFVEDP LFLVQTPHFFIN DPI+RNL L  +CPPENEMFYG IHRGLDR
Sbjct  245  SRDFLARTVGYFVEDPKLFLVQTPHFFINKDPIERNLGL--KCPPENEMFYGMIHRGLDR  302

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALEIHS+GW+SLY+DRAMIAGLQPE
Sbjct  303  WGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSKGWRSLYLDRAMIAGLQPE  362

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TFASFIQQRGRWA+GM+QML+LKNPLFRRGL   QRLCY+NSMSFWFFPL+R+++L+APL
Sbjct  363  TFASFIQQRGRWASGMIQMLMLKNPLFRRGLTPLQRLCYINSMSFWFFPLIRLVYLLAPL  422

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFF +EIFV T+ E +AY   Y+A+  +VQNA FAR RWPL+SE+YE+AQAPYLA AI
Sbjct  423  TYLFFSVEIFVTTWTEAMAYTLSYMAIVLMVQNATFARFRWPLISEIYEIAQAPYLATAI  482

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + T+LRPR+A+F VTAKDETL E+YISPI+ PLL  F L  +GV A + RW+AFPGDRSV
Sbjct  483  MRTVLRPRAAKFNVTAKDETLVEDYISPIFGPLLLLFGLTAAGVAALIFRWIAFPGDRSV  542

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT--ATVLD  609
            L+VVG WAVLN LLV  +LRAV+EKQQRRA+PRV+M+ PA+ ++ A  +R++T  A VLD
Sbjct  543  LIVVGTWAVLNFLLVSLSLRAVSEKQQRRASPRVEMQAPAQVKLAADDSRAVTLPAEVLD  602

Query  610  ASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA-RREGGTVM  668
            ASTSG R+ +     G+P    + G ++  +P F +AP LER VR  +R    + G
Sbjct  603  ASTSGARIRLGAMPRGEPIAMPQKGDVLVLRPLFDEAPHLERDVRAVVRGVFNKAGEGHT  662

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            +G+ F + QP+ VRE VA L+FG S +W   R    +  GLL G+  +  +   S+PKT
Sbjct  663  IGLQFLSDQPMDVREAVAQLVFGSSENWLAERMRGRKRKGLLAGLFYVFSLMLTSIPKTL  722

Query  729  RDFMDEPARRRRRH--EEPKEKQAHLLAFGTDFSTE  762
             DF+ EPARR +       K K AHL+AFG +F TE
Sbjct  723  GDFLREPARRTKSELTAHHKPKAAHLVAFGANFDTE  758


>TR:A0A0D0Q3P1 A0A0D0Q3P1_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Wenxinia marina DSM 24838 OX=1123501 GN=Wenmar_02203
PE=4 SV=1
Length=790

 Score = 954 bits (2467),  Expect = 0.0
 Identities = 491/772 (64%), Positives = 581/772 (75%), Gaps = 9/772 (1%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            R VP LL  LWV L V    L + P++ + QG +++ AV +VA LKPFA  +V RF LL+
Sbjct  11   RGVPELL--LWVLLAVVIAGLVSVPLSTNGQGFLSIVAVAVVACLKPFARLLVARFFLLA  68
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Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS+LV+RY+ WR+ ETLP P L  SF+ A++L  VET+SI +FFLN F+ ADPT  PFP
Sbjct  69   TASVLVLRYYLWRILETLPDPGLTVSFVVAIMLLVVETYSIMVFFLNAFIGADPTRPPFP  128

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
               + PE+LPTVDILVPSYNEPA+MLSVTLAAAKNMIYP+  RTVVLCDDGGTDQRC S D
Sbjct  129  PKVDPEDLPTVDILVPSYNEPAEMLSVTLAAAKNMIYPSAKRTVVLCDDGGTDQRCNSSD  188

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            PELA +A+ RR ELQ LC ELGV YSTR RNEHAKAGNMSAAL  L G+LVVVFDADHVP
Sbjct  189  PELAARARARRAELQALCAELGVKYSTRARNEHAKAGNMSAALADLNGDLVVVFDADHVP  248

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTV YFV +P+LFLVQTPHFFIN DPIQRNL L + CPPENEMFY  IHRGLDR
Sbjct  249  SRDFLARTVNYFVAEPELFLVQTPHFFINKDPIQRNLELSEACPPENEMFYSLIHRGLDR  308

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAAVLRRRALD  GGFAGETITEDAETALEIH+ GWKSLY+DRAMIAGLQPE
Sbjct  309  WGGAFFCGSAAVLRRRALDSVGGFAGETITEDAETALEIHASGWKSLYLDRAMIAGLQPE  368

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TFASFIQQRGRWA GMMQMLLLK PL RRGL + QR+CY+NSMSFW FPL+R+ +L  PL
Sbjct  369  TFASFIQQRGRWAAGMMQMLLLKRPLTRRGLSVPQRICYINSMSFWLFPLMRLFYLYVPL  428

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
            +YLFFGIEIFVATF+EV+AYM GYLAVSFLVQNAL+AR RWPL+SE+YEVAQAPYLA A+
Sbjct  429  VYLFFGIEIFVATFDEVIAYMLGYLAVSFLVQNALYARFRWPLISEIYEVAQAPYLALAV  488

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + T+LRPR A+F VTAKDETL++NYISP++ PL   FL  L+G++A  +RW  FPGDR+V
Sbjct  489  LRTVLRPRGAKFNVTAKDETLNQNYISPMHWPLTILFLTMLAGLVAFGIRWYTFPGDRAV  548

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
            L VVGGW + N +LVG A RAVAE+QQRRA+PRV M+  A   IP   + ++   + D S
Sbjct  549  LSVVGGWGIFNFILVGVAWRAVAERQQRRASPRVAMDEEATLSIPGSEHAAIPVRITDTS  608

Query  612  TSGVRLLVR---LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVM  668
            TSG  +LV    LPG G    AL  G  +   P      P L   +   + S +
Sbjct  609  TSGAGVLVEGNALPG-GATVAALR-GKTVILTPTLASNPTLSSPIAATVVSIKPAQEGQS  666

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            +GV+F+A QP+ VRETVA+LIFG+S +WR++R +T RP GLL G+A +L +    +P
Sbjct  667  LGVLFDAHQPMKVRETVAFLIFGDSENWRSIRHSTRRPKGLLAGLAYVLGLFFRGMPLVL  726

Query  729  RDFMDEPARRR--RRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSA  778
            R+F  EPARRR  + ++   EK AHLLAFG D       A E  +  A   A
Sbjct  727  REFWREPARRRDVQVNQVATEKPAHLLAFGVDVEERERLAAEEAEAEAAAEA  778


>TR:A0A6L7G5P3 A0A6L7G5P3_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudooceanicola albus OX=2692189 GN=bcsA PE=4 SV=1
Length=781

 Score = 954 bits (2465),  Expect = 0.0
 Identities = 479/745 (64%), Positives = 572/745 (77%), Gaps = 6/745 (1%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            +F+LW  LLVP  +L + P + + Q  + + AVV+VA LKPFA+++VPRF LL+ AS+LV
Sbjct  15   IFVLWCVLLVPIAVLISVPTSTAGQAFLGIVAVVIVAALKPFANRIVPRFFLLATASVLV  74

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            MRYW WR+ ETLP P+    F+ A++L  VET+SI +F LN F+SADPT R FP  + PE
Sbjct  75   MRYWIWRVIETLPEPSHPLPFIIAVILLLVETYSICVFMLNAFISADPTQRRFPPQVDPE  134

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
             LPTVDILVPSYNEP +MLS+TLAAAKNMIYP   RTVVLCDDGGTDQRC   +P++A+
Sbjct  135  NLPTVDILVPSYNEPTEMLSITLAAAKNMIYPKDKRTVVLCDDGGTDQRCNHSNPDIAEA  194

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
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            A+ RR ELQ LC  LGV YSTR +NE+AKAGNMSAA+E L G+LVVVFDADHVPSRDFLA
Sbjct  195  ARARRAELQDLCARLGVKYSTRAKNENAKAGNMSAAMEHLDGDLVVVFDADHVPSRDFLA  254

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
            RTVGYFV+DP LFLVQTPHFFINPDPIQRNL L  +CPPENEMFY  +HRGLDRWGGAFF
Sbjct  255  RTVGYFVDDPKLFLVQTPHFFINPDPIQRNLELSHKCPPENEMFYSTVHRGLDRWGGAFF  314

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR ALD  GGFAGETITEDAETALEIHS+GWKSLYIDRAMIAGLQPETFASFI
Sbjct  315  CGSAAVLRRAALDSVGGFAGETITEDAETALEIHSQGWKSLYIDRAMIAGLQPETFASFI  374

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
            QQRGRWATGMMQMLLLK PLFR+GL + QRLCY+NSMSFW FPL+R+ +L+ PL+YLFFG
Sbjct  375  QQRGRWATGMMQMLLLKGPLFRKGLRLQQRLCYINSMSFWLFPLIRLTYLLIPLVYLFFG  434

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EIFVA+F EV+AYM  YLA +FLVQNAL+AR RWP++SE+YEVAQAPYLA+A+  T+LR
Sbjct  435  VEIFVASFPEVMAYMLSYLATAFLVQNALYARTRWPMISEIYEVAQAPYLAKAVFKTVLR  494

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR+A FAVTAKDETL+ENYIS I+ PL   +L   +GV+A  +RWV FPGD SVL VVGG
Sbjct  495  PRAASFAVTAKDETLAENYISGIHWPLTVLWLGMAAGVVALAIRWVMFPGDHSVLAVVGG  554

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            WA+ N +LV  A RAVAEKQQRR++PRV M V          +  L A +LDASTSG R+
Sbjct  555  WALFNFILVSIAYRAVAEKQQRRSSPRVPMNVQGTFWASETTDEELPARILDASTSGARV  614

Query  618  LVRLPGVGD--PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            LV   GV +   H     G  I F+P FP++P+LE  VR ++ S        ++G++ +A
Sbjct  615  LVE--GVSNVWRHSEEIKGKKIWFKPHFPESPKLETRVRAKVMSVMTTPRGQVLGLLIDA  672

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEP  735
             Q + VRETVA+LIFG+S +WR MR A+    GLL G+  +L +     P+   DF  EP
Sbjct  673  DQDLKVRETVAFLIFGDSENWRRMRAASSNRKGLLGGLVYLLGLFVRGTPRLIADFAKEP  732

Query  736  ARRRR-RHEEPKEKQ-AHLLAFGTD  758
             RR R     P EK+ AHLLAFG D
Sbjct  733  GRRARIAATVPAEKKAAHLLAFGVD  757


>TR:A0A6L6IXM7 A0A6L6IXM7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus shanxieyensis OX=2675752 GN=bcsA PE=4 SV=1
Length=776

 Score = 953 bits (2463),  Expect = 0.0
 Identities = 478/756 (63%), Positives = 582/756 (77%), Gaps = 9/756 (1%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            RV   LL  LW  +L+P  +L+A PV+ +AQ ++ L AV LV +LKPF   + PR  L+
Sbjct  4    RVTQFLLLALWGLMLLPIFVLSAIPVSDAAQAMLGLFAVALVVILKPFTASIAPRMALIG  63

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS++V+RYWFWR+  TLP P L ASF+ A+LL  VET+SI +FFL GF++ADP DR  P
Sbjct  64   VASIVVLRYWFWRVTATLPEPGLSASFICAVLLLIVETYSILVFFLGGFITADPLDRGLP  123

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
              ++ E++P VDILVPSYNEP +MLS+TL+AAKNMIYPA  R VVLCDDGGTDQRC SPD
Sbjct  124  PKVELEDMPKVDILVPSYNEPVEMLSITLSAAKNMIYPASKRRVVLCDDGGTDQRCNSPD  183

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            PELA +A+ RR ELQ LC +LG++YSTR RNEHAKAGNMSAAL RL G+LVVVFDADHVP
Sbjct  184  PELAARARARRAELQALCADLGIIYSTRARNEHAKAGNMSAALARLDGDLVVVFDADHVP  243

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGLDR
Sbjct  244  SRDFLARTVGYFAQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGLDR  301

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAAV+RR+ALD  GGFAGETITEDAETALEIHS+GW+SLY+DRAMIAGLQPE
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Sbjct  302  WGGAFFCGSAAVIRRKALDSVGGFAGETITEDAETALEIHSQGWRSLYLDRAMIAGLQPE  361

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TF SFIQQRGRWA+GM+QML+LKNPLFRRGL   QRLCY+NSMSFWFFPL+R+ +++APL
Sbjct  362  TFVSFIQQRGRWASGMVQMLVLKNPLFRRGLKPLQRLCYINSMSFWFFPLIRLAYMLAPL  421

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFFGIEI V TF+E +AY+  Y+AV  LVQNA+F+R RWPL+SEVYE+AQAPYLA +I
Sbjct  422  TYLFFGIEIVVTTFQEAMAYVLSYMAVVLLVQNAIFSRYRWPLISEVYEIAQAPYLATSI  481

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + TLL+PR A+F VTAKDETL+E+YISPIY PL + F L L+GV+A + RW+AFPGDRSV
Sbjct  482  IKTLLKPRGAKFNVTAKDETLAEDYISPIYGPLAWLFALTLAGVIALIGRWIAFPGDRSV  541

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
            L VVG WAV+N+L+V  ALR+V+EKQQRRAAPRV++ +PA    P  G   + ATVLD S
Sbjct  542  LSVVGVWAVINLLMVSLALRSVSEKQQRRAAPRVELSLPAMVTWPGSGQHPIKATVLDVS  601

Query  612  TSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRI---RSARREGGTVM  668
            TSG +L +     G     +  G  I F+P F +AP LE+ V+  +    ++ ++G T
Sbjct  602  TSGAQLRLDQVPRGIGAVMVRQGDEISFRPSFANAPHLEQDVKAVVLVMSNSGKDGPT--  659

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            +G+   + QP A RE VA +IFG+S  W+  R AT +  GL+ G+  I+ +   S PKT
Sbjct  660  LGLRLLSDQPTAAREAVAQMIFGDSEVWQAQRHATRQGKGLIAGLFYIIGLMLRSFPKTI  719

Query  729  RDFMDEPARRRR--RHEEPKEKQAHLLAFGTDFSTE  762
            RDFM EPARRRR        ++ AHL+AFG DF  E
Sbjct  720  RDFMHEPARRRRVALTSNKAQRPAHLMAFGADFDQE  755


>TR:A0A399J2J0 A0A399J2J0_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudooceanicola sediminis OX=2211117 GN=bcsA PE=4
SV=1
Length=780

 Score = 952 bits (2462),  Expect = 0.0
 Identities = 478/751 (64%), Positives = 577/751 (77%), Gaps = 5/751 (1%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L +LW  +++P  +L + P + S Q  + + AV+LVALLKPF+  MVPRFLLL+ +++LV
Sbjct  15   LMVLWCLMMIPIAVLVSVPTSTSGQAFLGIIAVILVALLKPFSRYMVPRFLLLAVSTVLV  74

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            MRYW WRL ETLP  A+  SF+ A+LLF VET+SI +F LN F+SADPT R FP  + PE
Sbjct  75   MRYWLWRLLETLPDAAISLSFIIAVLLFMVETYSILVFMLNAFISADPTQRRFPPQVPPE  134

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            +LPTVDIL+PSYNEP +MLS+TLAAAKNMIYP   RTVVLCDDGGTDQRC S DPELA
Sbjct  135  DLPTVDILIPSYNEPIEMLSITLAAAKNMIYPVEKRTVVLCDDGGTDQRCESSDPELAAA  194

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            +++RR +LQ+LCR+LGV YSTR RNE+AKAGNMSAALE L G++VVVFDADHVPSRDFLA
Sbjct  195  SRKRRADLQRLCRQLGVKYSTRARNENAKAGNMSAALEDLTGDIVVVFDADHVPSRDFLA  254

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
            RTVGYFV+DP LFLVQTPHFFIN DPIQRNL L   CPPENEMFY +IHRGLDRWGGAFF
Sbjct  255  RTVGYFVDDPKLFLVQTPHFFINQDPIQRNLGLSRECPPENEMFYSQIHRGLDRWGGAFF  314

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAA+LRR ALD  GGFAGETITEDAETALEIHSRGWKSLY++RAMIAGLQPETFASFI
Sbjct  315  CGSAALLRRTALDSVGGFAGETITEDAETALEIHSRGWKSLYLNRAMIAGLQPETFASFI  374

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
            QQRGRWATGMMQMLLLKNPLFR+GL + QRLCY+NSMSFW FPL+R+ +LV PL+YLFFG
Sbjct  375  QQRGRWATGMMQMLLLKNPLFRKGLRLPQRLCYINSMSFWLFPLIRLTYLVVPLVYLFFG  434

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            IEIFVATF +V+AYM  YLAVSFLVQNAL++R RWPL+SE+YE+AQAPYL RA++ T+LR
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Sbjct  435  IEIFVATFPDVMAYMLSYLAVSFLVQNALYSRYRWPLISEIYEIAQAPYLFRAVLKTVLR  494

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR+A+F VTAKDETL ++YIS I+ PL   +LL LSGVLA + RW+ FPGDR VL VVGG
Sbjct  495  PRAAKFVVTAKDETLEQDYISQIHWPLTALWLLMLSGVLALIARWLMFPGDRVVLAVVGG  554

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTA--TVLDASTSGV  615
            WAV N +LV  + RAVAEKQQRR++PRV+M  P    +   G  ++ A   +LDAST G 
Sbjct  555  WAVFNFMLVSVSYRAVAEKQQRRSSPRVEMNAPGTMWV-GEGEEAVAAPIRILDASTRGA  613

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            RLL+              G  I F+P+F ++P LE  VR ++RS +      ++G++ EA
Sbjct  614  RLLIEETSKKAVSAQHLKGTKIYFRPQFSESPHLETKVRAQVRSVQSSPRGQILGLLLEA  673

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEP  735
             Q + V+ETVAYLIFG+S +WR +R +T    G+L G    L +     P    D   EP
Sbjct  674  DQNLKVQETVAYLIFGDSENWRRIRGSTEGGKGMLAGFGYALMLFVRGFPALMSDLAKEP  733

Query  736  AR-RRRRHEEPKEKQ-AHLLAFGTDFSTEPD  764
            AR    ++  P +K+ AHLLAFG +     D
Sbjct  734  ARLAAAQNAAPTDKKSAHLLAFGVNLEDPVD  764


>TR:A0ABS8CP10 A0ABS8CP10_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudogemmobacter faecipullorum OX=2755041 GN=bcsA
PE=4 SV=1
Length=775

 Score = 951 bits (2459),  Expect = 0.0
 Identities = 475/749 (63%), Positives = 582/749 (78%), Gaps = 7/749 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            LL LLW+  + P  +LA+ PV+ +AQG++ L+AV+LV LLKPFA+ ++ R  L+S +S++
Sbjct  10   LLLLLWLLAVAPVMVLASVPVSNAAQGMLGLAAVLLVVLLKPFANNIICRIALMSVSSVI  69

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RYW WR+  TLP PAL+ SF+ AL+L  VET+SI +FFLN F++ADP +R  P  + P
Sbjct  70   VLRYWIWRITATLPDPALNISFVLALVLLLVETYSILVFFLNAFINADPVERALPPRVAP  129

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E+LP+VDILVPSYNEP +ML++TL+AAKNMIYPARLRTVVLCDDGGTDQRC S D ELA 
Sbjct  130  EDLPSVDILVPSYNEPTEMLAITLSAAKNMIYPARLRTVVLCDDGGTDQRCNSADAELAA  189

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            K++ RR ELQ LC ELGV+YSTR +NEHAKAGNMSAAL +L G+LVVVFDADHVPSRDFL
Sbjct  190  KSRARRAELQALCAELGVIYSTRAKNEHAKAGNMSAALAKLDGDLVVVFDADHVPSRDFL  249

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            ARTVGYFVEDP LFLVQTPHFFIN DPI+RNL L   CPPENEMFYG+IH GLDRWGGAF
Sbjct  250  ARTVGYFVEDPKLFLVQTPHFFINKDPIERNLDLV--CPPENEMFYGRIHPGLDRWGGAF  307

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR+ALD  GGFAGETITEDAETALEIHS+GW+SLY+DRAMIAGLQPETFASF
Sbjct  308  FCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSKGWRSLYLDRAMIAGLQPETFASF  367

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWA+GMMQM +LKNPLFR+GL   QRLCY+NSM+FW FPLVRM +L+APL YLFF
Sbjct  368  IQQRGRWASGMMQMFMLKNPLFRKGLRPLQRLCYINSMAFWLFPLVRMTYLLAPLAYLFF  427

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            GIEIFV TF E +AY   Y+A+S LVQ+A+F+R RWPL+SE+YE+AQAPYL+ AI+ T+L
Sbjct  428  GIEIFVTTFREAMAYTLSYMAISLLVQSAVFSRYRWPLISEIYEIAQAPYLSGAIIRTIL  487

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            +PR A+F VTAKDETL E+YISPI  PLL  F L L+GVLA + RW+A+PGD SVL VVG
Sbjct  488  KPRGAKFNVTAKDETLVEDYISPIAGPLLALFGLMLAGVLALIFRWIAYPGDHSVLSVVG  547

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             WAV+N LLV  +LRAV+EKQQRRA+PRV++     A+    G   +   V D STSG+R
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Sbjct  548  TWAVINFLLVSLSLRAVSEKQQRRASPRVEVHETGSARWEGMGETMVPVEVFDVSTSGLR  607

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGT-VMVGVIFEA  675
            +  RL  +         G  + F+P+F  AP LER VR  +R+   + G    +G+ F
Sbjct  608  M--RLGSLPQGARLAAKGDELIFRPRFAHAPHLERDVRAVVRAVFNDSGKGTALGLQFVP  665

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEP  735
             QP+ VRE VA+++FG S +W  +R+ + R  GL  G+  + W+   SLPKT  DF+ EP
Sbjct  666  DQPMIVREAVAHMLFGSSENWLKIRQESRRGKGLTMGLLYVFWLTLTSLPKTIGDFIREP  725

Query  736  ARRRRR--HEEPKEKQAHLLAFGTDFSTE  762
            ARRR+   +E+   K AHL+AFG DF TE
Sbjct  726  ARRRKASLYEKQAPKPAHLVAFGADFDTE  754


>TR:A0A975PBI0 A0A975PBI0_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Gemmobacter fulvus OX=2840474 GN=bcsA PE=4 SV=1
Length=777

 Score = 951 bits (2457),  Expect = 0.0
 Identities = 479/772 (62%), Positives = 590/772 (76%), Gaps = 8/772 (1%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            R+  ++L L W+  ++P  +LA+ PV+ +AQG+  ++A+V+V LLKPFA  ++ R  ++S
Sbjct  5    RIRNIVLLLFWLTAMLPVMVLASIPVSNAAQGMFGIAALVIVLLLKPFAGNIICRISMMS  64

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS++ +RYW WR+  TLP P L+ASF+ A+ L  VET+SI +FFLN F++ADP +R  P
Sbjct  65   VASVIALRYWIWRVTSTLPDPGLNASFILAIALLVVETYSILVFFLNAFITADPVERALP  124

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
              ++PE LP+VDILVPSYNEP +ML+VTL+AA+NMIYPARLRTVVLCDDGGTDQRC SP+
Sbjct  125  PRVEPENLPSVDILVPSYNEPTEMLAVTLSAARNMIYPARLRTVVLCDDGGTDQRCNSPN  184

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
             ELA K++ RR ELQ LC ELGVVYSTR +NEHAKAGNMSAAL +L G+LVVVFDADHVP
Sbjct  185  AELAAKSKARRAELQALCAELGVVYSTRAKNEHAKAGNMSAALAKLNGDLVVVFDADHVP  244

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTVGYFVEDP LFLVQTPHFFIN DPI+RNL L  +CPPENEMFYGKIH GLDR
Sbjct  245  SRDFLARTVGYFVEDPKLFLVQTPHFFINKDPIERNLDL--KCPPENEMFYGKIHPGLDR  302

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAA+LRR+ALD  GGFAGETITEDAETALEIHS+GW+S+Y+DRAMIAGLQPE
Sbjct  303  WGGAFFCGSAALLRRKALDSVGGFAGETITEDAETALEIHSKGWRSIYLDRAMIAGLQPE  362

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TFASFIQQRGRWA+GMMQM +LKNPLFR GL   QRLCYLNSM+FW FPLVRM +L+APL
Sbjct  363  TFASFIQQRGRWASGMMQMFMLKNPLFRPGLKPFQRLCYLNSMAFWLFPLVRMTYLLAPL  422

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFF IEIFV TF E +AY   Y+AVS LVQNA+F+R RWPL+SEVYE+AQAPYLA AI
Sbjct  423  AYLFFSIEIFVTTFREAMAYTLSYMAVSLLVQNAVFSRHRWPLISEVYEIAQAPYLAGAI  482

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + T+LRPR A+F VTAKDETL E+YISP+  PL+  F L L+GV+A  VRW+A+PGD SV
Sbjct  483  IRTILRPRGAKFNVTAKDETLVEDYISPVSGPLVGLFFLMLAGVVALTVRWIAYPGDHSV  542

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
            L VVG WA++N LLV  +LRAV+EKQQRR++PRV M      +    G + L   V DAS
Sbjct  543  LSVVGTWAIINFLLVSLSLRAVSEKQQRRSSPRVAMHEAGFVRWEGSGEKMLPVEVYDAS  602

Query  612  TSGVRL-LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARRE-GGTVMV  669
            TSG+R+ +V LP        ++ G  + F+P FP AP LER VR  +R+   E G  + +
Sbjct  603  TSGLRMRMVGLPQEPGSRMVVK-GDEVVFRPSFPHAPHLEREVRALVRAVFNETGNGIGI  661

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            G+ +   QP+ VRE VA L+FG S +W  +R+ + R  GLL G+  +LW+  +S PKT
Sbjct  662  GLQYLPEQPMIVREAVAQLLFGSSENWLEIRQRSRRHKGLLAGLFYVLWLTLSSFPKTIG  721
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Query  730  DFMDEPARRRRR--HEEPKEKQAHLLAFGTDFSTEP-DWAGELLDPTAQVSA  778
            DF+ EPARRRR   +E+   + AHL+ F  DF  E    A + L P A + A
Sbjct  722  DFVREPARRRRSALYEKQSPRPAHLITFSADFDAEEYRLANDRLAPEAFIGA  773


>TR:A0A844WB24 A0A844WB24_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudooceanicola pacificus OX=2676438 GN=bcsA PE=4
SV=1
Length=776

 Score = 950 bits (2455),  Expect = 0.0
 Identities = 477/769 (62%), Positives = 590/769 (77%), Gaps = 7/769 (1%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +  + L L W  LL    L+ + P +  AQ L+ +S V++V LLKPFA+  V RF L++
Sbjct  4    IARITLLLAWGGLLAATLLVTSLPSSVPAQALLGISTVLVVMLLKPFAENTVARFALIAV  63

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
            AS++V+RYW WR+  TLP P +  S++ AL+LFAVET+SI +FFLN F++ADPT+R  P
Sbjct  64   ASVVVLRYWIWRMTTTLPEPGITPSYILALMLFAVETYSILVFFLNAFITADPTERAEPP  123

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
             +  E+LPTVDILVPSYNEP +MLSVTL+AAKN+IYP     VVLCDDGGTDQRC S DP
Sbjct  124  RVAVEKLPTVDILVPSYNEPIEMLSVTLSAAKNIIYPKDRMRVVLCDDGGTDQRCNSDDP  183

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
            ELA  +++RR +LQ+LC ELGV+YSTR RNEHAKAGNMSAAL RL G+LVVVFDADHVP+
Sbjct  184  ELAAASRKRRADLQKLCDELGVMYSTRARNEHAKAGNMSAALARLDGDLVVVFDADHVPT  243

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            RDFLARTVGYFVEDP LFLVQTPHFF+N DPI+RNL L   CPPENEMFY  IHRGLDRW
Sbjct  244  RDFLARTVGYFVEDPKLFLVQTPHFFLNQDPIERNLGL--TCPPENEMFYSMIHRGLDRW  301

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
            GGAFFCGSAAVLRR ALD  GGF+GETITEDAETAL+IH+ GW+SLY++RAMIAGLQPET
Sbjct  302  GGAFFCGSAAVLRREALDSVGGFSGETITEDAETALDIHATGWRSLYLNRAMIAGLQPET  361

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
            FASFI QRGRWATGMMQMLLLKNPLFRRGLG  QRLCY+NSM+FW FP++RM+++VAPL
Sbjct  362  FASFITQRGRWATGMMQMLLLKNPLFRRGLGPLQRLCYINSMAFWLFPIIRMVYMVAPLA  421

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            YLFFGIE+FVATF+E LA++  Y+A+SFLVQNALFAR RWPL+SEVYEVAQAPYLA+A++
Sbjct  422  YLFFGIEVFVATFDEALAFVLSYMAISFLVQNALFARYRWPLISEVYEVAQAPYLAKAVL  481

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
             T+L+PR+A F VTAKDETL E+ IS I RPL+  F L  +G+ A + RW+AFPGD  VL
Sbjct  482  KTVLKPRAASFKVTAKDETLLEDNISDIARPLVILFGLMAAGIGALIYRWLAFPGDHGVL  541

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAST  612
             VVG W + N +LV  +LRA  EKQQRR++PRV+M+VPA       G + L  TVLDAST
Sbjct  542  TVVGAWMIFNFMLVSLSLRATCEKQQRRSSPRVEMKVPATVWWEGSGKQPLNCTVLDAST  601

Query  613  SGVRLLV-RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
            SG RL V  +   G     +E+G +I F+P+F +A  LER VR  +R    +   +++GV
Sbjct  602  SGARLQVTNVASAGYAARVVESGEIITFRPQFEEASHLERPVRASVRKISEDKDGMILGV  661

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF  731
            +F   +P+ VRETVA+LIFG+S +W  +R++  +  G+L G+A ++W++ +SLP+T  D+
Sbjct  662  LFLPDEPMPVRETVAFLIFGDSDNWYRVRQSYTQKKGMLAGLAYVIWLSISSLPRTLGDY  721

Query  732  MDEPARRRRRHEE---PKEKQAHLLAFGTDFSTE-PDWAGELLDPTAQV  776
            M EPARRRR   E   PK K AHL+AFG  F  E    A + L PT  V
Sbjct  722  MREPARRRRLATEKTGPKTKPAHLVAFGATFEEEAKKQADKPLTPTQAV  770


>TR:A0A844H1W1 A0A844H1W1_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus limosus OX=913252 GN=bcsA PE=4 SV=1
```

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Length=778

 Score = 947 bits (2447),  Expect = 0.0
 Identities = 480/750 (64%), Positives = 580/750 (77%), Gaps = 9/750 (1%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L  LW  LLVP  +L A PV+ +AQ ++ L AV+LV LLKP +  +VPR +L++ AS++V
Sbjct  12   LLWLWALLLVPVFVLCAIPVSDAAQAMLGLGAVLLVILLKPLSRNIVPRMVLVAIASIVV  71

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RYWFWR+  TLP P L+ASF+ A++L   ET+SI +FFL  F++ADP DR  P  ++ E
Sbjct  72   LRYWFWRVTATLPDPGLNASFICAVILLVFETYSILVFFLGDFITADPLDRGLPPRVELE  131

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
             LPTVDILVPSYNEP +MLS+TL+AAKNMIYPA  R VVLCDDGGTDQRC SPDPELA +
Sbjct  132  NLPTVDILVPSYNEPVEMLSITLSAAKNMIYPASKRRVVLCDDGGTDQRCDSPDPELAAR  191

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A+ RR +LQ LC +LGV+YSTR +NEHAKAGNMSAAL RL G+LVVVFDADHVPSRDFLA
Sbjct  192  ARARRAQLQALCADLGVIYSTRAKNEHAKAGNMSAALARLDGDLVVVFDADHVPSRDFLA  251

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
            RTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGLDRWGGAFF
Sbjct  252  RTVGYFTQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGLDRWGGAFF  309

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAV+RR+ALD  GGFAGETITEDAETALEIHS+GW+SLY+DRAMIAGLQPETF SFI
Sbjct  310  CGSAAVIRRKALDSVGGFAGETITEDAETALEIHSQGWRSLYLDRAMIAGLQPETFVSFI  369

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
            QQRGRWA+GM+QML+LKNPLFRRGL   QRLCY+NSMSFWFFPL+R+++++APL YLFFG
Sbjct  370  QQRGRWASGMVQMLVLKNPLFRRGLKPLQRLCYINSMSFWFFPLIRLVYILAPLTYLFFG  429

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EI V TF+E +AY+  Y+AV  LVQ+ALF+R RWPL+SE+YE+AQAPYLA +I  TLLR
Sbjct  430  LEIVVTTFQEAMAYVLSYMAVVMLVQSALFSRYRWPLISEIYEIAQAPYLATSIFRTLLR  489

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR A+F VTAKDETLSE+YISPIY PL   FLL L+GV+A ++RW+AFPGDRSVL VVG 
Sbjct  490  PRGAKFNVTAKDETLSEDYISPIYGPLAGLFLLTLAGVVALVIRWIAFPGDRSVLSVVGV  549

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            WAV+N+L+V  +LRAV+EKQQRRAAPRV + +PA A     G   + ATVLD STSG  L
Sbjct  550  WAVINLLMVSLSLRAVSEKQQRRAAPRVTLHLPATASWDGAGRAPVKATVLDVSTSGASL  609

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRG---RIRSARREGGTVMVGVIFE  674
             +     G     +  G  I F+P F +AP LE+ VR     I +A  EG T  +G+
Sbjct  610  RLEHAPRGVGAVMVRQGEEICFRPSFANAPHLEQEVRAVVLAISTAAGEGTT--LGLRLV  667

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDE  734
              QP+AV+E VA +IFG+S  WR  REAT +  GL+ G+  IL +   S+P+T  DF+ E
Sbjct  668  GDQPVAVQEAVAQMIFGDSEVWRMQREATRQGKGLIAGLVYILGLMLTSIPRTLGDFLRE  727

Query  735  PARRRRR--HEEPKEKQAHLLAFGTDFSTE  762
            PARR+R          +  HLLAFG DF T+
Sbjct  728  PARRQRAALGANRGARPVHLLAFGADFDTD  757


>TR:A0ABT5TE18 A0ABT5TE18_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseinatronobacter alkalisoli OX=3028235 GN=bcsA PE=4
SV=1
Length=793

 Score = 946 bits (2446),  Expect = 0.0
 Identities = 477/775 (62%), Positives = 582/775 (75%), Gaps = 13/775 (2%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVPRFLLL  70
            R   V L LLWV L+VP  +LA  P +   Q L+ + AV +V + KPFA + +VPR  +L
Sbjct  9    RGAAVALGLLWVVLMVPIVVLAGTPTSTQVQALLGIIAVAIVLVAKPFARRHIVPRLAML  68
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Query  71   SAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPF  130
            + ASML++RYW WRL ETLP      SF+ ALLLFAVET++I++FFL  F++ADP D
Sbjct  69   AVASMLILRYWVWRLTETLPMLDAPVSFVVALLLFAVETYAIAVFFLTAFVNADPIDHDL  128

Query  131  PRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
            P+ ++  ELP+VDILVPSYNEP +MLS+TL+AAK + YP     VVLCDDGGTD+RC
Sbjct  129  PKRVRAAELPSVDILVPSYNEPVEMLSITLSAAKQIFYPRDKMRVVLCDDGGTDERCAHA  188

Query  191  DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
            DP +A  ++ RR ELQ++CREL V+Y+TR RNEHAKAGNMSAALE+L G+LVVVFDADHV
Sbjct  189  DPTIAAASRARRAELQKMCRELDVMYTTRRRNEHAKAGNMSAALEKLNGDLVVVFDADHV  248

Query  251  PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            PSRDFLARTVGYFVE+P LFLVQTPHFFIN DPIQRNL    +CP ENEMFY  IHRGLD
Sbjct  249  PSRDFLARTVGYFVENPRLFLVQTPHFFINLDPIQRNLGFARQCPSENEMFYANIHRGLD  308

Query  311  RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            RWGGAFFCGSAAVLRR ALDE GGF+GETITEDAETAL+IHSRGW+S+Y++RAMIAGLQP
Sbjct  309  RWGGAFFCGSAAVLRRAALDEVGGFSGETITEDAETALDIHSRGWESMYLNRAMIAGLQP  368

Query  371  ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
            ETFA+FIQQRGRWATGM+QMLLLKNPLFRRGL   QRLCY+NSMSFW FPLVR+ FLV P
Sbjct  369  ETFATFIQQRGRWATGMVQMLLLKNPLFRRGLSAQQRLCYVNSMSFWLFPLVRLGFLVIP  428

Query  431  LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L YLFFG+EIFVAT EEVLAYM  YL VSFLVQNALF+  RWPL+SEVYEVAQAPYL
Sbjct  429  LFYLFFGLEIFVATGEEVLAYMVSYLLVSFLVQNALFSHVRWPLISEVYEVAQAPYLGTQ  488

Query  491  IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
            I+ T+LRPR+A+FAVTAKDETLSEN+ISPIY PLL  F L  +G+ A ++RWV FPGDR+
Sbjct  489  ILKTILRPRAAKFAVTAKDETLSENFISPIYMPLLLLFALLAAGLGAAVLRWVIFPGDRT  548

Query  551  VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNR--SLTATVL  608
             + VVGGWA+ N LL G A+ +++EKQQRR+ PR+ ++ PA   +P   ++   L A ++
Sbjct  549  TIEVVGGWALFNFLLTGLAMGSISEKQQRRSVPRLAVDTPATVWLPGADDKGPELAARIV  608

Query  609  DASTSGVRLLVRLPGVGDPHPA----LEAGGLIQFQPKFPDAPQLERMVRGRIRSARREG  664
            DAST GVRL +R P  G P  A    LE G ++  +P+FPDA   E  +   IRS  R G
Sbjct  609  DASTGGVRLHLRTPDDGTPVAAQLQSLERGAVLSMRPQFPDAQDFEHNILVEIRSVSRSG  668

Query  665  GTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASL  724
              + +G+ F A QP+  RE+VA+LIF  S +WR +RE   RP GLL G+  +LW++  ++
Sbjct  669  EGLFLGLQFVADQPVKSRESVAFLIFSNSENWRRLRENETRPKGLLPGLFYVLWLSITTI  728

Query  725  PKTARDFMDEPARRRRRHEEPKEKQ--AHLLAFGTDFSTEPDWAGELLDPTAQVS  777
            P+T R+ + EPARRRR  ++  EK    H+L FG DF    D A    D T Q +
Sbjct  729  PRTLRELLREPARRRRGTDDSTEKDVPVHVLTFGADF----DPASPEADDTTQTT  779


>TR:A0A6L8VFE9 A0A6L8VFE9_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Frigidibacter albus OX=1465486 GN=bcsA PE=4 SV=1
Length=782

 Score = 946 bits (2444),  Expect = 0.0
 Identities = 478/742 (64%), Positives = 569/742 (77%), Gaps = 4/742 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            LLWV LLVP  LL + P + + Q L+++ AV+LV +LKPF ++   RF LL+ AS++V+R
Sbjct  20   LLWVMLLVPILLLTSVPTSNAGQALLSIVAVLLVVMLKPFTEQTAARFALLAVASVIVLR  79

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y  WRL ETLPP A   SF  A+LLFAVE +S   FFLN F++ADPT R  P  +   +L
Sbjct  80   YMVWRLLETLPPAAPTLSFTIAVLLFAVELYSNLAFFLNAFVNADPTTRKMPPQVSLRDL  139

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVDILVPSYNEP +ML++TL AAKNMIYP   RTVVLCDDGGTDQRC S +PELA  ++
Sbjct  140  PTVDILVPSYNEPTEMLAITLLAAKNMIYPVDKRTVVLCDDGGTDQRCNSDNPELAAASR  199
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Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             RR ELQQLC +LG++YSTR RNEHAKAGNMSAALERL G+LVVVFDADHVP+RDFLART
Sbjct  200  ARRAELQQLCADLGIMYSTRARNEHAKAGNMSAALERLNGDLVVVFDADHVPTRDFLART  259

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYFV+DP LFLVQTPHFFIN DP+QRNL    + P ENEMFY KIHRGLDRWGGAFFCG
Sbjct  260  VGYFVDDPKLFLVQTPHFFINDDPVQRNLGFSRKVPTENEMFYSKIHRGLDRWGGAFFCG  319

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR ALD  GGF+GETITEDAETAL+IHSRGWKSLYIDRAM+AGLQPETFASFIQQ
Sbjct  320  SAAVLRRAALDSVGGFSGETITEDAETALDIHSRGWKSLYIDRAMVAGLQPETFASFIQQ  379

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            RGRWATGMMQML+LKNPLFRRGL + QRLCY+NSMSFW FPL+RM +L+ PL+YLFFG+E
Sbjct  380  RGRWATGMMQMLILKNPLFRRGLRLPQRLCYINSMSFWLFPLIRMAYLLVPLVYLFFGVE  439

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IFVAT++EV+AYM GYLAVSFLVQNALF+R RWPLVSEV+E+AQAPYLA AI  T+LRPR
Sbjct  440  IFVATYDEVMAYMLGYLAVSFLVQNALFSRYRWPLVSEVFEIAQAPYLAAAIFRTVLRPR  499

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
            +A+F VTAKDE L E+YISPIY+PLLF  LL L+GV+A   RW+AFPGDR VL +VGGWA
Sbjct  500  AAKFNVTAKDEMLVEDYISPIYKPLLFLLLLMLAGVVALAARWIAFPGDRGVLAIVGGWA  559

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            V N LLV  ALRAV EKQQ RA+PRV M+VPA           L AT++DAS  G  L+
Sbjct  560  VFNFLLVSLALRAVCEKQQSRASPRVAMDVPATLTWEG-QTAPLQATIVDASVRGAGLVF  618

Query  620  RLP--GVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
            ++P    G     L    ++ F+P+FPDA  LE  +  R+R+  R    +++G+
Sbjct  619  QMPRGEDGSAGRPLALEDIVTFRPRFPDAQHLETDLGARVRNIIRTEKGLLIGLRMLPDP  678

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPAR  737
             +  R  +A+L FG S +W+ +REAT    GL+ G+  +L +   SLPKT  DF  EPAR
Sbjct  679  SMEARAAIAFLTFGASENWQRVREATRARKGLVAGLFYMLGLCLTSLPKTIADFAREPAR  738

Query  738  RRRRHEEPKEKQ-AHLLAFGTD  758
            RRR  E P+E++  HLLAF  D
Sbjct  739  RRRAAERPQEQRPVHLLAFTAD  760


>TR:A0A521D486 A0A521D486_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus laeviglucosivorans OX=1197861 GN=SAMN06265221_10619
PE=4 SV=1
Length=776

 Score = 943 bits (2438),  Expect = 0.0
 Identities = 472/748 (63%), Positives = 573/748 (77%), Gaps = 7/748 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            + L  LW   L+P  +L+A PV+ +AQ ++ + AV LV +LKPF   +VPR  L+  AS+
Sbjct  8    LFLLALWALTLLPVFVLSAIPVSDAAQAMLGMFAVALVVILKPFTSSIVPRMALIGIASI  67

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RYWFWR+  TLP P LDASF+ A++L  VET+SI +FFL GF++ADP DR  P  +
Sbjct  68   VVLRYWFWRVTATLPEPGLDASFICAIILLVVETYSILVFFLGGFITADPLDRGLPPKVD  127

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             E +P VDILVPSYNEP +MLS+TL+AAKNMIYPA  R VVLCDDGGTDQRC S DPELA
Sbjct  128  LEHMPRVDILVPSYNEPVEMLSITLSAAKNMIYPASKRRVVLCDDGGTDQRCNSADPELA  187

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +A+ RR ELQ LC +LG++YSTR +NEHAKAGNMSAAL RL G+LVVVFDADHVPSRDF
Sbjct  188  ARARARRAELQALCNDLGIIYSTRAKNEHAKAGNMSAALARLDGDLVVVFDADHVPSRDF  247

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            LARTVGYF +DP LFLVQTPH FINPDPIQRNL L  + PPENEMFYG IHRGLDRWGGA
Sbjct  248  LARTVGYFAQDPKLFLVQTPHHFINPDPIQRNLGL--KSPPENEMFYGMIHRGLDRWGGA  305
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Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAV+RR+ALD  GGFAGETITEDAETALEIHS+GW+SLY+DRAMIAGLQPETF S
Sbjct  306  FFCGSAAVIRRKALDSVGGFAGETITEDAETALEIHSQGWRSLYLDRAMIAGLQPETFVS  365

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FIQQRGRWA+GM+QML+LKNPLFRRGL   QRLCY+NSMSFWFFPL+R+ +++APL YLF
Sbjct  366  FIQQRGRWASGMVQMLVLKNPLFRRGLKPLQRLCYINSMSFWFFPLIRLAYMLAPLTYLF  425

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+EI V TF+E +AY+  Y+AV  LVQNA+F+R RWPL+SEVYE+AQAPYLA +I+ T+
Sbjct  426  FGVEIVVTTFQEAMAYVLSYMAVVLLVQNAIFSRYRWPLISEVYEIAQAPYLATSIIRTI  485

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L+PR A+F VTAKDETL+E+YISPIY PL   F L L+GV+A +VRW+AFPGDRSVL VV
Sbjct  486  LKPRGAKFNVTAKDETLAEDYISPIYGPLAGLFGLTLAGVIALIVRWIAFPGDRSVLSVV  545

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G WAV+N+L+V  ALR+V+EKQQRRAAPRV + +PA A     G   + ATV+D STSG
Sbjct  546  GVWAVINLLMVSLALRSVSEKQQRRAAPRVMLNLPATATWQGSGQYPVKATVMDVSTSGA  605

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREG--GTVMVGVIF  673
            +L +     G     +  G  I F+P F +AP LE+ VR  + S    G  GT + G+
Sbjct  606  QLRLDQAPRGIGAVMIRQGDEIAFRPSFANAPHLEQDVRAVVLSMSNTGKEGTTL-GLRL  664

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
               Q IA RE VA +IFG+S  W+  R+AT    GL+ G+  I+ +   S+PKT  DFM
Sbjct  665  VGDQSIAAREAVAQMIFGDSEVWQAQRDATRHGKGLIAGLLYIIGLMLTSIPKTIADFMR  724

Query  734  EPARRRR--RHEEPKEKQAHLLAFGTDF  759
            EPARRRR        ++ AHL+AFG DF
Sbjct  725  EPARRRRVAMTSNKSQRPAHLMAFGADF  752


>TR:A0A7L9WHZ9 A0A7L9WHZ9_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudooceanicola spongiae OX=2613965 GN=bcsA PE=4
SV=1
Length=779

 Score = 942 bits (2435),  Expect = 0.0
 Identities = 472/756 (62%), Positives = 570/756 (75%), Gaps = 5/756 (1%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L +LW  +++P G+L + P + S Q  + + AV +VALLKPFA  MVPRF LL+ A++LV
Sbjct  15   LMVLWCLMMIPIGVLVSVPTSTSGQAFLGIIAVAIVALLKPFARFMVPRFFLLAVATVLV  74

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            MRYW WRL ETLP P++  SF+ A+LLF VET+SI +F LN F+SADPT R FP  + PE
Sbjct  75   MRYWLWRLLETLPDPSISLSFIIAVLLFMVETYSILVFMLNAFISADPTQRRFPPQVPPE  134

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            +LPTVDIL+PSYNEP +MLS+TLAAAKNMIYP   RTVVLCDDGGTDQRC S DPELA
Sbjct  135  DLPTVDILIPSYNEPIEMLSITLAAAKNMIYPTDKRTVVLCDDGGTDQRCNSSDPELAAA  194

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            +++RR +LQ+LC+ LGV YSTR RNE+AKAGNMSAALE L GE+VVVFDADHVPSRDFLA
Sbjct  195  SRKRRADLQRLCKRLGVKYSTRARNENAKAGNMSAALEDLHGEIVVVFDADHVPSRDFLA  254

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
            RTVGYFV+DP LFLVQTPHFFIN DPIQRNL L   CPPENEMFY +IHRGLDRWGGAFF
Sbjct  255  RTVGYFVDDPKLFLVQTPHFFINQDPIQRNLGLSRECPPENEMFYSQIHRGLDRWGGAFF  314

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAA+LRR ALD  GGFAGETITEDAETALEIHSRGWKSLY++RAMIAGLQPETFASFI
Sbjct  315  CGSAALLRRAALDSVGGFAGETITEDAETALEIHSRGWKSLYLNRAMIAGLQPETFASFI  374

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
            QQRGRWATGMMQMLLLKNPLFR+GL   QRLCY+NSMSFW FPL+R+ +L+ PL+YLFFG
Sbjct  375  QQRGRWATGMMQMLLLKNPLFRKGLRFPQRLCYINSMSFWLFPLIRLTYLMVPLVYLFFG  434
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Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            IEIFVATF +V+AYM  YLAVSFL Q+AL++R RWPL+SE+YE+AQAPYL +A+  T+L 
Sbjct  435  IEIFVATFPDVMAYMLSYLAVSFLTQSALYSRYRWPLISEIYEIAQAPYLFKAVFKTVLS  494

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PRSA+FAVTAKDETL ++YISPI+ PL   ++  ++G++A  +RW  FPGD  VL VVGG
Sbjct  495  PRSAKFAVTAKDETLEQDYISPIHWPLTILWICMVAGIVALGIRWYLFPGDHPVLAVVGG  554

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTSGV  615
            WA+ N +LV  A RAVAEKQQRR++PRV+M  P        G++ + A V  LDAST G 
Sbjct  555  WAMFNFILVTIAYRAVAEKQQRRSSPRVEMNAPG-TMWAGDGDQLMEAPVRILDASTRGA  613

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            RLL+       P      G  I F+P+F ++P LE  V  ++ S +      ++G++ EA
Sbjct  614  RLLIEETSNRAPSTQQLKGSKIYFRPQFAESPHLETKVLAKVMSVQSSPRGQILGLLLEA  673

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEP  735
             Q +  +ETVAYLIFG+S +WR MR +T     ++ G    L +     P    D   EP
Sbjct  674  DQDLKAQETVAYLIFGDSENWRRMRMSTEASKSMIVGFGYALMLFVRGFPALMSDLAKEP  733

Query  736  ARRRRRH-EEPKEKQ-AHLLAFGTDFSTEPDWAGEL  769
             R    H   P EK+ AHLLAFG D   + D A E+
Sbjct  734  GRLAMVHATTPSEKKSAHLLAFGVDLEEQNDHAIEI  769


>TR:A0ABW2UIS3 A0ABW2UIS3_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Plastorhodobacter daqingensis OX=1387281 GN=bcsA PE=4
SV=1
Length=775

 Score = 940 bits (2429),  Expect = 0.0
 Identities = 491/774 (63%), Positives = 581/774 (75%), Gaps = 23/774 (3%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            R  P  +  LW+  LVP  +LA+ P + +AQ L+ LSAV+LVA+LKPF   +V R  LLS
Sbjct  5    RSFPRWILPLWLLALVPVFILASVPTSNAAQALLGLSAVLLVAILKPFTAHVVARVALLS  64

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS++V+RY  WR+  TLP   L  SF+ A+LL   ET+SI +FFLN F++ADP  R  P
Sbjct  65   IASIIVLRYLIWRVTATLPDADLTMSFVLAVLLLLTETYSIMVFFLNAFITADPVVRDLP  124

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
              +QPE+LPTVDILVPS+NEP +MLS+TL+AAKNMIYPARLR VVLCDDGGTDQRC + D
Sbjct  125  PQVQPEDLPTVDILVPSFNEPVEMLSITLSAAKNMIYPARLRRVVLCDDGGTDQRCNAAD  184

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            PELA  AQ+RRR+LQQLC +LGV+Y TR RNE AKAGNMSAALERL GELVVVFDADHVP
Sbjct  185  PELAAAAQDRRRQLQQLCSDLGVIYFTRARNERAKAGNMSAALERLDGELVVVFDADHVP  244

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTVGYF  DP LFLVQTPHFFIN DPI+RNL L  +CPPENEMFYGKIH GLDR
Sbjct  245  SRDFLARTVGYFRHDPRLFLVQTPHFFINRDPIERNLGL--KCPPENEMFYGKIHPGLDR  302

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALE+HS+GW+SLY+DRAMIAGLQPE
Sbjct  303  WGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEVHSKGWRSLYLDRAMIAGLQPE  362

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TFASFIQQRGRWA+GMMQML+LKNPL R+GL   QRLCY+NSM+FW FPLVR+ +L+APL
Sbjct  363  TFASFIQQRGRWASGMMQMLILKNPLMRKGLSPLQRLCYVNSMAFWLFPLVRLAYLIAPL  422

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFFG EIFV T+ E  AY+  Y+AV  LVQNALF+R RWP +SE+YE+AQAPYLA AI
Sbjct  423  TYLFFGFEIFVTTWREAAAYVLSYMAVVLLVQNALFSRHRWPFISEIYEIAQAPYLAGAI  482

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + T+LRPR A F VTAKDETL+E+YISPIYRPLL  F L ++GV+A ++RW AFPGDRSV
Sbjct  483  IRTVLRPRGATFKVTAKDETLAEDYISPIYRPLLIVFGLTVAGVVALILRWFAFPGDRSV  542
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Query  552   LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVP-------AEAQIPAFGNRSLT  604
             LLVVG WAVLN+LLV  ALRAV+EKQQRRAAPRV M  P       A A +P
Sbjct  543   LLVVGIWAVLNMLLVSIALRAVSEKQQRRAAPRVDMREPGALGWEGAPAPVP--------  594

Query  605   ATVLDASTSGVRL-LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGR-IRSARR  662
              TV+DASTSGV L +   PG   P     +G  +  +P FP A  LER VR   ++ +
Sbjct  595   VTVIDASTSGVALEIAGAPGTA-PARLPSSGSEVVLRPLFPHARHLERDVRATLLKVSTA  653

Query  663   EGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAA  722
               G  ++ + F A Q I +RE VA+LIFG S +W   R  T    GL+ G+A +L +
Sbjct  654   ASGATILNLKFVADQAIDMREAVAHLIFGSSENWLRQRSETQSGKGLIAGLAYVLVLIVT  713

Query  723   SLPKTARDFMDEPARRRR--RHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTA  774
             S+P T RDF+ EPARRRR  + +E   K AHL+AFG DF   P++  E    TA
Sbjct  714   SIPGTMRDFLREPARRRRLAQRQETDAKPAHLVAFGADFD-RPEYLEESPPVTA  766


>TR:A0A1G5DP34 A0A1G5DP34_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus tibetensis OX=336292 GN=SAMN05660710_00879
PE=4 SV=1
Length=772

 Score = 939 bits (2428),  Expect = 0.0
 Identities = 476/748 (64%), Positives = 574/748 (77%), Gaps = 21/748 (3%)

Query  21    LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
             LW+  L P  ++A+ P + +AQ ++ ++AV +VALLKPFA  ++PR  L++ +S++V+RY
Sbjct  14    LWLVALAPVIVMASVPTSNAAQAMLGVTAVAIVALLKPFAGTLMPRIALMAISSIIVLRY  73

Query  81    WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             + WR+  TLP P L  S++ A+LL   ET+SI +FFLN F++ADP +R  P  ++ E+LP
Sbjct  74    FVWRITSTLPDPDLSLSYVLAVLLLLTETYSILVFFLNAFITADPVERDLPPQVRAEDLP  133

Query  141   TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
             TVDILVPSYNEP +MLS+TL+AAKNMIYPARL+ VVLCDDGGTDQRC + DP LA  A+E
Sbjct  134   TVDILVPSYNEPVEMLSITLSAAKNMIYPARLKKVVLCDDGGTDQRCNAADPALADAARE  193

Query  201   RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
             RRR++Q+LCRELGV+YSTR RNEHAKAGNMSAAL RL GELVVVFDADHVPSRDFLARTV
Sbjct  194   RRRQMQELCRELGVIYSTRARNEHAKAGNMSAALARLDGELVVVFDADHVPSRDFLARTV  253

Query  261   GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
             GYF ++P LFLVQTPHFFIN DPI+RNL L   CPPENEMFYGKIH GLDRWGGAFFCGS
Sbjct  254   GYFAQNPKLFLVQTPHFFINSDPIERNLGLA--CPPENEMFYGKIHPGLDRWGGAFFCGS  311

Query  321   AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
             AAVLRR+ALD  GGFAGETITEDAETALEIHS+GW S+Y+DRAMIAGLQPETFASFIQQR
Sbjct  312   AAVLRRKALDSVGGFAGETITEDAETALEIHSKGWSSMYLDRAMIAGLQPETFASFIQQR  371

Query  381   GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             GRWATGMMQML+LKNPL R+GL   QRLCY+NSMSFW FPL+R+ +LVAPL YLFFG+EI
Sbjct  372   GRWATGMMQMLILKNPLLRKGLNPLQRLCYINSMSFWLFPLIRLAYLVAPLTYLFFGVEI  431

Query  441   FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
             FV T  E  AY+  Y+A+  LVQNA+FARQRWPL+SE+YE+AQAPYLA AI  T+LRPR+
Sbjct  432   FVTTANEAAAYVLSYMAIVLLVQNAVFARQRWPLISEIYEIAQAPYLAGAIFRTVLRPRA  491

Query  501   ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
             A+F VTAKDETL+E+YISPIYRPLL  F L ++GV+A + RW+AFPGDRSVLLVVG WAV
Sbjct  492   AKFNVTAKDETLAEDYISPIYRPLLILFALTVAGVVALIFRWIAFPGDRSVLLVVGIWAV  551

Query  561   LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL---  617
             LN+LLV  +LRAVAEKQQRRAAPRV M  PA     A  +  L  TV+DASTSG  +
Sbjct  552   LNMLLVSLSLRAVAEKQQRRAAPRVSMREPASLCWSAM-DAPLPVTVVDASTSGAGIELA  610

Query  618   ---LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGR-IRSARREGGTVMVGVIF  673
                 +RLP +             +  +P FP AP LER VR + ++++    G  ++ + F
Sbjct  611   GGSALRLPPLRSE---------VVLRPSFPHAPHLERDVRAQLLKTSSAASGATVLNLRF  661
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Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
             A Q I VRE VA+LIFG S  W   R AT    GL+ G+  +L +   S+P T RDF
Sbjct  662  VADQAIDVREAVAHLIFGSSDRWLQQRRATQSGKGLVAGLLYVLALILRSIPMTVRDFSR  721

Query  734  EPARRRRRHEE--PKEKQAHLLAFGTDF  759
            EPARRRR  +     E  AHL+AFG DF
Sbjct  722  EPARRRRLSQTKLSNEAPAHLVAFGADF  749


>TR:A0A159Z130 A0A159Z130_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Frigidibacter mobilis OX=1335048 GN=AKL17_1361 PE=4
SV=1
Length=759

 Score = 939 bits (2426),  Expect = 0.0
 Identities = 475/740 (64%), Positives = 566/740 (76%), Gaps = 13/740 (2%)

Query  27   VPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLF  86
            +P  LL + P + + Q L+++ AV+LV LLKPF+++   RF LL+ AS++V+RY  WRL
Sbjct  1    MPILLLTSVPTSNAGQALLSIVAVLLVVLLKPFSEQTAARFALLAIASVIVLRYLIWRLL  60

Query  87   ETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILV  146
            ETLPP A   SF  A+LLF VE +S  +FFLN F++ADPT R  P  +   +LPTVDILV
Sbjct  61   ETLPPAAPTLSFAIAVLLFTVELYSNLMFFLNAFINADPTTRKMPPRVSLRDLPTVDILV  120

Query  147  PSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQ  206
            PSYNEP +ML++TL AAKNMIYP   RTVVLCDDGGTDQRC S +PELA  ++ RR ELQ
Sbjct  121  PSYNEPTEMLAITLLAAKNMIYPVDKRTVVLCDDGGTDQRCNSDNPELAAASRHRRAELQ  180

Query  207  QLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVED  266
            QLCR+LG+VYSTR RNEHAKAGNMSAALERL G+LVVVFDADHVP+RDFLARTVGYFV+D
Sbjct  181  QLCRDLGIVYSTRARNEHAKAGNMSAALERLSGDLVVVFDADHVPTRDFLARTVGYFVDD  240

Query  267  PDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRR  326
            P LFLVQTPHFFIN DP+QRNL      P ENEMFY KIHRGLDRWGGAFFCGSAAVLRR
Sbjct  241  PKLFLVQTPHFFINDDPVQRNLGFSRNVPTENEMFYSKIHRGLDRWGGAFFCGSAAVLRR  300

Query  327  RALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATG  386
             ALD  GGF+GETITEDAETAL+IHSRGWKSLYIDRAM+AGLQPETFASFIQQRGRWA+G
Sbjct  301  AALDSVGGFSGETITEDAETALDIHSRGWKSLYIDRAMVAGLQPETFASFIQQRGRWASG  360

Query  387  MMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFE  446
            MMQML+LKNPLFR GL ++QRLCY+NSMSFW FPL+RM +L+ PL+YLFFGIEIFV+T+
Sbjct  361  MMQMLILKNPLFRSGLRLSQRLCYVNSMSFWLFPLIRMAYLLVPLVYLFFGIEIFVSTYA  420

Query  447  EVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVT  506
            EV+AYM GYLA+SFLVQNALF+R RWPLVSEV+EVAQAPYLA AI  T+LRPR+A+F VT
Sbjct  421  EVMAYMLGYLAISFLVQNALFSRYRWPLVSEVFEVAQAPYLAGAIFRTVLRPRAAKFNVT  480

Query  507  AKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLV  566
            AKDE L E+YISPIY+PLLF  LL L+GV+A + RW+AFPGDR VL +VGGWAV N LLV
Sbjct  481  AKDEMLVEDYISPIYKPLLFLLLLMLAGVVALVARWIAFPGDRGVLAIVGGWAVFNFLLV  540

Query  567  GFALRAVAEKQQRRAAPRVQMEVPA----EAQIPAFGNRSLTATVLDASTSGVRLLVRL-  621
              ALRAV EKQQ RA+PRV MEVPA    E Q     +  + AT++DAS  G  L+ ++
Sbjct  541  SLALRAVCEKQQSRASPRVTMEVPALLTWEGQ-----SAPIPATIVDASVRGAGLVFQMP  595

Query  622  -PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
             P  G     L    ++ F+P+FPDA  LE  +   +R+  R    V+VG+       +
Sbjct  596  RPAEGSAERMLALEDVVTFRPRFPDAQHLETDLGAVVRNITRTDKGVLVGLRMLPNPDLD  655

Query  681  VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPARRRR  740
             R  +A+L FG S +W+ +REAT    GLL G+  +LW+   SLPKT  DF  EPARR R
Sbjct  656  ARAAIAFLTFGASENWQRVREATRARKGLLAGILYVLWLCLTSLPKTVMDFAREPARRSR  715

Query  741  --RHEEPKEKQAHLLAFGTD  758
              RH   +++ AHLLAF  D
Sbjct  716  AARHPHEQQRPAHLLAFTAD  735
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>TR:A0A1H8GN18 A0A1H8GN18_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Loktanella fryxellensis OX=245187 GN=SAMN04488003_11714
PE=4 SV=1
Length=803

 Score = 937 bits (2423),  Expect = 0.0
 Identities = 471/748 (63%), Positives = 567/748 (76%), Gaps = 7/748 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V+  +LW+ L V    + + P +P AQ  +++ AV+ VA LKP+A  +V RF LL+ AS+
Sbjct  15   VVTTVLWLCLAVVIAAMVSFPTSPGAQAFLSIVAVITVAALKPYARLLVARFFLLATASI  74

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY+ WR+ +T+P   L  SF+ A++L  VET+SI +FFLN F+ ADPT RPFP  +
Sbjct  75   IVLRYYLWRILDTMPDAGLTISFIVAVMLLVVETYSIMVFFLNAFIGADPTRRPFPSTVA  134

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            P +LPTVDILVPSYNEP +MLSVTLAAAKNMIYPA  RTVVLCDDGGTDQRC S D  LA
Sbjct  135  PADLPTVDILVPSYNEPVEMLSVTLAAAKNMIYPADKRTVVLCDDGGTDQRCNSSDEGLA  194

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +A++RR ++  LC ELGV YSTR RNEHAKAGNMSAALE+L G+LVVVFDADHVPSRDF
Sbjct  195  ARAKQRRADMMALCAELGVTYSTRARNEHAKAGNMSAALEKLNGDLVVVFDADHVPSRDF  254

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            LARTV +FV+DP LFLVQTPHFFIN DPIQRNL L +  PPENEMFY  IHRGLDRWGGA
Sbjct  255  LARTVNHFVDDPQLFLVQTPHFFINKDPIQRNLELSEAAPPENEMFYSLIHRGLDRWGGA  314

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRRRALD  GGFAGETITEDAETALEIH+ GWKSLYIDRAMIAGLQPETFAS
Sbjct  315  FFCGSAAVLRRRALDSVGGFAGETITEDAETALEIHAAGWKSLYIDRAMIAGLQPETFAS  374

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FIQQRGRWA GMMQMLLLKNPLFR GLG+ QR+CY+NSMSFW FP++R+ +L  PL+YLF
Sbjct  375  FIQQRGRWAAGMMQMLLLKNPLFRSGLGLPQRICYINSMSFWLFPIMRLFYLYVPLVYLF  434

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FGIEIFVAT +EVLAYM GYLAVS+LVQNAL+AR RWPL+SE+YEVAQAPYLARA++ T+
Sbjct  435  FGIEIFVATLDEVLAYMLGYLAVSYLVQNALYARFRWPLISEIYEVAQAPYLARAVMRTI  494

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            +RPR A+F VTAKDE L ++YISPI+ PL   F + L+G++A  VRWVA+PGD SVL VV
Sbjct  495  IRPRDAKFNVTAKDEVLDKDYISPIHWPLTILFFVMLAGLIALGVRWVAYPGDHSVLAVV  554

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGWAV N LLV  A R+VAEKQQRRA+PRVQM+VP    +P   +      ++D STSGV
Sbjct  555  GGWAVFNFLLVSIAWRSVAEKQQRRASPRVQMDVPGRFWLPDDESAQAGVRIVDTSTSGV  614

Query  616  RLLV----RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
            R+L+     LPG G     L  G  I  +P   ++P LE  + G +R+  +     ++GV
Sbjct  615  RMLLDTGHGLPG-GLTAQTL-VGHPIVMRPTLEESPHLEAPITGVVRAVTQTARGTLIGV  672

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF  731
            +F+A  P+  RETVAYLIFG+S HWR++R  T  P GL+ G+A ++ +     P    D
Sbjct  673  VFDADNPMRARETVAYLIFGDSEHWRSIRHTTRAPKGLIAGLAYVMGLFLRGTPLLLIDM  732

Query  732  MDE-PARRRRRHEEPKEKQAHLLAFGTD  758
                 A R      P +K AHLLAFG D
Sbjct  733  WKSLRADRTGPDAGPGDKPAHLLAFGID  760


>TR:A0ABT5T3S5 A0ABT5T3S5_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseinatronobacter alkalisoli OX=3028235 GN=bcsA PE=4
SV=1
Length=809

 Score = 937 bits (2422),  Expect = 0.0
 Identities = 468/765 (61%), Positives = 583/765 (76%), Gaps = 14/765 (2%)
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Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVP  65
            A   LR   VLL  LW+A+++P   LA+ P + + QG + L AV++VA LKPF  K +V
Sbjct  6    ANRRLRPGEVLLAFLWLAVVIPLAFLASIPTSTAVQGALGLFAVLIVAALKPFTMKTIVA  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RF LL+ AS +VMRYWFWRL ETLP  +    F  A+ LFAVET++I +FF++ F++ADP
Sbjct  66   RFALLAIASAIVMRYWFWRLTETLPSVSNPLEFGIAVSLFAVETYAIWVFFVSSFVTADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
              R  P  +  + LPTVDILVPSYNEP DML+VTL+AAKNM YPA  RTVVLCDDGGTD+
Sbjct  126  IHRTLPPKVAAQSLPTVDILVPSYNEPTDMLAVTLSAAKNMHYPASKRTVVLCDDGGTDE  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC   +P++A KA+ RR+ELQ LC +LG+VYSTR RN HAKAGNMSAALERL GELVVVF
Sbjct  186  RCNHENPDIASKARARRKELQALCADLGIVYSTRARNVHAKAGNMSAALERLNGELVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVPSRDFLARTVGYFV DP LFLVQTPHFF+NPDPI RN+ L   CPPENEMFY +
Sbjct  246  DADHVPSRDFLARTVGYFVVDPKLFLVQTPHFFLNPDPIDRNIGLRADCPPENEMFYHQG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSA+VLRR ALD+ GGFAGETITEDAETALEIHSRGWKSLY+D AMI
Sbjct  306  HRGLDRWGGAFFCGSASVLRRAALDDVGGFAGETITEDAETALEIHSRGWKSLYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPETF +FI+QRGRWA GMMQ+L+LKNPL R+G+ + QRLCYLNSM+FW FPLVRM+
Sbjct  366  AGLQPETFVTFIEQRGRWAAGMMQLLMLKNPLRRKGMSLTQRLCYLNSMTFWLFPLVRMI  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFFG+ IFVAT +EVL YM  Y+A+SF+VQNAL+AR RWPL+SE+YE AQAP
Sbjct  426  FILAPLAYLFFGLHIFVATIQEVLVYMGAYMAISFMVQNALYARVRWPLISELYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+  ++ T+ +PR A+F VTAKDE L E+YISP+Y+PLLF ++L L GV+A  +RWV F
Sbjct  486  YLSGVVIKTIFKPRGAKFNVTAKDEVLIEDYISPLYKPLLFVWILSLMGVVAAGIRWVMF  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT-  604
            PGD+++L +VGGWAV N ++V  +LRA+AE+QQRR  PRV M VPA A I      S T
Sbjct  546  PGDQTILSIVGGWAVFNFVIVSASLRAIAERQQRRGVPRVDMNVPAVAAIGRNDMFSFTG  605

Query  605  ATVLDASTSGVRLLVRLPG----VGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSA  660
            ATVLD+STSG R+L+R PG    +G+   A+E G +  F P+FP +P LE  +R ++++
Sbjct  606  ATVLDSSTSGARILLR-PGPDTDMGE-FAAIEKGYIFYFTPEFPKSPHLENAIRVQVQNV  663

Query  661  RREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            +RE   ++VGV ++  QP+  RET+AYLIFG+SA W  +RE+  +P GLL G   ++++A
Sbjct  664  QRENNGIIVGVNYDPEQPMVARETIAYLIFGDSAVWEAVRESRNKPKGLLAGFGYVIYLA  723

Query  721  AASLPKTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDF  759
               +  T R    EPARR+R  E  +      +  AH+LAFG  F
Sbjct  724  VTGVYHTMRALAAEPARRKRAEERDRTEVGAIQAPAHILAFGEAF  768


>TR:A0A4V5MUU5 A0A4V5MUU5_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus gahaiensis OX=1706839 GN=bcsA PE=4 SV=1
Length=775

 Score = 937 bits (2422),  Expect = 0.0
 Identities = 484/755 (64%), Positives = 577/755 (76%), Gaps = 9/755 (1%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            R  P     LW+  ++P  +LA+ P + +AQ ++ +++V LVA LKPFA  +V R  L+S
Sbjct  5    RSFPRWFLPLWLVAIIPVLILASVPTSNAAQAMLGVASVALVAGLKPFAAHIVARIALMS  64

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS+ V+RY  WRL  TLP   L  SF+ A+LL   E +SI +FFLN F++ADP  R  P
Sbjct  65   IASVTVIRYLVWRLTSTLPDVDLSLSFVLAMLLLLTEIYSILVFFLNAFITADPVMRDLP  124
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Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
              ++ E+LPTVDILVPSYNEP +MLS+TL+AAKNMIYPARLR VVLCDDGGTDQRC S +
Sbjct  125  PQVRAEDLPTVDILVPSYNEPIEMLSITLSAAKNMIYPARLRRVVLCDDGGTDQRCNSDN  184

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            P LA+ AQ RR  LQQLCR+LGV+YSTR RNEHAKAGNMSAALERL GELVVVFDADHVP
Sbjct  185  PVLAKSAQARRAALQQLCRDLGVIYSTRARNEHAKAGNMSAALERLDGELVVVFDADHVP  244

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTVGYF +DP LFLVQTPHFFIN DPI+RNL L  +CPPENEMFYGKIH GLDR
Sbjct  245  SRDFLARTVGYFTQDPRLFLVQTPHFFINRDPIERNLGL--KCPPENEMFYGKIHPGLDR  302

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALEIHS+GW+S+Y+DRAMIAGLQPE
Sbjct  303  WGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSKGWRSMYLDRAMIAGLQPE  362

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TFASFIQQRGRWA GMMQML+LKNPL R+GL   QRLCY+NSMSFW FPL+RM +L+APL
Sbjct  363  TFASFIQQRGRWAAGMMQMLILKNPLLRKGLNPLQRLCYINSMSFWLFPLIRMAYLLAPL  422

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFFG+EIFV T  E  AY+  Y+A+  LVQNA+FARQRWPL+SE+YE+AQAPYLA AI
Sbjct  423  SYLFFGVEIFVTTLNEAAAYVLSYMAIVLLVQNAVFARQRWPLISEIYEIAQAPYLAGAI  482

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + T+LRPR+A F VTAKDETL+E+YISPIYRPLL  F L  +GV+A + RW+AFPGDRSV
Sbjct  483  IRTVLRPRAATFNVTAKDETLAEDYISPIYRPLLILFGLTAAGVVALIARWIAFPGDRSV  542

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
            L+VVG WAVLN+LLV  +LRAV+EKQQRRA+PRV M+     +      +++  TV DAS
Sbjct  543  LMVVGIWAVLNMLLVSISLRAVSEKQQRRASPRVAMQEKGSLRWEGSDGKAIPITVCDAS  602

Query  612  TSGVRLLVR-LPG-VGDPHPALEAGGLIQFQPKFPDAPQLERMVRG-RIRSARREGGTVM  668
            TSGV L +R LPG V    PAL +   + F+P FP AP LER VR   ++++    G V+
Sbjct  603  TSGVGLEMRELPGSVRLRPPALRSE--VIFRPAFPHAPHLERDVRAVLLKTSTAGSGAVV  660

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            + + F A Q I VRE VA+LIFG S HW   R AT    GL+ G+  +L +   S+P T
Sbjct  661  LNLQFVAEQDIDVREAVAHLIFGSSEHWLAQRRATQSGKGLIAGLFYVLRLTLTSIPLTV  720

Query  729  RDFMDEPARRRRRHEEPKEK--QAHLLAFGTDFST  761
            RDF  EPARRRR   +  +    AHL+AFG DF T
Sbjct  721  RDFAREPARRRRAALKAGQTAIPAHLVAFGADFDT  755


>TR:A0ABW4E1Y9 A0ABW4E1Y9_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus nototheniae OX=2489002 GN=bcsA PE=4 SV=1
Length=773

 Score = 937 bits (2421),  Expect = 0.0
 Identities = 478/761 (63%), Positives = 579/761 (76%), Gaps = 11/761 (1%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LW+  LVP  +LA+ P + +AQ ++ +++VV+V +LKPFA  +V R  L+S AS+ V+RY
Sbjct  14   LWLVALVPVMILASVPTSNAAQAMLGVASVVIVTVLKPFAAHIVARIALMSIASVTVIRY  73

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
              WR+  TLP      SF+ A+LL   E +SI +FFLN F++ADP  R  P  ++ E+LP
Sbjct  74   IVWRMTSTLPDVEFGVSFILAVLLLLTEIYSIFVFFLNAFITADPVVRDLPPQVRAEDLP  133

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVDILVPSYNEP +MLS+TL+AAKNMIYPARLR VVLCDDGGTDQRC SPDP+L++ A+
Sbjct  134  TVDILVPSYNEPIEMLSITLSAAKNMIYPARLRRVVLCDDGGTDQRCESPDPDLSKAARL  193

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RR +LQQLC++LGV+YSTR RNEHAKAGNMSAAL RL GELVVVFDADHVPSRDFLARTV
Sbjct  194  RRSQLQQLCQDLGVIYSTRARNEHAKAGNMSAALARLDGELVVVFDADHVPSRDFLARTV  253

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
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            GYF +DP LFLVQTPHFFIN DPI+RNL L  +CPPENEMFYGKIH GLDRWGGAFFCGS
Sbjct  254  GYFTQDPRLFLVQTPHFFINKDPIERNLGL--KCPPENEMFYGKIHPGLDRWGGAFFCGS  311

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR+ALD  GGFAGETITEDAETALEIHS+GW+S+Y+DRAMIAGLQPETFASFIQQR
Sbjct  312  AAVLRRKALDSVGGFAGETITEDAETALEIHSKGWRSMYLDRAMIAGLQPETFASFIQQR  371

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
            GRWA GMMQML+LKNPL R+GL   QRLCY+NSMSFW FPL+R+ +LVAPL YLFFG+EI
Sbjct  372  GRWAAGMMQMLILKNPLLRKGLNPLQRLCYINSMSFWLFPLIRLAYLVAPLTYLFFGVEI  431

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FV T  E  AY+  Y+AV  LVQNA+FARQRWPL+SE+YE+AQAPYLA AI+ T+LRPR+
Sbjct  432  FVTTLREAAAYVLSYMAVVLLVQNAVFARQRWPLISEIYEIAQAPYLAGAILRTVLRPRA  491

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
            A+F VTAKDETL+E+YISPIYRPLL  F L L+GV A + RW+AFPGDRSVL VVG WA+
Sbjct  492  AKFNVTAKDETLAEDYISPIYRPLLILFGLTLAGVAALVARWIAFPGDRSVLTVVGIWAI  551

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            +N+LLV  +LRAV+EKQQRRA+PRV M+   +  +      ++  TV DASTSGV L +R
Sbjct  552  INMLLVSISLRAVSEKQQRRASPRVAMQ--EKGSLRWDSGPAMPVTVFDASTSGVGLEMR  609

Query  621  -LPGVGDPH-PALEAGGLIQFQPKFPDAPQLERMVRG-RIRSARREGGTVMVGVIFEAGQ  677
                 G P  PA+   G + F+P FP AP LER VR   ++++    G  ++ + F + Q
Sbjct  610  ESAAAGRPRLPAIR--GEVVFRPSFPHAPHLERDVRAVLLKTSTAASGATVLNLQFVSEQ  667

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPAR  737
             I VRE VA+LIFG S HW   R  T +  GL+ G+  +LW+   SLPKT RDF  EPAR
Sbjct  668  DIDVREAVAHLIFGSSEHWLEQRRQTQQGKGLIAGLWYVLWLTLTSLPKTVRDFAKEPAR  727

Query  738  RRRRHEEPKEK--QAHLLAFGTDFSTEPDWAGELLDPTAQV  776
            RRR      +    AHL+AFG DF T        ++ P   +
Sbjct  728  RRRVALTAGQGAIPAHLVAFGADFDTPEHREERVMTPEEMI  768


>TR:A0A7Z0HYI9 A0A7Z0HYI9_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhabdonatronobacter sediminivivens OX=2743469 GN=bcsA
PE=4 SV=1
Length=814

 Score = 936 bits (2420),  Expect = 0.0
 Identities = 477/791 (60%), Positives = 587/791 (74%), Gaps = 11/791 (1%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVP  65
            A   LR   +LL +LW  +LVP  LL + P + + QG++ + AV++VA LKP+  K +V
Sbjct  6    ATRKLRAREILLVILWALVLVPILLLVSIPTSTAVQGVLGIFAVIVVAALKPWTMKNIVV  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RFLLL+ AS++VMRYW WRL ETLPP     SF+ A LLF VET++I +FF++ F++ADP
Sbjct  66   RFLLLAVASVVVMRYWSWRLTETLPPVDAPISFIAAALLFMVETYAIGVFFISSFITADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
              R  P  +   +LPTVDILVPSYNEP +MLS+TL+AA+NM YP   RTVVLCDDGGTDQ
Sbjct  126  VKRSLPPKVAVTDLPTVDILVPSYNEPIEMLSITLSAARNMHYPPEKRTVVLCDDGGTDQ  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC S DPELA+ A++RRR+LQ LCRELGVVYSTRERNEHAKAGNMSAALERL G+LVVVF
Sbjct  186  RCNSDDPELAEAARKRRRDLQALCRELGVVYSTRERNEHAKAGNMSAALERLDGDLVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVPSRDFLARTVGYFVEDP LFLVQTPHFF+NPDPI RN+ L   CPPENEMFY +
Sbjct  246  DADHVPSRDFLARTVGYFVEDPKLFLVQTPHFFLNPDPIDRNIGLRADCPPENEMFYHQG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSAAV+RR ALD+ GGFAGETITEDAETALEIHSRGWKSLY+D AMI
Sbjct  306  HRGLDRWGGAFFCGSAAVIRRAALDDVGGFAGETITEDAETALEIHSRGWKSLYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
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            AGLQPETF +FI+QRGRWA GMMQ+L LKNPL R+GL + QRLCYLNSM+FW FPLVRM
Sbjct  366  AGLQPETFTTFIEQRGRWAAGMMQLLRLKNPLRRKGLSLTQRLCYLNSMTFWLFPLVRMA  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFFG++IFVATF+EV+ YM  Y+ VSF+VQNAL+AR RWPL+SE+YE AQAP
Sbjct  426  FILAPLAYLFFGLQIFVATFQEVMVYMSSYMLVSFMVQNALYARVRWPLISELYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+  ++ TL +PR A+F VTAKDE L E+ I+PIY+PLL  + L   GV+A  +RW+ F
Sbjct  486  YLSGVVLRTLFKPRGAQFKVTAKDEVLDEDVITPIYQPLLIVWALAGLGVIAAGIRWMLF  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTA  605
            PGD ++L+VVGGWA+ N L++  ALR +AE+ QRRA+PRV ME PA A I       + A
Sbjct  546  PGDHTILMVVGGWAIFNFLILSAALRVIAERMQRRASPRVPMEAPAIAAIGREDYAFVKA  605

Query  606  TVLDASTSGVRLLVRLPGVGDPH--PALEAGGLIQFQPKFPDAPQLERMVRGRIRSARRE  663
            TV++ASTSG RLL++     D     AL  G +  F P+FP +P LE  VR ++++  ++
Sbjct  606  TVVNASTSGARLLLQPATEEDRRELAALVEGQVFYFTPEFPRSPHLENAVRVQVKTVDKD  665

Query  664  GGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAAS  723
                +VGV ++  QP+AVRETVA+LIFG+SA W  +R    +P  +  GM  +L +A  S
Sbjct  666  AKGFVVGVRYDPDQPMAVRETVAHLIFGDSAVWENIRAGRSKPKPMTVGMLYVLGLAVTS  725

Query  724  LPKTARDFMDEPARRRRRH------EEPKEKQAHLLAFGTDFSTEPDWAGELL--DPTAQ  775
            +  T R    EPARRRR        E  +   AHLLAFG  F  EP  +   +  DP A+
Sbjct  726  VYHTMRALAAEPARRRRARADERAAERERAVPAHLLAFGETFDPEPGPSATRIPFDPAAR  785

Query  776  VSARPNTVAWG  786
             S   + V  G
Sbjct  786  RSDAGHPVTGG  796


>TR:A0A4R2NMG1 A0A4R2NMG1_RHOAD Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhodovulum adriaticum OX=35804 GN=EV656_10620 PE=4
SV=1
Length=797

 Score = 935 bits (2417),  Expect = 0.0
 Identities = 468/755 (62%), Positives = 569/755 (75%), Gaps = 11/755 (1%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            LF LW+ + VP  +LA  P + + Q L+ + AV L+  LKPFADK+VPR  LL+ AS++V
Sbjct  19   LFGLWIVIFVPIAVLATTPTSTNVQALLGIVAVALIWGLKPFADKLVPRVALLAVASVVV  78

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RYW WRL ETLP P    S   AL+LF VET++I++FFLN  ++ADP  R  P  +  +
Sbjct  79   LRYWVWRLAETLPGPEDPFSLAAALVLFGVETYAIAVFFLNSLITADPCRRGLPPRVAED  138

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            +LPTVD+LVPSYNEP +MLS TL+AAK++IYP    TVVLCDDGGTDQRC   D ELA+
Sbjct  139  DLPTVDVLVPSYNEPTEMLSATLSAAKHIIYPQDKLTVVLCDDGGTDQRCNHADLELAKA  198

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            +++RR +LQ+LC +LGVVYSTR RNEHAKAGNMSAALE+L G+LVVVFDADHVPSRDFLA
Sbjct  199  SRQRRADLQKLCADLGVVYSTRARNEHAKAGNMSAALEKLDGDLVVVFDADHVPSRDFLA  258

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
            RTVGYFV++P LFLVQTPHFFIN DPI+RNL   ++CPPENEMFY  IHRGLDRWGGAFF
Sbjct  259  RTVGYFVQNPRLFLVQTPHFFINKDPIERNLGFHEKCPPENEMFYSVIHRGLDRWGGAFF  318

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR ALDEAGGF+GETITEDAETAL+IH+RGW+SLY+D AMIAGLQPETFASFI
Sbjct  319  CGSAAVLRREALDEAGGFSGETITEDAETALDIHARGWESLYLDHAMIAGLQPETFASFI  378

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QRGRWATGM+QMLLLKNP+FR GL + QR CYLNSMSFW FP++R+ FL+ PLIYLFFG
Sbjct  379  LQRGRWATGMLQMLLLKNPIFRPGLTLFQRFCYLNSMSFWLFPVIRLSFLLIPLIYLFFG  438

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
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            +EIFVAT++EVLA+   YL  S+LVQNAL++R RWP++SEVYEVAQ PYL  +I+ TLLR
Sbjct  439  LEIFVATYQEVLAFAITYLLTSYLVQNALYSRVRWPMLSEVYEVAQTPYLVMSIIQTLLR  498

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR+A F VTAKDETL  +YISPI+RPL + FLL  +GV+A + RW AFPGDR VL+VVGG
Sbjct  499  PRAATFKVTAKDETLDTDYISPIFRPLFYLFLLMAAGVVAFIARWFAFPGDREVLMVVGG  558

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQI-----PAFGNRSLTATVLDAST  612
            W + N LLVG +LRAV+EKQQRR APRV M   A  ++     P+     L AT+ DAST
Sbjct  559  WGIFNFLLVGISLRAVSEKQQRRGAPRVNMAKQAVVRLGGRLDPSDSAPVLAATITDAST  618

Query  613  SGVRLLVRLPGVGDPH----PALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVM  668
            SGVRL ++ P  G P      A+   G  I F+P+FP+A  LE  V   +++A   G   +
Sbjct  619  SGVRLEIKRPPAGSPAQQDLAAMTQGARICFRPRFPEAQHLETFVEAEVQAAFSSGPDAV  678

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            +GV     QP++ RE VAYLIFG+S +WR MR    +P G L GMA  L +    +P+T
Sbjct  679  LGVRLVPDQPLSTREAVAYLIFGDSENWRRMRRDEKQPRGFLRGMAYFLGLCITGIPRTI  738

Query  729  RDFMDEPARRRRRHEEPK--EKQAHLLAFGTDFST  761
             D   EPAR RR     +  E   HLLAFG DFS+
Sbjct  739  VDLAREPARLRRERLSGRVHEAPVHLLAFGADFSS  773


>TR:A0A2K8KH18 A0A2K8KH18_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseinatronobacter bogoriensis subsp. barguzinensis
OX=441209 GN=bcsA PE=4 SV=1
Length=810

 Score = 933 bits (2412),  Expect = 0.0
 Identities = 468/784 (60%), Positives = 586/784 (75%), Gaps = 14/784 (2%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMV-P  65
            A   L +  + L L WVAL+VP  +LA+ P +   QG + + AV++VA LKPF  K +
Sbjct  6    ANRKLSLNEIFLALAWVALVVPLVILASIPTSTLVQGAMGVFAVLMVAALKPFCSKKILA  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RFLLL+ AS +V+RYWFWR+ ETLPP  +  SF  A+ LF VET++I +FF++ F+SADP
Sbjct  66   RFLLLAIASAVVLRYWFWRILETLPPMDMPVSFAIAVALFMVETYAIFVFFISSFISADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
             DR  P  +    LPTVDILVPSYNEP +ML+VTL+AAKNM YP + RTVVLCDDGGTDQ
Sbjct  126  VDRALPPKVSAANLPTVDILVPSYNEPTEMLAVTLSAAKNMHYPPQKRTVVLCDDGGTDQ  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC   DPE+A+ A++RR +LQQLC ELGVVYSTR RNEHAKAGNMSAALERL G+LVVVF
Sbjct  186  RCNHEDPEIARAARQRRIDLQQLCAELGVVYSTRPRNEHAKAGNMSAALERLNGDLVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVPSRDFLARTVGYFVEDP LFLVQTPHFF+NPDP++RN+ L   CPPENEMFY
Sbjct  246  DADHVPSRDFLARTVGYFVEDPKLFLVQTPHFFLNPDPVERNIGLRADCPPENEMFYHLG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSA+VLRR ALD+ GGFAGETITEDAETALEIHSRGWKSLY+D AMI
Sbjct  306  HRGLDRWGGAFFCGSASVLRRAALDDVGGFAGETITEDAETALEIHSRGWKSLYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPETF SFIQQRGRWA GMMQ+L+LKNPL R+G+ + QRLCYLNSM+FW FPLVRM
Sbjct  366  AGLQPETFVSFIQQRGRWAAGMMQLLMLKNPLRRKGMSLTQRLCYLNSMTFWLFPLVRMT  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFFG+EIFVAT  EVL YM  Y+AVSF+VQNAL+AR RWPL+SE+YE AQAP
Sbjct  426  FILAPLAYLFFGLEIFVATINEVLVYMSAYMAVSFMVQNALYARVRWPLLSEIYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+  ++ TLL+PR A+F VTAKDE L EN+ISP+++PLL  + +   G++A  +RWV F
Sbjct  486  YLSGVVIKTLLKPRGAKFNVTAKDEVLEENFISPLFKPLLVVWAIVGLGLVAAGIRWVLF  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT-  604
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            PGD ++L+VVGGWAV N +++  +LRA++E+QQRR  PRV+M+VPA A     G  S +
Sbjct  546  PGDHTILMVVGGWAVFNFMILSASLRAISERQQRRGVPRVEMQVPAVAAFGRDGKFSFSA  605

Query  605  ATVLDASTSGVRLLVRLPGVGD---PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSAR  661
            AT++D+STSG  L + +PG         A++ G ++ F P+FP +P LE  +R ++++
Sbjct  606  ATIVDSSTSGAGLKL-IPGPDTDLAEMAAIKPGYVLYFTPEFPKSPHLENAIRVQVKNVE  664

Query  662  REGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
            R    +++GV ++  QP+ VRET+A+LIFG+SA W  MR    +P+ LL GMA +  +A
Sbjct  665  RTSSGLVLGVRYDPEQPMIVRETIAHLIFGDSAVWEKMRADRNKPMPLLKGMAYVAGLAF  724

Query  722  ASLPKTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDFSTEPDWAGELLDPTAQ  775
             S+  T +    EPARRR   E  +       + AHLLAFG  F  +PD      DP+
Sbjct  725  TSVYHTVKALSAEPARRRAAQERARLGEIEAAQPAHLLAFGEAF--DPDITNPGFDPSLG  782

Query  776  VSAR  779
            V  +
Sbjct  783  VDGQ  786


>TR:A0A4Z1CKA7 A0A4Z1CKA7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paracoccus liaowanqingii OX=2560053 GN=bcsA PE=4 SV=1
Length=775

 Score = 932 bits (2408),  Expect = 0.0
 Identities = 480/755 (64%), Positives = 575/755 (76%), Gaps = 9/755 (1%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            R  P     LW+  +VP  +LA+ P + +AQ ++ +++V LVA LKPFA  +V R  L+S
Sbjct  5    RSFPRWFLPLWLVAIVPVLILASVPTSNAAQAMLGVASVALVAGLKPFAAHIVARIALMS  64

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
             AS+ V+RY  WRL  TLP   L  SF+ A+LL   E +SI +FFLN F++ADP  R  P
Sbjct  65   IASVTVIRYLVWRLTSTLPDVDLTLSFVLAMLLLLTEFYSILVFFLNAFITADPVMRDLP  124

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
              ++ E+LPTVDILVPSYNEP +MLS+TL+AAKNMIYPARLR VVLCDDGGTDQRC S D
Sbjct  125  PQVRAEDLPTVDILVPSYNEPIEMLSITLSAAKNMIYPARLRRVVLCDDGGTDQRCESSD  184

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            P +A+ A++RR +LQQLC +LGV+YSTR RNEHAKAGNMSAAL RL GELVVVFDADHVP
Sbjct  185  PVMAKAAKQRRAQLQQLCLDLGVIYSTRARNEHAKAGNMSAALARLDGELVVVFDADHVP  244

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            SRDFLARTVGYF +DP LFLVQTPHFFIN DPI+RNL L  +CPPENEMFYGKIH GLDR
Sbjct  245  SRDFLARTVGYFTQDPRLFLVQTPHFFINRDPIERNLGL--KCPPENEMFYGKIHPGLDR  302

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            WGGAFFCGSAAVLRR+ALD  GGFAGETITEDAETALEIHS+GW+S+Y+DRAMIAGLQPE
Sbjct  303  WGGAFFCGSAAVLRRKALDSVGGFAGETITEDAETALEIHSKGWRSMYLDRAMIAGLQPE  362

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TFASFIQQRGRWA GMMQML+LKNPL R+GL   QRLCY+NSMSFW FPL+RM +L+APL
Sbjct  363  TFASFIQQRGRWAAGMMQMLILKNPLMRKGLNPLQRLCYINSMSFWLFPLIRMAYLLAPL  422

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFFG+EIFV T  E  AY+  Y+A+  LVQNA+FARQRWPL+SE+YE+AQAPYLA AI
Sbjct  423  SYLFFGVEIFVTTLNEAAAYVLSYMAIVLLVQNAVFARQRWPLISEIYEIAQAPYLAGAI  482

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            + T+LRPR+A+F VTAKDETL+E+YISPIYRPLL  F L  +GV+A + RW+AFPGDRSV
Sbjct  483  IRTVLRPRAAKFNVTAKDETLAEDYISPIYRPLLILFGLTAAGVVALIARWIAFPGDRSV  542

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
            L+VVG WAVLN+LLV  +LRAV+EKQQRRA+PRV M+     +      +++  TV DAS
Sbjct  543  LMVVGIWAVLNMLLVSISLRAVSEKQQRRASPRVAMQEKGSLRWDGSDGQAIPVTVCDAS  602

Query  612  TSGVRLLVR-LPGVGDPH-PALEAGGLIQFQPKFPDAPQLERMVRG-RIRSARREGGTVM  668
            TSGV L +R LPG      PAL +   + F+P FP AP LER VR   ++++    G V+
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Sbjct  603  TSGVGLEMRDLPGAARLRAPALRSE--VIFRPDFPHAPHLERDVRAVLLKTSTAGSGAVV  660

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            + + F A Q   VRE VA+LIFG S HW   R  T    GL+ G+  +L +   SLP T
Sbjct  661  LNLQFVAEQDFDVREAVAHLIFGSSEHWLAQRRDTQSGKGLVAGLFYVLKLTLTSLPLTV  720

Query  729  RDFMDEPARRRRRHEEPKEK--QAHLLAFGTDFST  761
            RDF  EPARRRR   +  +    AHL+AFG DF T
Sbjct  721  RDFAREPARRRRAAMKAGQTAIPAHLVAFGADFDT  755


>TR:A0A543KFX0 A0A543KFX0_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseinatronobacter monicus OX=393481 GN=BD293_2634
PE=4 SV=1
Length=810

 Score = 930 bits (2404),  Expect = 0.0
 Identities = 468/777 (60%), Positives = 583/777 (75%), Gaps = 15/777 (2%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVP  65
            A   L +  VLL L W AL+VP  +LA+ P + + QG + + AV+ VA LKPF  K +V
Sbjct  6    ANRKLNLTEVLLALAWFALVVPIAILASIPTSTAVQGALGVFAVLAVAALKPFTSKKIVA  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RFLLL+ AS +VMRYWFWR+ ETLPP  +  SF  A+ LF VET++I +FF++ F+SADP
Sbjct  66   RFLLLAIASAVVMRYWFWRVTETLPPLDMPVSFTIAMALFIVETYAIFVFFISSFISADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
             +R  P  +    LPTVDILVPSYNEP +ML+VTL+AAKNM YPA+ RTVVLCDDGGTDQ
Sbjct  126  VERSLPPKVAAANLPTVDILVPSYNEPTEMLAVTLSAAKNMHYPAQKRTVVLCDDGGTDQ  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC S DPELA+ +++RR +LQ+LC +LGVVYSTR +NE+AKAGNMSAALERL G+LVVVF
Sbjct  186  RCNSEDPELARASRQRRADLQELCAQLGVVYSTRPKNENAKAGNMSAALERLDGDLVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVPSRDFLARTVGYFVEDP LFLVQTPHFF+NPDPI+RN+ L   CPPENEMFY
Sbjct  246  DADHVPSRDFLARTVGYFVEDPKLFLVQTPHFFLNPDPIERNIGLRADCPPENEMFYHLG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSA+VLRR ALD+ GGFAGETITEDAETALEIHSRGWKS+Y+D AMI
Sbjct  306  HRGLDRWGGAFFCGSASVLRRAALDDVGGFAGETITEDAETALEIHSRGWKSIYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPETF S IQQRGRWA GMMQ+L+LKNPL R+G+ + QRLCYLNSM+FW FPLVRM
Sbjct  366  AGLQPETFVSLIQQRGRWAAGMMQLLMLKNPLRRKGMSLTQRLCYLNSMTFWLFPLVRMT  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFFG++IFVAT +EVL YM GY+AVSF+VQNAL+AR RW LVSE+YE AQAP
Sbjct  426  FILAPLAYLFFGLQIFVATIQEVLVYMGGYMAVSFMVQNALYARVRWSLVSELYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+  ++  L +PR A+F VTAKDE L E++ISP+++PLL  + +   GVLA  VRWV F
Sbjct  486  YLSGVVIKILFKPRGAKFNVTAKDEVLEEDFISPMFKPLLVLWAVAGLGVLAAAVRWVLF  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT-  604
            PGD ++L +VGGWAV N ++V  ALRA++E+QQRR  PR + + PA A     G  S +
Sbjct  546  PGDHTILSIVGGWAVFNFIIVSAALRAISERQQRRGVPRFETQAPAVAAFGRDGQFSFSA  605

Query  605  ATVLDASTSGVRLLVRLPGVGD---PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSAR  661
            AT+LD+STSG R+ + LPG         A+  G +  F P+FP +P LE  +R ++++
Sbjct  606  ATILDSSTSGARIKL-LPGPDTDLAEMTAITPGYVFYFTPEFPKSPHLENAIRVQVKNIE  664

Query  662  REGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
            R    +++GV F+  QP+ VRET+AYLIFG+SA W  +RE+  +P+ +L GMA I+ +A
Sbjct  665  RTNSGLILGVRFDPDQPMIVRETIAYLIFGDSAVWERVRESKNKPMPMLKGMAYIVMLAF  724

Query  722  ASLPKTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDFS---TEPDWAGEL  769
             S+  T      EPARRR  HE  +       + AHLLAFG  F    T P++A  +
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Sbjct  725  TSVYHTMHALAAEPARRRAAHERARMGEIGAAQPAHLLAFGEAFDPAITNPEFAANM  781


>TR:A0A1H2XT79 A0A1H2XT79_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseicitreum antarcticum OX=564137 GN=SAMN04488238_104306
PE=4 SV=1
Length=890

 Score = 929 bits (2401),  Expect = 0.0
 Identities = 468/778 (60%), Positives = 581/778 (75%), Gaps = 9/778 (1%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVP  65
            A  PL+   +L+F +W+ L++P     + P + + QG++ L+AV++VA+LKP  ++ MV
Sbjct  6    ANRPLKTGEMLIFAIWLLLMIPLLAFVSIPTSTAVQGILGLAAVLVVAVLKPVTNRNMVA  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RF LLS AS++VMRYW WR+ ETLP P    SF  A+LLFAVET++I +FFL+ F++ADP
Sbjct  66   RFALLSIASLVVMRYWSWRVMETLPAPEYPVSFAAAMLLFAVETYAIMVFFLSSFMTADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
             +R  P  +   +LPTVDILVPSYNEP +MLSVTL+AAKNM YPA  RTVVLCDDGGTDQ
Sbjct  126  IERTLPPKVAAADLPTVDILVPSYNEPVEMLSVTLSAAKNMHYPAHKRTVVLCDDGGTDQ  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC S D  LA++++ RRR LQ LC +LGV+Y TR RNE AKAGNMS+ALERL G+LVVVF
Sbjct  186  RCNSDDAGLAERSRARRRALQALCNDLGVLYMTRARNESAKAGNMSSALERLNGDLVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVP+RDFLARTVGYFV+DP LFLVQTPHFF+NPDPI RN+ L   CPPENEMFY +
Sbjct  246  DADHVPARDFLARTVGYFVQDPKLFLVQTPHFFLNPDPIDRNIGLRKDCPPENEMFYHQG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSAAVLRR ALD  GGFAGETITEDAETALEIHS+GWKSLY+D AMI
Sbjct  306  HRGLDRWGGAFFCGSAAVLRREALDSVGGFAGETITEDAETALEIHSQGWKSLYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPETF SFI+QRGRWATGMMQ+L+LKNPL R+GL + QRLCYLNSM+FW FPLVR+
Sbjct  366  AGLQPETFTSFIEQRGRWATGMMQLLILKNPLRRKGLSMTQRLCYLNSMTFWLFPLVRLT  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFFG++IFVAT +EVL YM  Y+A+SF+VQNAL+ R RWPL+SE+YE AQAP
Sbjct  426  FILAPLAYLFFGLQIFVATIQEVLVYMTSYMAISFMVQNALYGRVRWPLISELYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YLA AI  T  RPR+A+F VTAKDE L E+Y+SPIY PLL  ++L   GV+A  VRW+ +
Sbjct  486  YLASAIFKTFWRPRAAKFNVTAKDEVLEEDYLSPIYAPLLTIWVLAGLGVIAAGVRWMLY  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTA  605
            PGD ++L++VGGWAV N L+V  +LR +AE+QQRRA PRV M+VPA A +     + ++A
Sbjct  546  PGDHNILMIVGGWAVFNFLIVSASLRVLAERQQRRAVPRVPMQVPAVAALGRSVEQFVSA  605

Query  606  TVLDASTSGVRLLVRLPGVGDPH--PALEAGGLIQFQPKFPDAPQLERMVRGRIRSARRE  663
            TVLDASTSG RL +R      P     +E G +  F P+FP +P LE  VR +++S  R
Sbjct  606  TVLDASTSGARLSLRPSPETRPEDLAKIEKGFVFFFTPEFPKSPHLENAVRVQVQSVVRS  665

Query  664  GGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAAS  723
            G + +VGV ++  QP+ VRETVA+LIFG+SA W  +R    R  GLL GM  ++ +A +
Sbjct  666  GNSYVVGVKYDPDQPMIVRETVAHLIFGDSAVWEAIRAGRTRQKGLLVGMGYVVVLAFSG  725

Query  724  LPKTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDFSTEPDWAGELLDPTAQ  775
            +  TA    +EPAR RR  E  +         AHLLAFG  F   P      + P A+
Sbjct  726  IWHTAIAIKNEPARLRRLRERERISGRSEAVPAHLLAFGEAFDPPPAARPVPISPAAR  783


>TR:A0A2W7Q1E3 A0A2W7Q1E3_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseinatronobacter thiooxidans OX=121821 GN=LY56_02043
PE=4 SV=1
Length=810
```

```
 Score = 926 bits (2392),  Expect = 0.0
 Identities = 458/766 (60%), Positives = 582/766 (76%), Gaps = 10/766 (1%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPF-ADKMVP  65
            A   LR+  + L L+WVAL+VP  +LA+ P + + QG + + AV+ VA LKPF + K+V
Sbjct  6    ANRKLRLTEIALVLMWVALVVPLAILASVPTSTAVQGALGVFAVLAVAALKPFTSSKIVA  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RFLLL+ AS +VMRYWFWR+ ETLPP  +  SF  A+ LF VET++I +FF++ F++ADP
Sbjct  66   RFLLLAIASAVVMRYWFWRVTETLPPMDMPISFGIAVALFIVETYAIFVFFISSFITADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
             +R  P  +    LPTVDILVPSYNEP +ML+VTL+AAKNM YPA+ RTVVLCDDGGTDQ
Sbjct  126  INRALPPKVAAANLPTVDILVPSYNEPTEMLAVTLSAAKNMHYPAQKRTVVLCDDGGTDQ  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC   DPE+A+ A++RR +LQ+LC ELG+VYSTR +NEHAKAGNMSAALERL G+LVVVF
Sbjct  186  RCNHEDPEIARIARQRRADLQELCAELGIVYSTRPKNEHAKAGNMSAALERLNGDLVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVPSRDFLARTVGYFVEDP LFLVQTPHFF+NPDP++RN+ L   CPPENEMFY
Sbjct  246  DADHVPSRDFLARTVGYFVEDPKLFLVQTPHFFLNPDPVERNIGLRSDCPPENEMFYHLG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSA+VLRR ALD+ GGFAG+TITEDAETALEIHSRGWKSLY+D AMI
Sbjct  306  HRGLDRWGGAFFCGSASVLRRAALDDVGGFAGDTITEDAETALEIHSRGWKSLYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPETF SFIQQRGRWA GMMQ+L+LKNPL R+G+ + QRLCYLNSM+FW FPLVRM
Sbjct  366  AGLQPETFVSFIQQRGRWAAGMMQLLMLKNPLRRKGMSLTQRLCYLNSMTFWLFPLVRMT  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFFG++IFVAT +EVL YM  Y+A+SF+VQNAL+AR RWPL+SE+YE AQAP
Sbjct  426  FILAPLAYLFFGLQIFVATIQEVLVYMGAYMAISFMVQNALYARVRWPLLSEIYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+  +V TL +PR A+F VTAKDE L E++ISP+++PLL  +++   GVLA  VRWV F
Sbjct  486  YLSGVVVKTLFKPRGAKFNVTAKDEVLEEDFISPLFKPLLVLWMIAGLGVLAAAVRWVLF  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSL-T  604
            PGD ++L +VGGWA+ N +++  +LRA+AE+QQRR  PRV+M  PA A     G  S
Sbjct  546  PGDHNILSIVGGWAIFNFVILSASLRAIAERQQRRGVPRVEMHAPAVAAFGRDGKFSFAA  605

Query  605  ATVLDASTS--GVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARR  662
            ATV+D+STS  G+RL+           A++ G ++ F P+FP +P LE  +R ++++  R
Sbjct  606  ATVVDSSTSGAGIRLVAGPDTDLGEMAAIKPGYVMYFTPEFPKSPHLENAIRVQVKNVER  665

Query  663  EGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAA  722
                +++GV ++  QP+ VRET+A+LIFG+SA W  +R +  +P+ LL GM  I+ +A +
Sbjct  666  TNSGLVLGVRYDPEQPMFVRETIAHLIFGDSAVWEAIRASKNKPMPLLKGMGYIVTLAFS  725

Query  723  SLPKTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDFSTE  762
            S+   T    + EPARRR   E  +       + AH+LAFG  F  E
Sbjct  726  SVYHTMSALVAEPARRRAAMERARLGEIEAAQPAHMLAFGEAFDPE  771


>TR:A0A2T7UYD8 A0A2T7UYD8_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pararhodobacter aggregans OX=404875 GN=bcsA PE=4 SV=1
Length=800

 Score = 914 bits (2361),  Expect = 0.0
 Identities = 453/749 (60%), Positives = 565/749 (75%), Gaps = 9/749 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA-DKMVPRFLLLSAASMLVM  78
            LLW+ L+V    L + P +   Q  + +++ ++V  LKP A + MV RF ++S AS LV+
Sbjct  16   LLWLGLMVLVAGLVSVPTSIQVQATLGIASFLVVVALKPVAMESMVARFAMMSIASTLVL  75

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RYW WR+ ETLPP     SF+ A++LF VET++I +FFL+ F++ADP +R  P  +   +
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Sbjct  76   RYWAWRVTETLPPVTDVISFIPAIVLFLVETYAIGVFFLSAFMTADPVNRTLPPRVAASD  135

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LPTVDILVPSYNEP +ML+VTL+AAKNM YP   RTVVLCDDGGTDQRC S +PELA+KA
Sbjct  136  LPTVDILVPSYNEPVEMLAVTLSAAKNMHYPEHKRTVVLCDDGGTDQRCNSDNPELAEKA  195

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            ++RRR+L QLC ELGV+YSTRERN HAKAGNMSAALE+L G++VVVFDADHVPSRDFLAR
Sbjct  196  RKRRRDLIQLCAELGVMYSTRERNVHAKAGNMSAALEKLDGDIVVVFDADHVPSRDFLAR  255

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYFVEDP LFLVQTPHFF+NPDPI RN+ L D CPPENEMFY   HRGLDRWGGAFFC
Sbjct  256  TVGYFVEDPKLFLVQTPHFFLNPDPIDRNIGLRDDCPPENEMFYHLSHRGLDRWGGAFFC  315

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR+ALDEAGGFAG+TITEDAETAL IH+RGWKSLY+D AMIAGLQPETF SFI+
Sbjct  316  GSAALLRRKALDEAGGFAGDTITEDAETALGIHARGWKSLYVDHAMIAGLQPETFVSFIE  375

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QRGRWATGMMQ+L+LKNPL  RGL + Q+LCYLNSM+FW FPLVRM F++APL+YLFFG+
Sbjct  376  QRGRWATGMMQLLILKNPLKYRGLSLTQKLCYLNSMTFWLFPLVRMTFILAPLMYLFFGL  435

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVAT  EV  YM  Y+AV+FL+QNAL+ + RWPLVSE+YE AQAPYLA AI  T   P
Sbjct  436  QIFVATIGEVAVYMTSYMAVNFLIQNALYGKVRWPLVSEIYETAQAPYLAAAIFKTFWNP  495

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R A+F VTAKDE L E+++SPIY+PL+F F L L GV+A  VRWV FPGD ++++VVGGW
Sbjct  496  RGAKFNVTAKDEVLEEDFVSPIYKPLIFIFALTLLGVVAAAVRWVMFPGDHNIIMVVGGW  555

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
            A+ N LLVG ++RAVAE+QQRRA PRV + VPA   +       + ATV+DASTSG RL+
Sbjct  556  AIYNFLLVGASMRAVAERQQRRAVPRVPVNVPATVALGLDHPVFMPATVVDASTSGCRLV  615

Query  619  VRLPGVGDPHPAL--EAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            +R   + D    +         F P+FP +P LE  VR +++S  REG  V +GV F+
Sbjct  616  LRSKPLADGTTPVMPRVADTFYFTPEFPRSPHLENAVRVQVQSVTREGEAVALGVKFDPT  675

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPA  736
            QP+ VRET+A++IFG+SA W  +R    + +GL+ GM  +  ++   +  T R   +EPA
Sbjct  676  QPMIVRETIAHMIFGDSASWEAIRARRHKKMGLIRGMLYVFQLSFQGIYHTLRALAEEPA  735

Query  737  RRRRRHEEPKEKQ------AHLLAFGTDF  759
            R++R  E  +  Q      AH++AFG  F
Sbjct  736  RQQRVRERERNAQVTRTVPAHMMAFGEAF  764


>TR:A0A2U2CA05 A0A2U2CA05_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pararhodobacter marinus OX=2184063 GN=bcsA PE=4 SV=1
Length=805

 Score = 907 bits (2345),  Expect = 0.0
 Identities = 459/752 (61%), Positives = 564/752 (75%), Gaps = 15/752 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA-DKMVPRFLLLSAASMLVM  78
            L W  LL     L + P +   Q  + ++A V VA+LKP A D MV RF ++S AS LV+
Sbjct  19   LFWFGLLALVAGLVSVPTSIQVQATLGIAAFVTVAMLKPVASDNMVARFTMMSIASTLVL  78

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RYW WR+ ETLPP +   SF+ AL+LF VET++I +FFL+ F++ADP  R  P  +   +
Sbjct  79   RYWAWRVTETLPPVSDVLSFIPALVLFLVETYAIGVFFLSAFMTADPVKRSLPPRVAAAD  138

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LPTVDILVPSYNEP +ML+VTL+AAKNM YPA  RTVVLCDDGGTDQRC S DPELA+KA
Sbjct  139  LPTVDILVPSYNEPTEMLAVTLSAAKNMHYPAHKRTVVLCDDGGTDQRCNSDDPELAEKA  198

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            ++RRR+L  LC ELGV+YSTRE+N HAKAGNMSAALE+L G++VVVFDADHVP+RDFLAR
Sbjct  199  RKRRRDLIALCNELGVMYSTREKNVHAKAGNMSAALEKLDGDIVVVFDADHVPARDFLAR  258
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Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYFVEDP LFLVQTPHFF+NPDPI RN+     CPPENEMFY   HRGLDRWGGAFFC
Sbjct  259  TVGYFVEDPKLFLVQTPHFFLNPDPIDRNVGFARDCPPENEMFYHLSHRGLDRWGGAFFC  318

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR+ALDEAGGFAG+TITEDAETAL IH+RGWKS+Y+D AMIAGLQPETF SFI+
Sbjct  319  GSAALLRRKALDEAGGFAGDTITEDAETALGIHARGWKSIYVDHAMIAGLQPETFVSFIE  378

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QRGRWATGMMQ+L+LKNPL  RGL I Q+LCYLNSM+FW FPLVRM F++APL+YLFFG+
Sbjct  379  QRGRWATGMMQLLILKNPLKFRGLSITQKLCYLNSMTFWLFPLVRMTFIIAPLMYLFFGL  438

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVAT EEV  YM  Y+AV+F++QNAL+ R RWPL+SE+YE AQAPYLA AI  T   P
Sbjct  439  QIFVATIEEVAVYMTSYMAVNFMIQNALYGRVRWPLISEIYETAQAPYLAAAIFKTFWNP  498

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R A+F VTAKDE L E+++SPIY+P+LF F L   GV+A  VRWV FPGD+++++VVGGW
Sbjct  499  RGAKFNVTAKDEVLIEDFVSPIYKPMLFIFALTFLGVVAAGVRWVLFPGDQNIIMVVGGW  558

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRS---LTATVLDASTSGV  615
            AV N LLVG ALRA+AE+QQRR+ PRV + VPA   I AFG  +   L ATV+DASTSG
Sbjct  559  AVYNFLLVGAALRAIAERQQRRSVPRVPVNVPA---IVAFGTENPVFLGATVVDASTSGC  615

Query  616  RLLVR-LPGVGDPHPAL-EAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIF  673
            R++VR  P      P +        F P+FP +P LE  +R ++ S  REG +V +GV F
Sbjct  616  RMIVRNKPNADGVAPEIPRVTDTFYFTPEFPKSPHLENAIRVQVMSVTREGDSVALGVKF  675

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
            +  QP+ VRE++A++IFG+SA W  +R +  + +GLL GM  +L ++ A +  T R
Sbjct  676  DPSQPMRVRESIAHMIFGDSASWEAIRASRHKKMGLLRGMYYVLTLSLAGIYATMRALAA  735

Query  734  EPAR--RRRRHEEP----KEKQAHLLAFGTDF  759
            EPAR  R +  E+       K    +AFG  F
Sbjct  736  EPARLARAKAREDADVAVTRKPIQAMAFGETF  767


>TR:A0A2T8HWD3 A0A2T8HWD3_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pararhodobacter oceanensis OX=2172121 GN=bcsA PE=4
SV=1
Length=805

 Score = 907 bits (2344),  Expect = 0.0
 Identities = 451/753 (60%), Positives = 562/753 (75%), Gaps = 9/753 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA-DKMVPRFLLLSAASMLVM  78
            +LW+ +L     L + P +    Q  + +++V++VA LKP A D MV RF ++S AS LVM
Sbjct  19   ILWILVLGLIAALVSVPTSIQVQATLGIASVIVVAALKPVAMDSMVARFAMMSVASTLVM  78

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RYW WR+ ETLPP     SF+ A+ LF VET++I++FFL+GF++ADP  R  P  +   +
Sbjct  79   RYWAWRVTETLPPIDDPISFIPAIFLFFVETYAIAVFFLSGFMTADPIKRGLPPKVAARD  138

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LPTVDILVPSYNEP +ML+VTL+AAKNM YPA  RTV+LCDDGGTDQRC   +PE+A+ +
Sbjct  139  LPTVDILVPSYNEPIEMLAVTLSAAKNMHYPAHKRTVILCDDGGTDQRCNHENPEIAEAS  198

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            ++RRR++  LC ELGVVYSTR RNEHAKAGNMSAALE+  GELVVVFDADHVPSRDFLAR
Sbjct  199  RKRRRDMIALCNELGVVYSTRPRNEHAKAGNMSAALEKQNGELVVVFDADHVPSRDFLAR  258

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYFVEDP LFLVQTPHFF+NPDPI RN+   D CPPENEMFY   HRGLDRWGGAFFC
Sbjct  259  TVGYFVEDPKLFLVQTPHFFLNPDPIDRNVGFRDDCPPENEMFYHLSHRGLDRWGGAFFC  318

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAAVLRR+ALDEAGGFAG+TITEDAETAL+IH  GWKS+Y+D AMIAGLQPETF SFI+
Sbjct  319  GSAAVLRRQALDEAGGFAGDTITEDAETALQIHRNGWKSIYVDHAMIAGLQPETFVSFIE  378
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  Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
              QRGRWATGMMQ+L+LKNPL  +GL   QRLCYLNSM+FW FPLVRM F++APL YLFFG+
  Sbjct  379  QRGRWATGMMQLLILKNPLRGKGLSFTQRLCYLNSMTFWLFPLVRMTFILAPLAYLFFGL  438

  Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
              +IFVAT EEV  YM  Y+AV+F++QNAL+ + RWPL+SE+YE AQAPYL++AI  T+  P
  Sbjct  439  QIFVATIEEVAVYMTSYMAVNFMIQNALYGKVRWPLISEIYETAQAPYLSKAIFKTVANP  498

  Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
              R A+F VTAKDE L E+++SPIY+PL+  F+L L GV+A  VRW  +PGD ++++VVGGW
  Sbjct  499  RGAKFNVTAKDEILEEDFVSPIYKPLVLIFVLTLLGVVAAAVRWFLYPGDHNIIMVVGGW  558

  Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
              AV N LLVG ALRA++E+QQRR  PRV   + A   +        +ATV+DASTSG R++
  Sbjct  559  AVYNFLLVGAALRAISERQQRRQVPRVPTNISATVALGGNTPVFQSATVVDASTSGCRIV  618

  Query  619  VRLPGV--GDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              +R      G   P    G    F P+FP +P LE  VR +++S  REG +V VGV F+
  Sbjct  619  LRPRSTPDGAASPLPVKGETFYFTPEFPKSPHLENAVRVQVQSVIREGDSVAVGVRFDPA  678

  Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPA  736
              QP+ VRETVA++IFG+SA W  +R    + +GL+ GM  +L ++   +  T R   DEPA
  Sbjct  679  QPMVVRETVAHMIFGDSASWEAIRATRNKKMGLIVGMLYVLKLSVEGIVNTLRALADEPA  738

  Query  737  RRRR---RHEE---PKEKQAHLLAFGTDFSTEP  763
              R +R   R E+    + + AHLLAFG  F   P
  Sbjct  739  RLKRVAAREEKIVVVESQPAHLLAFGEAFDPPP  771


  >TR:A0ABT0LZK6 A0ABT0LZK6_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
  OS=Roseinatronobacter domitianus OX=2940293 GN=bcsA PE=4
  SV=1
  Length=809

   Score = 901 bits (2329),  Expect = 0.0
   Identities = 458/792 (58%), Positives = 580/792 (73%), Gaps = 15/792 (2%)

  Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVP  65
              A   L+   + L  LW A+++P   L++ P + + QG + L AV+ VA+LKPF  K +V
  Sbjct  6    ANRRLKPGEIFLAFLWFAIVIPLAFLSSIPTSNAVQGALGLFAVLGVAVLKPFTMKSIVA  65

  Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
              RF LL+ AS +VMRYWFWR+  TLPP      SF  A+ LF VET++I +FF++ F++ADP
  Sbjct  66   RFALLAIASAIVMRYWFWRVTSTLPPIDEPLSFAIAVALFIVETYAICVFFVSSFITADP  125

  Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
               +R  P  +    LPTVDILVPSYNEP +MLSVTL+AAKNM YP   RTVVLCDDGGTD+
  Sbjct  126  VERKLPPKVAASSLPTVDILVPSYNEPIEMLSVTLSAAKNMHYPQNKRTVVLCDDGGTDE  185

  Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
              RC S DP  AQ A++RR +LQ LC ELG+VYSTRERN +AKAGNMSAALERL G+LVVVF
  Sbjct  186  RCNSDDPVKAQAARKRRADLQALCAELGIVYSTRERNINAKAGNMSAALERLDGDLVVVF  245

  Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
              DADHVP+RDFLARTVGYFV DP LFLVQTPHFF+NPDP+ RN+ L   CPPENEMFY +
  Sbjct  246  DADHVPARDFLARTVGYFVVDPKLFLVQTPHFFLNPDPVDRNIGLRADCPPENEMFYHQG  305

  Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
              H+GLDRWGGAFFCGSA+VLRR ALD  GGFAGETITEDAETALEIHS+GWKSLY+D AMI
  Sbjct  306  HKGLDRWGGAFFCGSASVLRRAALDSVGGFAGETITEDAETALEIHSQGWKSLYVDHAMI  365

  Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
              AGLQPETF SFI+QRGRWATGMMQ+L LKNPL R+G+ ++QRLCYLNSM+FW FPLVRM
  Sbjct  366  AGLQPETFTSFIEQRGRWATGMMQLLRLKNPLRRKGMSLSQRLCYLNSMTFWLFPLVRMT  425

  Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
              F++APL YLFF ++IFVAT +EV  YM  Y+A+SF+VQN L+AR RWPL+SE+YE AQAP
  Sbjct  426  FILAPLAYLFFELQIFVATIQEVAVYMSSYMAISFMVQNGLYARVRWPLISELYETAQAP  485
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Query  486   YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
             YL+  ++ T+ RPR A+F VTAKDE L E+++SPIYRPLL  + + L GVLA  +RWV F
Sbjct  486   YLSGVVLRTIFRPRGAKFNVTAKDEVLEEDFLSPIYRPLLVLWGITLLGVLAGAIRWVLF  545

Query  546   PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT-  604
             PGD ++L++VGGWA+ N +++  AL A+ E++QRRA PRV+M VPA A I A    + T
Sbjct  546   PGDHNILMIVGGWAIFNFIILSAALGAIGERRQRRAVPRVEMNVPAVAAIGAGEQYTFTA  605

Query  605   ATVLDASTSGVRLLVRLPGVG---DPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSAR  661
             ATVLD+STSG +L + +PG          LE G +  F P+FP +P LE  VR ++ +
Sbjct  606   ATVLDSSTSGCKLKL-IPGPDTDLTELTRLEKGTVFYFTPEFPKSPHLENAVRVQVVNIS  664

Query  662   REGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
             R+   V++GV ++  Q + VRET+A+LIFG+SA W  +RE+  +P+ LL GM  ++ +A
Sbjct  665   RDPSGVVLGVRYDPEQSLIVRETIAHLIFGDSAVWERVRESRNKPMPLLKGMGYVVSLAF  724

Query  722   ASLPKTARDFMDEPARRRRRHEEPKE------KQAHLLAFGTDFSTEPDWAGELLDPTAQ  775
              S+    R  ++EPARR+R  E  +E        AH+LAFG  F        E + P  Q
Sbjct  725   TSVAHVMRMIVNEPARRKRAEEREREVAIVEDHPAHILAFGETFDPV---LSEPVHPMKQ  781

Query  776   VSARPNTVAWGS  787
             +  R  + A G+
Sbjct  782   MLTRSESAARGA  793


>TR:A0A0N8K7F3 A0A0N8K7F3_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseibaca calidilacus OX=1666912 GN=bcsA PE=4 SV=1
Length=806

 Score = 898 bits (2320),  Expect = 0.0
 Identities = 451/760 (59%), Positives = 568/760 (75%), Gaps = 12/760 (2%)

Query  11    LRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVPRFLL  69
             LR   ++L LLW A+++P   LA+ P + + QG + L AV+ VA+LKPF  K +V RF L
Sbjct  10    LRPGEIVLALLWFAIVIPLAFLASIPTSNAVQGALGLFAVLGVAVLKPFTMKSIVARFAL  69

Query  70    LSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRP  129
             L+ AS +VMRYWFWR+  TLPP     SF  A+ LF VET++I +FF++ F++ADP +R
Sbjct  70    LAMASAIVMRYWFWRITSTLPPFDEPLSFTIAVALFIVETYAICVFFVSSFITADPIERK  129

Query  130   FPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMS  189
              P  +    LPTVDILVPSYNEP +MLSVTL+AAKNM YP   RTVVLCDDGGTD+RC S
Sbjct  130   LPPKVAASSLPTVDILVPSYNEPVEMLSVTLSAAKNMHYPQNKRTVVLCDDGGTDERCNS  189

Query  190   PDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADH  249
              DP  AQ A++RR +LQ LC ELG+VYSTR +N +AKAGNMSAALERL GELVVVFDADH
Sbjct  190   DDPVKAQAARKRRADLQALCAELGIVYSTRAQNLNAKAGNMSAALERLDGELVVVFDADH  249

Query  250   VPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGL  309
             VP+RDFLARTVGYFV DP LFLVQTPHFF+NPDP+ RN+ L   CPPENEMFY + HRGL
Sbjct  250   VPARDFLARTVGYFVVDPKLFLVQTPHFFLNPDPVDRNIGLRADCPPENEMFYHQGHRGL  309

Query  310   DRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQ  369
             DRWGGAFFCGSA+VLRR ALD  GGFAGETITEDAETALEIHS+GWKSLY+D AMIAGLQ
Sbjct  310   DRWGGAFFCGSASVLRRAALDSVGGFAGETITEDAETALEIHSKGWKSLYVDHAMIAGLQ  369

Query  370   PETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVA  429
             PETF +FI+QRGRWATGMMQ+L LKNPL R+G+ ++QRLCYLNSM+FW FPLVRM F++A
Sbjct  370   PETFTTFIEQRGRWATGMMQLLRLKNPLRRKGMSLSQRLCYLNSMTFWLFPLVRMTFILA  429

Query  430   PLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLAR  489
             PL YLFF ++IFVAT EEV  YM  Y+A+SF+VQN L+AR RWPL+SE+YE AQAPYL+
Sbjct  430   PLAYLFFELQIFVATIEEVAVYMSSYMAISFMVQNGLYARVRWPLISELYETAQAPYLSG  489

Query  490   AIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDR  549
              ++ T+ +PR A+F VTAKDE L E+++SPIYRPLL  + + L GV+A  +RW+ FPGD
Sbjct  490   VVLRTIFKPRGAKFNVTAKDEVLEEDFLSPIYRPLLVLWGITLLGVIAAGIRWLLFPGDH  549
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Query  550  SVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT-ATVL  608
            ++L++VGGWAV N +++  AL A+ E++QRR  PRV+M VPA A I A  + + T ATVL
Sbjct  550  NILMIVGGWAVFNFIILSAALGAIGERRQRRVVPRVEMNVPAVAAIGAGEHYTFTAATVL  609

Query  609  DASTSGVRLLVRLPGVGD---PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGG  665
            D+STSG +L +  PG          LE G +  F P+FP +P LE  VR ++ +  R+
Sbjct  610  DSSTSGCKLKL-TPGPDTDLAELERLEKGAVFYFTPEFPKSPHLENAVRVQVVNISRDPS  668

Query  666  TVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLP  725
             V++GV ++  QP+ VRET+A+LIFG+SA W  +RE+  +P+ +L GM  +  +A  S+
Sbjct  669  GVVLGVRYDPEQPMIVRETIAHLIFGDSAVWERVRESRNKPMPMLKGMGYVFTLAFTSVA  728

Query  726  KTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDF  759
               R   +EPARR+R  E  +      E  AH+LAFG  F
Sbjct  729  HVMRMIANEPARRKRAEERERKVAIVEEHPAHILAFGEAF  768


>TR:A0A6B2JZH4 A0A6B2JZH4_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudoroseicyclus tamaricis OX=2705421 GN=bcsA PE=4
SV=1
Length=791

 Score = 895 bits (2312),  Expect = 0.0
 Identities = 446/761 (59%), Positives = 553/761 (73%), Gaps = 3/761 (0%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LWVALL+P   L + P     Q  +++ AV+ VA LKPFA  +VPRF LL+ AS++VMRY
Sbjct  30   LWVALLLPIATLVSVPTDVGGQAFLSIVAVLAVAALKPFARMLVPRFFLLATASVIVMRY  89

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
              WR+FETLP P    SF+ A+ L A E +++ +FFL+ F+++DPT RPFP  + PE LP
Sbjct  90   ALWRVFETLPEPGFTLSFICAVTLLAAEAYAVLVFFLSSFITSDPTRRPFPPTVAPERLP  149

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TV++LVPSYNEP +ML +TLAA KNM+YPA   TVVLCDDGGTDQRC   D   A  A+
Sbjct  150  TVNVLVPSYNEPTEMLRITLAACKNMVYPAEKLTVVLCDDGGTDQRCNDSDKAKATAARA  209

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RR ELQ LC ELGV+YSTR RNEHAKAGNMSAAL RL G+LVVVFDADHVP+RDFLARTV
Sbjct  210  RRAELQALCAELGVMYSTRARNEHAKAGNMSAALARLDGDLVVVFDADHVPTRDFLARTV  269

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYFVEDP LFLVQTPHFF+N DPI RNL L +  PPENEMFY  IHRGLDRW GAFFCGS
Sbjct  270  GYFVEDPKLFLVQTPHFFLNKDPIMRNLELSENVPPENEMFYSFIHRGLDRWDGAFFCGS  329

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR ALD  GGF+GETITEDAETAL+IH+ GW+S+Y++RAMIAGLQPETFASFIQQR
Sbjct  330  AAVLRRAALDSVGGFSGETITEDAETALDIHASGWRSMYLNRAMIAGLQPETFASFIQQR  389

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
            GRWATGMMQ++LLKNP+FRRGL +AQRLCY+NSM+ W FP++R++FL APL YLFFG EI
Sbjct  390  GRWATGMMQIMLLKNPMFRRGLTMAQRLCYINSMACWLFPIIRLIFLCAPLAYLFFGAEI  449

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
             VATF+E +AYM GYLAVSFLVQNAL++R RWPL+SE+YE+AQ PYLA+A++ TL++PR
Sbjct  450  LVATFQEAMAYMLGYLAVSFLVQNALYSRFRWPLMSEIYEIAQTPYLAQAVIKTLIKPRG  509

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
            A+F VTAKDETL  ++ISP + PL   + LC +GV A +VRWV FPGDRSVL VVGGWAV
Sbjct  510  AKFNVTAKDETLDNDFISPAHWPLTILWGLCAAGVAALVVRWVNFPGDRSVLSVVGGWAV  569

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
             N +LV  + RAVAE++QRRA+PRV M VPA A +P   +  + A +LDASTSG+R+++
Sbjct  570  FNFILVSISWRAVAERKQRRASPRVNMNVPAMAWLPGAPDEKVAAHILDASTSGMRVMLD  629

Query  621  LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
             P    P     +G  +  +P F  +P LE  +   +    +       G +  A Q +
Sbjct  630  EPLGDTPIGKRSSGMELVVRPYFEGSPHLEADINLTVICFHQRPDGPQAGSVINADQSVK  689
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Query  681  VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPARRRR  740
             +E VA+LIFG+S +WR  R  +   IGL+ G+    ++     PK    F+ EP RRR
Sbjct  690  AQEAVAHLIFGDSENWRNTRYVSQGGIGLIRGLGYAAYLFLNGTPKLIAAFIREPMRRRT  749

Query  741  --RHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSAR  779
                 +P + QAH+LAFG D            D  A++  +
Sbjct  750  VVAKRDPSD-QAHILAFGVDIEERERMLARAQDHVAKLQGQ  789


>TR:A0A3B0MB29 A0A3B0MB29_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseinatronobacter ekhonensis OX=254356 GN=bcsA PE=4
SV=1
Length=809

 Score = 892 bits (2306),  Expect = 0.0
 Identities = 449/764 (59%), Positives = 568/764 (74%), Gaps = 12/764 (2%)

Query  7    ARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADK-MVP  65
            A   L+   V+L LLW A+++P   LA+ P + + QG + L AVV VALLKP+  K +V
Sbjct  6    ANRRLKPGEVVLALLWFAIVIPLAFLASIPTSNAVQGGLGLFAVVCVALLKPWTMKTIVA  65

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
            RF LL+ AS +VMRYWFWR+  TLPP     SF  A+ LFAVET++I +FF++ F++ADP
Sbjct  66   RFALLAIASSIVMRYWFWRITSTLPPMDEPLSFAIAVALFAVETYAICVFFVSSFITADP  125

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
             +R  P  +    LPTVDILVPSYNEP +MLSVTL+AAKNM YP   RTVVLCDDGGTD+
Sbjct  126  IERKLPPKVAASSLPTVDILVPSYNEPIEMLSVTLSAAKNMHYPPHKRTVVLCDDGGTDE  185

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            RC S D   A  A++RR +LQ LC ELG+VYSTR  N +AKAGNMSAA+ERL G+LVVVF
Sbjct  186  RCNSDDSIKAHAARKRRADLQALCAELGIVYSTRAENINAKAGNMSAAMERLNGDLVVVF  245

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVP+RDFLARTVGYFV DP+LFLVQTPHFF+NPDP+ RN+ L   CPPENEMFY +
Sbjct  246  DADHVPARDFLARTVGYFVVDPNLFLVQTPHFFLNPDPVDRNIGLRADCPPENEMFYHQG  305

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRWGGAFFCGSA+VLRR ALD  GGFAGETITEDAETALEIHS+GWKSLY+D AMI
Sbjct  306  HRGLDRWGGAFFCGSASVLRRAALDSVGGFAGETITEDAETALEIHSQGWKSLYVDHAMI  365

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPETF SFI+QRGRWATGMMQ+L LKNPL R+G+ ++QRLCYLNSM+FW FPLVRM
Sbjct  366  AGLQPETFTSFIEQRGRWATGMMQLLRLKNPLRRKGMSLSQRLCYLNSMTFWLFPLVRMT  425

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            F++APL YLFF ++IFVAT EEV  YM  Y+A+SF+VQN L+AR RWPL+SE+YE AQAP
Sbjct  426  FILAPLAYLFFELQIFVATIEEVAVYMSSYMAISFMVQNGLYARTRWPLISELYETAQAP  485

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+  ++ T+ +PR A+F VTAKDE L E+++SPI+RPLL  + + L GV+A  VRW  F
Sbjct  486  YLSGVVLRTIFKPRGAKFNVTAKDEVLEEDFLSPIHRPLLILWGIALLGVVAAAVRWFMF  545

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT-  604
            PGD ++L++VGGWA+ N +++  AL A+ E++QRRA PRV M VPA A +      + T
Sbjct  546  PGDHNILMIVGGWAIFNFVILSAALGAIGERRQRRAVPRVDMVVPAVAAVGQGEYYTFTA  605

Query  605  ATVLDASTSGVRLLVRLPGVGD---PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSAR  661
            ATVLD+STSG +L +  PG          LE G +  F P+FP +P LE  VR ++ +
Sbjct  606  ATVLDSSTSGAKLKL-TPGPDTDIAELTRLEKGSVFYFTPEFPKSPHLENAVRVQVVNIS  664

Query  662  REGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
            R+   +++GV ++  QP+ VRET+A+LIFG+SA W  +RE+  +P+ LL GM  +L +A
Sbjct  665  RDPSGLVLGVRYDPDQPLIVRETIAHLIFGDSAVWERVRESRNKPMPLLKGMGYVLMLAF  724

Query  722  ASLPKTARDFMDEPARRRRRHEEPK------EKQAHLLAFGTDF  759
            +S+    R   +EPARR+R  E  +      ++ AH+LAFG  F
Sbjct  725  SSVAHVMRMIANEPARRKRAEERERDTAIVDDQPAHILAFGEAF  768
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>TR:A0A4R6A107 A0A4R6A107_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Palleronia sediminis OX=2547833 GN=bcsA PE=4 SV=1
Length=806

 Score = 888 bits (2295),  Expect = 0.0
 Identities = 440/744 (59%), Positives = 552/744 (74%), Gaps = 11/744 (1%)

Query  2    TVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFAD  61
            T  ++A   + +   L   +W+A+     +LAA PV+   Q L+ ++ +++V   +PF+ 
Sbjct  4    TAASRAGRQVPLDRALYLTMWLAVGACIAVLAALPVSTWTQALLGVTGLLIVIASRPFSR  63

Query  62   KMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFL  121
              V RF++L+ AS +V+RYW WRL ETLP P    SF+ ALLLFA ET++I IFF+ GF+
Sbjct  64   VPVVRFIMLATASTMVLRYWIWRLTETLPSPDEPLSFVAALLLFATETYTIGIFFMTGFM  123

Query  122  SADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDG  181
            +ADP  R  P  +   +LPTV++LVPSYNEPA ML+VTL+AAKNM YP     VVLCDDG
Sbjct  124  TADPITRAPPATVNARDLPTVNVLVPSYNEPASMLAVTLSAAKNMHYPPDKMIVVLCDDG  183

Query  182  GTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGEL  241
            GTD+RC   DP +A+KA +RR +LQ++C ELGV+YSTRERNEHAKAGNMSAAL RL G+L
Sbjct  184  GTDERCNHEDPAIAEKAVKRRAQLQEMCAELGVLYSTRERNEHAKAGNMSAALARLDGDL  243

Query  242  VVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMF  301
            V VFDADHVPSRDFLART G+FVE  DLFLVQTPHFF+NPDPIQRN+ L D CPPENEMF
Sbjct  244  VAVFDADHVPSRDFLARTAGHFVERDDLFLVQTPHFFLNPDPIQRNIGLVDNCPPENEMF  303

Query  302  YGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYID  361
            YG +H+GLDRW G FFCGSAA++RR ALD  GGF+GETITEDAETAL+IH+ GWKSLY++
Sbjct  304  YGHVHQGLDRWEGTFFCGSAALIRRAALDSVGGFSGETITEDAETALDIHATGWKSLYVN  363

Query  362  RAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPL  421
             AMIAGLQPETF SFIQQRGRWATGMMQML+LKNP+FR+GL  +QRLCYLNSM+FWFFP+
Sbjct  364  HAMIAGLQPETFVSFIQQRGRWATGMMQMLILKNPIFRKGLRFSQRLCYLNSMTFWFFPI  423

Query  422  VRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEV  481
            VRM+F++APL+YLFFG+EIFVAT++EVLAYM  Y+AVSF+VQNALF   RWPL+SE+YE 
Sbjct  424  VRMIFILAPLLYLFFGLEIFVATYQEVLAYMATYIAVSFVVQNALFNSYRWPLMSELYET  483

Query  482  AQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVR  541
             QAPYL+ A++ T L+PR+A+F VTAKDE L E+ ISPI RPLL  FLL L+GV A + R
Sbjct  484  TQAPYLSSAVIKTFLKPRAAKFNVTAKDEVLDEDMISPIARPLLILFLLMLAGVAAAVFR  543

Query  542  WVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNR  601
            W+ FPGDR VL +VGGWA+ N +L+G AL+ V EKQQRR  PRV +E PAE  +    +R
Sbjct  544  WIMFPGDREVLQLVGGWALFNFMLIGAALQTVHEKQQRRGVPRVPLEEPAEVSLAGHPDR  603

Query  602  SLTATVLDASTSGVRLLVR-----LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGR  656
             + A V DAS SG ++L++     LPG       +  G  +  +P   DAP L   +RG 
Sbjct  604  LMGARVCDASLSGAQILIKNGPEILPG------QIAEGAPLIVRPVLEDAPSLSHPIRGT  657

Query  657  IRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARI  716
            IR AR+EG  + +G  F   QP  V ETV +LI+G+S+ W   REA    +GLL GM  I
Sbjct  658  IRWARKEGAHIRLGYEFTEDQPRIVAETVGHLIYGKSSRWAARREAYFSEMGLLGGMFYI  717

Query  717  LWMAAASLPKTARDFMDEPARRRR  740
              ++   + +TAR  + EP RRRR
Sbjct  718  FRLSLRGMVRTARALIAEPGRRRR  741


>TR:A0A934IKG0 A0A934IKG0_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Palleronia pontilimi OX=1964209 GN=bcsA PE=4 SV=1
Length=809

 Score = 859 bits (2219),  Expect = 0.0
 Identities = 428/736 (58%), Positives = 538/736 (73%), Gaps = 7/736 (1%)

Query  21   LWVALLVPFG----LLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
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             +W++L +  G    +LA+ P++  AQ L+ ++ V+ V LL+P AD+  PRF LLS A  +
Sbjct  17   IWISLWLVVGFVCVVLASIPISTWAQALLGVAGVLGVVLLRPLADQAAPRFALLSIAGAM  76

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
             V+RYW WR+ ETLP      S +FA LL   ET++I IFFL  F+++DP  RP P  ++
Sbjct  77   VLRYWIWRVTETLPGLDSPISLVFATLLLLTETYAICIFFLTAFMTSDPLTRPMPPTVRV  136

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             +ELPTV++LVPSYNEPA ML +TLAAA+NM YP     VVLCDDGGTD+R  S DP+ ++
Sbjct  137  DELPTVNVLVPSYNEPASMLKITLAAARNMHYPPDKMCVVLCDDGGTDERIASDDPQKSK  196

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             ++ ERR ELQ LC +LGVVYSTR RNEHAKAGNMSAALERL G+LV VFDADHVPSRDFL
Sbjct  197  QSAERRAELQALCADLGVVYSTRARNEHAKAGNMSAALERLDGDLVAVFDADHVPSRDFL  256

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
             ART GYFV+  DLFLVQTPHFF+NPDPI RN+ L D CPPENEMFYG +HRGLDRW G F
Sbjct  257  ARTAGYFVKHEDLFLVQTPHFFLNPDPIMRNVGLVDNCPPENEMFYGHVHRGLDRWHGTF  316

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
             FCGSAA++RRRALD  GGF+GETITEDAETAL+IH+ GW+S+Y++RAMIAGLQPETF SF
Sbjct  317  FCGSAALIRRRALDSVGGFSGETITEDAETALDIHATGWRSIYVNRAMIAGLQPETFTSF  376

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
             I+QRGRWA GMMQMLLLKNPL R+GLG+ QRLCY+NSM+FWFFP++RM FL+APL YLFF
Sbjct  377  IEQRGRWAAGMMQMLLLKNPLMRKGLGVTQRLCYINSMTFWFFPIIRMTFLLAPLCYLFF  436

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             G+EIFVAT  EV+AYM  Y+A SF+VQNALF R RWPL+SE+YE AQAPYL+RA++ T L
Sbjct  437  GLEIFVATRSEVVAYMATYVATSFIVQNALFNRSRWPLMSELYETAQAPYLSRAVLKTFL  496

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             +PR A+F VTAKDETL E  I+PI  PLL+TF L ++GV+A  +R+  FPGDR VL VVG
Sbjct  497  KPRGAKFNVTAKDETLDEASITPIAGPLLWTFALMVAGVVAAGIRYYLFPGDREVLQVVG  556

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             GWAV N++L+G AL  + E QQRR APRV +E PA   +    NR L   VLD S SG++
Sbjct  557  GWAVFNLILIGAALPCLRETQQRRGAPRVPLEEPALVALAGHPNRKLGGVVLDGSLSGMQ  616

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
             + + +   G     +  G  I+  P   +AP L   + G IR  RRE   ++VG+ ++
Sbjct  617  VKI-VSDEGIAPGQITEGAPIKVLPALAEAPALAHPIAGHIRWTRREDKAILVGIEYDED  675

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPA  736
             QP  V ET+  +I+G+S+ W   RE     +GLL G+  IL ++      T +  M EPA
Sbjct  676  QPNIVAETIGQMIYGKSSRWAARREHYFHEMGLLGGLGYILRLSVTGTFTTLKALMAEPA  735

Query  737  RRRRRHEEPKEKQAHL  752
             RR+    E +   AH+
Sbjct  736  RRKA--AEARRLNAHV  749


>TR:A0A1H8CQY7 A0A1H8CQY7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Palleronia pelagia OX=387096 GN=SAMN04488011_10238
PE=4 SV=1
Length=807

 Score = 849 bits (2193),  Expect = 0.0
 Identities = 442/760 (58%), Positives = 537/760 (71%), Gaps = 15/760 (2%)

Query  6    KARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP  65
             K+   L +       LWV +     +LA+ P++  AQ L+ ++ V+ V LL+P AD+  P
Sbjct  5    KSNRQLPIAEAASVSLWVLVGAIGVILASIPISTWAQALLGVTGVLCVVLLRPMADRAAP  64

Query  66   RFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP  125
             RF LL+ A  LV+RYW WR+ ETLP      SF  A+LL   ET++I +FFL  F++ADP
Sbjct  65   RFALLAIAGALVLRYWIWRVTETLPGLDAPLSFTCAMLLLITETYAILVFFLTTFMTADP  124

Query  126  TDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQ  185
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              RP P  ++ +ELPTVD+LVPSYNEPA ML VTLAA +NM YPA    VVLCDDGGTDQ
Sbjct  125  LTRPVPPTVRVDELPTVDVLVPSYNEPAAMLKVTLAACRNMHYPAEKLRVVLCDDGGTDQ  184

Query  186  RCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVF  245
            R  S DP  A+ A  RR ELQ LC +LGV+YSTR RNEHAKAGNMSAAL  L G+LV VF
Sbjct  185  RVNSEDPATARAAAARRAELQALCADLGVLYSTRARNEHAKAGNMSAALALLDGDLVAVF  244

Query  246  DADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKI  305
            DADHVPSRDFLART GYF++  DLFLVQTPHFF+NPDPI RN+     CPPENEMFYG I
Sbjct  245  DADHVPSRDFLARTAGYFLKHDDLFLVQTPHFFLNPDPIMRNVGTVSHCPPENEMFYGHI  304

Query  306  HRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMI  365
            HRGLDRW GAFFCGSAA++RR ALD  GGF+GETITEDAETAL+IH+ GW+S+Y++RAMI
Sbjct  305  HRGLDRWDGAFFCGSAALIRRDALDSVGGFSGETITEDAETALDIHASGWRSIYVNRAMI  364

Query  366  AGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMM  425
            AGLQPE+F SFIQQRGRWATGMMQMLLLKNPL RRGL + QRLCY+NSMSFWFFPLVRM+
Sbjct  365  AGLQPESFVSFIQQRGRWATGMMQMLLLKNPLMRRGLSVTQRLCYVNSMSFWFFPLVRMV  424

Query  426  FLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAP  485
            FL+APL YLFFG+EIFVAT  EV+AYM  Y+A SF+VQNALF R RWPL+SE+YE AQAP
Sbjct  425  FLLAPLAYLFFGLEIFVATRAEVVAYMATYVATSFIVQNALFNRTRWPLMSELYETAQAP  484

Query  486  YLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAF  545
            YL+RA++ T  +PR+ARF VTAKDETL E  ISPI  PL + F L   GV+A  VR+  +
Sbjct  485  YLSRAVLRTFAKPRAARFNVTAKDETLDETAISPIAAPLFWLFGLLALGVVAAGVRYSLY  544

Query  546  PGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTA  605
            PGDR VL VVGGWAV N++LVG AL  V E QQRR APRV+++ PA   +    NR + A
Sbjct  545  PGDREVLQVVGGWAVFNLVLVGAALACVRETQQRRGAPRVKLDEPAIVALAGHPNRKMAA  604

Query  606  TVLDASTSGVRLLVRLPGVGDPHPALEA-GGLIQFQPKFPDAPQLERMVRGRIRSARREG  664
            TV+D S SG+ L   + G  D  P   A G  ++  P   +AP L   + G +R +RRE
Sbjct  605  TVIDGSLSGLSL--EIAGGPDIAPGQVAEGAPLRVLPALVEAPSLAHPISGHVRWSRRER  662

Query  665  GTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASL  724
            G + +G+ ++  QP  V ETVA +I+G+S+ W  MR+      GLL G   IL++   SL
Sbjct  663  GKIAMGIAYDENQPTIVAETVAQMIYGKSSRWAAMRDHYFHEKGLLGG---ILYIPRLSL  719

Query  725  PKTARDF---MDEPARRRRRHEE------PKEKQAHLLAF  755
              T   F     EP RRRR  +         E  AH++AF
Sbjct  720  RGTVSAFAALAAEPGRRRRAAQRALHSTIALEPPAHIVAF  759


>TR:A0A1M6JMZ7 A0A1M6JMZ7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Palleronia salina OX=313368 GN=SAMN04488012_11038
PE=4 SV=1
Length=808

 Score = 849 bits (2193),  Expect = 0.0
 Identities = 433/741 (58%), Positives = 528/741 (71%), Gaps = 7/741 (1%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LWV +     +LA+ P++  AQ L+ ++ V+ V LL+P AD+  PRF LL+ A  LV+RY
Sbjct  21   LWVLVGAIGVILASIPISTWAQALLGVTGVLCVVLLRPMADRAAPRFALLAIAGALVLRY  80

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
            W WR+ ETLP      SF  A+LL   ET++I +FFL  F++ADP  RP P  ++ +ELP
Sbjct  81   WIWRVTETLPGLDAPLSFTCAMLLLITETYAILVFFLTTFMTADPLTRPVPPTVRVDELP  140

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVD+LVPSYNEPA ML VTLAA +NM YPA    VVLCDDGGTDQR  S DP  A+ A E
Sbjct  141  TVDVLVPSYNEPAAMLKVTLAACRNMHYPAEKLRVVLCDDGGTDQRINSEDPATARAAAE  200

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RR ELQ LC +LGV+YSTR RNEHAKAGNM+AAL  L G+LV VFDADHVPSRDFLART
Sbjct  201  RRAELQALCADLGVIYSTRARNEHAKAGNMTAALALLDGDLVAVFDADHVPSRDFLARTA  260

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
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            GYF++  DLFLVQTPHFF+NPDPI RN+     CPPENEMFYG IHRGLDRW GAFFCGS
Sbjct  261  GYFLKHDDLFLVQTPHFFLNPDPIMRNVGTVSHCPPENEMFYGHIHRGLDRWDGAFFCGS  320

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AA++RR ALD  GGF+GETITEDAETAL+IH+ GW+S+Y++RAMIAGLQPE+F SFIQQR
Sbjct  321  AALIRRDALDSVGGFSGETITEDAETALDIHASGWRSIYVNRAMIAGLQPESFVSFIQQR  380

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
            GRWATGMMQMLLLKNPL RRGL + QRLCY+NSMSFWFFPLVRM+FL+APL YLFFG+EI
Sbjct  381  GRWATGMMQMLLLKNPLMRRGLSVTQRLCYVNSMSFWFFPLVRMVFLLAPLAYLFFGLEI  440

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FVAT  EV+AYM  Y+A SF+VQNALF R RWPL+SE+YE AQAPYL+RA++ T  +PR+
Sbjct  441  FVATRAEVVAYMATYVATSFIVQNALFNRTRWPLMSELYETAQAPYLSRAVLRTFAKPRA  500

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
            ARF VTAKDETL E  ISPI  PL + F L   GV+A  VR+  +PGDR VL VVGGWAV
Sbjct  501  ARFNVTAKDETLDETAISPIAAPLFWLFGLLALGVVAAGVRYSLYPGDREVLQVVGGWAV  560

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
             N++LVG AL  V E QQRR APRV+++ PA   +    NR + ATV+D S SG+ L +
Sbjct  561  FNLVLVGAALACVRETQQRRGAPRVKLDEPAIVALAGHPNRKMAATVIDGSLSGLSLEI-  619

Query  621  LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
              G       +  G  ++  P   +AP L   + G +R +RRE G + +G+ ++  QP
Sbjct  620  ADGPDIAPGQVAEGAPLRVLPALVEAPSLAHPISGHVRWSRRERGKIAMGIAYDENQPTI  679

Query  681  VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPARRRR  740
            V ETVA +I+G S+ W  MR+      GLL G+  IL ++             EP RRRR
Sbjct  680  VAETVAQMIYGRSSRWAAMRDHYFHEKGLLGGILYILRLSLRGTVSAFAALAAEPGRRRR  739

Query  741  RHEE------PKEKQAHLLAF  755
              +         E  AH++AF
Sbjct  740  AAQRALHSTIALEPPAHIVAF  760


>TR:A0A2T5JTB7 A0A2T5JTB7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Cereibacter azotoformans OX=43057 GN=C8J28_12216 PE=4
SV=1
Length=806

 Score = 844 bits (2180),  Expect = 0.0
 Identities = 429/750 (57%), Positives = 534/750 (71%), Gaps = 6/750 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAASM  75
            LL L   +  +P  +L + P    AQGL  ++ ++LVA+LKPF  + +P RFL+L+ A
Sbjct  16   LLILAVASGTIPLIMLLSVPSDTLAQGLFGVTTILLVAVLKPFTWRSMPLRFLMLATAGT  75

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RYW WRLFETLP      S   A +LFAVET++I +FFLN FL ADP  R  P  +
Sbjct  76   VVLRYWMWRLFETLPSSDNPVSLAAAWMLFAVETYAILLFFLNAFLLADPLKRGMPEMVP  135

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             + LPTVDILVPSYNEP ++LSVTLAAA+N+ YP  L  VVLCDDGGTDQ+C S DP  A
Sbjct  136  VDRLPTVDILVPSYNEPIELLSVTLAAARNIHYPPHLLNVVLCDDGGTDQKCTSSDPAEA  195

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            + AQ RR+ LQ+LC  LGV Y TRERN  AKAGN+++AL R +GE V VFDADH+PS DF
Sbjct  196  EAAQARRKALQELCERLGVTYLTRERNVSAKAGNLNSALGRTQGEFVAVFDADHIPSSDF  255

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            LART+G+ V+DP LFLVQTPHFFIN DPIQRNL L + CP ENEMFY  I +GLDRW GA
Sbjct  256  LARTIGFLVKDPKLFLVQTPHFFINKDPIQRNLDLPESCPAENEMFYALIQKGLDRWDGA  315

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRR AL+  GGF+G+TITEDAETAL+IH+RGW SLYI RA+IAGLQPETF+S
Sbjct  316  FFCGSAALLRRAALNAVGGFSGQTITEDAETALDIHARGWNSLYIGRALIAGLQPETFSS  375

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
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            FIQQRGRWA GMMQ+L LKNP+FR GL +AQRLCY NSMS+WFFP+VR++FL++PL+YLF
Sbjct  376  FIQQRGRWAAGMMQILRLKNPIFRPGLTLAQRLCYYNSMSYWFFPVVRLIFLLSPLLYLF  435

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG++IFVATFEE L Y   YL VSFLVQNALF+R RWPL+SEVYE+AQ PYL RA +  L
Sbjct  436  FGLQIFVATFEEALVYTLTYLVVSFLVQNALFSRVRWPLISEVYEIAQTPYLIRATLGAL  495

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            LRP+  RF VTAKDET++++++SPIYRPLL  FLL  +GV A  +RWV  P DR V+++V
Sbjct  496  LRPKGFRFQVTAKDETVADSFLSPIYRPLLALFLLMAAGVAAAGLRWVFLPDDRQVVMIV  555

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGWA+ N L+ GF+LRAV EK+QRR APRV + V A    P  G  ++   V+DAST G
Sbjct  556  GGWALFNFLITGFSLRAVVEKRQRRVAPRVDLSVRASLD-PGEGEAAVPVEVVDASTYGA  614

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            RL  RL          + G  I FQP+ PD P+  R +   +RS + EG  + +G+ F
Sbjct  615  RL--RLTDAAHRRLRFKPGQTITFQPEIPDVPRASRWISCEVRSLQPEGSDLYLGLRFLP  672

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF--MD  733
             Q  +VRE VA L+F +S+ W   R + +   GLL GMA + W A  ++P+T+ D   +
Sbjct  673  DQDPSVREAVACLVFSDSSLWEKTRRSALAGRGLLAGMAYVFWRAGTTIPRTSLDMIRLS  732

Query  734  EPARRRRRHEEPKEKQAHLLAFGTDFSTEP  763
              A       E K    H+LAFG D    P
Sbjct  733  WTAPPEEADSEAKGPAPHILAFGQDPDDPP  762


>TR:A0A2R8BTT8 A0A2R8BTT8_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Palleronia abyssalis OX=1501240 GN=bcsA_1 PE=4 SV=1
Length=809

 Score = 843 bits (2179),  Expect = 0.0
 Identities = 421/731 (58%), Positives = 530/731 (73%), Gaps = 3/731 (0%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            VL  +LW+       +LAA P++  AQ L+ ++ V++   L+P +DK   RF+LL+ A
Sbjct  17   VLWMVLWILTGAVVIVLAAMPISTWAQALLGVTGVLICVALRPMSDKAPMRFVLLAVAVT  76

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RYW WR  ETLP      S  FA++L A ET++I +  L  F++ADP  RP P  +
Sbjct  77   MVLRYWIWRATETLPGWDSPISMTFAVMLLATETYTIFVLLLTCFMTADPVTRPAPPTVS  136

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              ELPTVD+LVPSYNEP+ ML+VTL+AAKNM YP     VVLCDDGGTDQR    D  +A
Sbjct  137  TRELPTVDVLVPSYNEPSAMLAVTLSAAKNMHYPKDKLRVVLCDDGGTDQRINHEDQSIA  196

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            + A ERR ELQ+LC +LGV+YSTRERNE+AKAGNMSAAL RL GELV VFDADHVPSRDF
Sbjct  197  KAAVERRAELQKLCADLGVIYSTRERNENAKAGNMSAALARLDGELVAVFDADHVPSRDF  256

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            LART GYFV D  LFLVQTPHFF+NPDPI RN+ L   CPPENEMFYG +HRGLDRW G
Sbjct  257  LARTAGYFVHDAKLFLVQTPHFFLNPDPINRNIGLVPHCPPENEMFYGHVHRGLDRWDGT  316

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA++RR ALD  GGF+GETITEDAETAL+IH+ GWKS+Y++RAMIAGLQPE+F S
Sbjct  317  FFCGSAALMRRAALDSVGGFSGETITEDAETALDIHAAGWKSIYVNRAMIAGLQPESFVS  376

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FIQQRGRWA+GM+QMLLLKNPL R GLG+ QRLCY+NSM+FWFFP+VR+ FL+APL+YLF
Sbjct  377  FIQQRGRWASGMIQMLLLKNPLLRSGLGMTQRLCYINSMAFWFFPVVRLSFLMAPLLYLF  436

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+EIFVAT+ EV+AYM  Y+ V+F+VQNALF R RWPL+SE+YE AQAPYLA A++ TL
Sbjct  437  FGLEIFVATYSEVIAYMVTYVLVNFIVQNALFNRSRWPLMSELYETAQAPYLAGAVMKTL  496

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            ++PR A+F VTAKDETL E+ ISPI  PLL  F L   GV    +R+V FPGDR VL +V
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Sbjct  497  VKPRGAKFNVTAKDETLDEDLISPIAGPLLAVFGLLAVGVAVAGMRYVMFPGDREVLQIV  556

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGWAV N++LVG +L+ + EKQQRR  PRV+M  PA+  +     R +   ++DAS SGV
Sbjct  557  GGWAVFNLILVGASLQCIHEKQQRRGTPRVRMTEPADVALAGNPERLMRGRIVDASNSGV  616

Query  616  RLLVRLPGVGDPHPA-LEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
               V LP   D  P  +  G  I F+P   DAP L   ++G +R +RR+G  +++G+
Sbjct  617  --CVTLPMGQDIRPGQVVLGAPIAFRPLLEDAPTLAHPIKGTVRWSRRDGAEILIGIEIA  674

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDE  734
              QP  + ETV +LI+G S  W  +RE+  + +GL+ G+  +  ++   + +TAR    E
Sbjct  675  RDQPWIIAETVGHLIYGRSTRWAKVRESYFQEMGLIGGLVYVCKLSGQGVVRTARALAAE  734

Query  735  PARRRRRHEEP  745
            PARRR +   P
Sbjct  735  PARRRGKTNVP  745


>TR:A0A1H3MQ75 A0A1H3MQ75_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Citreimonas salinaria OX=321339 GN=SAMN05444340_11817
PE=4 SV=1
Length=803

 Score = 834 bits (2155),  Expect = 0.0
 Identities = 418/745 (56%), Positives = 532/745 (71%), Gaps = 7/745 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            LL + L+VP  LL   P +   QGL+  SAV+LV  LKPFA  +VPR  LL+ A ++V R
Sbjct  19   LLGLVLIVPITLLVITPSSDLVQGLLGFSAVLLVIALKPFASHLVPRLALLAIAGVIVTR  78

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y  WR+  TLP P    ++  A++L  +ETFS+ +FF+   ++ D   R  P  ++  +L
Sbjct  79   YLSWRILYTLPAPDQPVAYAAAVVLLGIETFSVLVFFMTSLVNIDYVTRRQPGKIRMGQL  138

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VD+LVPSYNEP +ML++TLAAAKNM YP     VVLCDDGGTDQ+  +PDP  A+ A+
Sbjct  139  PRVDVLVPSYNEPTEMLAITLAAAKNMYYPKDKLRVVLCDDGGTDQKINAPDPAKAEAAR  198

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             RR +L +LCR+LGV+YSTR RNEHAKAGNM+AAL RL G+LV +FDADHVP+RDFLART
Sbjct  199  TRREDLTRLCRDLGVMYSTRARNEHAKAGNMTAALSRLNGDLVAIFDADHVPTRDFLART  258

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYFVE P LFL+QTPHFF+NPDPI+RNL L  +CP ENEMFYG IH+GLD   GAFFCG
Sbjct  259  VGYFVERPKLFLLQTPHFFLNPDPIERNLQLSPKCPTENEMFYGAIHKGLDSMRGAFFCG  318

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAA+LRRRALDEAGGF+GETITEDAETAL+IH++GW+SLY+DRAM+AGLQPETF+SFIQQ
Sbjct  319  SAALLRRRALDEAGGFSGETITEDAETALDIHAKGWESLYLDRAMVAGLQPETFSSFIQQ  378

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            RGRWATGM+QMLLLKNPLFRRGLG+ QRLCYLNSMSFW FP+VR+ +L+ PL YL FG+E
Sbjct  379  RGRWATGMIQMLLLKNPLFRRGLGLTQRLCYLNSMSFWLFPIVRLAYLIIPLFYLVFGLE  438

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IFV T  E L YM  YL V+FLVQN LF+R RWPL+SE+YE+AQAPYLA+ IV T++RPR
Sbjct  439  IFVTTRTEALVYMVSYLMVAFLVQNTLFSRHRWPLISEIYEIAQAPYLAKQIVKTVMRPR  498

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
            +A+F VTAKDE L  +++S IY PLL    +  +GV     RW+AFPGDR ++ +VG WA
Sbjct  499  AAKFNVTAKDEQLDNDFVSEIYPPLLTLTAITGAGVALAAARWLAFPGDRPIVEIVGAWA  558

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNR--SLTATVLDASTSGVRL  617
            + N LL   ALRA  E+QQRRA PRV +  P   Q+    ++   + A + D ST G+R+
Sbjct  559  LFNFLLCVLALRATCERQQRRAMPRVALNRPCTVQMVDANDQVIEVPAVIEDGSTQGLRI  618

Query  618  LVRLPGVGDPH----PALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIF  673
              R   + D        L+    +  +P+ P+A  LE  +  R+ +          GV
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Sbjct  619  AFRAQALSDGELVALHCLQTDMFLAVRPQIPEADMLEAEIIVRVTNPYPSSTGFAFGVRV  678

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
            EA QP+A+   +A++++G+S  WR MRE      GL+HG+  +L MA AS+P+TA DF+
Sbjct  679  EADQPVAMYSCLAHVVYGDSEVWRRMREDERAERGLVHGILYVLSMAVASIPRTAGDFLR  738

Query  734  EPARRRRRHEEPKEKQAHLLAFGTD  758
            EPARRR       E  A +LAF T+
Sbjct  739  EPARRRALAAAETE-SAQILAFATE  762


>TR:A0A1G8LIV2 A0A1G8LIV2_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Salipiger marinus OX=555512 GN=SAMN04487993_1006179
PE=4 SV=1
Length=772

 Score = 819 bits (2116),  Expect = 0.0
 Identities = 419/773 (54%), Positives = 549/773 (71%), Gaps = 11/773 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAAS  74
            +LL L+W+ALLVP   LAA PVA   Q L+AL+ + ++  LKPF  K +  RF +L+AAS
Sbjct  1    MLLMLVWLALLVPVLFLAATPVATVVQALLALTVLAILFALKPFVQKSLRVRFFVLAAAS  60

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             LV+RYWFWRL ETLP P    SF+ AL+LF  E+F++ +FFL   ++ADPT  P P+ +
Sbjct  61   TLVLRYWFWRLTETLPSPEDPVSFIAALVLFGAESFTVVLFFLTALITADPTTPPLPKRM  120

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
            +  E PTVD+LVPSYNEP ++L+VTLAAA  M+YP   +TVVLCDDGGTDQ+C SPDP+
Sbjct  121  RRSEAPTVDVLVPSYNEPPELLAVTLAAAMQMVYPEGRKTVVLCDDGGTDQKCASPDPKA  180

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A++AQERR +LQ +C ++GVVY+TR RNEHAKAGN+++AL++L+GELV++ DADHVPSR+
Sbjct  181  AKEAQERRAQLQAMCEQMGVVYTTRARNEHAKAGNLNSALQKLRGELVLILDADHVPSRE  240

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FLART GYFVE+P LFLVQTPHFF N DPI+RN+ L + CP ENEMFY +IHRGLDR GG
Sbjct  241  FLARTAGYFVENPKLFLVQTPHFFTNRDPIERNIGLPETCPSENEMFYTEIHRGLDRLGG  300

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAA++RR+ALD+ GG +G TITEDAETAL+IHSRGW+SLY+D AMIAGLQPETFA
Sbjct  301  AFFCGSAALIRRKALDDVGGISGRTITEDAETALDIHSRGWESLYLDHAMIAGLQPETFA  360

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QRGRWATGMMQML+LKNPLFR GL + QR+CYLNSMS+W FPLVRM+FL++PL YL
Sbjct  361  SFITQRGRWATGMMQMLILKNPLFRPGLTMLQRVCYLNSMSYWLFPLVRMIFLLSPLFYL  420

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FFG+E+FV T++EVLAY+  +L V FL+QNALF++ RWPL+SEVYE+AQ PYL +A+  T
Sbjct  421  FFGLEVFVVTYDEVLAYILPHLLVGFLIQNALFSKVRWPLISEVYEIAQTPYLLKAVFNT  480

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +LRP +A F VTAKDETL +++ISP+++PLL   LL  +G++A  +RW  FPGDR+V+L+
Sbjct  481  VLRPNAATFKVTAKDETLDKDFISPVFQPLLMLNLLLFAGLVAAAMRWSLFPGDRTVVLI  540

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW + N LL   +LR+V E+Q+R   PR  +  PA   + A       A  L  S SG
Sbjct  541  VGGWNLYNFLLAALSLRSVFERQRRLQKPRTVIRAPARVWL-AGQPEETAAPALVRSISG  599

Query  615  VRLLVRLPGVGDPHPAL---EAGGLIQFQPKFPDAPQLERMVRGRI-RSARREGGTVMVG  670
              L + L    D  PAL   +    I    + P A  LE+ ++G++ +S R   G    G
Sbjct  600  KGLRLELQLGPDTDPALLEIKPDAEIMVHLEIPKARALEQTLQGKVTQSDRGRMGAERHG  659

Query  671  --VIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
              V F+  Q IA     A+L++G+S  W   R+A  +  GL+ G+  +L  A  SLP T
Sbjct  660  LAVTFDESQMIAASAMTAWLVYGDSKKWHAARKAVPQRRGLVPGILFVLRKAIVSLPVTV  719

Query  729  RDFMDEPARRRRRHEEPKE---KQAHLLAFGTDFSTEPDWAGELLDPTAQVSA  778
               +  P+  R    + +    +Q  +  F  D   + D +G      A+V A
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Sbjct  720  IGLLRAPSSARAAKTDDRRSSVEQQAIDQFLADDPRDDDGSGYFDSDEAEVRA  772


>TR:W4HF89 W4HF89_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseivivax marinus OX=1379903 GN=ATO8_21086 PE=4 SV=1
Length=783

 Score = 807 bits (2085),  Expect = 0.0
 Identities = 410/732 (56%), Positives = 512/732 (70%), Gaps = 11/732 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAASML  76
            L LLW+ L+VP   LA+ P + S Q L+A+  V ++ ++KPF    +P R  +L+ AS+
Sbjct  9    LALLWIGLMVPILFLASVPTSVSVQALMAVVTVTIIFVMKPFVAANMPLRLSVLAVASVF  68

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RYW WRL ETLP      S   ALLLF  ETF++ +FFL   ++ADP   P P  L+
Sbjct  69   VLRYWIWRLVETLPSIDDPISLAAALLLFGAETFTVGLFFLTALITADPVTHPLPPRLKL  128

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             E+P+VDILVPSYNE   +L+VTLAAAKN+ YP   +TVVLCDDGGTDQRC   DPE+A+
Sbjct  129  SEVPSVDILVPSYNESDQLLAVTLAAAKNITYPDDKKTVVLCDDGGTDQRCAHADPEIAK  188

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             +QERR  LQ+LC +LGVVYSTR RNEHAKAGN++AALE L+GEL++V DADHVP+RD L
Sbjct  189  TSQERRARLQKLCADLGVVYSTRARNEHAKAGNLNAALETLEGELLLVLDADHVPTRDIL  248

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
             RTVGYF E+P LFLVQTPHFF N DPI+RNLAL + CP ENEMFY +IHRGLDR GGAF
Sbjct  249  TRTVGYFSENPRLFLVQTPHFFTNRDPIERNLALPETCPSENEMFYSEIHRGLDRLGGAF  308

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRRRALDE GG AG+TITEDAETALEIHSRGW+S+YI+RAM+AGLQPETFASF
Sbjct  309  FCGSAAILRRRALDEVGGIAGDTITEDAETALEIHSRGWESIYIERAMVAGLQPETFASF  368

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            IQQRGRWATGM+QML+LKNP+ R GL + QRLCYLNSMSFW FPLVR +FL++PL+YLFF
Sbjct  369  IQQRGRWATGMIQMLILKNPILRSGLSLTQRLCYLNSMSFWLFPLVRTVFLLSPLLYLFF  428

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+EIFV T EEVLAY+  YL + F++QNALFA  RWP +SEVYE+AQ PYL RA+  T+L
Sbjct  429  GLEIFVVTGEEVLAYILPYLLIGFMIQNALFASVRWPQISEVYEIAQTPYLLRAVFETVL  488

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            RPR A F VTAKD+TL   ++SPIYRPL      L L+G++A L+RW+AFPGDR V+ +VG
Sbjct  489  RPRGATFKVTAKDDTLDSAFLSPIYRPLTLMTGLLLAGLIAGLIRWIAFPGDRGVIQIVG  548

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQI----PAFGNRSLTATVLDAST  612
             W + N LL  FALRAV E+  R   PR  +  PA   +       G   L  T++ A+
Sbjct  549  AWNLYNFLLAAFALRAVFERPWRLVKPRTAVSTPARLALSGDETGAGATMLDVTIIAATA  608

Query  613  SGVRLLVRLPGVGDP-----HPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTV  667
              V+L +  P  GD            G L    P     PQLE  +   I         +
Sbjct  609  GSVQLRLD-PDSGDSATRDWKKLSIKGALATLTPILEKTPQLEAPLEVSISDVSSGADGI  667

Query  668  MVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKT  727
             VG++ +    IA     A +++G+S+ W   R+   +   LL G+  +L  +  S+PK+
Sbjct  668  RVGLVVDPAHMIAASHLSATVVYGDSSRWHFFRKVRPQSSTLLAGLVYVLAKSVVSIPKS  727

Query  728  ARDFMDEPARRR  739
              DF+ EPARRR
Sbjct  728  VYDFLREPARRR  739


>TR:A0A1G7E198 A0A1G7E198_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Salipiger thiooxidans OX=282683 GN=SAMN04488105_10561
PE=4 SV=1
Length=785

 Score = 797 bits (2059),  Expect = 0.0
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 Identities = 420/783 (54%), Positives = 539/783 (69%), Gaps = 23/783 (3%)

Query  6    KARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFAD-KMV  64
            + R  L    VLL LLW+ALL    +LAA P+A   + L AL  V  + LLK FA
Sbjct  3    RERKRLGAGMVLLILLWLALLAVIVVLAATPIATPVEALFALVGVSSIWLLKRFASTNRQ  62

Query  65   PRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSAD  124
             RF++L+ AS+ VMRYW WRL ETLP      SF  A++LF  ETF++++FFL   ++AD
Sbjct  63   ARFIVLAIASVFVMRYWIWRLAETLPSQDDPLSFAAAVVLFGAETFTVALFFLTALVTAD  122

Query  125  PTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTD  184
            P DR  P+P++P ++P+VDILVPSYNEP ++L+VTLAAAK +IYP   +TVVLCDDGGTD
Sbjct  123  PIDRDPPKPMRPSQVPSVDILVPSYNEPPELLAVTLAAAKQVIYPEGRKTVVLCDDGGTD  182

Query  185  QRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVV  244
            QRC  PDP++++ AQERR+ LQ+LCR++G+VYSTR RNEHAKAGN++AAL+RL G+LV++
Sbjct  183  QRCNHPDPDISRGAQERRKLLQELCRDMGIVYSTRARNEHAKAGNLNAALQRLSGDLVLI  242

Query  245  FDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGK  304
             DADHVPSRD LART GYFVE+P LFLVQTPHFF N DPI+RN+ L + CP ENEMFY
Sbjct  243  LDADHVPSRDILARTAGYFVENPRLFLVQTPHFFTNRDPIERNIGLPETCPSENEMFYST  302

Query  305  IHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAM  364
            IHRGLDR GGAFFCGSAA+LRR+ALDE GG +G TITEDAETAL+IHSRGW+S+Y++RAM
Sbjct  303  IHRGLDRLGGAFFCGSAALLRRKALDEVGGISGVTITEDAETALDIHSRGWESMYLNRAM  362

Query  365  IAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRM  424
            IAGLQPETFASFIQQRGRWATGMMQ+L+LKNPLFR GL +AQR CYLNSMS+W FP+VRM
Sbjct  363  IAGLQPETFASFIQQRGRWATGMMQILILKNPLFRSGLSLAQRFCYLNSMSYWLFPVVRM  422

Query  425  MFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQA  484
             FL++PL YLFFG+++FV   +EV+AY+  YL V+FLVQN LFAR RWPL+SEVYE+AQ
Sbjct  423  TFLLSPLFYLFFGLQVFVVQPDEVMAYILPYLLVAFLVQNGLFARVRWPLISEVYEIAQT  482

Query  485  PYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVA  544
            PYL  A+  T+LRP +A+F VTAKDE+L  ++ISP+ +PL  T LL   G++A  +RW
Sbjct  483  PYLLMAVFKTMLRPHAAKFNVTAKDESLDNDFISPVMKPLFITTLLMFGGLVAAGIRWYM  542

Query  545  FPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLT  604
            +PGDR ++ +VGGWA+ N +L   +LR+V E+Q+R   PR ++ VPA     +  + +
Sbjct  543  YPGDRLIVQIVGGWALFNFILTVLSLRSVFERQRRLRKPRTEIMVPAAVWSESKTDGAGV  602

Query  605  ATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQ------FQPKFPDAPQLERMVR---G  655
            + VL  S+           + D   A E  G+I+        P  P AP LE  +R
Sbjct  603  SAVLRMSSGRTMQFT----LNDDDEAREGLGMIRSGDRLVLCPVIPAAPDLEHHLRLHVT  658

Query  656  RIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMAR  715
            R+    + G    V V  E GQ I   E  AYL++G S  W   REA  +  GL+ G+
Sbjct  659  RVSHDEQAGRGTAVTVEVEDGQLIPASEITAYLVYGNSEKWVAAREALPQARGLISGIVF  718

Query  716  ILWMAAASL-PKTARDFMDEPARRRRRHEEPK---EKQA--HLLAFGTDFSTEPDWAGEL  769
            +L ++  S+ P          A +  R +E +   EK A  H LA   D    P  A E
Sbjct  719  VLRLSVGSIVPSVLALVTHRAAPQHSRKDEDRNTVEKTAIEHYLA---DRGALPAPATEF  775

Query  770  LDP  772
            L P
Sbjct  776  LVP  778


>TR:A0A1I1VMK9 A0A1I1VMK9_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseivivax sediminis OX=936889 GN=SAMN04515678_103303
PE=4 SV=1
Length=784

 Score = 793 bits (2048),  Expect = 0.0
 Identities = 398/730 (55%), Positives = 518/730 (71%), Gaps = 6/730 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAASM  75
            +L L WVAL++P   LA+ P + + Q L+A+    ++  LKPF    +P RF++L+ AS+
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Sbjct  14   ILVLAWVALMLPILFLASVPTSVTVQALLAIVTCAVLFTLKPFVRASLPMRFVVLAVASV  73

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
             V+RYW WRL +TLP      S   A+LLFA ETF++ +FFL   ++ADP D P P  L+
Sbjct  74   FVLRYWIWRLVDTLPSLDDPLSLAPAILLFAAETFTVGLFFLTALITADPVDHPPPPRLK  133

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              ++P+VDILVPSYNE  ++L+VTLAAAKN+ YP   + +VLCDDGGTDQRC   DP +A
Sbjct  134  LSDVPSVDILVPSYNESDELLAVTLAAAKNVTYPEEKKRLVLCDDGGTDQRCAHSDPAIA  193

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q ++ERR  LQ LC ELGV+Y+TR RNE AKAGN++AAL+ + GELV++ DADHVP+RD
Sbjct  194  QASRERRARLQALCEELGVIYTTRARNESAKAGNLNAALQHIDGELVLILDADHVPTRDI  253

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L RTVGYF E+P LFLVQTPHFF N DPI+RNLAL + CP ENEMFY +IHRGLDR GGA
Sbjct  254  LTRTVGYFSENPRLFLVQTPHFFTNRDPIERNLALPEVCPSENEMFYSEIHRGLDRLGGA  313

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRRRALDE GG AGETITEDAETALEIHSRGW+S+Y++ AM+AGLQPETFAS
Sbjct  314  FFCGSAAILRRRALDEVGGIAGETITEDAETALEIHSRGWESMYLEHAMVAGLQPETFAS  373

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FIQQRGRWATGM+QML+LKNP+FRRGL + QR+CYLNSMSFW FP+VR +FL +PL+YLF
Sbjct  374  FIQQRGRWATGMIQMLILKNPIFRRGLSLTQRVCYLNSMSFWLFPVVRTIFLASPLLYLF  433

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+EIFV T EEVLAY+  YL + F+VQNALF+  RWP +SEVYE+AQ PY+ RA++ T+
Sbjct  434  FGLEIFVVTSEEVLAYILPYLLIGFMVQNALFSNVRWPQISEVYEIAQTPYILRAVIGTV  493

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            +RPR+A F VTAKD+ L   ++SPIY PL+    L L+GV+A ++RW+AFPGDR+V+ +V
Sbjct  494  MRPRAATFKVTAKDDELDHAFLSPIYLPLVVLTGLLLAGVIAGVIRWIAFPGDRAVVQIV  553

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W V N LL  FALRAV E+  R   PR  +  PA   +   G  +   T++ A+ + V
Sbjct  554  GAWNVYNFLLAAFALRAVFERPWRLVKPRTAVSAPARLAVED-GATAFDVTIIAATANAV  612

Query  616  RLLV--RLPGVG--DPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
            +L +   L G    D   +   G      P  P  P+LE+ +   I   R     + +GV
Sbjct  613  QLQLDSELRGADGRDWQNSGWEGKAASLTPILPKTPELEQPLPVVIEDIRTGVDGISLGV  672

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF  731
               +   +      A +++G+S+ W   R+   +   LL G+A IL  +  S+P +A DF
Sbjct  673  TVASEHMVPASRLAATIVYGDSSRWHFFRKVRSQGSTLLAGLAYILGKSLVSIPMSALDF  732

Query  732  MDEPARRRRR  741
            + EPARRRR+
Sbjct  733  LREPARRRRQ  742


>TR:S9QL88 S9QL88_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Salipiger mucosus DSM 16094 OX=1123237 GN=Salmuc_03684
PE=4 SV=1
Length=792

 Score = 789 bits (2038),  Expect = 0.0
 Identities = 401/736 (54%), Positives = 516/736 (70%), Gaps = 12/736 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAASM  75
            LL  +WVALLVP   LA+ P + + QGL+A+   + +  LKPF    +P RF +L+ AS+
Sbjct  14   LLLPVWVALLVPILFLASVPTSVTVQGLLAIVTCIAIFALKPFVHGSLPVRFAVLAIASV  73

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
             V+RYW WRL ETLP      S   AL+LFA ETF++ +FFL+  ++ADP   P P  L+
Sbjct  74   FVLRYWIWRLLETLPSLDDPLSLAAALVLFAAETFTVGLFFLSALVTADPVSHPPPPRLK  133

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              E+P+VDILVPSYNE  ++L+VTLAAAK + YP   +TVVLCDDGGTDQRC   DP +A
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Sbjct  134  LTEVPSVDILVPSYNESDELLAVTLAAAKRVTYPEDKKTVVLCDDGGTDQRCNHADPAIA  193

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              A+ERR  LQ LC ++GVVY+TR RNE AKAGN++AAL+ L GE+V+V DADHVP+RD
Sbjct  194  AAARERRARLQALCEKMGVVYTTRARNESAKAGNLNAALKELDGEIVLVLDADHVPTRDI  253

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L RTVGYF E+P LFLVQTPHFF N DPI+RNLAL + CP ENEMFY +IHRGLDR GGA
Sbjct  254  LTRTVGYFAENPRLFLVQTPHFFTNRDPIERNLALPEVCPSENEMFYTEIHRGLDRLGGA  313

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRRRALDE GG AGETITEDAETALEIHSRGW+S+Y++ AM+AGLQPETFAS
Sbjct  314  FFCGSAALLRRRALDEVGGIAGETITEDAETALEIHSRGWESMYVEHAMVAGLQPETFAS  373

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FIQQRGRWATGM+QML+LKNPLFR+GL + QR+CY+NSMSFW FPLVR +FL++P++YLF
Sbjct  374  FIQQRGRWATGMIQMLILKNPLFRKGLSLPQRVCYINSMSFWLFPLVRTVFLLSPMVYLF  433

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+EIFV T EEVLAY+  YL + F++QNAL+A  RWP VSEVYE+AQ PY+ RA++ T+
Sbjct  434  FGLEIFVVTAEEVLAYILPYLLIGFMIQNALYANVRWPQVSEVYEIAQTPYVLRAVIGTI  493

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            LRPR+A F VTAKD+ L   ++SPI RPL+    L L+G++A +VRW+ FPGDR+V+ +V
Sbjct  494  LRPRAATFKVTAKDDGLDHAFLSPIARPLVLLAGLLLAGLVAGVVRWIYFPGDRAVVQIV  553

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQI---PAFGN----RSLTATVL  608
            G W   N LL  FALRAV E+  R   PR  +  PA   +   P  G+     +L  T++
Sbjct  554  GAWNAYNFLLAAFALRAVFERPWRLVKPRTAVSTPARLTLEPDPDAGDTDEATTLDVTII  613

Query  609  DASTSGVRLLVRLPGVGDPHPALEAGG----LIQFQPKFPDAPQLERMVRGRIRSARREG  664
             AS + V+L + +   G      + GG     +   P  P AP+LE  +   I   R
Sbjct  614  AASAAAVQLQLDVAPGGAEGREWQDGGWEGRAVTLAPVLPKAPELEEPLPATIGDVRGGV  673

Query  665  GTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASL  724
              + +G+       +      A++++G+S+ W   R+   +   LL G   +L  +  S+
Sbjct  674  DGIRIGLEVAPDHIVPASRLAAHIVYGDSSRWHFFRKVRPQGTTLLTGFVYVLGKSLVSV  733

Query  725  PKTARDFMDEPARRRR  740
            PK+  DF  EPARRRR
Sbjct  734  PKSLFDFAREPARRRR  749


>TR:A0A1U7D471 A0A1U7D471_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Salipiger profundus OX=1229727 GN=Ga0080559_TMP2107
PE=4 SV=1
Length=789

 Score = 784 bits (2024),  Expect = 0.0
 Identities = 413/772 (53%), Positives = 525/772 (68%), Gaps = 20/772 (3%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLL  70
            R+   +L LLW+ALLVP   LA+ P +  AQGL+AL   VL+ +LKPF    +P RF +L
Sbjct  3    RISVSVLVLLWLALLVPIVFLASVPTSIIAQGLMALCICVLIYVLKPFVSASMPVRFFVL  62

Query  71   SAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPF  130
            + A++ V+RYW WRL ETLP      S   AL+LF  ETF++ +FFL   +S DP D
Sbjct  63   AVAAVFVLRYWLWRLLETLPALDDPVSLAAALVLFGAETFTVGLFFLTALVSGDPVDHAP  122

Query  131  PRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
            P  ++  + PTVDIL+PSYNEPAD+L+VTLAAAKN+ YP   + VVLCDDGGTDQRC
Sbjct  123  PPKVKLRDAPTVDILIPSYNEPADLLAVTLAAAKNVTYPDDKKVVVLCDDGGTDQRCAHS  182

Query  191  DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
            DPE+A++A+ERR ELQ+LCRELGVVY+TR RNEHAKAGN++ AL+ LKGELV+V DADHV
Sbjct  183  DPEVAREARERRAELQELCRELGVVYTTRARNEHAKAGNLNEALKSLKGELVLVLDADHV  242

Query  251  PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            P+RDFLARTVGYF E+P LFLVQTPHFF N DPI+RNLA  +  P ENEMFYG+IHRGLD
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Sbjct  243  PTRDFLARTVGYFAENPRLFLVQTPHFFTNRDPIERNLAFSEALPSENEMFYGQIHRGLD  302

Query  311  RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            R GGAFFCGSAA+LRRRALDE GG +GETITEDAETAL+IHSRGW+S+Y+D AMIAGLQP
Sbjct  303  RLGGAFFCGSAALLRRRALDEVGGISGETITEDAETALDIHSRGWESMYLDYAMIAGLQP  362

Query  371  ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
            ETFASFIQQRGRWATGM+QML+LKNP+FR GL   +RLCYLNSMSFW FP+VRM+FL++P
Sbjct  363  ETFASFIQQRGRWATGMIQMLILKNPIFRSGLPFTKRLCYLNSMSFWLFPVVRMIFLLSP  422

Query  431  LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L+YLFFG+EIFV T  EVL ++  YL + F+VQNALF+  RWP VSEVYE+AQ PYL  A
Sbjct  423  LLYLFFGLEIFVVTPAEVLGFILPYLLIGFMVQNALFSHVRWPQVSEVYEIAQTPYLLGA  482

Query  491  IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
            I++T+ +PR+A F VTAKDE+L   ++SPI  PLL    L L+G++A ++RWVA+PGDR+
Sbjct  483  IISTIRKPRAASFKVTAKDESLDRAFMSPIAMPLLALTGLLLAGLVAGVLRWVAYPGDRA  542

Query  551  VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPA-------------EAQIPA  597
            V+ +VG W V N +L  +ALR+V E+  R   PR  + VPA             EA
Sbjct  543  VVQIVGAWNVYNFILAAWALRSVFERPWRLVRPRTAVSVPARLTISWPENAAEGEATPDT  602

Query  598  FGNRSLTATVLDASTSGVRLLVRLPGVGD---PHPALEAGGLIQFQPKFPDAPQLERMVR  654
              +      V+  S +   L VRLP   +      A +AG      P   +AP  E  +
Sbjct  603  DSDTGEGVEVVIVSATPKSLSVRLPAGAEGDIVKRASDAGASASILPAVENAPAPEGPLP  662

Query  655  GRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMA  714
              +   + +    +  +       I      A +++G+S  W   R+   R   L+ G A
Sbjct  663  VTVGVLKSDTSGYLCMLDIPESAMIDASRFAAAVVYGDSGRWEFFRKTVPRSSTLVTGFA  722

Query  715  RILWMAAASLPKTARDFMDEPARRRRR-HEEPKE--KQAHLLAFGTDFSTEP  763
             ++  A  SLP T  D + EP RRR+   ++  E  + A   A GT+    P
Sbjct  723  YVIGKALMSLPVTVLDLLREPERRRQAVFDDAAEIPRDAFAAAKGTEARNRP  774


>TR:A0ABT2KUL7 A0ABT2KUL7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Alloyangia mangrovi OX=1779329 GN=bcsA PE=4 SV=1
Length=784

 Score = 783 bits (2021),  Expect = 0.0
 Identities = 399/726 (55%), Positives = 509/726 (70%), Gaps = 10/726 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAAS  74
            +LLF +WVAL VP   LA+ P++ S QGL+AL A VL+  LKPF    +  RF+++S A
Sbjct  13   LLLFGVWVALAVPLLFLASVPISVSTQGLLALVACVLIYGLKPFVGTRISVRFVVMSIAG  72

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
            + V+RYW WR FETLP      S   AL+LF  ETF++ +FFL   ++ADP   P P P+
Sbjct  73   VFVLRYWLWRAFETLPSLDDPISLAAALVLFGAETFTVGLFFLTALITADPVTHPRPEPI  132

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
            +  ++PTVDILVPSY+E  ++L+VTLAAAK + YP   +TVVLCDDGGTDQRC   DP +
Sbjct  133  KLSDVPTVDILVPSYDESPELLAVTLAAAKRVSYPEDRKTVVLCDDGGTDQRCNHSDPAI  192

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            +++A  RR  LQ LC ELGVVY+TR RNEHAKAGN++AAL+++ GELV++ DADHVP+ D
Sbjct  193  SERALARRARLQALCDELGVVYTTRARNEHAKAGNLNAALQKVNGELVLILDADHVPTPD  252

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FLARTVGYF E P LFLVQTPHFF N DPI+RNLAL + CP ENEMFY +IHRGLDR GG
Sbjct  253  FLARTVGYFAERPRLFLVQTPHFFTNRDPIERNLALPENCPSENEMFYSEIHRGLDRLGG  312

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAA+LRR+ALDE GG +GETITEDAETAL+IH+RGW+SLY+D AMIAGLQPETFA
Sbjct  313  AFFCGSAALLRRKALDEVGGISGETITEDAETALDIHARGWESLYLDHAMIAGLQPETFA  372

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFIQQRGRWATGM+QML+LKNP+FR GL +AQRLCYLNSMSFW FPL+R +FL++PL+YL
Sbjct  373  SFIQQRGRWATGMIQMLILKNPIFRSGLTMAQRLCYLNSMSFWLFPLIRTIFLLSPLLYL  432
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Query  435   FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
             FFG+EIFV   EEV  Y+  YL + F+VQNALF+  RWP +SEVYE+AQ PY+ +A+V T
Sbjct  433   FFGLEIFVVDPEEVFVYILPYLLIGFMVQNALFSEVRWPQISEVYEIAQTPYILKALVET  492

Query  495   LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
             +LRPR A F VTAKD +L   ++SPIYRPL     L L+G+ A   RW AFPGDRSV+ +
Sbjct  493   VLRPRGASFKVTAKDGSLEHAFLSPIYRPLTLLVALLLAGLAAGAYRWYAFPGDRSVVQI  552

Query  555   VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAE----AQIPAFGNRSLTATVLDA  610
             VG WA+ N +L  +ALRAV E+ +R   PR  +  P      A +      +   T+L A
Sbjct  553   VGAWALYNFVLAAYALRAVFERPRRLIRPRTAVSAPGRITLLAPVSEADREAQDVTILSA  612

Query  611   STSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARR--EGGTVM  668
             S    +L ++  G  +   A  AG  I   P  P AP LE  +   I   R   EG  +
Sbjct  613   SPERFQLQLK-DGTHEAWSAEHAGAAIALVPSLPKAPDLETALPMTISEVRSGVEGTVIE  671

Query  669   VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
             + V  E    +   +  A++++G+S  W+  R+   +   L+ G+  +L  +A SLP+T
Sbjct  672   LNVAPE--HMVQAAQLTAHVVYGDSRRWQFFRKFHAQSSTLVAGLLYVLAKSAISLPQTL  729

Query  729   RDFMDE  734
              DF  E
Sbjct  730   FDFARE  735


>TR:X7EDY9 X7EDY9_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Roseivivax halodurans JCM 10272 OX=1449350 GN=OCH239_05490
PE=4 SV=1
Length=777

 Score = 781 bits (2018),  Expect = 0.0
 Identities = 397/730 (54%), Positives = 510/730 (70%), Gaps = 10/730 (1%)

Query  18    LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA-DKMVPRFLLLSAASML  76
             L ++W+AL+VP   LA+ P +  AQGL+AL+   ++ +LKPF     + RF +L+ AS+
Sbjct  9     LAIIWIALMVPVLFLASVPTSIVAQGLMALTTCAVIYVLKPFVTSNALVRFFVLALASVF  68

Query  77    VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
             V+RYW WRL ETLP      S   AL+LF  ETF++ +FFL   ++ DP + P P  ++
Sbjct  69    VLRYWLWRLLETLPSTDSPLSLAAALVLFGAETFTVGLFFLTALVTGDPVENPPPPKVKL  128

Query  137   EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
              + P VDILVPSYNEP D+L+VTLAAAKN+ YPA  +TVVLCDDGGTDQRC   DPE+A+
Sbjct  129   RDAPRVDILVPSYNEPDDLLAVTLAAAKNVTYPADKKTVVLCDDGGTDQRCAHADPEIAR  188

Query  197   KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             +A+ERR  LQ+LC EL VVY+TR RNEHAKAGN++ AL+ L GELV+V DADHVP+RDFL
Sbjct  189   QARERRARLQKLCAELDVVYTTRARNEHAKAGNLNEALKTLDGELVLVLDADHVPTRDFL  248

Query  257   ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
             ARTVGYF E+P LFLVQTPHFF N DPI+RNL   + CP ENEMFYG+IHRGLDR GGAF
Sbjct  249   ARTVGYFTENPRLFLVQTPHFFTNRDPIERNLGFKETCPSENEMFYGQIHRGLDRLGGAF  308

Query  317   FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
             FCGSAA+LRR ALDE GG +GETITEDAETAL+IH+RGW+S+Y+D AMIAGLQPETFASF
Sbjct  309   FCGSAALLRRSALDEVGGISGETITEDAETALDIHARGWESMYLDYAMIAGLQPETFASF  368

Query  377   IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
             IQQRGRWATGM+QML+LKNP+FR GL I +RLCYLNSMSFW FPL+R +FLV+PLIYLFF
Sbjct  369   IQQRGRWATGMIQMLILKNPVFRSGLTIGKRLCYLNSMSFWLFPLIRTIFLVSPLIYLFF  428

Query  437   GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             G++IFV    EVL Y+  YL + F+VQNALFA  RWP +SEVYE+AQ PYL  A++ T+
Sbjct  429   GLQIFVVNPAEVLGYILPYLLIGFMVQNALFANVRWPQISEVYEIAQTPYLFAALIETVR  488

Query  497   RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
              PR A F VTAKD+TL   ++SPI  PL+    L L+G++A + R++AFPGDR+V+ +V
Sbjct  489   HPRGASFKVTAKDDTLDRAFMSPIAMPLMVLTGLLLAGIVAAVARYIAFPGDRTVVQIVA  548
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Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGN--RSLTATVLDASTSG  614
             W V N LL   ALRAV E+  R   PR  + VPA   IP   +    L  T++ AS +
Sbjct  549  AWNVYNFLLAALALRAVFERPARLVRPRTAVFVPARLHIPGADDDAADLETTIISASPTV  608

Query  615  VRLLVRLPGVGDPH---PALEAGGLI--QFQPKFPDAPQLERMVRGRIRSARREGGTVMV  669
            ++   RL     P    P  E    +  +  P  P +P L+  +   +   R +   +++
Sbjct  609  IQ--ARLAAGALPKGLAPGSEGAAPMRGKLSPVLPKSPALQTPLNVTVNEVRSDPDGLLL  666

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             +   A Q +      A +++G+S+ W   R+   R   L+ G+A +L  AA SLPKT
Sbjct  667  ELGISAEQMVDASRLTAVIVYGDSSRWEFFRKVVPRSSTLVAGLAYVLGKAALSLPKTTL  726

Query  730  DFMDEPARRR  739
            D + EP RR+
Sbjct  727  DLLREPGRRQ  736


>TR:S9RNV7 S9RNV7_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Salipiger mucosus DSM 16094 OX=1123237 GN=Salmuc_04572
PE=4 SV=1
Length=782

 Score = 780 bits (2015),  Expect = 0.0
 Identities = 408/776 (53%), Positives = 525/776 (68%), Gaps = 16/776 (2%)

Query  8    RSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFAD-KMVPR  66
            R  + +   LL LLW+ LL    +LAAAP+A S Q  +A+ +V L+ LLK F       R
Sbjct  5    RGFMSIAIALLGLLWLLLLAIIIILAAAPIAVSVQAFLAIISVALIWLLKRFVPVNRQVR  64

Query  67   FLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPT  126
            FL+L+ AS+ VMRYW WR+FETLP P    SF  A+LL   E+F++++FFL   ++ DP
Sbjct  65   FLVLAIASVFVMRYWIWRVFETLPSPEDPVSFAAAVLLLGAESFTVALFFLTCLVTGDPC  124

Query  127  DRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQR  186
            DR  P+ +   ++P+VDILVPSYNEP ++L+VTLAAAK +IYP   +TVVLCDDGGTDQR
Sbjct  125  DRAPPKLMHVSQVPSVDILVPSYNEPPELLAVTLAAAKQIIYPEGKKTVVLCDDGGTDQR  184

Query  187  CMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFD  246
            C  PD E+A  A+ERR  LQ LCR++ +VYSTR RNEHAKAGN++AAL+ L G+LV++ D
Sbjct  185  CNHPDKEIANAARERRETLQSLCRDMDIVYSTRARNEHAKAGNLNAALKHLDGDLVLILD  244

Query  247  ADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIH  306
            ADHVPSRDFLART GYFVE P LFLVQTPHFF N DPI+RN+ L + CP ENEMFY  IH
Sbjct  245  ADHVPSRDFLARTAGYFVEKPRLFLVQTPHFFTNRDPIERNIGLPETCPAENEMFYTTIH  304

Query  307  RGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIA  366
            RGLDR GG FFCGSAA+LRR ALDE GG +G TITEDAETAL+IHSRGW+SLY++RAM A
Sbjct  305  RGLDRLGGTFFCGSAALLRRAALDEVGGISGVTITEDAETALDIHSRGWESLYLNRAMSA  364

Query  367  GLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMF  426
            GLQPETFASFIQQRGRWATGMMQ+LLLKNPLFR GL + QRLCYLNSMS+W FP+VRM+F
Sbjct  365  GLQPETFASFIQQRGRWATGMMQILLLKNPLFRSGLSLTQRLCYLNSMSYWLFPVVRMIF  424

Query  427  LVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPY  486
            L++PL YLFFG++IFV   + V+AY+  YL ++ LVQN LFAR RWPL+SEVYE+AQ PY
Sbjct  425  LISPLFYLFFGLQIFVVQPDGVMAYILPYLLIAMLVQNGLFARVRWPLISEVYEIAQTPY  484

Query  487  LARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFP  546
            L +A+  T + PRSA+F VTAKDETL + +ISP+  PLL T L+ L+G++A  +RW  FP
Sbjct  485  LLKAVFKTFISPRSAKFNVTAKDETLEDEFISPVLVPLLLTTLVLLAGIVAAALRWYLFP  544

Query  547  GDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTAT  606
            GDRSV+ +VGGWA+ N+LL   ALR+V E+Q+R   PR  +  PA        + S T
Sbjct  545  GDRSVVQIVGGWALFNLLLAILALRSVIERQRRLLKPRTAIMAPASLWPEGQHSGSATDV  604

Query  607  VLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLER---MVRGRIRSARRE  663
            VL A  S  ++           +  +  G  +  +PK  DAP+L+    +   R
Sbjct  605  VLRA-ISARKMRFVFADDDRKNEMIGEGARLVIRPKIDDAPELQHELTITLTRAEDPSDN  663
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Query  664  GGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAAS  723
             G  +     +    IA  E  A+L++G+S  W   REA  R  GL+ G+  +L ++  S
Sbjct  664  AGRRLWSADIDRDHLIAASEITAHLVYGDSEKWMAAREAVPRSRGLISGIVFVLRLSLTS  723

Query  724  LPKTARDF-------MDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDP  772
            +  +A           D P  R R   E +  + +L     D +++ D +   L P
Sbjct  724  IVPSAIALFTYRGAPQDNPEDRYRNANETEAIKYYL----ADNTSDSDLSAAFLLP  775


>TR:A0A285IR92 A0A285IR92_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudooceanicola antarcticus OX=1247613 GN=bcsA PE=4
SV=1
Length=782

 Score = 776 bits (2005),  Expect = 0.0
 Identities = 396/728 (54%), Positives = 503/728 (69%), Gaps = 3/728 (0%)

Query  9    SPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFAD-KMVPRF  67
            S L  V +LL   W  L VP   LA+ P++   QGL+AL    L+  LKPF   K+  R
Sbjct  6    SSLSAVRLLLLCTWAILAVPLFFLASVPISVGTQGLLALVTSALIYGLKPFVGFKISIRV  65

Query  68   LLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTD  127
            +++S A + V+RYW WRLFETLP      S   AL+LFA ETF++ +FFL  F+++DP
Sbjct  66   IVMSVAGVFVLRYWLWRLFETLPALDDPVSLAAALVLFAAETFTVIVFFLTAFITSDPVT  125

Query  128  RPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRC  187
               P+P++  E P+VDILVPSY+E  ++L+VTLAAAK + YP   +TVVLCDDGGTDQRC
Sbjct  126  HAKPQPIKLSEAPSVDILVPSYDESPELLAVTLAAAKRITYPDDKKTVVLCDDGGTDQRC  185

Query  188  MSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDA  247
             S DPE A  A+ERR  LQ LC ELGVVY+TR RNEHAKAGN++AAL++L GELV++ DA
Sbjct  186  NSDDPERAAAAKERRATLQALCAELGVVYTTRARNEHAKAGNLNAALQKLTGELVLILDA  245

Query  248  DHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHR  307
            DHVP+ +FLARTVGYF E+P LFLVQTPHFF N DPI+RNLAL + CP ENEMFY +IHR
Sbjct  246  DHVPTPEFLARTVGYFAENPRLFLVQTPHFFTNRDPIERNLALPEHCPSENEMFYSEIHR  305

Query  308  GLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAG  367
            GLDR GGAFFCGSAA+LRRRALDE GG +GETITEDAETAL+IHSRGW+SLY+D AMIAG
Sbjct  306  GLDRMGGAFFCGSAALLRRRALDEVGGISGETITEDAETALDIHSRGWESLYLDHAMIAG  365

Query  368  LQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFL  427
            LQPETFASFIQQRGRWATGM+QML+LKNP+FR GL  AQRLCY+NSMSFW FPL+RM+FL
Sbjct  366  LQPETFASFIQQRGRWATGMIQMLILKNPMFRSGLSFAQRLCYVNSMSFWLFPLIRMIFL  425

Query  428  VAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYL  487
            ++PL+YLFFG+EIFV    EV  Y+  YL + F+VQNALF+  RWP +SEVYE+AQ PY+
Sbjct  426  LSPLLYLFFGLEIFVVDANEVFVYILPYLLIGFMVQNALFSNVRWPQISEVYEIAQTPYI  485

Query  488  ARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPG  547
              A++ T+  PR A F VTAKD TL   ++SPIYRPL     L L+G+LA   RW AFPG
Sbjct  486  LSALIETVRNPRGATFKVTAKDGTLEHAFLSPIYRPLTLLVALLLAGLLAGAYRWYAFPG  545

Query  548  DRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPA-FGNRSLTAT  606
            DR+V+ +VG WA+ N +L  +ALRAV E+ +R   PR  +  PA   + A     S  AT
Sbjct  546  DRAVVQIVGAWALYNFMLAAYALRAVFERPRRLTRPRTAISTPARISLAADAAGPSHEAT  605

Query  607  VLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGT  666
            ++ AS   ++L +   G       L  G  +   P  P+ P LE  +   + + RR
Sbjct  606  IVAASPEAIQLKL-AEGAPAGWNDLAMGTEVSLLPVLPETPDLEVALPLTLSALRRGVDG  664

Query  667  VMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPK  726
             ++       Q I      A +++G+S  W+  R+   +   L+ G+  +L  +A S+P+
Sbjct  665  TVLTFDVPPEQMIPAARLTAQVVYGDSRRWQFFRKVHPQGSTLVAGLLYVLMKSALSMPQ  724

Query  727  TARDFMDE  734
            T  DF  E
Sbjct  725  TIYDFARE  732
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>TR:A0A5B8FXL0 A0A5B8FXL0_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Paroceanicella profunda OX=2579971 GN=bcsA PE=4 SV=1
Length=801

 Score = 765 bits (1975),  Expect = 0.0
 Identities = 408/764 (53%), Positives = 512/764 (67%), Gaps = 17/764 (2%)

Query  23   VALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWF  82
            + +L     LA+ P++  AQ ++A+ AV++VALLKP A+  V RF+LLS A  +V+RY F
Sbjct  19   ITILAAVVFLASVPLSTPAQAVVAICAVLVVALLKPAANLPVVRFILLSVAGFIVLRYLF  78

Query  83   WRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ-PEELPT  141
            WR+  TLP  A   S + A +L   E  +I +FFL+ F++A P DRP P  +   EELPT
Sbjct  79   WRISYTLPFDADIPSQIAAFVLLVAEMQAICVFFLSAFVTAQPADRPLPPVIDYAEELPT  138

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+LVPSYNEPADMLSVTLAAA  M YP     ++LCDDGGTDQRC   DP+LA  ++ R
Sbjct  139  VDVLVPSYNEPADMLSVTLAAASMMRYPRDRLKIILCDDGGTDQRCNHADPDLAAASRRR  198

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
            R ELQ +CRELGV+Y+TRERN  AKAGNMS+ALE L GELVVVFDADHVP++DFL RTVG
Sbjct  199  RAELQDMCRELGVIYATRERNVGAKAGNMSSALENLDGELVVVFDADHVPTQDFLERTVG  258

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            +F+ DP LFLVQTPHFFIN DPI+RNL L DRCPPENEMFYG I  G+D WG   FCGSA
Sbjct  259  HFIADPKLFLVQTPHFFINKDPIERNLGLSDRCPPENEMFYGIIQPGIDNWGSTLFCGSA  318

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            A+LRR+ALDEAGGFAGE+ITEDAETAL+IH+RGW S+Y++ A+IAGLQPETF+SFI QR
Sbjct  319  AILRRQALDEAGGFAGESITEDAETALDIHARGWHSMYVNHAVIAGLQPETFSSFIGQRS  378

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RWA+GMMQ+ LLKNP+F+RGL I QRLCYLN + FW FPLVRM+FL APL YLFFG+EIF
Sbjct  379  RWASGMMQIFLLKNPIFKRGLTIYQRLCYLNMIGFWLFPLVRMVFLCAPLAYLFFGLEIF  438

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A  E+   Y+  YL VS +VQN LF R RWPL+SE+YE AQ PYLAR++++T  RPRS
Sbjct  439  SANVEQFSVYVLSYLVVSLMVQNTLFRRYRWPLISELYETAQTPYLARSVLSTFWRPRSP  498

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAKDETL +  ISPI RPL+  FLL  +G++A  VR+  FPGDR  + +V  WAV
Sbjct  499  SFNVTAKDETLDKESISPIARPLILLFLLMTAGIVAGAVRYALFPGDRDAVTIVASWAVF  558

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N ++VG AL AV EK QRRA PRV   V   A +         AT+LD S  G R+ V L
Sbjct  559  NFIVVGTALGAVCEKPQRRARPRV--SVREAATLFTDDGLEYAATLLDVSMGGTRIEVPL  616

Query  622  ----PGVGDP-HPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
                 G G     AL  G  +  +P   D       +   + S  R    ++VG+ + A
Sbjct  617  GGPTKGAGSALLTALRPGQKVTVRPLLKDEGAPNAPILCHVASVTRSPHALIVGLSYAAT  676

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKT----ARDFM  732
            Q  + R +VA ++F +S  W+  R  T    GLL G+   LW+A  ++P +     RD +
Sbjct  677  QARSARFSVASIMFRDSLLWQAKRLQTRDGPGLLMGILYYLWLAIRTIPASVISIVRDIL  736

Query  733  DEPARRRRRHEEPKEKQAHLLAFGTD----FSTEPDWAGELLDP  772
              P            +QAH   FG +    F+  P   G +++P
Sbjct  737  -TPKPDNTGEIRAVIEQAHPFRFGVELQPSFADSPRPVGTMINP  779


>TR:A0A1H9WKQ1 A0A1H9WKQ1_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Tranquillimonas rosea OX=641238 GN=SAMN04490244_11182
PE=4 SV=1
Length=783

 Score = 749 bits (1933),  Expect = 0.0
 Identities = 383/749 (51%), Positives = 495/749 (66%), Gaps = 10/749 (1%)
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Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LW   +    ++A+ P   + Q L+ +  VV V +L+ +A  +  R  +L  AS++V+RY
Sbjct  17   LWFISVACVLVMASIPTTITVQALLGVVTVVSVLVLRHYAHNLAARMAMLGIASVVVLRY  76

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
            WFWR+  TLP      SF+ ALLLF VETF+I IFFL  F+ ADP     P P+    LP
Sbjct  77   WFWRVLHTLPGLDDPVSFVAALLLFMVETFAIGIFFLGNFIMADPVRHKRPAPVSVGALP  136

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
             VD+L+P+ +EP D+L+VTLAAA+NM YP  L  VVLCDDGGTD RC +PDP  A  A++
Sbjct  137  RVDVLIPTLDEPRDLLAVTLAAARNMAYPPELVKVVLCDDGGTDARCGNPDPVKAAAARK  196

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RRRELQ+LC ELG +Y TR  N  AKAGN++ AL RL GELVV+FDADH P+RDFLARTV
Sbjct  197  RRRELQELCDELGCIYMTRPENRSAKAGNLNEALSRLDGELVVIFDADHAPTRDFLARTV  256

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF E+  LFLVQTPHFF+N DP+ RNL LG+  PPENEMFYG++H GLDRWGGAFFCGS
Sbjct  257  GYFAENEKLFLVQTPHFFLNDDPVARNLHLGEDTPPENEMFYGQLHEGLDRWGGAFFCGS  316

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR ALDE GG +G TITEDAETAL IHSRGW+S+Y++ AM+AGLQPETFASF+QQR
Sbjct  317  AAVLRRTALDEVGGISGNTITEDAETALTIHSRGWESMYLNHAMVAGLQPETFASFLQQR  376

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
            GRWATGMMQ+L  K P  +RG+   Q+LCY NSM++W FPL R++ L+APL YLFFGIE+
Sbjct  377  GRWATGMMQLLTSKFPFAQRGMRPFQQLCYFNSMTYWLFPLFRLVLLLAPLTYLFFGIEL  436

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FV T  E LAYM  YL +S++VQN L+   R P +SE+YE+AQ PYL RA++  L RP+S
Sbjct  437  FVTTASEALAYMSSYLIISYVVQNTLYGTTRRPFLSEIYEIAQTPYLVRAVIGALARPKS  496

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
            A F VT+K ET++E+ +S + RPL+  F L LSGV     RW A PGDR +L +VG W +
Sbjct  497  ASFKVTSKTETVTESVLSDVARPLILLFALMLSGVAVLAWRWYALPGDREILQIVGFWVI  556

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
             N LL G ALRAV E +QRRA+PR  + +PA A   A   ++L AT+ D S  G RL++
Sbjct  557  ANALLTGAALRAVVEARQRRASPRCAVTIPAIAGDSATEGQNLPATITDISYGGARLVLL  616

Query  621  LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
                   H + +    ++F P            + G I + R EGG +++G+ F   Q  A
Sbjct  617  PRPDQKAHRSYKPSERLRFMPSKSFGFDAAAPINGEIANVRTEGGRLVLGMKFAEDQTGA  676

Query  681  VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPARRRR  740
               T+A ++ G+S  W  +R +    +GL+ G  R+  +A A +  T    +   A R +
Sbjct  677  GLRTIAAMLNGDSERWAAIRASRSSHVGLIRGALRMFVLAFAGIGSTVSLVLRPGAMRPK  736

Query  741  RHE----------EPKEKQAHLLAFGTDF  759
            R E           P E QA + A  T F
Sbjct  737  RVEAAESAGWVGHAPIESQAFIDADNTPF  765


>TR:A0A2R8C0P2 A0A2R8C0P2_9RHOB Cellulose synthase catalytic subunit [UDP-forming]
OS=Palleronia abyssalis OX=1501240 GN=bcsA_2 PE=4 SV=1
Length=785

 Score = 714 bits (1843),  Expect = 0.0
 Identities = 370/715 (52%), Positives = 482/715 (67%), Gaps = 26/715 (4%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            L VAL+V F   A+   + S Q L+ L AV  + +L+P+      R + L  AS++ +RY
Sbjct  20   LSVALVVFF---ASVSTSVSVQALLGLLAVAAILILRPYISSPTGRMIFLGIASIVALRY  76

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
            WFWRL  TLP      SF  A LLF +ET++I +FFL  F+ ADP  R  P P++  +LP
Sbjct  77   WFWRLLNTLPSLDDPISFAAASLLFGIETYAIGVFFLGNFIMADPVRRAPPPPVEANDLP  136
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Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            +VD+L+PSYNEP D+L++TLAAA N+ YP    T+VLCDDGGTDQRC  PDP  A+ AQ+
Sbjct  137  SVDVLIPSYNEPTDLLAITLAAACNLDYPRDKLTIVLCDDGGTDQRCSDPDPGKARAAQQ  196

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RRR+L +LCR+LGV Y TR  N  AKAGN++ AL  L GELVV+FDADH P+ DFL RTV
Sbjct  197  RRRDLFELCRKLGVTYRTRPFNRSAKAGNLNEALAHLSGELVVIFDADHAPTPDFLMRTV  256

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF ++P LFLVQTPHFF+N DP+ RNL LG   PPENEMFY ++H GLDRWGGAFFCGS
Sbjct  257  GYFSQNPRLFLVQTPHFFLNDDPVARNLGLG-AAPPENEMFYRQLHEGLDRWGGAFFCGS  315

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRRRALDE GG +G +ITEDAETAL+IH RGW+SLY++ AMIAGLQPETFASF+QQR
Sbjct  316  AAVLRRRALDEVGGISGTSITEDAETALQIHGRGWESLYVNHAMIAGLQPETFASFLQQR  375

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
            GRWATGM+Q+L+ +NP    GL + QRLCY NSM +W FP+ R++ L+APL Y+FFG+E+
Sbjct  376  GRWATGMIQLLMTRNPFTMPGLSLFQRLCYFNSMVYWLFPVFRLILLMAPLSYVFFGVEL  435

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FV +  E LAYM  YL +++LVQN LF   R P +SE+YE+AQAPYLARA++  ++ PR
Sbjct  436  FVTSASEALAYMLSYLTITYLVQNTLFGASRHPFLSEIYEIAQAPYLARAVIGAIVNPRK  495

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
            A F VT+KDET+ E+ IS ++ PL   F + ++G++    R+ AFPGDRSVL +VG W +
Sbjct  496  ADFKVTSKDETIYEDTISDVFAPLAGLFAILIAGLVVIGWRYYAFPGDRSVLELVGAWVI  555

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL-V  619
             N  L G ALRAV E +QRR APR        AQI A G+  L ++  +A  + V +  V
Sbjct  556  FNTALTGAALRAVMEVRQRRQAPR--------AQIAAAGSLVLRSSRPEAPGTPVSIRDV  607

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERM----------VRGRIRSARREGGTVMV  669
               G G       AGG    QP F D   L  +          +  R+ + R E G  ++
Sbjct  608  SYGGAGLSLKTARAGG---GQPFFLDDKVLLALAEDGAAASAPIEARVANVRVESGETIL  664

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASL  724
            G+ F+AGQ       T+A L+ G SA W   R    +  GL+ G+AR++ +A + +
Sbjct  665  GLAFDAGQAAGGLRTIARLLNGSSARWEAARARRGKHQGLVAGLARLVVLALSGI  719


>TR:A0A285CYE8 A0A285CYE8_9RHOB Cellulose synthase (UDP-forming) OS=Cereibacter
ovatus OX=439529 GN=SAMN05878503_111118 PE=4 SV=1
Length=751

 Score = 682 bits (1759),  Expect = 0.0
 Identities = 392/764 (51%), Positives = 487/764 (64%), Gaps = 27/764 (4%)

Query  1    MTVRAKARSPLRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFA  60
            MT +   R     + +LL  LW+ LLVP  LLAAAPVAP+AQGL AL AV LVA L P A
Sbjct  1    MTAQPPRRRTGPALRILLAGLWLLLLVPALLLAAAPVAPAAQGLFALLAVALVAALLPVA  60

Query  61   DKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGF  120
            D+  PR LLL+ A  + +RYWFWRLFETLP  A DA F+ AL+LF  ET +I + FL
Sbjct  61   DRTGPRLLLLATAGAVTLRYWFWRLFETLPAVAPDAGFVVALVLFLAETCAIGLLFLEAC  120

Query  121  LSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDD  180
            L   P  RP   P++PE LP VDILV S +EPADML++TLAAAKNM+YPARLRTVVL D+
Sbjct  121  LLVGPLRRPEAPPVKPETLPGVDILVTSSDEPADMLAITLAAAKNMVYPARLRTVVLYDE  180

Query  181  GGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGE  240
            GGTD RC S D   A  A+ RR  LQQ+C +LGVVY+TR  N   + G ++AAL  +  +
Sbjct  181  GGTDARCASADAGSAAAARARRAGLQQMCHDLGVVYATRPGNAGGRGGALNAALACVSRD  240

Query  241  LVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEM  300
            LV+V +  HVPSRDFLARTVG+F  DP L LVQTPHFFINPDP+QRNL LG   P  +E
Sbjct  241  LVLVLEGCHVPSRDFLARTVGHFAADPRLALVQTPHFFINPDPVQRNLGLGPGWPAASER  300

Query  301  FYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYI  360
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             +G I  GLDRWGGA FCGSA VLRRRALDE GGFA +   ED +T+L +H RGW+SLY
Sbjct  301  LFGAILPGLDRWGGAVFCGSAGVLRRRALDEIGGFAEKPGAEDLQTSLALHVRGWRSLYH  360

Query  361  DRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFP  420
            DR MIAG+QPETFA  I  RGR   G++++L   +PL  RGL ++QRL YL  +     P
Sbjct  361  DRVMIAGVQPETFAGQIAARGRRIAGLLRLLAAGHPLRHRGLCLSQRLGYLVRLGEGLRP  420

Query  421  LVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYE  480
            L+ ++FL+APL +L  G+    A FE++LA+  GYLAV  +++ ALF R   PL S V E
Sbjct  421  LLLLVFLLAPLAHLLAGVRFLSAGFEDLLAHGSGYLAVGLMLRRALFDRHAPPLASLVQE  480

Query  481  VAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLV  540
             AQAP     ++  L   R A    +                PL     LCL+GVLA +
Sbjct  481  AAQAP---SVVLAALFGDRLAGARASV---------------PLWAVTGLCLAGVLAGIA  522

Query  541  RWVAFPGD-RSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFG  599
            +  A P +  +V L +  WA  N++++   +RA  +K QRR  PRVQM+V AE   PA
Sbjct  523  QLRAAPAEAAAVPLAMTLWAGFNLVVLAAGMRAGLDKCQRRTMPRVQMQVSAEVHCPAED  582

Query  600  NRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRS  659
             R + ATVLDAST GVRLL+ LP      PA+  G  ++F+PKFPDAPQLERMV G +R+
Sbjct  583  VRPMNATVLDASTRGVRLLLPLP---PGAPAIGLGTGVRFRPKFPDAPQLERMVSGHVRA  639

Query  660  ARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWM  719
            A R GG V +GV  + GQP AVRETVA LIFG+SA W   R+AT R  GLL     ILW+
Sbjct  640  AVRMGGMVTLGVALDPGQPSAVRETVACLIFGDSAAWLRRRQATQRTKGLLREGLLILWL  699

Query  720  AAASLPKTARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEP  763
            A  +LP      +    R  R H  P ++ AH LAFG     +P
Sbjct  700  AVGALPVV---LLRATGRCGRSH--PSDRPAHPLAFGAAPCPDP  738


>TR:A0A8B2NZA1 A0A8B2NZA1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Acuticoccus sediminis OX=2184697 GN=bcsA PE=4 SV=1
Length=769

 Score = 633 bits (1633),  Expect = 0.0
 Identities = 347/777 (45%), Positives = 488/777 (63%), Gaps = 27/777 (3%)

Query  11   LRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLL  70
            +R++ +LL+ L VA+++    LA  PV+ +   + ++  ++++A+LK F  +   R ++L
Sbjct  1    MRLLTLLLWFLMVAIII---FLATQPVSLTTHFVTSMIVIIIIAILKMFDRRGALRAVVL  57

Query  71   SAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPF  130
            +  + +V+RY +WR   T+PP    A+F+  ++L+A E +S+ + F++ F  ADP +RP
Sbjct  58   ALGTAVVLRYVYWRTSSTIPPIDELANFIPGIILYAAEMYSVFMLFVSLFTIADPLNRP-  116

Query  131  PRPLQPEEL-PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMS  189
             R L P+ + PTVDI +PSYNE  ++L+ T++AA+ + YP    TV L DDGGTDQR  S
Sbjct  117  RRTLAPDSIRPTVDIFIPSYNESPELLATTISAARQIDYPEDRFTVYLLDDGGTDQRIDS  176

Query  190  PDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADH  249
            P+P+LA +A ERRR LQQLCR+LGV Y TR +N HAKAGN++  L    GE VVV DADH
Sbjct  177  PNPQLAAQAAERRRTLQQLCRDLGVNYLTRAQNVHAKAGNLNNGLAHSTGEFVVVLDADH  236

Query  250  VPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGL  309
             PSRDFL  T+GYF  DP LFLVQTPHFFINPDP++ NL   +R P ENEMFYG I +GL
Sbjct  237  APSRDFLNETIGYFAADPRLFLVQTPHFFINPDPLEHNLETWNRMPSENEMFYGVIQKGL  296

Query  310  DRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQ  369
            D+W  +FFCGSAAVLRR AL+E+GGF+G +ITEDAETAL +H+RGW S Y+DR MIAGLQ
Sbjct  297  DKWNASFFCGSAAVLRREALEESGGFSGLSITEDAETALGLHARGWNSAYVDRPMIAGLQ  356

Query  370  PETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVA  429
            PETFASFI QR RW  GM+Q+L+L NPL +RGL I QR+CYL+S+ +W FP  R+ FL +
Sbjct  357  PETFASFIGQRSRWCQGMLQILMLNNPLLKRGLSIPQRICYLSSILYWLFPFSRLAFLFS  416

Query  430  PLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLAR  489
            PL YLFFG+ IF A+  E  AY   Y+ V+ L+QN  ++R RWP +SE+YE  Q+ YL R
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Sbjct  417  PLAYLFFGLSIFDASGAEFAAYTTTYIVVNILMQNYNWSRVRWPFISELYETIQSIYLGR  476

Query  490  AIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDR  549
            A++  +L+PR+  F VT K ET   + IS +  P    F +  +G++A + R +A P D
Sbjct  477  ALIAVILKPRAPSFKVTTKGETTRFSRISELGGPFYVIFFILTAGLVAMVWRLIAVPSDS  536

Query  550  SVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLD  609
             V LVVGGW + N+LL+G AL  VAE++Q R++ RV +E PAE     +G+R + A + D
Sbjct  537  GVSLVVGGWNLFNMLLMGAALGVVAERRQLRSSQRVSIERPAEI---IYGDRVIPARIDD  593

Query  610  ASTSGVRLLVRLPGVGDPHPALEAGGLI--QFQPKFPDAPQLERMVRGRIRSARREGGTV  667
             S +G R+LV    +     ++ AG  I  +FQ     AP     +   +RS  R+ G +
Sbjct  594  VSVNGARILVPANAL----RSIRAGEQITMRFQTM---APLPTNELPLTVRSVVRDDGGM  646

Query  668  MVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKT  727
             +G  F    P   +  VA L+F  S  W   + +  + IG++ G+   + +A     +
Sbjct  647  SLGSEFAVEDPRQYK-LVADLVFANSDEWIRFQASRRKNIGVVRGVIAFVRVALFQTVRG  705

Query  728  ARDFMDEPARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARPNTVA  784
                  +P +  RR           L  G+D    P       DP+A VS   +T A
Sbjct  706  LSYLFRKPPKNARRQN---------LDGGSDMPAPPPHNFSGADPSAVVSGTGSTAA  753


>TR:A0A934IJL6 A0A934IJL6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Acuticoccus mangrovi OX=2796142 GN=bcsA PE=4 SV=1
Length=777

 Score = 628 bits (1620),  Expect = 0.0
 Identities = 344/769 (45%), Positives = 471/769 (61%), Gaps = 13/769 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+FLLW+A       L   PV+ +   + ++  V+++A+LK F  K + R ++L+  + +
Sbjct  4    LVFLLWLATTAVVIFLVTQPVSLNTHFITSMVIVIIIAVLKMFDRKGMLRAIVLALGTAV  63

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR F T+PP     +F+  +LL+A E +S+ + FL+ F  ADP +RP  + L+P
Sbjct  64   VLRYVYWRTFTTIPPVEELQNFIPGILLYAAEMYSVLMLFLSMFAIADPLNRP-KKTLKP  122

Query  137  EE-LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            +   PTVDI VP++NE A +L+ TL+AAK + YP+    V L DDGGTDQRC S DP  A
Sbjct  123  DSPKPTVDIFVPTFNEDAQLLATTLSAAKQIDYPSDRMNVFLLDDGGTDQRCESADPRAA  182

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              AQERRRELQQL R+LGV Y TR  N +AKAGN++  L    GE VVVFDADH PSRDF
Sbjct  183  AAAQERRRELQQLARDLGVNYLTRSANINAKAGNLNNGLAHSTGEFVVVFDADHAPSRDF  242

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  T+GYF +DP LFLVQTPHFFINPDP++ NL   +R P ENEMFYG + +GLD+W
Sbjct  243  LQETIGYFYDDPQLFLVQTPHFFINPDPLEHNLETWNRMPSENEMFYGVMQKGLDKWNAT  302

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL+E  GFAG +ITED ET+L +H++GW S Y+DR MIAGLQPETFA+
Sbjct  303  FFCGSAAVLRRSALEEVSGFAGTSITEDCETSLGLHAQGWNSAYVDRPMIAGLQPETFAN  362

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GM Q+LLLKNPLF+ GL +AQR+CYL+SM +W FP  R+ FL +PL YLF
Sbjct  363  FIGQRSRWAQGMTQILLLKNPLFKGGLSLAQRICYLSSMFYWLFPFARLTFLFSPLFYLF  422

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+ IF A+  E  AY   Y+ V+ L+QN +++R RWP +SE+YE  Q+ YL RA+   +
Sbjct  423  FGLSIFDASGAEFAAYTITYILVNILLQNYIWSRVRWPFISELYETIQSVYLIRALGAVV  482

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P+   F VT K ET   + IS +  P    F +  +GV+AT+ R V  P    + +VV
Sbjct  483  LNPKRPSFKVTTKGETNRRSRISELGGPFYVIFFILAAGVVATIYRLVFQPFAADIAMVV  542

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW + N+LL+G AL  VAE++Q R + RV ++ PAE     +G+R + A + D S +G
Sbjct  543  GGWNLFNILLMGAALGVVAERRQLRTSQRVSIDRPAEI---IYGDRVIPAKIDDVSITGA  599
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Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            R+LV    +    P  +   +++FQP    AP     +   +RS  R+ G   +G  F
Sbjct  600  RILVPGNVLRQIKPGEQI--IMRFQPM---APLASNELPLTVRSVVRDEGGAALGSEFTV  654

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEP  735
              P    E VA L+F  S  W   + +  + IG   G+   + +A   + +
Sbjct  655  VDP-RQYELVADLVFANSDEWVRFQASRRKDIGAFRGIVEFISLAVFQMVRGLSYLFTTA  713

Query  736  ARRRRRHEEPKEKQAHLLAFGTDFSTEPDWAGELLDPTAQVSARPNTVA  784
            A R +R  +        +      S  P + G   DP A V++     A
Sbjct  714  APRGQRGGDAPAASPASVPQAQAQSRRPAFVG--ADPNAVVTSGAGATA  760


>TR:A0ABU0F8I6 A0ABU0F8I6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Labrys monachus OX=217067 GN=J3R73_000469 PE=4 SV=1
Length=732

 Score = 608 bits (1569),  Expect = 0.0
 Identities = 334/719 (46%), Positives = 451/719 (63%), Gaps = 24/719 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L  LLW    +   ++   P++     +   + V+ +ALLK F    V R + L+  + +
Sbjct  5    LAVLLWACASLLVFVVVTLPISQQTHLIAGTAVVIAMALLKAFKPTGVWRLIALALGTSI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPT-DRPFPRPLQ  135
            V+RY +WR   TLPP     +F+F LL++  E + + +  L+ F+ A P   R  PR L
Sbjct  65   VLRYVYWRTTSTLPPINQPENFVFGLLVYLAEMYCVGMLALSLFVVATPLPSRRAPR-LA  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             +ELPTVD+ VPSYNEP DML+ TLAAA+ + YPA    V L DDG TDQ+      ELA
Sbjct  124  DDELPTVDVFVPSYNEPPDMLARTLAAARGIDYPADKINVFLLDDGSTDQKRSDERIELA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +A+ R  +LQ LC +LGV Y TR RNEHAKAGN++  L    GE+VVVFDADH P+RDF
Sbjct  184  AEAERRHADLQDLCAKLGVHYLTRARNEHAKAGNLNNGLAHSTGEIVVVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  T+G+F ++P LF+VQTPHFF+NPDP++RNL    + P ENEMFYG I RGLD+W  +
Sbjct  244  LHSTIGFFRDEPLLFMVQTPHFFLNPDPVERNLRTFLKMPSENEMFYGIIQRGLDKWNAS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA LRR AL E  GF G +ITED ETA+E+HSRGW S+YID+ +IAGLQP TFAS
Sbjct  304  FFCGSAAALRRSALAETDGFKGRSITEDCETAMELHSRGWHSIYIDKPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+LL + P  +RGL I QRLCY++S+ FWFFPL R+MFL+APL YLF
Sbjct  364  FIVQRSRWAQGMMQILLFQRPFMKRGLSIPQRLCYMSSIMFWFFPLARIMFLIAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IFVA+  E L+Y   Y+ V+ ++QN L+   RWP VSE+YE AQ+ YL  A+V+ L
Sbjct  424  FDLQIFVASGAEFLSYTLSYMFVNLMMQNYLYGSYRWPWVSELYEYAQSLYLLPALVSVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VTAKDE++  + +S I  PL   F++ L G++ T+++ +A PG   V LVV
Sbjct  484  LHPSKPTFRVTAKDESVQTSRLSEIAWPLFAFFVVLLFGIVMTVLKLIAEPGKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W +LNVLL G AL  VAE+ + +++ RV +E   E  +   G+R L AT+ + S +G
Sbjct  544  GMWNLLNVLLAGCALGVVAERGEAQSSQRVSVERRCELLV---GDRILPATIQNVSANGA  600

Query  616  RLLVRLPGVGDPHPALEAGGLI---QFQPKFPDAPQLE--RMVRGRIRSARREGGTVMVG  670
               +RLPG         A G+I   Q   +F     LE   ++   +R      GT  +G
Sbjct  601  --AIRLPG--------SAEGIIKDGQISIRFATLTPLEGDPLLPSHVRRVAMHQGTTTIG  650

Query  671  VIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            V F   +P+  R  VA L++  S  W   ++A     GLL G    +W  A ++ +T R
Sbjct  651  VRFLTTEPMHYR-LVADLLYANSDRWTAFQKARRYNPGLLRG---TIWFYALAIRQTVR  705
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>TR:A0ABT0DB64 A0ABT0DB64_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter crimeensis OX=2579147 GN=bcsA PE=4 SV=1
Length=730

 Score = 608 bits (1568),  Expect = 0.0
 Identities = 340/690 (49%), Positives = 437/690 (63%), Gaps = 11/690 (2%)

Query  32   LAAAPVAPSAQGLIALSAVVLVA-LLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLP  90
            L   P++  A  LIA S VVLV  LLK FA   VPR + LS  S +V+RY +WR   TLP
Sbjct  20   LITLPISLQAH-LIAGSIVVLVIILLKLFAPVGVPRLIALSLGSTIVLRYIYWRTTSTLP  78

Query  91   PPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYN  150
            P +    F+  ++L+  E +S+ +  L+ F+ + P        L PE+LPTVD+ VP+YN
Sbjct  79   PISQIEDFIPGIMLYLAELYSVGMLCLSLFVVSSPAPPRTAPALTPEQLPTVDVFVPTYN  138

Query  151  EPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCR  210
            E A +L+ TLAAAK M YPA   TV L DDGGTDQ+C   DP  AQ+AQ RRREL +LC
Sbjct  139  EDASLLASTLAAAKAMDYPADKFTVWLLDDGGTDQKCHQDDPLGAQEAQNRRRELGELCE  198

Query  211  ELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLF  270
             LGV Y TR RNEHAKAGN++  L    GELV VFDADH P+R FL  TVGYF +D  LF
Sbjct  199  GLGVRYLTRRRNEHAKAGNLNNGLANSTGELVAVFDADHAPARSFLHETVGYFRQDERLF  258

Query  271  LVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALD  330
            LVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W GAFFCGSAA+LRR AL
Sbjct  259  LVQTPHFFINPDPLERNLDTFDHMPSENEMFYGIIQRGLDKWDGAFFCGSAALLRREALA  318

Query  331  EAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQM  390
            E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQPETFASFI QR RWA GM Q+
Sbjct  319  ETNGFSGISITEDCETALELHSRGWHSVYVDKPLIAGLQPETFASFIGQRSRWAQGMYQI  378

Query  391  LLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLA  450
            L  + P  +RG+  AQRLCY++SM FWFFP+ RM+FL++PL YL FG+EIF A+  E LA
Sbjct  379  LRFRFPPLKRGITFAQRLCYMSSMLFWFFPISRMIFLISPLFYLVFGLEIFNASGAEFLA  438

Query  451  YMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDE  510
            Y   Y+ V+ L+QN L+ R RWP +SE+YE  Q+ YL  A+++ ++ PR   F VTAK E
Sbjct  439  YTSTYMLVNLLMQNYLYGRYRWPWISELYEYIQSVYLLPALLSVMMNPRKPTFKVTAKGE  498

Query  511  TLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFAL  570
            TL+E+++S I +P    F L      + T+ R +  P    V  VVGGW +LN+++ G AL
Sbjct  499  TLTESHVSEIGKPFFILFGLMTLAAVLTVWRVINDPFTADVTAVVGGWNILNMIIAGCAL  558

Query  571  RAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPA  630
              V+E+Q RR   RV +    E       + S  A V D S  G    VR  G   P
Sbjct  559  GVVSERQNRRRTHRVNLFRRCEF---ILDDVSYPAVVEDVSIGGAS--VRAAGANLPQVE  613

Query  631  LEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIF  690
                  I+F+P+  D    +  V  +IR+ +R+G   + G  FEA  P+  R  +A L+F
Sbjct  614  RGKMAAIRFKPQ-ADIEVSDLPV--QIRNMKRDGNGQLFGCQFEAQVPLHHR-LIADLMF  669

Query  691  GESAHWRTMREATMRPIGLLHGMARILWMA  720
              +A W   +E+     G+L G  R L +A
Sbjct  670  ANAAEWSKFQESRRYNPGVLRGTFRFLVIA  699


>TR:A0ABQ1IAD8 A0ABQ1IAD8_9PROT Cellulose synthase catalytic subunit [UDP-forming]
OS=Tistrella bauzanensis OX=657419 GN=celA PE=4 SV=1
Length=777

 Score = 602 bits (1553),  Expect = 0.0
 Identities = 328/717 (46%), Positives = 446/717 (62%), Gaps = 13/717 (2%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLK---PFADKMVPRFL  68
            R+  + L +LW   +V     AA PV+  AQ ++ +  +V +ALLK      +  + R +
Sbjct  4    RLGRLALIILWCVSVVALLAAAAQPVSLPAQIVLMVVLLVAMALLKGRRSHEEGSIRRTI  63

Query  69   LLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDR  128
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            L+   + +V RY  WR   TLPP     +F+  ++L+  E ++I +FF+N F+  DP  R
Sbjct  64   LVMIGAFVVARYLAWRTLSTLPPTDDLLAFIPGIILYGAEIYAIVMFFVNNFVVIDPVTR  123

Query  129  PFPR-PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRC  187
              P  P   E+LP++D+ VPSYNE   ++  TL  A+ M YPA   TV L DDGGTD +
Sbjct  124  KSPPLPEAAEDLPSIDVFVPSYNEDDALIETTLIGARRMWYPAERVTVYLLDDGGTDAKR  183

Query  188  MSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDA  247
             S DP+ A +A+ER   LQ +C  LGV Y TRE N HAKAGN++AAL   +G+L+ VFDA
Sbjct  184  HSADPQEAMRARERHERLQAMCSRLGVRYLTRENNAHAKAGNLNAALRHSQGDLIAVFDA  243

Query  248  DHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHR  307
            DHVP+RDFL  T G+F++DP LFLVQTPHFF++PDP++RNL   +R P ENEMFYG I R
Sbjct  244  DHVPTRDFLMATAGFFLKDPKLFLVQTPHFFLSPDPLERNLGTFERMPSENEMFYGMIQR  303

Query  308  GLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAG  367
            GLDRW  AFFCGSAA+LRR  L+E GGF+G ++TEDAETAL++H+RG+ S+Y  + +IAG
Sbjct  304  GLDRWNAAFFCGSAALLRRACLEEIGGFSGSSVTEDAETALDLHARGYNSVYFGKPLIAG  363

Query  368  LQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFL  427
            LQPE+FA+FI QR RWA GM Q+ ++KNPL +RGL + QRL YL S  FW FP  R+MFL
Sbjct  364  LQPESFAAFIGQRSRWAQGMTQIFIMKNPLIKRGLTLGQRLSYLASSMFWLFPFSRLMFL  423

Query  428  VAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYL  487
            +APL YL+FG+EI+ AT  E  AY   YLA S ++QNAL  R RWPL+SE+YE++Q+ +
Sbjct  424  IAPLFYLYFGLEIYRATAAEFAAYTLTYLAASLVIQNALNGRFRWPLISELYELSQSLHT  483

Query  488  ARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPG  547
            + AIVTT++ PR   F VTAK  TL+ +++SP+ RPLL    L L GV AT+ R+V  P
Sbjct  484  SVAIVTTIVNPRKPTFKVTAKGATLTHDHVSPLARPLLVVIGLLLLGVAATIWRYVMEPS  543

Query  548  DRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV  607
             R V+LVVG W + N+LL   AL  V E  Q R+APR  +  PA  +I           +
Sbjct  544  TRDVVLVVGFWNLFNMLLALAALGVVCEHAQHRSAPRAVVRRPARIRIDGV---IYDGAL  600

Query  608  LDASTSGVRLLVRLPGVGDPHPALEAGGLI---QFQPKFPDAPQLERMVRGRIRSAR-RE  663
            LD S  G RL +    V     +     L+      P  P A +  R V   +R  R  +
Sbjct  601  LDVSQGGARLALPAKLVPGGRVSGRVAHLLVDDLIAPTHPSAAE-ARAVPVEMRYGRPDD  659

Query  664  GGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             G + +G+ F A      +E V  L++G SA W  +     R  G+L G+   L ++
Sbjct  660  DGNIQIGLRF-AATTETEKEAVVDLVYGSSALWSELLARRHRRPGILRGLTHFLGLS  715


>TR:A0ABU9YIC2 A0ABU9YIC2_9PROT Cellulose synthase catalytic subunit [UDP-forming]
OS=Tistrella arctica OX=3133430 GN=bcsA PE=4 SV=1
Length=776

 Score = 601 bits (1550),  Expect = 0.0
 Identities = 328/717 (46%), Positives = 445/717 (62%), Gaps = 13/717 (2%)

Query  12   RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLK---PFADKMVPRFL  68
            R+  + L +LW   +V     AA PV+  AQ ++    +V + LLK      D  + R +
Sbjct  5    RLGRLALIILWCVSVVALLAAAAQPVSLPAQIVLMAMLLVAMTLLKGRRSHEDGSIRRTI  64

Query  69   LLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDR  128
            L+   + +V RY  WR   TLPP     +F+  ++L+  E ++I +FF+N F+  DP  R
Sbjct  65   LVMIGAFVVARYLAWRTLSTLPPTDDLLAFIPGIVLYGAEIYAIVMFFVNNFVVIDPVTR  124

Query  129  PFPR-PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRC  187
              P  P   E+LP++D+ VPSYNE   ++  TL  A+ M YPA   TV L DDGGTD +
Sbjct  125  KSPPLPEAAEDLPSIDVFVPSYNEDDALIETTLIGARRMWYPAERVTVYLLDDGGTDAKR  184

Query  188  MSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDA  247
             S DP+ A +A+ER   LQ +C  LGV Y TRE N HAKAGN++AAL   +G+L+ VFDA
Sbjct  185  HSADPQEAMRARERHERLQAMCSRLGVRYLTRENNAHAKAGNLNAALRHSQGDLIAVFDA  244

Query  248  DHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHR  307
            DHVP+RDFL  T G+F++DP LFLVQTPHFF++PDP++RNL   +R P ENEMFYG I R
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Sbjct  245  DHVPTRDFLMATAGFFLKDPKLFLVQTPHFFLSPDPLERNLGTFERMPSENEMFYGMIQR  304

Query  308  GLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAG  367
            GLDRW  AFFCGSAA+LRR  L+E GGF+G ++TEDAETAL++H+RG+ S+Y  + +IAG
Sbjct  305  GLDRWNAAFFCGSAALLRRACLEEIGGFSGSSVTEDAETALDLHARGYNSVYYGKPLIAG  364

Query  368  LQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFL  427
            LQPE+FA+FI QR RWA GM Q+ ++KNPL +RGL + QRL YL S  FW FP  R+MFL
Sbjct  365  LQPESFAAFIGQRSRWAQGMTQIFIMKNPLIKRGLKLGQRLSYLASSMFWLFPFSRLMFL  424

Query  428  VAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYL  487
            +APL YL+FG+EI+ AT  E +AY   YLA S ++QNAL  R RWPL+SE+YE++Q+ +
Sbjct  425  IAPLFYLYFGLEIYRATAAEFVAYTLTYLAASLVIQNALNGRFRWPLISELYELSQSLHT  484

Query  488  ARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPG  547
            + AIVTT++ PR   F VTAK  TL+ +++SP+ RPLL    L L GV AT+ R+V  P
Sbjct  485  SVAIVTTIVNPRKPTFKVTAKGATLAHDHVSPLARPLLVVVGLLLLGVAATVWRYVMEPS  544

Query  548  DRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV  607
             R V+LVVG W + N+LL   AL  V E  Q R+APR  +  PA  +I          +
Sbjct  545  TRDVVLVVGFWNLFNMLLALAALGVVCEHAQHRSAPRAVVRRPARIRIDGV---IYDGAL  601

Query  608  LDASTSGVRLLVRLPGVGDPHPALEAGGLI---QFQPKFPDAPQLERMVRGRIRSAR-RE  663
            LD S  G RL +    V     +     L+      P  P A +  R V   +R  R  +
Sbjct  602  LDVSQGGARLALPAKLVPGGRVSGRVAHLLVDDLIAPTHPSAAE-ARAVPVEMRYGRPDD  660

Query  664  GGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             G + +G+ F A      +E V  L++G SA W  +     R  G+L G+   L ++
Sbjct  661  DGNIQIGLRF-AATTETEKEAVVDLVYGSSALWSELLARRHRRPGILRGLTHFLGLS  716


>TR:I3TJI5 I3TJI5_TISMK Cellulose synthase catalytic subunit [UDP-forming]
OS=Tistrella mobilis (strain KA081020-065) OX=1110502 GN=bcsA
PE=4 SV=1
Length=778

 Score = 601 bits (1549),  Expect = 0.0
 Identities = 335/715 (47%), Positives = 442/715 (62%), Gaps = 17/715 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLK---PFADKMVPRFLLLSAAS  74
            L L+WV  LV     AA PV+  AQ ++ +  +  +A+LK      D  V R +L+
Sbjct  11   LGLIWVLALVALLAAAAQPVSLPAQIVLMILLLAAMAVLKGTRAHEDASVRRTMLVMIGG  70

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR-P  133
             +V RY  WR   TLPP     +F+  L+L+A E ++I +FF+N F+  DP  R  P  P
Sbjct  71   FIVARYLCWRTLSTLPPLDDPFAFVPGLVLYAAEVYAIVMFFVNNFVVIDPVTRMSPPLP  130

Query  134  LQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPE  193
              P ELPTVD+ VPS+NE   ++  TL  AK M YPA    V L DDG TD + MS DP+
Sbjct  131  EDPAELPTVDVFVPSFNEDDGLIETTLIGAKRMWYPADRLNVYLLDDGSTDMKRMSADPQ  190

Query  194  LAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSR  253
              A KA+ER   L+ +C  LGV Y TRE N HAKAGN++AAL    G+L+ VFDADHVP+R
Sbjct  191  EALKARERHERLKVMCARLGVHYLTRETNAHAKAGNLNAALPETHGDLIAVFDADHVPTR  250

Query  254  DFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWG  313
            DFL  TVG+F +DP LFLVQTPHFF++PDP++RNL   +R P ENEMFYG I RGLDRW
Sbjct  251  DFLLATVGFFRKDPKLFLVQTPHFFLSPDPLERNLKTFERMPSENEMFYGMIQRGLDRWN  310

Query  314  GAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETF  373
            GAFFCGSAA+LRR  L+E GGF+G +ITEDAETAL++H+RG+ S+Y  + +IAGLQPE++
Sbjct  311  GAFFCGSAALLRRACLEEVGGFSGLSITEDAETALDLHARGYNSVYYGKPLIAGLQPESY  370

Query  374  ASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIY  433
            A+FI QR RWA GM Q+ ++KNPL +RGL + QRLCYL S  FW FP  R+MFL+APL Y
Sbjct  371  AAFIGQRSRWAQGMTQIFMMKNPLIKRGLRLPQRLCYLASSMFWLFPFSRLMFLIAPLFY  430

Query  434  LFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVT  493
            LFFG+EI+ AT  E   Y   YL  S ++QNAL  R RWPL+SE+YE++Q+ + + AIV
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Sbjct  431  LFFGLEIYRATAAEFAGYTLTYLVASLMIQNALNGRFRWPLISELYELSQSLHTSVAIVK  490

Query  494  TLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLL  553
            T++ PR   F VTAK ETL+ +++SP+ +PL+    L + G+ A L RW   P  R VLL
Sbjct  491  TMIDPRKPVFRVTAKGETLAHDHVSPLAKPLVGVVGLLILGMGAALWRWWMEPATRDVLL  550

Query  554  VVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTS  613
            VV  W   N+LL   AL  V E  Q RAAPRV ++ PA   I           +LD S
Sbjct  551  VVTFWNTFNLLLASAALGVVCEHAQHRAAPRVMVKRPARILI---DGTLYEGALLDLSQG  607

Query  614  GVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQ-----LERMVRGRIRSAR-REGGTV  667
            G RL +  P    P   L AG   +       AP        R V   +R  R  + G +
Sbjct  608  GARLAI--PARQAPKGRL-AGRFAELLVDELTAPAHLATGEARPVPVEMRYGRPDDAGNI  664

Query  668  MVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAA  722
             +G+ F   +  A +E +  L++G SA W  +     R  G++ G+A  + ++AA
Sbjct  665  QIGLRF-MPETDAAKEAIVDLVYGSSALWAELLSRRHRRPGVVRGVAHFIRLSAA  718


>TR:A0ABX0VEN0 A0ABX0VEN0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga terricola OX=2719797 GN=bcsA PE=4 SV=1
Length=732

 Score = 599 bits (1545),  Expect = 0.0
 Identities = 326/715 (46%), Positives = 442/715 (62%), Gaps = 16/715 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W        LL A P++  A  +  L  V  + +LK F  + + R + L+  + +
Sbjct  5    LIVAFWAVAAAIIVLLVALPISLQAHLIAGLVVVASMVVLKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   TLPP    A+++ A LL+A E +S+ + FL+ F+ ++P     P  +
Sbjct  65   VLRYVFWRTTSTLPPITELANYIPAFLLYAAEMYSVMMLFLSLFVVSNPLGSRKPPQVDY  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
              LPTVD+ VPSYNE A +L+ TLAAAK M YPA   TV L DDGGTDQ+C   D  LA+
Sbjct  125  SHLPTVDVFVPSYNESASLLASTLAAAKAMSYPADKVTVWLLDDGGTDQKCEQHDAILAR  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  L V Y TR+RNEHAKAGN++ ALE   G+LV VFDADH P+R+FL
Sbjct  185  EARERRAELQALCAALDVKYLTRKRNEHAKAGNLNNALENSTGDLVAVFDADHAPARNFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF    DLFLVQTPHFFINPDP++RNL       P ENEMFYG I RGLD+W  AF
Sbjct  245  EETVGYFNTQKDLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGWKS+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGLSITEDCETALELHSRGWKSIYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GM+Q++  + PLF+RGL + QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMIQIMRYRFPLFKRGLSLPQRLCYMSSALFWLFPFTRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF+A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFIASGGEFLAYTTTYMIVNFMMQNYLYGRFRWPWISDLYEFIQMVYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VT+K+ET+  N +S +  P    F + + GV+AT+VR  A P    V LV G
Sbjct  485  NPSKPTFKVTSKNETMDRNRVSELGAPYFIIFGILVLGVIATIVRVWAEPYKADVTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W ++N+++ G AL  V+E+  RR + RV  E P            + A + D S  G+
Sbjct  545  AWNLVNLIIAGCALGVVSERATRRHSHRVVAERPCRF---LMDGEFVHAMIRDVSVGGIS  601

Query  617  LLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            LL+    +    P L+ G  G ++F+P + D P  +  +  R  S   +G  V++G  F
Sbjct  602  LLLSESAL----PGLKRGALGTLEFKP-YSDLPTNQLPMEVRKMSMDDKG--VLIGCRFL  654
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Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
               P   R  +A L+F  +  W   ++   + IG+L G    LW    ++ +T R
Sbjct  655  TETPDHHR-LIADLVFANAEQWSHFQKRRHQDIGILRG---TLWFLTVAIYQTGR  705


>TR:A0ABW9YW44 A0ABW9YW44_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga arsenatis OX=2692265 GN=bcsA PE=4 SV=1
Length=731

 Score = 599 bits (1544),  Expect = 0.0
 Identities = 324/713 (45%), Positives = 440/713 (62%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W    +    L A P++  A  +  L+ V  + +LK F  + V R + L+  + +
Sbjct  5    LIVAFWAVAAILIVSLVALPISLQAHLVAGLTVVACMIILKFFRARGVWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP    A+F+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEVANFIPGFLLYLAEMYSVMMLFLSLFVVSSPLGSRKAPQVDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
              LPTVD+ VPSYNE A++L+ TLAAAK M YPA   TV L DDGGTD++C S +P  AQ
Sbjct  125  HNLPTVDVFVPSYNESAELLATTLAAAKAMTYPADRLTVWLLDDGGTDEKCNSLNPITAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R+FL
Sbjct  185  QARERRAELQALCASLEVRYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARNFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            A TVGYF+ D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  AETVGYFITDKNLFLVQTPHFFINPDPLERNLGTFHTMPSENEMFYGVIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGISITEDCETALELHSRGWTSVYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P  +RGL ++QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPLKRGLKLSQRLCYMSSTLFWLFPFSRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN LF R RWP +S++YE  Q  YL  AI++ +
Sbjct  425  SLEIFTASGGEFLAYTFTYMMVNFMMQNYLFGRYRWPWISDLYEYIQTLYLLPAILSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VT+K+ET+ ++ +S + +P    F + + GV+AT VR  A P    + LV G
Sbjct  485  NPSKPTFRVTSKNETMDQSRVSELGKPYFIIFGILVLGVIATGVRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN+++ G AL  V+E+  RR + RV++E P + ++   G+  + A + D S  G R
Sbjct  545  AWNILNLIIAGCALGVVSERATRRQSHRVRVERPCQFRV---GDEVVEAVLRDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            L   +P   +P     A G + FQP F + P     V   IR    +   +++G  F
Sbjct  602  L--HVPPSAEPGLKKGAAGTLSFQP-FANLPIQHLPV--EIRKVGMDDEGLLLGCRFMIE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             P   R+ +A L+F  +  W   +      IG+L G    +W    +  +T R
Sbjct  657  NP-EHRKMIADLVFANADQWSEFQRNRHYDIGVLRG---TIWFFMVAFYQTGR  705


>TR:A0AAE3VR52 A0AAE3VR52_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Amorphus orientalis OX=649198 GN=J2S73_003691 PE=4
SV=1
Length=771

 Score = 598 bits (1543),  Expect = 0.0
 Identities = 320/706 (45%), Positives = 437/706 (62%), Gaps = 11/706 (2%)
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Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            +L+ + W    +    L   PV  +   + A+    L+A+ K F  +   R ++L+  +
Sbjct  4    ILIVVAWAVAALVVIFLVTQPVDINTHFITAMLVAALIAIFKNFKREGALRLIVLALGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   T+PP A    F+  ++L+  E +S+ +  L+ F  ADP DRP    L
Sbjct  64   IVLRYVYWRTTSTIPPVAQLEDFIPGIILYVAEMYSVFMLCLSLFAVADPLDRPKAPVLP  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             E+ PT+D+ VP+YNE  ++L+ TLAAA  M YP     V L DDGGTDQ+C   DPE A
Sbjct  124  DEDQPTIDVFVPTYNEEPELLATTLAAALQMDYPKEKFIVYLLDDGGTDQKCEDDDPEKA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +AQ RRRELQQL R+LG  Y TR +N HAKAGN++  L    GEL+VVFDADH P+RDF
Sbjct  184  AEAQARRRELQQLARDLGARYLTRAKNLHAKAGNLNNGLAHSHGELIVVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L +TVG F +D  LFLVQTPHFFINPDP++RNL   DR P ENEMFYG I RG D+W G+
Sbjct  244  LKQTVGLFRQDKKLFLVQTPHFFINPDPLERNLETWDRMPSENEMFYGMIQRGFDKWDGS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL+EAGGF+G +ITEDAE+ALE+HSRGW S Y+DR MIAGLQPETFAS
Sbjct  304  FFCGSAAVLRRAALEEAGGFSGVSITEDAESALELHSRGWHSAYVDRPMIAGLQPETFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GM+Q++LLK P  + GL I QRLCYL +  FW FP  R+ FL APL YLF
Sbjct  364  FIGQRSRWAQGMLQIILLKRPFLKSGLKIQQRLCYLAASMFWIFPFARLTFLFAPLAYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IF A+  E  AY   Y+ ++ L+QN L++  RWP +SE+YE  Q+ YL RA+   L
Sbjct  424  FSLQIFNASGAEFAAYTMTYMLINILLQNYLYSNVRWPFISELYETIQSVYLIRALGGVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VTAK E  +++ IS +  P    F + +  +L T+ R    P    + +VV
Sbjct  484  LNPTKPTFKVTAKGEATTKSRISELGWPFYIIFFILVFALLVTIWRVWTQPYISDIAIVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW V N++++G AL  V+E++  R + RV +E  AE  +   G+  + A + D S +G
Sbjct  544  GGWNVFNLIIMGAALGVVSERRNLRQSQRVTIERKAEILV---GDEVVPAKIDDVSVTGT  600

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQL-ERMVRGRIRSARREGGTVMVGVIFE  674
            R+LV    + +    L+ G  +    +F    QL    +  ++ S  R+ G   +G  F
Sbjct  601  RILVPSNALRN----LKRGQEVNM--RFETRSQLASNTLPLKVMSIMRDEGGQALGCRFV  654

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              +P+  R  VA L+F +S  W   +++  + IG+L G+     MA
Sbjct  655  TEEPLHFR-LVADLVFADSDEWVRFQQSRRKDIGVLRGIIEFFVMA  699


>TR:A0A1M7ZQE2 A0A1M7ZQE2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudoxanthobacter soli DSM 19599 OX=1123029 GN=SAMN02745172_03799
PE=4 SV=1
Length=722

 Score = 598 bits (1543),  Expect = 0.0
 Identities = 315/702 (45%), Positives = 444/702 (63%), Gaps = 9/702 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            L W    V    L   P++  A  ++ +  V+++  +K F    + R + L+  + +++R
Sbjct  8    LAWGLTTVVVLFLITQPISLQAHLIVGIIVVLVLTAIKWFPSVGLRRQVFLALGTTIILR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   T+PP     +F+  ++L+  E +S+ +  L+ F  ADPT R    P  PE
Sbjct  68   YVYWRSTSTIPPINQPENFIPGVILYIFEMYSVLMLALSLFTVADPTARKPAPPPAPETA  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VDI +P+YNE   +L+ T+AAA  + YP     V L DDGGTDQ+C S +   A +AQ
Sbjct  128  PSVDIFIPTYNEDEILLATTVAAAVALDYPKDRLKVYLLDDGGTDQKCNSSNAAAALEAQ  187
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Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +RR  LQ++C +LG  Y TR RNEHAKAGN++AALE+  G+LV VFDADH P+RDFL  T
Sbjct  188  QRRVALQKMCADLGATYLTRARNEHAKAGNLNAALEKTNGDLVAVFDADHCPTRDFLQNT  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VG+FV DP LFLVQTPHFFINPDP++ NL   +R P ENE FYG + RGLDRW  +FFCG
Sbjct  248  VGFFVADPKLFLVQTPHFFINPDPLEHNLNTFERMPSENEQFYGMVQRGLDRWDASFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAA+LRR+AL    GF+G +ITED ETALE+H++GW S+Y+++ MIAGLQPETFA+FI Q
Sbjct  308  SAALLRRQALKITNGFSGVSITEDCETALELHAQGWHSVYLEKPMIAGLQPETFANFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GM+Q+L+LKNP+ R GL +AQRLCY+ +  FW FP+ R++FL++PL+YLFFG++
Sbjct  368  RSRWAQGMLQILILKNPIGRPGLTLAQRLCYMTNPLFWLFPIGRLVFLISPLLYLFFGLQ  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF ++  E  AY   Y+ V+ ++QN L+ + RWP +SE+YE  Q+ YL RAIV  +L PR
Sbjct  428  IFSSSGGEFFAYTFTYMIVNMMIQNYLYGKYRWPWISELYEYIQSIYLFRAIVAVVLNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VT+K +TL EN +S +  P    F + L GV AT+ R  + P    + +VVGGW
Sbjct  488  KPTFKVTSKGDTLDENQVSELAAPYFIMFAILLVGVGATVWRMYSQPYLSDITMVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            V N+L+   A+  VAE++  R APRV+M    E +   F  + + A + D S  GVRL
Sbjct  548  VFNLLMAAAAIGVVAERRNLRRAPRVEMSRTGELE---FDGQVVPAMIEDGSMGGVRLRP  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
             +P   D  P   +  +++F+ K         MV   +R+  R+G  V  G      +P+
Sbjct  605  LIP--MDREPERMSKVVLRFETKSDIPNDGLPMV---VRNVARDGEGVHFGCQPTREKPV  659

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
             V+  +A L+FG+S  W   ++   R IG+LHG    L +AA
Sbjct  660  HVK-LIADLVFGDSTQWSNFQQRRRRTIGVLHGTLFYLHLAA  700


>TR:A0ABW4YSG6 A0ABW4YSG6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter oerskovii OX=459519 GN=bcsA PE=4 SV=1
Length=734

 Score = 598 bits (1542),  Expect = 0.0
 Identities = 329/728 (45%), Positives = 446/728 (61%), Gaps = 12/728 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVM  78
            +LW+   +    L   P++  A  ++    V+ + LLK F     V R + L+  + +V+
Sbjct  8    VLWMLASLVVIFLITLPISLQAHLIVGSIVVLAMILLKTFGPPTGVFRVIALALGTAIVL  67

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY +WR   TLPP      F+   +L+  E +S+ + FL+ F+ + P   P P P  P E
Sbjct  68   RYVYWRTTSTLPPVNQIEDFIPGFMLYVAEMYSVFMLFLSLFVVSSPVP-PRPTPPLPAE  126

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            +PTVD+ +P+YNE   +L+ T+AAAK M YPA   TV L DDGGT+Q+C   +   A++A
Sbjct  127  VPTVDVFIPTYNEDYALLANTVAAAKGMDYPADKLTVWLLDDGGTEQKCNQDNAAKAKEA  186

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            QERRREL  LC  LG  Y TR RNEHAKAGNM+  LE   G++VVVFDADH P+R FL
Sbjct  187  QERRRELSALCEGLGARYLTRARNEHAKAGNMNNGLEHSTGDIVVVFDADHAPARSFLQE  246

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            T+G+F ED DLFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  +FFC
Sbjct  247  TIGHFAEDKDLFLVQTPHFFINPDPLERNLDTFDVMPSENEMFYGIIQRGLDKWDASFFC  306

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR AL E  GF+G TITED ETAL +H+RGW+S+Y+++ +IAGLQPE+FASFI
Sbjct  307  GSAALLRRTALKETNGFSGVTITEDCETALGLHARGWRSIYVEKPLIAGLQPESFASFIG  366
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Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RWA GMMQ+L+   P F+RGL + QRLCY++SM FW FP  R+MFL++PL YLFF +
Sbjct  367  QRSRWAQGMMQILIFHAPFFKRGLSLPQRLCYMSSMLFWLFPYPRLMFLISPLFYLFFSL  426

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            E+F A+  E LAY   Y+ V+ L+QN L+ + RWP +SE+YE  Q+ YL  AI++ +  P
Sbjct  427  EVFNASGAEFLAYTSTYMLVNLLMQNYLYGKYRWPWISEIYEYIQSIYLLPAILSVIANP  486

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VT+K E ++E+ +S I RP    F + ++ +  ++ R +  P +  V++VVGGW
Sbjct  487  RKPTFNVTSKGENMAESRVSEIGRPFFIIFAVLVAALFVSIYRALTEPFNADVIIVVGGW  546

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             VLN+L+ G AL  V+E++ RR   RV +    E  I      +  ATV D ST G R
Sbjct  547  NVLNLLIAGCALGVVSERRNRRRTHRVNLLRRCEMTINGI---TYPATVEDGSTGGAR--  601

Query  619  VRL-PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
            VRL  G+G   P  E G   Q + K P A   +  +   IR+   +   V+ G  FE
Sbjct  602  VRLAEGIG--RPDFERGQEAQMRFK-PHADLGDEALPLSIRNVEEDKQGVVFGCQFEPKT  658

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPAR  737
            P+  R  VA LIF  +  WR  +E+  R  G+L G  R +  A     +    F+
Sbjct  659  PMHYR-LVADLIFANADEWRKFQESRRRNPGVLFGTLRFIRQALYHTGRGLSYFVHLQRL  717

Query  738  RRRRHEEP  745
             R R   P
Sbjct  718  WRERRRNP  725


>TR:A0ABY5RQ61 A0ABY5RQ61_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga terrae OX=2740529 GN=bcsA PE=4 SV=1
Length=731

 Score = 598 bits (1541),  Expect = 0.0
 Identities = 324/713 (45%), Positives = 436/713 (61%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+  LW    V    + A P++  A  +  L+ V  + +LK F  + + R + L+  + +
Sbjct  5    LIVALWAVAAVLIVSIVALPISLQAHLVAGLTVVACMIILKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP    ASF+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEVASFIPGFLLYLAEMYSVMMLFLSLFVVSSPLKSRKAPQIDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LPTVD+ VPSYNE AD+LS TLAAAK M YP+   TV L DDGGTD++C S +   AQ
Sbjct  125  ENLPTVDVFVPSYNEGADLLSTTLAAAKAMTYPSDKVTVWLLDDGGTDEKCNSSNAAAAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  + V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  185  QARERRAELQALCAVMDVKYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  D +LFLVQTPHFFINPDP++RNL       P ENEMFYG I RGLD+W  AF
Sbjct  245  TETVGYFTTDKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSVYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P F+RGL I+QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPFKRGLKISQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
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             P    F VTAK+E++ E+ +S +  P    F + + GV+AT +R  A P    + LV G
Sbjct  485  NPSKPTFKVTAKNESMEESRVSELGTPYFIIFGILILGVIATGIRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W VLN+++ G AL  V+E+  RR + RV++E P        G+  + A + D S  G R
Sbjct  545  AWNVLNLVIAGCALGVVSERATRRQSHRVRVERPCRF---IMGDEIIDAVLKDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              V +P   +P       G ++FQP F   P   + +   IR    +   +++G  F
Sbjct  602  --VHVPPSAEPKLKKGTSGTLEFQP-FSSLP--IQHLPMEIRKVGMDDKGLLLGCRFMIE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +P   R  +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  657  KP-EHRRMIADLVFANADQWSKFQKNRHHDIGVLRG---TLWFFMVAFYQTGR  705


>TR:A0A6A7Y2A8 A0A6A7Y2A8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Segnochrobactrum spirostomi OX=2608987 GN=bcsA PE=4
SV=1
Length=721

 Score = 597 bits (1540),  Expect = 0.0
 Identities = 326/723 (45%), Positives = 447/723 (62%), Gaps = 20/723 (3%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LW+A +     L   P+   A  ++ +  V+++ L+K F  + V R + L+  + +V+RY
Sbjct  9    LWIAAMALVVFLITEPINLQAHLIVGVIVVIVLGLIKFFGPQGVFRQVFLALGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   T+PP     +F+  ++L+  E +++    L+ F  ADP  RP P   +PE  P
Sbjct  69   AYWRTTSTIPPINQLENFIPGVILYVFEMYNVLALGLSLFTVADPLSRPSPPRAKPELAP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVDI +P+YNE  D+L+ T+AAA+ + YPA    V L DDGGTDQ+C S DP  A++AQ
Sbjct  129  TVDIFIPTYNESEDLLATTVAAARAIDYPADRFKVYLLDDGGTDQKCNSDDPMTAREAQR  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RR  L+QLC +LG  Y TR RNEHAKAGN++  L    G+LV VFDADH P+RDFL  TV
Sbjct  189  RRASLKQLCADLGAHYITRPRNEHAKAGNLNHGLSHTSGDLVAVFDADHCPARDFLNETV  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            G+F+EDP LFLVQTPHFFINPDP++ NLA  ++ P ENE FYG + RGLDRW  AFFCGS
Sbjct  249  GFFLEDPKLFLVQTPHFFINPDPLEHNLATFEKMPSENEQFYGMVQRGLDRWNAAFFCGS  308

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AA+LRR AL +  GF+G +ITED ETALE+HS GW S+Y+D+ +IAGLQPETFASFI QR
Sbjct  309  AALLRREALRQTNGFSGVSITEDCETALELHSLGWHSVYVDKPLIAGLQPETFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ+LLLKNP+ RRGL  +QRLCY+ +  FW FP  R+ F+ +PL+YLFFG++I
Sbjct  369  SRWAQGMMQILLLKNPVRRRGLKFSQRLCYITNAMFWLFPAGRLTFMFSPLLYLFFGLQI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            F ++  E +AY   Y+ V+ ++QN L+ R RWP +SE+YE  QA YL RA+V  +  PR
Sbjct  429  FNSSGGEFMAYTSSYMLVNLMMQNYLYGRYRWPWISELYEYIQAVYLLRALVAVVANPRK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VT K ETL  + IS +  P    F L ++GV  T  R    P    + +VVGGW V
Sbjct  489  PTFKVTNKGETLDVSRISELGGPYFIIFALLIAGVGMTFYRLWTQPYLADITVVVGGWNV  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
             N+LL G AL  V+EK+  R APRV + +PAE +I       + A + D S  G+R+
Sbjct  549  FNLLLAGAALGVVSEKRNLRQAPRVDLSIPAEIEIDGV---RMPALIEDGSMGGIRVRPL  605

Query  621  LPGVGDPHPALEAGGLIQFQPK----FPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
                 DP    + G ++  + K     P+   L   VRG  R A  EG  + +G
Sbjct  606  DKPTRDP----KQGDVVVVRHKTRATIPN-DGLSLTVRGVSRDA--EG--LHLGCQVSTR  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPA  736
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            +   VR  +A +++ ++A W+       R IG+L G    L+  + +L ++AR
Sbjct  657  EATQVR-LLADIVYADAAQWQRFLAKRRRGIGVLRG---TLFFLSIALFQSARGIAYLGR  712

Query  737  RRR  739
            RR+
Sbjct  713  RRK  715


>TR:I4YT33 I4YT33_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga lotononidis OX=864069 GN=MicloDRAFT_00036790
PE=4 SV=1
Length=731

 Score = 597 bits (1539),  Expect = 0.0
 Identities = 322/713 (45%), Positives = 440/713 (62%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W    V    + A P++  A  +  L+ V  + +LK F  + + R + L+  + +
Sbjct  5    LIVAFWAVAAVLIISIVALPISIQAHLVAGLTVVACMIILKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP    ASF+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEIASFIPGFLLYLAEMYSVMMLFLSLFVVSSPLKSRKAPQIDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LPTVD+ VP+YNE +D+L+ TLAAAK M YPA   TV L DDGGTD++C S + + AQ
Sbjct  125  ENLPTVDVFVPTYNEGSDLLATTLAAAKAMTYPADKFTVWLLDDGGTDEKCNSSNAKAAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  + V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  185  EARERRAELQALCEVMDVKYLTRARNLHAKAGNLNNGLENSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF +D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  METVGYFTKDKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSVYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P  +RGL I+QRLCY++S  FW FP  R  FL++PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPLKRGLKISQRLCYMSSSMFWLFPFSRFCFLISPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+E++ E+ +S +  P    F + + GV+AT +R  A P    + LV G
Sbjct  485  NPSKPTFKVTAKNESMEESRVSELGTPYFIIFGILILGVIATGIRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W VLN+++ G AL  V+E+  RR + RV++E P    I   G+ ++ A V D S  G R
Sbjct  545  AWNVLNLIIAGCALGVVSERATRRHSHRVRVERPCRFII---GDEAIDAVVRDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              V +P   +P     A G ++FQP F + P   + +   IR    +   +++G  F
Sbjct  602  --VHVPPSAEPKLKKGAAGTLEFQP-FSNLP--IQHLPMEIRKVGMDDKGLLLGCRFLIE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +P   R  +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  657  KP-EHRRMIADLVFANADQWSQFQKNRHHDIGVLRG---TLWFFMVAFYQTGR  705


>TR:A0A931BPR7 A0A931BPR7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga alba OX=2791025 GN=bcsA PE=4 SV=1
Length=731
```

```
 Score = 597 bits (1538),  Expect = 0.0
 Identities = 321/713 (45%), Positives = 438/713 (61%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W        LL A P++  A  +  L  V  + +LK F  + + R + L+  + +
Sbjct  5    LIVAFWAVAATIIVLLVALPISLQAHLIAGLVVVASMIVLKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   TLPP     +++ A+LL+  E +S+ + FL+ F+ + P     P  +
Sbjct  65   VLRYVFWRTTSTLPPITELTNYIPAILLYLAEMYSVIMLFLSLFVVSSPLRSRKPPRIDH  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
              +PTVD+ VPSYNE A +L+ TLAAAK M YPA   TV L DDGGTDQ+C  PD  LA+
Sbjct  125  SNVPTVDVFVPSYNENASLLASTLAAAKAMSYPAGKMTVWLLDDGGTDQKCEQPDAVLAR  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  L V Y TR RNEHAKAGN++ ALE   G+L+ VFDADH P+R+FL
Sbjct  185  EARERRVELQALCAALDVNYITRARNEHAKAGNLNNALEHSTGDLIAVFDADHAPARNFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  + +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  EETVGYFGTEKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSIYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GM+Q++  + PLF+RGL + QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMIQIMRYRFPLFKRGLKLPQRLCYMSSAMFWLFPFTRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  AI++ +
Sbjct  425  SLEIFTASGGEFLAYTSTYMMVNFMMQNYLYGRYRWPWISDLYEFIQTVYLLPAIMSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+ET+ +N +S +  P    F + + GV+AT++R  A P    V LV G
Sbjct  485  NPSKPTFKVTAKNETMDKNRVSELGAPYFIIFGVLVLGVIATIIRIWAEPYKADVTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W ++N+++ G AL  V+E+  RR + RV  E P        G++ + AT+ D S  G+
Sbjct  545  AWNLMNLIIAGCALGVVSERATRRQSHRVIAERPCRF---IMGDQLVDATIRDVSVGGIS  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              +RL     P     A G ++F P + D P     +   +R    +   V++G  F
Sbjct  602  --IRLSQSALPGLKRGAFGTLEFTP-YSDLP--TNQLPMEVRKMGMDDKGVLIGCRFLTE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             P   R  +A L+F  +  W   ++   + IG+L G    LW    ++ +T R
Sbjct  657  TPEQHR-LIADLVFANAEQWSHFQKRRHQDIGILRG---TLWFITVAIYQTGR  705


>TR:A0AAW9RRK9 A0AAW9RRK9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microbaculum marinum OX=1764581 GN=bcsA PE=4 SV=1
Length=724

 Score = 597 bits (1538),  Expect = 0.0
 Identities = 322/707 (46%), Positives = 445/707 (63%), Gaps = 19/707 (3%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQ---GLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            + W+            PV+  A    GL+ + A++L+ LL+P     + R + L+  + +
Sbjct  7    VFWILSAACVLFFVTQPVSLQAHLTAGLLVMVAIILLKLLRPTG---MWRHIALALGTAI  63

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   TLPP +   +F+ ALLL+  E + + +F ++ F  +DP   P P    P
Sbjct  64   VLRYIFWRTTSTLPPVSQLENFIPALLLYVAELYCVGMFAISLFTVSDPL-APRPARENP  122

Query  137  EE--LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
            +    PTVD+ VPSYNE  D+L +TLAAAK M YP+   TV L DDGGTDQ+C + D  +
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Sbjct  123  KNGYFPTVDVFVPSYNEDYDLLGITLAAAKAMDYPSDRFTVWLLDDGGTDQKCEADDASV  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A  AQ+RR  LQ+LC  L V Y TR RNEHAKAGN++  L   K ELV V DADH P+RD
Sbjct  183  AIVAQQRRANLQKLCESLDVRYLTRARNEHAKAGNLNNGLAHSKAELVAVLDADHAPTRD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL +TVGYF EDP LFLVQ+PHFF+NPDP++RNL      P ENEMFYG I RGLD+W  
Sbjct  243  FLTQTVGYFAEDPKLFLVQSPHFFLNPDPLERNLDTFGTMPSENEMFYGVIQRGLDKWNA  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            +FFCGSAAVLRR AL+E  GF+G +ITED ETA+++H+RGW S+Y+DR +IAGLQP TF+
Sbjct  303  SFFCGSAAVLRRAALEEGSGFSGVSITEDCETAIDLHARGWNSVYVDRPLIAGLQPLTFS  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            +FI QR RWA GM+Q++LLK P+ +RGL  +QRLCY +S  +W FP  R++FL++PL YL
Sbjct  363  AFIGQRSRWAQGMIQIMLLKRPVLKRGLTFSQRLCYASSTLYWLFPFARLIFLISPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IF A+ EE LAY+  Y+ ++ ++QN ++ R RWP +SE+YE  Q+ +L RA ++ 
Sbjct  423  FFSLKIFNASGEEFLAYIAIYMIINVIMQNYMYGRYRWPWISELYEYIQSVHLVRAAISA  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +L P    F VTAKDE+L E+ IS +  P    F + L GV  T+ R +  P D  + LV
Sbjct  483  ILHPTKPTFKVTAKDESLEESRISELAAPFYMIFAILLFGVGVTVWRVLEQPYDADITLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW + N+++VG AL  V+E++  R   RV +   AEA    FG +S  ATVLDAST G
Sbjct  543  VGGWNLFNLIIVGCALGVVSERRDLRRNIRVALARRAEA---TFGGQSHAATVLDASTGG  599

Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            VRL   +PGV      +E G  +  +   P +    + +   ++ A   G  V++G   
Sbjct  600  VRL--SIPGVESGR--IEEGSTLLLRLVRPRSEAANQPIELTVQRATHNGEGVVLGC--R  653

Query  675  AGQPIAVR-ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
               P A     +A +I+ +S+ W   +      IG+L G  + L+MA
Sbjct  654  VASPTADDFRVIADMIYADSSKWSEFQNRRRVNIGVLWGTIQFLFMA  700


>TR:A0ABT0DL41 A0ABT0DL41_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter koreensis OX=266121 GN=bcsA PE=4 SV=1
Length=735

 Score = 597 bits (1538),  Expect = 0.0
 Identities = 327/700 (47%), Positives = 434/700 (62%), Gaps = 12/700 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVMR  79
            LW    V    L   P++  A  +     VV +A+LK F    V R + L+  + +V+R
Sbjct  9    LWAIASVVVVFLITLPISLQAHLIAGCIVVVAMAILKTFGPATSVLRKIALALGTAIVLR  68

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP +    F+   +L+  E +S+ + FL+ F+ + P       P+ P E 
Sbjct  69   YVYWRTTSTLPPISQLEDFIPGFMLYLAEMYSVFMLFLSLFVVSAPMAPRKAPPIPPGEH  128

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVD+ +P+YNE  ++L+ T++AA +M YPA   T+ L DDGG+DQ+C   DPE A  A 
Sbjct  129  PTVDVFIPTYNEEPELLASTVSAALSMDYPADKLTIWLLDDGGSDQKCQQDDPEKAAAAM  188

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +RR +LQ+LC  LGV Y TR RNEHAKAGN++  L+   G+LVVVFDADH P+RDFL  T
Sbjct  189  QRRADLQKLCEGLGVNYLTRARNEHAKAGNLNNGLKFSSGDLVVVFDADHAPTRDFLTNT  248

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF++D +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCG
Sbjct  249  VGYFLQDENLFLVQTPHFFINPDPLERNLGTFDFMPSENEMFYGIIQRGLDKWDAAFFCG  308

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL E  GF+G TITEDAETALE+HSRGW S+Y+D+ MIAGLQPETFASFI Q
Sbjct  309  SAAVLSRRALGETNGFSGITITEDAETALELHSRGWHSIYVDKPMIAGLQPETFASFIGQ  368
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Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+LL   P  +RGL + QRLCY +S  FW F   R+MFL++PL YLFF +E
Sbjct  369  RSRWAQGMMQILLFHFPPGKRGLTLPQRLCYCSSTFFWLFSYPRLMFLISPLFYLFFSLE  428

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ L+QN L+   RWP VSE+YE  QA YL  AI++ L  P 
Sbjct  429  IFNASGAEFLAYTTTYMMVNLLMQNYLYGHYRWPWVSEIYEYIQAVYLMPAIISVLANPN  488

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAK ET+ E ++S I RP    F + L GV  T  R V  P +  +++VVGGW 
Sbjct  489  KPTFNVTAKGETMDEGHVSEIGRPFFIIFGILLIGVGVTGWRLVTEPFNHDIIVVVGGWN  548

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+LL G AL  V+E++ RR + RV +    +  +      +  AT+ D S  G R+  
Sbjct  549  LLNLLLAGCALGVVSERRNRRRSHRVDLLRRCDILV---DGEAYAATIDDGSLGGARV--  603

Query  620  RLPGVGDPHPALEAGGLI--QFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
              P      P LE G ++  +F+P   + P     V   IR+  R    +++G  F+  Q
Sbjct  604  -RPAANVVLPELERGRVVSLRFRPLAENIPIDTLPV--TIRNVERTADGLLIGCQFQPDQ  660

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL  717
            P+  R  +A LIF  S  W+  +++     G+L G  R +
Sbjct  661  PLHYR-LIADLIFANSNEWKKFQDSRRTNPGVLLGTIRFV  699


>TR:A0AAV4Z1B0 A0AAV4Z1B0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium bullatum OX=570505 GN=bcsA PE=4 SV=1
Length=820

 Score = 596 bits (1537),  Expect = 0.0
 Identities = 313/702 (45%), Positives = 439/702 (63%), Gaps = 6/702 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L + +W+   V    L + P++   Q  ++L A+  + +L  F D    RF+ L+  S++
Sbjct  5    LRWTVWLVSTVAVLALLSQPISTQDQLAMSLCAMAAMIVLWIFFDNPPARFVFLALGSLV  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR+  TLP P+   SF F L+L   E + + I F++  ++ADP  R  P    P
Sbjct  65   VLRYMFWRVTNTLPSPSDPVSFGFGLVLLLGELYCVFILFISLIINADPLRRSTPPMGAP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E+LPTVDI VPSYNE A +LS TL+AAK + YPA    V L DDGGTDQ+C  PDP  AQ
Sbjct  125  EDLPTVDIFVPSYNEDAGILSTTLSAAKLIDYPADKLHVWLLDDGGTDQKCADPDPAKAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A +RR ELQ LC  LGV Y TR RN+HAKAGN++  L+  +GE++VV DADHVP R FL
Sbjct  185  EAIQRRSELQALCMALGVTYLTRSRNQHAKAGNLNNGLKHSQGEIIVVLDADHVPFRSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              T+G+F  DP LFLVQTPH F+NPDPI+RNL   DR P ENEMFY    RGLD+W G+F
Sbjct  245  RETIGHFAADPRLFLVQTPHAFLNPDPIERNLRTFDRMPSENEMFYSVTQRGLDKWNGSF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRRRALDEAGGF+G TITED ETA E+HSRGW S+Y+D  +IAGLQP+T  +F
Sbjct  305  FCGSAALLRRRALDEAGGFSGVTITEDCETAFELHSRGWNSIYVDTPLIAGLQPDTLVAF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GM Q+L+LKNPLF+RGL   Q+L YL+SM+FWFFP+ RM+F+ AP++++FF
Sbjct  365  IGQRSRWCQGMFQILMLKNPLFKRGLHPIQKLAYLSSMTFWFFPVPRMIFMFAPMLHIFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL RAI++ ++
Sbjct  425  DLKIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLFRAIISVIV  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VTAK   L ++++SP+  P    + + L G    L R++  PG  +++LVVG
Sbjct  485  SPRKPTFNVTAKGAALDQDHLSPMAWPYFAVYFILLIGCGTALYRYLFEPGVTNLMLVVG  544
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Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W   N+L  G AL   AE++   A+P + ++         FG R+L   +  AS  G
Sbjct  545  LWNFFNLLTAGVALGVAAERRTTEASPSLAIDRQGRL---VFGGRALDVAIERASALG--  599

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              +R    G P  A     + Q      D   ++  +   I    + G  V+V + F+
Sbjct  600  CTIRFGAEGLPPGAGSTHRMGQLSVVPIDGAPVQVPLPVEIGEITQSGDEVVVTLQFQPL  659

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILW  718
             P      +A L++G++      +++  R   +L G  +++W
Sbjct  660  DPKGY-GALASLMYGDAGALLRFQQSRRRHKNILSGTLQLIW  700


>TR:A0A5N7MPM9 A0A5N7MPM9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga tunisiensis OX=2108360 GN=bcsA PE=4 SV=1
Length=731

 Score = 595 bits (1535),  Expect = 0.0
 Identities = 320/713 (45%), Positives = 433/713 (61%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W    V    + A P++  A  +  L+ V  + +LK F  + + R + L+  + +
Sbjct  5    LIVAFWAVAAVLIISIVALPISLQAHLVAGLTVVACMIILKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP     SF+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEVTSFIPGFLLYLAEMYSVMMLFLSLFVVSSPLKSRKAPQIDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            + LPTVD+ VPSYNE AD+L+ TLAAAK M YPA   TV L DDGGTD++C S     A
Sbjct  125  QNLPTVDVFVPSYNENADLLATTLAAAKGMTYPADKVTVWLLDDGGTDEKCNSSTANAAH  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  + V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  185  QARERRAELQALCAAMDVKYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  TETVGYFTTDKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSVYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P F+RGL I+QRLCY++S  FW FP  R  FL++PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPFKRGLKISQRLCYMSSSMFWLFPFSRFCFLISPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  GLEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+E++ E+ +S +  P    F + + GV+AT +R  A P    + LV G
Sbjct  485  NPSKPTFKVTAKNESMEESRVSELGTPYFIIFGILILGVIATGIRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W VLN+++ G AL  V+E+  RR + RV++E P        G+  + A + D S  G R
Sbjct  545  AWNVLNLIIAGCALGVVSERATRRQSHRVRVERPCRF---VLGDEIIDAVLKDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              V +P   +P       G ++FQP F   P   + +   IR    +   +++G  F
Sbjct  602  --VHVPPSAEPKLKKGTSGTLEFQP-FSSLP--VQHLPMEIRKVGMDDRGLLLGCRFMTE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +P   R  +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  657  KP-EHRRMIADLVFANADQWSEFQKNRHHDIGVLRG---TLWFFMVAFYQTGR  705
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>TR:A0A9W6NDQ8 A0A9W6NDQ8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter defluvii OX=1282440 GN=celA PE=4 SV=1
Length=734

 Score = 595 bits (1533),  Expect = 0.0
 Identities = 329/706 (47%), Positives = 439/706 (62%), Gaps = 12/706 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVL-VALLKPFADKM-VPRFLLLSAAS  74
            L+ +LW+   V    L   P++  A  LIA S VVL + LLK F     V R + L+  +
Sbjct  5    LIAVLWMLASVVIVFLITLPISLQAH-LIAGSIVVLAMILLKTFGPPTGVFRVIALALGT  63

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP      F+   +L+  E +S+ + FL+ F+ + P   P P P
Sbjct  64   AIVLRYVYWRTTSTLPPINQIEDFIPGFMLYIAEMYSVFMLFLSLFVVSSPVP-PRPTPP  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P  +PTVD+ +P+YNE   +L+ T+AAAK M YPA   TV L DDGGTDQ+C   +
Sbjct  123  LPANVPTVDVFIPTYNEDMALLANTVAAAKGMDYPADKLTVWLLDDGGTDQKCNQDNAAK  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A +AQ+RRREL  LC  LG  Y TR RNEHAKAGNM+  LE   G+LVVVFDADH P+R
Sbjct  183  ALEAQQRRRELSALCEGLGARYLTRARNEHAKAGNMNNGLEHSTGDLVVVFDADHAPART  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVG+F +D +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W
Sbjct  243  FLKETVGHFAQDENLFLVQTPHFFINPDPLERNLDTFDVMPSENEMFYGIIQRGLDKWDA  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            +FFCGSAAVLRR AL E  GF+G TITED ETAL +HSRGW+S+Y+++ +IAGLQPE+FA
Sbjct  303  SFFCGSAAVLRRAALKETNGFSGVTITEDCETALGLHSRGWRSIYVEKPLIAGLQPESFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+   P F+RGL + QRLCY++SM FW FP  R+MFLV+PL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFHVPFFKRGLSLPQRLCYMSSMLFWLFPYPRLMFLVSPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF +E+F A+  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  Q+ YL  AI++
Sbjct  423  FFSLEVFNASGAEFLAYTSTYMLVNLLMQNYLYGRYRWPWISELYEYIQSIYLLPAILSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  PR   F VT+K E + E ++S I RP    F + ++ ++ ++ R +  P +  V++V
Sbjct  483  IANPRKPTFNVTSKGENIHEGHVSEIGRPFFIIFAVLVAALIVSIYRALTEPFNADVIIV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW VLN+L+ G AL  V+E++ RR   RV ++   E  I A    +  A V D ST G
Sbjct  543  VGGWNVLNLLIAGCALGVVSERRNRRRTHRVNLQRRCEIIIDAI---TYAAMVEDGSTGG  599

Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
             R+ +   GV  P          ++F P     P +  +    IR+   +   V+ G  FE
Sbjct  600  ARIRL-AEGVKGPDFERGQQAQLRFTPHADIGPDVLPL---SIRNIEHDKDGVVFGCQFE  655

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
               P   R  VA LIF  +  WR  +E+  +  G+L G  R +  A
Sbjct  656  PQTPTHYR-LVADLIFANADEWRKFQESRRKNPGVLLGTLRFIRQA  700


>TR:A0A838BJA9 A0A838BJA9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga mediterraneensis OX=2754695 GN=bcsA PE=4
SV=1
Length=731

 Score = 594 bits (1531),  Expect = 0.0
 Identities = 321/713 (45%), Positives = 436/713 (61%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W    V    + A P++  A  +  L+ V  + +LK F  + + R + L+  + +
Sbjct  5    LIVAFWAVAAVLIISIVALPISIQAHLVAGLTVVACMIILKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
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            V+RY FWR   T+PP     SF+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEITSFIPGFLLYLAEMYSVMMLFLSLFVVSSPLKSRTAPQIDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LPTVD+ VPSYNE AD+L+ TLAAAK M YP    TV L DDGGTD++C S + + AQ
Sbjct  125  ENLPTVDVFVPSYNEGADLLATTLAAAKAMTYPEDKVTVWLLDDGGTDEKCNSSNAKTAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  + V Y TR RN HAKAGN++  L+   G+LV VFDADH P+R FL
Sbjct  185  EARERRAELQALCEVMDVKYLTRARNLHAKAGNLNNGLDNSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF +D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  METVGYFTKDKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSVYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P  +RGL I+QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPLKRGLKISQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+E+++E+ +S +  P    F + + GV+AT VR  A P    + LV G
Sbjct  485  NPSKPTFKVTAKNESMAESRVSELGTPYFIIFGILILGVIATGVRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W VLN+++ G AL  V+E+  RR + RV++E P        G+ ++ A V D S  G R
Sbjct  545  AWNVLNLIIAGCALGVVSERATRRHSHRVRVERPCRF---IMGDEAIDAVVRDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              V +P   +P       G ++FQP F   P   + +   IR    +   +++G  F
Sbjct  602  --VHVPPSAEPKLKKGTSGTLEFQP-FSSLP--VQHLPMEIRKVGMDDKGLLLGCRFLIE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +P   R  +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  657  KP-EHRRMIADLVFANADQWSQFQKNRHHDIGVLRG---TLWFFMVAFYQTGR  705


>TR:A0ABY3DNB5 A0ABY3DNB5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter moscoviensis OX=2597768 GN=bcsA PE=4
SV=1
Length=735

 Score = 592 bits (1526),  Expect = 0.0
 Identities = 319/701 (46%), Positives = 435/701 (62%), Gaps = 12/701 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAASMLVM  78
            +LW    +    L   P++  A  +     VV + LLK F   + P R + L+  + +V+
Sbjct  8    VLWAIASLVVVFLITLPISLQAHLIAGCIVVVAMILLKMFGPPVGPLRTVALALGTAIVL  67

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY +WR   T+PP      F+   LL+  E +S+ + FL+ F+ + P       P+  ++
Sbjct  68   RYVYWRTTSTIPPITQIEDFIPGFLLYLAEMYSVFMLFLSLFVVSAPMPERSAPPIPADQ  127

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            +P+VD+ +P+YNE   +L+ T++AA +M YPA   TV L DDGGTDQ+C   D   A  A
Sbjct  128  VPSVDVFIPTYNEDPHLLASTISAALSMDYPADKFTVWLLDDGGTDQKCEQDDHVQAAAA  187

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
             +RR ELQ+LC  LG  Y TR +NEHAKAGN++  L+  + ELV VFDADH P+RDFL
Sbjct  188  VKRRAELQELCAGLGARYLTRAKNEHAKAGNLNNGLQHSQAELVAVFDADHAPTRDFLTN  247

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
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               TVGYF++D +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFC
Sbjct  248   TVGYFLQDENLFLVQTPHFFINPDPLERNLGTFDTMPSENEMFYGIIQRGLDKWDAAFFC  307

Query  319   GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
             GSAAVL RRAL+E  GF+G TITED ETALE+HSRGW S+Y+++ MIAGLQPE++ASFI
Sbjct  308   GSAAVLSRRALNETNGFSGVTITEDCETALELHSRGWHSIYVEKPMIAGLQPESYASFIG  367

Query  379   QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
             QR RWA GMMQ+L    P  +RGL +AQRL Y +S  FW FP  R+MFL++PL YLFF +
Sbjct  368   QRSRWAQGMMQILRFHFPPGKRGLTLAQRLSYCSSTLFWLFPYSRLMFLISPLFYLFFSL  427

Query  439   EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
             EIF A+  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  QA YL  A++  L  P
Sbjct  428   EIFNASGAEFLAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQAIYLFPALIAVLANP  487

Query  499   RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
             R   F VTAK ET+ E ++S I RP    F + + G L T+ R +  P ++ V++VVGGW
Sbjct  488   RKPTFKVTAKHETMEEGHVSEIGRPFFIIFAVLIVGALLTIWRLLTEPFNQDVIIVVGGW  547

Query  559   AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
              +LN+LL G AL  V+E++ RR + RV +    E         +  A + D S  G R+
Sbjct  548   NLLNLLLAGCALGVVSERRNRRRSHRVNLARRGEL---VLNGTAYPAIIEDGSLGGARV-  603

Query  619   VRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
                P      P LE G  GL++F+P  P+   ++ +  G IR+  R    V++G  F+
Sbjct  604   --RPAANVTLPDLERGTVGLLRFRPLAPNI-SVDSLPVG-IRNVERNDDDVLIGCQFQPD  659

Query  677   QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL  717
             QP+  R  +A LIF  S  W+  +++     G+L G  R +
Sbjct  660   QPLHYR-LIADLIFANSDEWKKFQDSRRNNPGVLMGTIRFV  699


>TR:A0ABV6Y867 A0ABV6Y867_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga arabica OX=1128671 GN=bcsA PE=4 SV=1
Length=731

 Score = 592 bits (1526),  Expect = 0.0
 Identities = 322/713 (45%), Positives = 434/713 (61%), Gaps = 12/713 (2%)

Query  17    LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
             L+  LW    +    L   P++  A  +  L+ V  + ++K F  + + R + L+  + +
Sbjct  5     LIVALWAVAAILIVSLVVLPISLQAHLVAGLTVVACMIIIKFFRAQGIWRQIALALGTAI  64

Query  77    VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
             V+RY FWR   T+PP    A+F+   LL+  E +S+ + FL+ F+ + P     P  + P
Sbjct  65    VLRYVFWRTTSTIPPITEVANFIPGFLLYLAEMYSVMMLFLSLFVVSSPMPSRKPPQIDP  124

Query  137   EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
               LPTVD+ VPSYNE AD+L+ TLAAAK M YP    TV L DDGGTD++C S +   A
Sbjct  125   HNLPTVDVFVPSYNEGADLLATTLAAAKAMTYPEDKLTVWLLDDGGTDEKCSSQNALAAL  184

Query  197   KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             +A+ERR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R+FL
Sbjct  185   QARERRAELQALCAALDVRYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARNFL  244

Query  257   ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
               TVGYF  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  +F
Sbjct  245   TETVGYFTADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDASF  304

Query  317   FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
             FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGWKS Y+D+ +IAGLQP++FASF
Sbjct  305   FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWKSAYVDKPLIAGLQPDSFASF  364

Query  377   IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
             I QR RWA GMMQ+L  K P F+RGL ++QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365   IGQRSRWAQGMMQILRYKFPPFKRGLKLSQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFF  424

Query  437   GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
              +EIF A+  E  AY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
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Sbjct  425  SLEIFTASGGEFFAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYVQTIYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VT+K+ET+ E+ IS +  P    F + L GV+AT VR  A P    + LV G
Sbjct  485  NPSKPTFKVTSKNETMDESRISELGTPYFIIFGILLLGVVATGVRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN+++ G AL  V+E+  RR + RV++E P        G+  + A + D S  G R
Sbjct  545  AWNILNLIVAGCALGVVSERATRRQSHRVRVERPCRF---VMGDEIIDAILRDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              V +P   +P     A G I+FQP F + P     V   IR    +   +++G  F
Sbjct  602  --VHVPPSVEPRLKKGAAGTIEFQP-FANLPVQHLPV--EIRKVGMDDDGLLLGCRFMI-  655

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +    R+ +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  656  EKAEHRKMIADLVFANADQWSEFQKNRHYDIGVLRG---TLWFFMVAFYQTGR  705


>TR:A0A5S9P898 A0A5S9P898_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Starkeya nomas OX=2666134 GN=bcsA PE=4 SV=1
Length=735

 Score = 592 bits (1526),  Expect = 0.0
 Identities = 319/701 (46%), Positives = 435/701 (62%), Gaps = 12/701 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVP-RFLLLSAASMLVM  78
            +LW    +    L   P++  A  +     VV + LLK F   + P R + L+  + +V+
Sbjct  8    VLWAIASLVVVFLITLPISLQAHLIAGCIVVVAMILLKMFGPPVGPLRTVALALGTAIVL  67

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY +WR   T+PP      F+   LL+  E +S+ + FL+ F+ + P       P+  ++
Sbjct  68   RYVYWRTTSTIPPITQIEDFIPGFLLYLAEMYSVFMLFLSLFVVSAPMPERSAPPIPADQ  127

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            +P+VD+ +P+YNE   +L+ T++AA +M YPA   TV L DDGGTDQ+C   D   A  A
Sbjct  128  VPSVDVFIPTYNEDPHLLASTISAALSMDYPADKFTVWLLDDGGTDQKCEQDDHVQAAAA  187

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
             +RR ELQ+LC  LG  Y TR +NEHAKAGN++  L+  + ELV VFDADH P+RDFL
Sbjct  188  VKRRAELQELCAGLGARYLTRAKNEHAKAGNLNNGLQHSQAELVAVFDADHAPTRDFLTN  247

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF++D +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFC
Sbjct  248  TVGYFLQDENLFLVQTPHFFINPDPLERNLGTFDTMPSENEMFYGIIQRGLDKWDAAFFC  307

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAAVL RRAL+E  GF+G TITED ETALE+HSRGW S+Y+++ MIAGLQPE++ASFI
Sbjct  308  GSAAVLSRRALNETNGFSGVTITEDCETALELHSRGWHSIYVEKPMIAGLQPESYASFIG  367

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RWA GMMQ+L    P  +RGL +AQRL Y +S  FW FP  R+MFL++PL YLFF +
Sbjct  368  QRSRWAQGMMQILRFHFPPGKRGLTLAQRLSYCSSTLFWLFPYSRLMFLISPLFYLFFSL  427

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            EIF A+  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  QA YL  A++  L  P
Sbjct  428  EIFNASGAEFLAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQAIYLFPALIAVLANP  487

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VTAK ET+ E ++S I RP    F + + G L T+ R +  P ++ V++VVGGW
Sbjct  488  RKPTFKVTAKHETMEEGHVSEIGRPFFIIFAVLIVGALLTIWRLLTEPFNQDVIIVVGGW  547

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             +LN+LL G AL  V+E++ RR + RV +     E         +  A + D S  G R+
Sbjct  548  NLLNLLLAGCALGVVSERRNRRRSHRVNLARRGEL---VLNGTAYPAIIEDGSLGGARV-  603

Query  619  VRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
               P      P LE G  GL++F+P  P+   ++ +  G IR+  R    V++G  F+
Sbjct  604  --RPAANVTLPDLERGTVGLLRFRPLAPNI-SVDSLPVG-IRNVERNDDDVLIGCQFQPD  659
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Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL  717
            QP+  R  +A LIF  S  W+  +++     G+L G  R +
Sbjct  660  QPLHYR-LIADLIFANSDEWKKFQDSRRNNPGVLMGTIRFV  699


>TR:A0AAE3N3P0 A0AAE3N3P0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ectorhizobium quercum OX=2965071 GN=bcsA PE=4 SV=1
Length=729

 Score = 591 bits (1524),  Expect = 0.0
 Identities = 330/703 (47%), Positives = 436/703 (62%), Gaps = 12/703 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L  LLW         LA  PV    Q +     +++VA +K    +   R +LL+  + +
Sbjct  5    LNLLLWAPCAALMVFLAFLPVDARTQLVTTFLVLLIVATMKYLRMEGASRLVLLALGTSI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP-RPLQ  135
            V+RY +WR   TLPP    ++F+  LL++  E +S+ + FL+ F+ + P     P R L
Sbjct  65   VLRYVYWRTTSTLPPVNQPSNFIPGLLVYLAEMYSVFMLFLSLFIVSMPLPPRKPYRTLA  124

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             +ELP+VDI VPSYNE   +L+ TLAAA+N+ YP    TV L DDGGT+Q+  S +   A
Sbjct  125  DDELPSVDIFVPSYNEEESLLANTLAAARNIDYPPEKVTVWLLDDGGTEQKRHSTNLLEA  184

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            + A++R   LQ LC++LGV Y TR RNEHAKAGN++  L+   G+LV VFDADH P+RDF
Sbjct  185  KSAEKRHASLQALCQQLGVRYLTRARNEHAKAGNLNNGLQHSTGDLVAVFDADHAPARDF  244

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  A
Sbjct  245  LRETVGYFNDDPRLFLVQTPHFFINPDPVERNLNTFSTMPSENEMFYGIIQRGLDKWNAA  304

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL+EA GF+G +ITED ETALE+HSRGW S+Y+D  +IAGLQP TFAS
Sbjct  305  FFCGSAAVLRREALNEAEGFSGLSITEDCETALELHSRGWNSIYVDVPLIAGLQPATFAS  364

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ++  + PLF+ GL +AQRLCY++S  FW FP  RM+FL+APL YLF
Sbjct  365  FIGQRSRWAQGMMQIMRFRFPLFKGGLSLAQRLCYMSSTMFWLFPFPRMIFLIAPLCYLF  424

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F   +IF A+  E +AY   Y+ V+ L+QN L+   RWPL+SE+YE  Q+ +L  A+V+
Sbjct  425  FDRQIFTASGGEFMAYTLSYMLVNLLIQNYLYGSYRWPLISELYEYIQSVHLLPAVVSVA  484

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              PR   F VTAKDE+++E+ +S I RP    FL+ +  V  T  R    P    V LVV
Sbjct  485  FNPRKPTFKVTAKDESIAESRLSEISRPFFIIFLVLVIAVFVTAYRLYTEPYKFDVTLVV  544

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN++L G AL  VAE+ +R+++ RV +    E    A G+    A + + S +G
Sbjct  545  GGWNLLNLVLAGCALGVVAERGERQSSRRVTVNRRGEF---AIGDTWYPAMIENVSVNGA  601

Query  616  RLLVRLPGVGDPHP-ALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
             + V      D  P   +A G ++FQP     P     +   IR A+ +G  V VG  F
Sbjct  602  SIQV---FTRDSAPFQRDAPGRMRFQPNGRSEP---GELPVDIRHAQHDGDIVTVGCRFL  655

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL  717
             G P+   E VA LIF  S  W   ++A  R  G+L G  R L
Sbjct  656  PGTPLH-HELVADLIFANSEQWSLFQQARRRNPGVLRGTLRFL  697


>TR:A0A5P9JZD0 A0A5P9JZD0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga thermotolerans OX=2651334 GN=bcsA PE=4
SV=1
Length=737

 Score = 590 bits (1521),  Expect = 0.0
 Identities = 323/715 (45%), Positives = 441/715 (62%), Gaps = 16/715 (2%)
```

```
Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W        LL A P++  A  +  L  V  + +LK F  + V R + L+  + +
Sbjct  5    LIVAFWAVAATLILLLVALPISLQAHLIAGLVVVSCMIVLKFFRAQGVWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   TLPP     +++ ALLL+  E   + + FL+ F+ + P     P  L
Sbjct  65   VLRYVFWRTTSTLPPITELTNYIPALLLYVAEMLCVVMLFLSLFVVSSPLPSRRPPRLDE  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LP+VD+ VPSYNE A +L+ TLAAAK M YPA   TV L DDGGTDQ+C S D   A+
Sbjct  125  ENLPSVDVFVPSYNESASLLASTLAAAKAMNYPADKLTVWLLDDGGTDQKCQSTDKAQAE  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ LC  L V Y TR +N HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  185  EARARRAELQALCAALDVKYLTRAKNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  + +LFLVQTPHFFINPDP++RNL   +  P ENEMFYG I RGLDRW GAF
Sbjct  245  EETVGYFSTEKNLFLVQTPHFFINPDPLERNLGTFETMPSENEMFYGIIQRGLDRWNGAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRR AL E  GF+G +ITED ETALE+H+RGWKS+Y+D+ +IAGLQP+TFASF
Sbjct  305  FCGSAALLRREALLETNGFSGISITEDCETALELHARGWKSIYVDKPLIAGLQPDTFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GM+Q++  + P F+RGL +AQRLCY +SM FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMIQIMRYRFPPFKRGLTLAQRLCYTSSMMFWLFPFTRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFLAYTSTYMMVNFMMQNYLYGRYRWPWISDLYEFIQTVYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+E++S++ +S +  P    F L + GV+AT+VR  A P    V LV G
Sbjct  485  NPSKPTFKVTAKNESMSQSRVSELGAPFFIIFGLLVLGVVATVVRLWAEPYKADVTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN+++ G AL  V+E+  RR + RV+++          G++ + AT+ D S  G+
Sbjct  545  AWNLLNLIIAGCALGVVSERGTRRQSHRVRVQRQCRF---IMGDKIVDATIRDVSVGGIS  601

Query  617  LLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            L +    +    P L+ G  G ++F P + D P  +  +  R  S   +G  V++G  F
Sbjct  602  LRLSQSAL----PGLKKGALGTLEFTP-YSDLPLNQLPMEVRKMSMDEKG--VLIGCRFL  654

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
               P   R  +A L+F  +  W   ++   + IG+L G    +W  + +  +T R
Sbjct  655  TETPEHHR-LIADLVFANADQWSEFQKRRHQDIGILRG---TIWFFSVAAYQTGR  705


>TR:A0A1G6ABI6 A0A1G6ABI6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Bauldia litoralis OX=665467 GN=SAMN02982931_00409
PE=4 SV=1
Length=733

 Score = 590 bits (1521),  Expect = 0.0
 Identities = 324/712 (46%), Positives = 441/712 (62%), Gaps = 13/712 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L LLW         L   P++  AQ +     V  +  LK    + + R + L+  + +V
Sbjct  6    LGLLWAVAATAALFLITLPISLQAQLIAGSLVVAAMIALKVVRPEGIWRLMALALGTAIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY +WR  +T+PP     +F+   LL+  E +++ + FL+ F+ A P     P P+ P+
Sbjct  66   LRYVYWRTTQTIPPINQLENFVPGALLYGAELYNVFMLFLSLFVVARPLPSRRPPPM-PD  124

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            ELPTVDI VP+YNE AD+L+ TLAAAK M YPA   T+ L DDGGTDQ+C S   E A
Sbjct  125  ELPTVDIYVPTYNEGADLLATTLAAAKGMDYPADKFTIWLLDDGGTDQKCNSDKVEEAVV  184
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Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            AQ+RR ELQ+LC +L V Y TR RNEHAKAGN++  L+   GELV VFDADH P+RDFL 
Sbjct  185  AQQRRAELQKLCEDLEVNYLTRARNEHAKAGNLNNGLDHSTGELVAVFDADHAPARDFLV  244

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TV YF ED  LFLVQTPHFFINPDP++RNL   ++ P ENEMFYG I RGLD+W  +FF
Sbjct  245  ETVSYFSEDEKLFLVQTPHFFINPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNASFF  304

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVL+R AL E  GF+G +ITED ETALE+H+RGW S+Y+D+ +IAGLQP TFASFI
Sbjct  305  CGSAAVLKRTALAETNGFSGVSITEDCETALELHARGWHSVYVDKPLIAGLQPTTFASFI  364

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P  +RGL ++QRL Y++S  FW FP+ R++FLV+PL YLFFG
Sbjct  365  GQRTRWAQGMMQILRFRFPPGKRGLKLSQRLSYMSSTLFWLFPIPRIIFLVSPLFYLFFG  424

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
             EIFVA+  E  AY   Y+ V+ ++QN L+ R RWP +SE+YE+ Q+ YL  A+++ L+ 
Sbjct  425  AEIFVASGGEFAAYTLMYMIVNLMMQNYLYGRYRWPWISELYELIQSVYLLPALISVLMN  484

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            P    F VTAKDE L  NYIS +  P    F + L+GV  T+ R V  P D  V LVVG 
Sbjct  485  PARPTFKVTAKDEKLDRNYISELGGPFYIIFAILLAGVAMTVWRLVTQPYDADVALVVGA  544

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W ++N+L+VG AL  V+E++  +++ RV +    + +   +G+  + A++ D S  G R 
Sbjct  545  WNIMNLLMVGCALGVVSERRNPQSSHRVVISRRCDFR---YGDEVIPASIEDVSIGGAR-  600

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
             +++ G   PH        I F+P        E  +   IRS+  E   +++G  F    
Sbjct  601  -IKVLGTAIPHIDKTRSCSICFEPLSDIG---ETCLPLTIRSSVMEDNALIIGGRFSPAN  656

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                R  +A L+F  S  W   +E+    IG++ G    LW    S+ ++ R
Sbjct  657  ASHYR-LIADLLFANSKQWSDFQESRRVNIGIIKG---TLWFLKLSIIQSGR  704


>TR:A0A6P1YML2 A0A6P1YML2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter pratisalsi OX=1745854 GN=bcsA PE=4 SV=1
Length=735

 Score = 589 bits (1519),  Expect = 0.0
 Identities = 318/704 (45%), Positives = 438/704 (62%), Gaps = 14/704 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVMR  79
            LW    +    L   P++  A  +     V+++ LLK FA  + + R + L+  + +V+R
Sbjct  9    LWAIASLVVVFLITLPISLQAHLIAGCIVVLVMILLKTFAPPVGIFRMIALALGTAIVLR  68

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP +   +F+   +L+  E +S+ + FL+ F+ + P  R    P+  ++ 
Sbjct  69   YVYWRTTSTLPPISEIENFIPGFMLYIAEMYSVFMLFLSLFVVSSPMPRRPTPPIPADQT  128

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVD+ VP+YNE  D+L+ T++AA  M YPA   TV L DDGGTDQ+C   DP  A++A+
Sbjct  129  PTVDVFVPTYNESEDLLASTVSAALGMDYPADKFTVWLLDDGGTDQKCQQDDPTAAEEAR  188

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +RR +L++LC  LG  Y TR RNEHAKAGN++  LE   G+LVVVFDADH P+RDFL  T
Sbjct  189  QRRADLEKLCEGLGARYLTRARNEHAKAGNLNNGLEHSTGDLVVVFDADHAPTRDFLKET  248

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VG+FV++ DLFLVQTPHFFI+PDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  249  VGFFVQEEDLFLVQTPHFFISPDPLERNLDTFENMPSENEMFYGIIQRGLDKWDSAFFCG  308

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL E  GF+G TITEDAETALE+HSRGW S+Y+D+ MIAGLQP++FASFI Q
Sbjct  309  SAAVLSRRALKETNGFSGVTITEDAETALELHSRGWHSIYVDKPMIAGLQPDSFASFIGQ  368
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  Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
              R RWA GMMQ+L    P  +RGL + QRL Y +S  FW F   R+MFL++PL YLFF ++
  Sbjct  369  RSRWAQGMMQILRFHMPPLKRGLSMPQRLSYCSSTLFWLFSYPRLMFLISPLFYLFFSLQ  428

  Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
              IF A+  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  QA YL  A+++ +L P 
  Sbjct  429  IFTASGAEFLAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQAVYLLPALISVILNPS  488

  Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
              S  F VTAK ETL E ++S I RP    F + +   L T+ R +  P +  VL+VVG W 
  Sbjct  489  SPTFKVTAKGETLDEGHVSQIGRPFFIIFAVLIVAFLVTIYRLLTEPFNADVLIVVGAWN  548

  Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
              VLN+++ G AL  V+E++ RR   RV++    E  I      S   ++ D S  G R+  
  Sbjct  549  VLNIVIAGCALGVVSERRNRRRTHRVELMRRGELLI---DGESYAVSIDDGSLGGARI--  603

  Query  620  RLPGVGDPHPALEAG--GLIQFQPKFPD-APQLERMVRGRIRSARREGGTVMVGVIFEAG  676
                P      P +E G   L++F P   + A     MV   IR+   +   +++G  F   
  Sbjct  604  -RPNSNVKLPEIERGATALLRFTPLANNIAINTVPMV---IRNVEYDDEGILLGCQFAPD  659

  Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              QP+  R  ++ LIF  S  W   +++  +  G+L G  R + M+
  Sbjct  660  QPLHHR-LISDLIFANSDEWEKFQQSRRKNPGVLIGTIRFIRMS  702


  >TR:A0ABS0XZ43 A0ABS0XZ43_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
  OS=Microvirga splendida OX=2795727 GN=bcsA PE=4 SV=1
  Length=731

   Score = 588 bits (1517),  Expect = 0.0
   Identities = 319/713 (45%), Positives = 435/713 (61%), Gaps = 12/713 (2%)

  Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
              L+  LW    +    L   P++  A  +  L+ V  + ++K F  + + R + L+  + +
  Sbjct  5    LIVALWAVAAILIVSLVVLPISLQAHLVAGLTVVACMIIKFFRAQGIWRQIALALGTAI  64

  Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
              V+RY FWR   T+PP    A+F+   LL+  E +S+ + FL+ F+ + P        + P
  Sbjct  65   VLRYVFWRTTSTIPPITELANFIPGFLLYLAEMYSVMMLFLSLFVVSSPMPSRKAPQIDP  124

  Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
                LPTVD+ VPSYNE A++L+ TLAAAK + YP    TV L DDGGTD++C S +   AQ
  Sbjct  125  HNLPTVDVFVPSYNESAELLATTLAAAKALTYPDDKLTVWLLDDGGTDEKCSSQNAIAAQ  184

  Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
              +A+ERR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R+FL
  Sbjct  185  QARERRAELQALCAALDVRYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARNFL  244

  Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              A TVGYF  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  +F
  Sbjct  245  AETVGYFTADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDASF  304

  Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
              FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGWKS Y+D+ +IAGLQP++FASF
  Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWKSAYVDKPLIAGLQPDSFASF  364

  Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
              I QR RWA GMMQ+L  K P F+RGL ++QRLCY++S  FW FP  R  FLV+PL YLFF
  Sbjct  365  IGQRSRWAQGMMQILRYKFPPFKRGLKLSQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFF  424

  Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
               +EIF A+  E  AY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
  Sbjct  425  SLEIFTASGGEFFAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYVQTIYLLPAVLSVIA  484

  Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
               P    F VT+K+ET+ E+ +S +  P    F + L GV+AT VR  A P    + LV G
  Sbjct  485  NPSKPTFKVTSKNETMDESRVSELGTPYFIIFGILLLGVVATGVRVWAEPYKADLTLVTG  544

  Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
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             W +LN+++ G AL  V+E+  RR + RV++E P        G+  + A + D S  G R
Sbjct  545  AWNILNLVIAGCALGVVSERATRRQSHRVRVERPCRF---VMGDEIIDAVLRDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            L   +P   +P     A G ++FQP F + P     V   IR    +   +++G  F
Sbjct  602  L--HVPPSVEPSLKKGASGTLEFQP-FANLPIQHLPV--EIRKVGMDDDGLLLGCRFMI-  655

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +    R+ +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  656  EKAEHRKMIADLVFANADQWSEFQKNRHYDIGVLRG---TLWFFMVAFYQTGR  705


>TR:A0A7W6IBP8 A0A7W6IBP8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga flocculans OX=217168 GN=GGR34_000157 PE=4
SV=1
Length=731

 Score = 588 bits (1516),  Expect = 0.0
 Identities = 316/713 (44%), Positives = 437/713 (61%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+  LW    +    L   P++  A  +  L+ V  + +LK F  + V R + L+  + +
Sbjct  5    LIVALWAVAAILIVSLIVLPISLQAHLIAGLTVVACMIILKFFRAQGVWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP    ASF+  +LL+  E +S+ + FL+ F+ + P        +
Sbjct  65   VLRYVFWRTTSTIPPITDVASFIPGILLYFAEMYSVLMLFLSLFVVSSPLSSRKAPQIDT  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            + LPTVD+ VPSYNE +D+L+ TLAAAK M YP    TV L DDGGTD++C SP+  +AQ
Sbjct  125  QNLPTVDVFVPSYNEGSDLLATTLAAAKAMDYPGDKLTVWLLDDGGTDEKCNSPNTIVAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ LC  L V Y TR RN HAKAGN++  LE   G+L+ VFDADH P+R FL
Sbjct  185  EARARRAELQALCEALEVRYLTRARNVHAKAGNLNNGLEHSTGDLIAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVG+F  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  TETVGHFTADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP+TFASF
Sbjct  305  FCGSAAVLRREALQETNGFSGLSITEDCETALELHSRGWTSVYVDKPLIAGLQPDTFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ++  K P F+RGL ++QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMMQIMHYKFPAFKRGLKLSQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E  AY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFFAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAVLSVVA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+ET+ ++ IS +  P    F + + GV+AT VR    P    + LV G
Sbjct  485  NPSKPTFKVTAKNETMDQSRISELGMPYFIIFGILVLGVIATGVRVWMEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN+++ G AL  V+E+  RR + RV++E P        G+ ++ A ++D S  G R
Sbjct  545  AWNILNLIVAGCALGVVSERATRRQSHRVRVERPCRF---IMGDEAVDAVLVDVSVGGGR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            L   +P   +P+      G+++FQP F + P  +  +   IR    +   +++G  F
Sbjct  602  L--HVPPSAEPNLKKGTSGILEFQP-FSNLPVQQLPL--EIRKVNMDDKGLLLGCRFVI-  655

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +    R  +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  656  EKHEHRRMIADLVFANADQWSEFQKNRHHDIGVLRG---TLWFFMVAFYQTGR  705
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>TR:A0A1H9NI49 A0A1H9NI49_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Faunimonas pinastri OX=1855383 GN=SAMN05216548_11625
PE=4 SV=1
Length=728

 Score = 588 bits (1515),  Expect = 0.0
 Identities = 321/713 (45%), Positives = 438/713 (61%), Gaps = 15/713 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L LLW        L+   P+   A  +I +  V  + +LK    +   R + L+  + +V
Sbjct  6    LVLLWALAAAAVMLIITLPINLQAHLIIGILVVATMIILKMMKPEGNFRLIALALGTAIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY +WR   TLPP    A+F+   +L+  E +S+ + F++ F+ + P  +    P+ PE
Sbjct  66   LRYVYWRTTSTLPPLNEPANFIPGFMLYCGEMYSVFMLFVSLFVVSSPLPKRVAPPIDPE  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
             +P VDI VP+YNE A++L++TLAAAK M YP     V L DDGG+DQ+C SPD   A
Sbjct  126  NIPFVDIFVPTYNEDAELLTMTLAAAKAMDYPTDKFKVWLLDDGGSDQKCNSPDVATAVA  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            AQERR EL  L  ELGV Y TR RNEHAKAGN++  L    G +VVVFDADH P+R FL
Sbjct  186  AQERRAELTALAEELGVTYLTRARNEHAKAGNLNNGLNHSHGSIVVVFDADHSPARSFLQ  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             T+GYF +DP LFLVQTPHFFINPDP++RNL   +  P ENEMFYG I RGLD+W  +FF
Sbjct  246  ETIGYFAQDPKLFLVQTPHFFINPDPLERNLQTFEFMPSENEMFYGLIQRGLDKWDASFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAA+LRR AL++  GF+G +ITED ETALE+HS GW SLY+D+ +IAGLQP+TFASFI
Sbjct  306  CGSAALLRREALEQTNGFSGISITEDCETALELHSSGWHSLYVDKPLIAGLQPDTFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P  +RGL + QRLCY++S  FW FPL R+MFL+APL YLFF
Sbjct  366  GQRTRWAQGMMQILRFRFPPGKRGLNLWQRLCYMSSTLFWLFPLPRLMFLIAPLFYLFFS  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EIF A+  E +AY   Y+ V+ L+QN L+ R RWP VSE+YE  Q+ YL  A+++ +
Sbjct  426  LEIFTASGAEFMAYTFSYMIVNLLMQNYLYGRFRWPWVSELYEFIQSVYLFPALLSVVAN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR   F VTAK E+L+E+ IS I +P    F + L GV AT+ R +  P    V +VVG
Sbjct  486  PRKPTFNVTAKGESLAEDRISEIGKPFYIIFAVLLVGVAATVWRIIEQPYKADVTIVVGA  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN+++ G +L  V+E+  RR + RV ++         FG +++ A V + S  G
Sbjct  546  WNILNLIMAGCSLGVVSERSTRRLSHRVDVQRRCSFH---FGEQTIPAMVENVSIGG---  599

Query  618  LVRLPGVGDPHPALE-AGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              R+  VG     ++ A   I F+P      +   MV   IR+   E G +++G  F
Sbjct  600  -ARVRAVGHLQNVVKGAAASITFEPLSSLEVKTLPMV---IRNTFNEEGGLILGCQFMPT  655

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             P   R+ +A L+F  +  W  ++EA    +G+L G      W    S+ +T R
Sbjct  656  TP-QHRQLIADLVFANADQWTKIQEARRTNVGVLRG---TWWFLTTSIYQTGR  704


>TR:D7A7Y7 D7A7Y7_ANCN5 Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter novellus (strain ATCC 8093 / DSM 506 / JCM
20403 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIMB 10456) OX=639283
GN=Snov_3170 PE=4 SV=1
Length=735

 Score = 586 bits (1511),  Expect = 0.0
 Identities = 325/703 (46%), Positives = 433/703 (62%), Gaps = 12/703 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVMR  79
            LW    +    L   P++  A  +     VV + LLK F   + +PR + L+  + +V+R
Sbjct  9    LWAISSLVVVFLITLPISLQAHLIAGCIVVVAMILLKTFGPPVGMPRTIALAIGTAVVLR  68
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Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   T+PP      F+   +L+  E +S+ + FL+ F+ + P        +  +++
Sbjct  69   YVYWRTTSTIPPITQLEDFIPGFMLYLAEMYSVFMLFLSLFVVSAPMPVRTAPAIPADQI  128

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVD+ +PSYNE A +L+ T++AA ++ YPA   TV L DDGGTDQ+C   DP+ A  A
Sbjct  129  PTVDVFIPSYNEDASLLASTVSAALSLDYPADKFTVWLLDDGGTDQKCEQDDPDQAAAAI  188

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             RR ELQQLC  LG  Y TR RNEHAKAGN++  L    G+LVVVFDADH P+RDFL  T
Sbjct  189  ARRAELQQLCAGLGARYLTRARNEHAKAGNLNNGLAHSTGDLVVVFDADHAPTRDFLTNT  248

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF+ED +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCG
Sbjct  249  VGYFLEDENLFLVQTPHFFINPDPLERNLGTFDFMPSENEMFYGIIQRGLDKWDAAFFCG  308

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL E+ GF+G TITED ETALE+HSRGW S+Y+D+ MIAGLQP+++ASFI Q
Sbjct  309  SAAVLSRRALGESNGFSGVTITEDCETALELHSRGWHSIYVDKPMIAGLQPDSYASFIVQ  368

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L    P  +RGL +AQRLCY +S  FW FP  R+MFL++PL YLFF +E
Sbjct  369  RSRWAQGMMQILRFHFPPGKRGLTLAQRLCYCSSTFFWLFPYSRLMFLISPLFYLFFSLE  428

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ L+QN L+ R RWP VSE+YE  Q+ YL  A+V+ L  PR
Sbjct  429  IFNASGAEFLAYTTTYMLVNLLMQNYLYGRYRWPWVSELYEYIQSIYLFPALVSVLANPR  488

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAK E + E ++S I  P    F + + GV+ T+ R +  P +  V++VVGGW
Sbjct  489  KPTFKVTAKGEHMDEGHVSEIGPPFFIIFGILVLGVVLTIWRLLTEPFNHDVIIVVGGWN  548

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+LL G AL  V+E++ RR   RV +    E  I      +  A + D S  G R  V
Sbjct  549  LLNLLLAGCALGVVSERRNRRRTHRVDLLRRGEIVI---NGVAYPAAIEDGSLGGAR--V  603

Query  620  RLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
            RL       P  E G  GL++F+P   + P    ++   IR+  R     ++G  F   Q
Sbjct  604  RL-AANVTVPEFERGTVGLLRFRPLATNIP--IDVLPVAIRNVERGAEGALLGCQFHPDQ  660

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            P+  R  +A LIF  S  W+   ++     G+L G  R + +A
Sbjct  661  PLHYR-LIADLIFANSNEWQKFLDSRRNNPGVLMGTIRFVRVA  702


>TR:A0A1G5GZ94 A0A1G5GZ94_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga guangxiensis OX=549386 GN=SAMN02927923_01670
PE=4 SV=1
Length=731

 Score = 586 bits (1510),  Expect = 0.0
 Identities = 327/714 (46%), Positives = 431/714 (60%), Gaps = 16/714 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L  LW    +   LL A P++     +  L  V  + +LK F  + V R + LS  + +V
Sbjct  6    LVALWAVAAMLIVLLVALPISLQTHLVAGLVVVACMIVLKFFRAQGVWRIIALSLGTAIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY FWR   T+PP    ASF+ A+LL+  E +S+ + FL+ F+ + P     P  + P
Sbjct  66   LRYVFWRTTSTIPPITEIASFIPAILLYIAEMYSVMMLFLSLFVVSSPMPSRKPPKIDPH  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
             LPTVD+ VPSYNE A +L+ TLAAAK M YP    TV L DDGGTD++C S +P  A+
Sbjct  126  NLPTVDVFVPSYNEDASLLATTLAAAKAMNYPDGKFTVWLLDDGGTDEKCNSANPHAAEA  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A+ RR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  186  ARARRAELQTLCAALDVKYLTRARNLHAKAGNLNNGLENSTGDLVAVFDADHAPTRSFLE  245
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Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVG+F  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AFF
Sbjct  246  ETVGFFSADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP+TFASFI
Sbjct  306  CGSAAVLRREALQETNGFSGLSITEDCETALELHSRGWSSVYVDKPLIAGLQPDTFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P  +RGL + QRL Y++S  FW FP  R  FL++PL YLFF
Sbjct  366  GQRSRWAQGMMQILSFRFPPLKRGLKLTQRLAYMSSTLFWLFPFSRFAFLLSPLCYLFFS  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  AI++ +
Sbjct  426  LEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAIISVIAN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR   F VT+K E++ E+ +S +  P    F + L GV+AT VR    P    + LV G
Sbjct  486  PRKPTFKVTSKGESMLESRVSELGMPYFIIFGILLLGVVATGVRVWLEPYKADLTLVTGA  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W VLN+++ G AL  V+E+  RR + RV+ +         FG+  + A+V D S  G RL
Sbjct  546  WNVLNLIIAGCALGVVSERASRRMSHRVRTDRVCRF---LFGDEVIEASVRDISVGGARL  602

Query  618  LVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
             V         P L+ G  G ++F P   D P     V   IR    +   +++G  F
Sbjct  603  HV----APSNEPTLKKGALGTLEFMP-HADLPVQTMPV--EIRKVGMDDNGLLLGCRFLI  655

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             +P   R  VA L+F ++  W   ++   + IG+L G    LW    SL +T R
Sbjct  656  DKPEHHR-LVADLVFADADQWSAFQKRRHQDIGVLRG---TLWFFMVSLYQTGR  705


>TR:A0A839ZFC9 A0A839ZFC9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter tetraedralis OX=217068 GN=FHS55_003982
PE=4 SV=1
Length=735

 Score = 586 bits (1510),  Expect = 0.0
 Identities = 317/695 (46%), Positives = 432/695 (62%), Gaps = 12/695 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVMR  79
            LW    +    L   P++  A  +     V+ + +LK F   + + R + L+  + +V+R
Sbjct  9    LWAIASLIVVFLITLPISLQAHLIAGCIVVLAMIVLKTFGPPVGIFRMIALALGTAIVLR  68

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F    +L+  E +S+ + FL+ F+ + P       P+   E+
Sbjct  69   YVYWRTTSTLPPITELGNFTIGFMLYIGEMYSVFMLFLSLFVVSSPMPERKAPPIPEGEV  128

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VDI VPSYNE  D+L+ TL+AA ++ YP    TV L DDGGTDQ+C   D   A +AQ
Sbjct  129  PKVDIFVPSYNEDPDLLASTLSAALSIDYPVDRFTVWLLDDGGTDQKCEQDDSVKALEAQ  188

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +RR ELQ++C  LG  Y TR RNEHAKAGN++  L+   G+LV VFDADH P+RDFL +T
Sbjct  189  KRRVELQRICDGLGCRYLTRARNEHAKAGNLNNGLKHSDGDLVAVFDADHAPTRDFLKQT  248

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF+E  +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCG
Sbjct  249  VGYFLEQENLFLVQTPHFFINPDPLERNLNTFDFMPSENEMFYGIIQRGLDKWDSAFFCG  308

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAA++ R+AL E  GF G TITEDAETALE+HSRGW S+Y+DR ++AGLQPETFASFI Q
Sbjct  309  SAALVNRKALAETNGFQGITITEDAETALELHSRGWHSIYVDRPLVAGLQPETFASFIGQ  368

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L    P  +RGL + QRLCY++S  FW FP  R+MFL++PL YLFF +E
Sbjct  369  RSRWAQGMMQILRFHVPPLKRGLSLQQRLCYMSSTLFWLFPYPRLMFLISPLFYLFFSLE  428
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Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E  AY   Y+ V+ L+QN L+ R RWP +SE+YE  QA YL  A+++ L+ PR
Sbjct  429  IFNASGAEFFAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQAIYLLPALISVLINPR  488

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAK ETL E ++S I RP    F + +  +L T+ R +  P +  V++VVG W
Sbjct  489  KPTFNVTAKGETLDEGHVSEIGRPFFIIFAVLIVALLVTIWRLLTEPFNADVIIVVGAWN  548

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E++ RR A RV +     +  I    + S  AT+ D S  G R+
Sbjct  549  LLNILIAGCALGVVSERRNRRRAHRVDLMRRCDLII---NDVSYPATIDDGSLGGARV--  603

Query  620  RLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
              P      P L+ G   L++F+P   + P     +   IR+A R+   +++G  F   Q
Sbjct  604  -RPNANVTMPELDRGQPALLRFKPLAANIP--IDTLPFTIRNADRDADGLLIGGEFAPDQ  660

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHG  712
            P+  R  ++ LIF  S  W+  +E+  +  G+L G
Sbjct  661  PLHYR-LISDLIFANSDQWKKFQESRRKNPGVLRG  694


>TR:A0ABS0HRY2 A0ABS0HRY2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga terrestris OX=2791024 GN=bcsA PE=4 SV=1
Length=731

 Score = 585 bits (1508),  Expect = 0.0
 Identities = 318/713 (45%), Positives = 430/713 (60%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+  LW    +    L   P++  A  +  L+ V  + ++K F  + + R + L+  + +
Sbjct  5    LIVALWAVAAILIVSLVVLPISLQAHLVAGLTVVACMIIIKFFRAQGIWRQIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP    A+F+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEVANFIPGFLLYLAEMYSVMMLFLSLFVVSSPMPSRKAPQIDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
              LPTVD+ VPSYNE AD+L+ TLAAAK M YPA   TV L DDGGTD++C S +   A
Sbjct  125  HNLPTVDVFVPSYNEGADLLATTLAAAKAMTYPADKLTVWLLDDGGTDEKCSSQNALAAL  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ERR ELQ LC  L + Y TR RN HAKAGN++  L+    +LV VFDADH P+R+FL
Sbjct  185  QARERRAELQALCTALDIRYLTRARNLHAKAGNLNNGLDHSTSDLVAVFDADHAPARNFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AF
Sbjct  245  TETVGYFTADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSAYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P F+RGL ++QRLCY++S  FW FP  R  FLV+PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPFKRGLKLSQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E  AY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFFAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYVQTIYLLPAVLSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VT+K+ET+ E+ +S +  P    F + L GV+AT VR  A P    + LV G
Sbjct  485  NPSKPTFKVTSKNETMDESRVSELGTPYFIIFGILLLGVVATGVRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN+++ G AL  V+E+  RR + RV++E P        G   + A + D S  G R
Sbjct  545  AWNILNLIIAGCALGVVSERATRRLSHRVRVERPCRF---VMGGEVIDAVLRDVSVGGAR  601
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Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
              V +P   +P     A G I+FQP F + P     V   IR    +   +++G  F
Sbjct  602  --VHVPPSVEPRLKKGAAGTIEFQP-FANLPIQHLPV--EIRKVGMDDDGLLLGCRFMI-  655

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +    R+ +A L+F  +  W   +      IG+L G    LW    +  +T R
Sbjct  656  EKAEHRKMIADLVFANADQWSDFQRNRHYDIGVLRG---TLWFFMVAFYQTGR  705


>TR:A0A936ZID1 A0A936ZID1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga aerilata OX=670292 GN=bcsA PE=4 SV=1
Length=731

 Score = 585 bits (1507),  Expect = 0.0
 Identities = 319/713 (45%), Positives = 432/713 (61%), Gaps = 12/713 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+   W         L A P++  A  +  L+ V  + +LK F  + + R + L+  + +
Sbjct  5    LIVAFWAVAAALIISLVALPISLQAHLVAGLTVVACMIILKFFRAQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   T+PP    A+F+   LL+  E +S+ + FL+ F+ + P        + P
Sbjct  65   VLRYVFWRTTSTIPPITEVANFIPGFLLYLAEMYSVMMLFLSLFVVSSPMRSRKAPQIDP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
              LPTVD+ VPSYNE AD+L+ TLAAAK M YP+   TV L DDGGTD++C S D   AQ
Sbjct  125  HNLPTVDVFVPSYNEGADLLATTLAAAKAMTYPSDKVTVWLLDDGGTDEKCNSADIIKAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  185  EARARRAELQALCASLEVKYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  D +LFLVQTPHFFINPDP++RNL+     P ENEMFYG I RGLD+W  AF
Sbjct  245  TETVGYFSIDKNLFLVQTPHFFINPDPLERNLSTFQTMPLENEMFYGVIQRGLDKWDAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETALE+HSRGW S+Y+D+ +IAGLQP++FASF
Sbjct  305  FCGSAAVLRREALQETNGFSGVSITEDCETALELHSRGWTSIYVDKPLIAGLQPDSFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  K P  +RGL ++QRLCY++S  FW FP  R  FL++PL YLFF
Sbjct  365  IGQRSRWAQGMMQILRYKFPPLKRGLKLSQRLCYMSSTLFWLFPFSRFCFLISPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  425  SLEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPAVLSVVA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VT+K+E++ E+ +S +  P    F + + GV+AT VR  A P    + LV G
Sbjct  485  NPSKPTFKVTSKNESMEESRVSELGTPYFIIFGILVLGVVATGVRVWAEPYKADLTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W VLN+++ G AL  V+E+  RR + RV++E P        G   + A + D S  G R
Sbjct  545  AWNVLNLVIAGCALGVVSERASRRQSHRVRVERPCRF---VMGTEVIDAMLKDVSVGGAR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            L   +P   +P     A G ++FQP F + P     V   IR    +   +++G  F
Sbjct  602  L--HVPPSAEPSLKRGAAGTLEFQP-FSNLPVQHLPV--EIRKVGMDDKGLLLGCRFMIE  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +P   R  +A L+F  +  W   ++     IG+L G    +W    +  +T R
Sbjct  657  KP-EHRRLIADLVFANADQWSEFQKNRHHDIGVLRG---TIWFFMVAFYQTGR  705


>TR:A0A7W4YYH0 A0A7W4YYH0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga lupini OX=420324 GN=FHR70_003395 PE=4 SV=1
Length=725
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```
 Score = 584 bits (1505),  Expect = 0.0
 Identities = 315/709 (44%), Positives = 431/709 (61%), Gaps = 12/709 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LW    +    L   P++  A  +  L+ V  + ++K F  + + R + L+  + +V+RY
Sbjct  3    LWAVAAILIVSLVVLPISLQAHLVAGLTVVACMIIIKFFRAQGIWRQIALALGTAIVLRY  62

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             FWR   T+PP    A+F+   LL+  E +S+ + FL+ F+ + P        + P  LP
Sbjct  63   VFWRTTSTIPPITEVANFIPGFLLYLAEMYSVMMLFLSLFVVSSPMPSRKAPQIDPHNLP  122

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVD+ VPSYNE A++L+ TLAAAK M YP    TV L DDGGTD++C S +   +Q+A+E
Sbjct  123  TVDVFVPSYNEGAELLATTLAAAKAMTYPEDKLTVWLLDDGGTDEKCSSQNAIASQQARE  182

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R+FL  TV
Sbjct  183  RRAELQALCAALDVRYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARNFLTETV  242

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  +FFCGS
Sbjct  243  GYFTADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDASFFCGS  302

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR AL E  GF+G +ITED ETALE+HSRGW S Y+D+ +IAGLQP++FASFI QR
Sbjct  303  AAVLRREALQETNGFSGVSITEDCETALELHSRGWTSAYVDKPLIAGLQPDSFASFIGQR  362

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ++  K P F+RGL ++QRLCY++S  FW FP  R  FLV+PL YLFF +EI
Sbjct  363  SRWAQGMMQIIRYKFPPFKRGLRLSQRLCYMSSSMFWLFPFSRFCFLVSPLCYLFFSLEI  422

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            F A+  E  AY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +  P
Sbjct  423  FTASGGEFFAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYVQTIYLLPAVLSVIANPSK  482

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VT+K+ET+ E+ +S +  P    F + L GV+AT VR  A P    + LV G W +
Sbjct  483  PTFKVTSKNETMDESRVSELGTPYFIIFGILLLGVVATGVRVWAEPYKADLTLVTGAWNI  542

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LN+++ G AL  V+E+  RR + RV++E P        G+  + A + D S  G RL
Sbjct  543  LNLIIAGCALGVVSERATRRQSHRVRVERPCRF---VMGDEVIDAVLRDVSVGGARL--H  597

Query  621  LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
            +P   +P     A G ++FQP F + P     V   IR    +   +++G  F   +
Sbjct  598  VPPSVEPRLKKGAAGTLEFQP-FANLPIQHLPV--EIRKVGMDDNGLLLGCRFMI-EKAE  653

Query  681  VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             R+ +A L+F  +  W   ++     IG+L G    LW    +  +T R
Sbjct  654  HRKMIADLVFANADQWSEFQKNRHYDIGVLRG---TLWFFMVAFYQTGR  699


>TR:A0A178Y421 A0A178Y421_SINSA Cellulose synthase catalytic subunit [UDP-forming]
OS=Sinorhizobium saheli OX=36856 GN=ATB98_06710 PE=4
SV=1
Length=725

 Score = 584 bits (1505),  Expect = 0.0
 Identities = 327/709 (46%), Positives = 433/709 (61%), Gaps = 16/709 (2%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            ++    W  + +    L   PV    Q + ++  V  +AL+K        R + L+  S
Sbjct  4    IVTLAAWALIALCLVALITLPVNLQTQLIASVLVVTFMALIKLMKAGGKWRLIALAFGSA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR  ETLPP     +F+    LL+  E +++ +  L+ F+ A P      R
Sbjct  64   MVLRYIYWRTTETLPPFNQPENFIPGFLLYLAELYNVMMLALSLFVVAMPLPSRPSRAAT  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
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            P + P VD+ VPSYNE   +L+ TLAAAK M YPA   TV L DDGGT Q+  S +   A
Sbjct  124  PGKYPKVDVFVPSYNEDIGLLANTLAAAKGMDYPAEKLTVWLLDDGGTLQKRNSTNLIEA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q+A +R R+LQ+LC +L V Y TRERNEHAKAGN++  ++   G+L+ VFDADH P+RDF
Sbjct  184  QRAAQRHRDLQKLCSDLNVRYLTRERNEHAKAGNLNNGMQHSNGDLIAVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  A
Sbjct  244  LLETVGYFEDDPRLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR+AL++ GGF+G +ITED ETAL +HSRGWKS+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLRRKALEDTGGFSGLSITEDCETALALHSRGWKSVYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L+ + PLF+ GL I QRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILMFRMPLFKGGLSIPQRLCYMSSTLFWLFPFSRTIFLFAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IF A+  E LAY   Y+ V+  +QN L+   RWP +SE+YE AQ  +L  A+V+ L
Sbjct  424  FDLQIFTASGGEFLAYTLVYMLVNLTMQNYLYGSFRWPWISELYEYAQTVHLLPAVVSVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              PR   F VTAKDE++ E+ +S I RP    F +  + VL T+ R  + P    V LVV
Sbjct  484  ANPRKPTFKVTAKDESVRESRLSEISRPFFVIFAVLFAAVLITVYRVYSEPDKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN++L G AL  V+E+ +R A+ RV++    E    A G     ATV D S  G
Sbjct  544  GGWNLLNLILAGCALGVVSERGERAASRRVKVSRRCEF---AVGEEWYPATVEDVSAHGA  600

Query  616  RLLV-RLPGVGDPHPALEAGGLIQFQPKFPD-APQLERMVRGRIRSARREGGTVMVGVIF  673
            R+ V  LPG G    A++    I+F+P   D  P+    +    IR+    G   ++G  +
Sbjct  601  RVQVYGLPGDG---LAIDTRARIRFEPYSGDGTPETLPLT---IRNVEVSGDLTIIGCRY  654

Query  674  EAGQPIAVR--ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
                P A R    VA LIF  S  W   +       GLL G    LW+A
Sbjct  655  ---TPEAARHHSLVADLIFANSEQWSEFQHMRRYNPGLLRGTLWFLWLA  700


>TR:A0ABU0LWP2 A0ABU0LWP2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter amanitiformis OX=217069 GN=QOZ99_004031
PE=4 SV=1
Length=735

 Score = 584 bits (1505),  Expect = 0.0
 Identities = 316/695 (45%), Positives = 432/695 (62%), Gaps = 12/695 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVMR  79
            LW    +    L   P++  A  +     V+ +  LK F   + + R + L+  + +V+R
Sbjct  9    LWAIASLIVVFLITLPISLQAHLIAGCIVVLAMIALKTFGPPVGIFRMIALALGTAIVLR  68

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP +   +F    +L+  E +S+ + FL+ F+ + P       P+   E+
Sbjct  69   YVYWRTTSTLPPISELGNFTIGFMLYIGEMYSVFMLFLSLFVVSSPMPERKAPPIPEGEV  128

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VDI VPSYNE  D+L+ TL+AA ++ YP    TV L DDGGTDQ+C   D   A +AQ
Sbjct  129  PKVDIFVPSYNEDPDLLASTLSAALSIDYPVDRFTVWLLDDGGTDQKCEQDDSVKALEAQ  188

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +RR ELQ++C  LG  Y TR RNEHAKAGN++  L+   G+LV VFDADH P+RDFL +T
Sbjct  189  QRRVELQRICDGLGCRYLTRARNEHAKAGNLNNGLKHSDGDLVAVFDADHAPTRDFLKQT  248

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF+E  +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCG
Sbjct  249  VGYFLEQENLFLVQTPHFFINPDPLERNLNTFDFMPSENEMFYGIIQRGLDKWDSAFFCG  308

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
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            SAA++ R+AL E  GF G TITEDAETALE+HSRGW S+Y+DR ++AGLQPETFASFI Q
Sbjct  309  SAALVNRKALAETNGFQGITITEDAETALELHSRGWHSIYVDRPLVAGLQPETFASFIGQ  368

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L    P  +RGL + QRLCY++S  FW FP  R+MFL++PL YLFF +E
Sbjct  369  RSRWAQGMMQILRFHVPPLKRGLTLQQRLCYMSSTLFWLFPYPRLMFLISPLFYLFFSLE  428

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E  AY   Y+ V+ L+QN L+ R RWP +SE+YE  QA YL  A+++ L+ P+
Sbjct  429  IFNASGAEFFAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQAIYLLPALISVLINPK  488

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAK ETL E ++S I RP    F + +  +L T+ R +  P +  V++VVG W
Sbjct  489  KPTFNVTAKGETLDEGHVSEIGRPFFIIFAVLIVALLVTIWRLLTEPFNADVIIVVGAWN  548

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E++ RR A RV +    +  I    + S  AT+ D S  G R+
Sbjct  549  LLNILIAGCALGVVSERRNRRRAHRVDLMRRCDLII---NDVSYPATIDDGSLGGARV--  603

Query  620  RLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
              P      P L+ G   L++F+P   + P     +   IR+A R+   +++G  F   Q
Sbjct  604  -RPNANVTMPELDRGQPALLRFKPLAANIP--IDTLPFTIRNADRDADGLLIGGEFAPDQ  660

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHG  712
            P+  R  ++ LIF  S  W+  +E+  +  G+L G
Sbjct  661  PLHYR-LISDLIFANSDQWKKFQESRRKNPGVLRG  694


>TR:A0ABU5I6Q2 A0ABU5I6Q2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Fulvimarina uroteuthidis OX=3098149 GN=bcsA PE=4 SV=1
Length=742

 Score = 583 bits (1503),  Expect = 0.0
 Identities = 301/600 (50%), Positives = 402/600 (67%), Gaps = 7/600 (1%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            W+   + F +L   PV+  AQ  IA +A+ +   +     + V R++ LSA S++V RY
Sbjct  10   WLFFALSFLILVQQPVSVDAQWNIAATALAVATAIYIIRLEGVWRYVFLSAISIVVFRYA  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   T+P P    SF+ A+LL+  E + + +  L+ F+ ADP +RP       EELP+
Sbjct  70   YWRTTSTIPSPDDLISFIPAILLYGAEMYCLLMLALSLFVVADPIERPRAAQFPDEELPS  129

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VPSYNE +D+LS+TLAAAK + YPA    + L DDGTDQ+ +S D   A  A +R
Sbjct  130  VDVFVPSYNESSDILSLTLAAAKGLDYPAEKLRIFLLDDGGTDQKRLSSDKAAASAAIDR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
              ELQ LC ELGV Y TR  N HAKAGN++  L   +G+LVVVFDADH P+R+FL  TVG
Sbjct  190  HHELQHLCTELGVTYLTRSANVHAKAGNLNNGLLHSRGDLVVVFDADHAPAREFLRETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            +F+ED  LFLVQTPHFF NPDP++RNL+     P ENEMFYG+I +GLD+W  AFFCGSA
Sbjct  250  HFIEDRKLFLVQTPHFFANPDPLERNLSTFQHMPSENEMFYGQIQKGLDKWNSAFFCGSA  309

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVLRR AL++ GGF+G +ITED ETAL++HSRGW SLY+DR M+ GLQP+T ASFI QR
Sbjct  310  AVLRRSALEQVGGFSGVSITEDCETALDLHSRGWNSLYVDRPMVVGLQPDTVASFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RW  GM+Q++LLKNPLFR GL + QRLCY++SM FWFFP VR+ FLVAPL+ + F ++IF
Sbjct  370  RWCRGMLQIMLLKNPLFRSGLSLPQRLCYMSSMMFWFFPFVRLAFLVAPLLLILFDLKIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A+ +E +AY   YL    L++N L+ R RWP VS++YE  Q+ YL RAIV+ +L PR
Sbjct  430  DASVDEFIAYSVSYLIAGELLRNYLYGRVRWPWVSDLYEYVQSVYLLRAIVSVILNPRRP  489

Query  502  RFAVTAKDETLSENYISPIYRP--LLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
             F VTAK +TL  N +S +  P   +F  LL  +GV+A   R+   P    +LLVVG W
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Sbjct  490  TFNVTAKGQTLDRNQLSELAWPYFAIFGVLLFATGVVA--YRFQTEPEIGGMLLVVGAWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+++ G AL  V E+ +RR  PR+  +   E Q+  FG+  +  +V D S  G ++ V
Sbjct  548  LLNLIVAGAALGVVTERMERRQTPRLASQ--REGQL-FFGDERIDVSVEDVSLGGAKVTV  604


>TR:A0ABT5YPN5 A0ABT5YPN5_9PROT Cellulose synthase catalytic subunit [UDP-forming]
OS=Aquibaculum arenosum OX=3032591 GN=bcsA PE=4 SV=1
Length=741

 Score = 582 bits (1501),  Expect = 0.0
 Identities = 324/727 (45%), Positives = 450/727 (62%), Gaps = 19/727 (3%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            +  LWV +L+   +LA  P++  AQ  ++++  V + ++         R L    AS +V
Sbjct  1    MLALWVLILLIHLVLAGQPLSADAQIALSMTLFVALIVIGRLPRTSFFRVLFCGVASFMV  60

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR-PLQP  136
            +RY  WR   T+PP     +F+  ++L+  E +++ +FF++ F+  DP  RP  +    P
Sbjct  61   LRYLIWRTQNTIPPVEDIYAFVPGVVLYGAEVYAMLMFFISLFIVIDPMRRPVAKLDDDP  120

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             + P+VD+ VP+Y+E   +L+ TL+AA  M YP    TV L DDGGTDQ+  +     +
Sbjct  121  SKAPSVDVFVPTYDEDPHILAATLSAASRMRYPQGRMTVYLLDDGGTDQKRRA-----SA  175

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A +R + L+++CRELGVVY TRERNEHAKAGN++AAL + +GEL+ V DADH P+ DFL
Sbjct  176  DAVKRGKLLEEMCRELGVVYLTRERNEHAKAGNLNAALPKTRGELIAVLDADHAPTEDFL  235

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVG+F + P LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLDRWG +F
Sbjct  236  ENTVGHFADKPKLFLVQTPHFFINPDPLERNLNTFDYMPGENEMFYGVIQRGLDRWGASF  295

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR+AL++ GGF+G TI ED ET++++H+ GW+SLYID+ MIAGLQPETF+SF
Sbjct  296  FCGSAAVLRRQALEQVGGFSGRTIVEDCETSVDLHALGWESLYIDKPMIAGLQPETFSSF  355

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            + QR RW  GM+Q+ LLKNPLFRRGL + QRL YL+S  FWFF   R+ F + PL YLFF
Sbjct  356  MSQRIRWGQGMVQIFLLKNPLFRRGLDLGQRLGYLSSNLFWFFGFARLTFFLMPLFYLFF  415

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+ ++ AT  E LAY   Y+ V+ L  + LF R RWPL+SE+YE  QA ++ARA+++ +L
Sbjct  416  GLAVYSATAAEFLAYTTFYIGVTLLTSSYLFGRTRWPLLSELYEFIQATFMARALISVML  475

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            +P +  F VTAK ET+ +N +S   RPL         G++AT+ R+ A+P  + ++LVVG
Sbjct  476  KPTAPSFNVTAKGETVDKNKLSQQARPLFIITGFLTLGLIATVWRYFAYPDTQDIVLVVG  535

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GW +   LL    LR V E++Q R APRVQ+E P    I     R L A ++DAS  GV+
Sbjct  536  GWNLFGFLLAVQGLRVVCERKQVRRAPRVQIEEPVALMIGE--ERRLPAYIVDASIMGVK  593

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            +L  LP         LE+  L     K     +    +R ++R+ R E   + +G  F
Sbjct  594  VL--LPRGAASQEELESYPLAVSFVK--PGEEASGRLRIQLRNVRVEEEGIAIGAEFV--  647

Query  677  QPIAVR-ETVAYLIFGESAHWRTMREA-TMRPIGLLHGMARILWMAAASLPKTAR---DF  731
            +P       +A LIF  S  W    E    R  G++ G+ R L  +A S+   AR
Sbjct  648  EPTGAEFGMIAELIFISSNRWVAFLEGRRARSPGVVMGVLRFLLGSALSIYYVARFLLKL  707

Query  732  MDEPARR  738
             D P+ R
Sbjct  708  QDAPSPR  714


>TR:A0A1E3H446 A0A1E3H446_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobrevis pamukkalensis OX=1439726 GN=bcsA PE=4
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SV=1
Length=667

 Score = 581 bits (1498),  Expect = 0.0
 Identities = 304/601 (51%), Positives = 391/601 (65%), Gaps = 3/601 (0%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            LL + +    + F  L A PV  + Q ++ ++ V  + L+ P A K   R L ++ A  +
Sbjct  5    LLTVAFALAALVFLALVAQPVGAAGQLVVGMTLVAAMLLIWPLARKGAGRLLFVALALGV  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V RY +WR   TLP P+    F+  +LL+ VE FS+ + F++ F+ ADP +R   R
Sbjct  65   VGRYVYWRSTSTLPDPSDLVDFIPGVLLYGVEMFSVLMLFVSLFVIADPKERAEIRVDDD  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             +LPTVD+ VPSYNE AD+L+ TLAAA  M YPA    V L DDGGTDQ+C S DP  A
Sbjct  125  ADLPTVDVFVPSYNESADLLATTLAAAVAMDYPAEKLRVYLLDDGGTDQKCQSDDPVTAH  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A+ RR EL++LCR+LGV Y TRE+N  AKAGNM+AAL R  G+LV VFDADH P R FL
Sbjct  185  AARARRTELRELCRDLGVTYLTREKNVSAKAGNMNAALPRTTGDLVAVFDADHAPVRSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVG+F+EDP LFLVQTPHFF+NPDPI++NL+L    P ENEMFYG I +GLDRW  AF
Sbjct  245  RLTVGHFLEDPRLFLVQTPHFFLNPDPIEKNLSLFKSMPSENEMFYGVIQKGLDRWNSAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRR AL++AGGF G TITED ETAL +H+RGW S YID  +IAGLQPETF+SF
Sbjct  305  FCGSAALLRRAALEDAGGFDGVTITEDCETALTLHARGWNSRYIDTPLIAGLQPETFSSF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GMMQ+L+LKNPLFR GL +AQR+CYL+S  FW F + RM F+VAPL+++FF
Sbjct  365  IGQRSRWCRGMMQILILKNPLFRAGLSLAQRVCYLSSSLFWLFSITRMTFVVAPLLHIFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EI+ A  +E +AY   Y+  + ++QN LF R RWP +SE+YE  Q+ YL RAIV+ +L
Sbjct  425  SLEIYEANLQEFIAYTCVYMLANMMLQNYLFGRVRWPWMSELYEYVQSVYLTRAIVSVVL  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR    F VTAK  TL    +S    P    F L L        +RW   P  R +L VVG
Sbjct  485  NPRRPTFNVTAKGLTLDREQLSEFALPYFAIFGLLLVAAGVAGLRWWMEPASRDLLAVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W  LN+L+ G AL  V+E+ +RR   R+ +   +   +           V D S+ G R
Sbjct  545  LWNGLNLLIAGLALGVVSERAERRRNQRLDI---SRKGVLTLAGTPFPVLVEDVSSGGAR  601

Query  617  L  617
            +
Sbjct  602  V  602


>TR:A0ABV2MXA9 A0ABV2MXA9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aquamicrobium terrae OX=1324945 GN=ABID37_001648 PE=4
SV=1
Length=730

 Score = 581 bits (1498),  Expect = 0.0
 Identities = 322/716 (45%), Positives = 437/716 (61%), Gaps = 16/716 (2%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            ++L ++W         + + P+   A  +     + ++  +K F  +   R + LS  +
Sbjct  5    LVLGIMWALAAACVIFIVSMPINLQAHLIAGTIVLAVMIAMKMFRPEGTWRLVALSLGTA  64

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   T+PP +   +F+  LLL+  E +S+ +  L+ F+ A P        +
Sbjct  65   IVLRYVYWRTTSTIPPVSQLENFIPGLLLYLAEMYSVFMLALSLFIVARPLPSRPAIEVA  124

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              ELP+VD+ +PSYNEPA +L+ T+AAAK M YP    TV L DDGGT Q+  + D   A
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Sbjct  125  EAELPSVDVFIPSYNEPAVLLADTVAAAKAMDYPPDRLTVWLLDDGGTVQKRNADDVATA  184

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q AQER  ELQQLC +LG  Y TRERNEHAKAGN++  L    G+L+ VFDADH P+R F
Sbjct  185  QAAQERHLELQQLCADLGAHYLTRERNEHAKAGNLNNGLAHSSGDLIAVFDADHAPARSF  244

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF EDP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +
Sbjct  245  LRETVGYFNEDPRLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAS  304

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL+E  GFAG +ITED ETA+E+HSRGW S+Y+D+ +IAGLQP TFAS
Sbjct  305  FFCGSAAVLRREALEETDGFAGISITEDCETAVELHSRGWNSVYVDKPLIAGLQPATFAS  364

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L  + P  +RGL + QRLCY++S  FW FP  R +FL+APL YLF
Sbjct  365  FIGQRSRWAQGMMQILRFRFPPLKRGLSLPQRLCYMSSTLFWLFPFPRTIFLLAPLFYLF  424

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IF A+  E LAY   Y+ V+ ++QN L+ R RWP +SE+YE  Q+ +L  A+++ +
Sbjct  425  FDLQIFTASGGEFLAYTLSYMVVNLMMQNYLYGRFRWPWISELYEYIQSVHLLPAVISVM  484

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR   F VTAKDE++S + +S + RP    F L L GV  T  R  A P    V LVV
Sbjct  485  LNPRKPTFKVTAKDESISTSRLSELSRPFFLIFALLLVGVGVTAWRVYAEPWKADVTLVV  544

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRS--LTATVLDASTS  613
            GGW +LN+++ G AL  V+E+++R A  RV++    E     FG     L A + D S +
Sbjct  545  GGWNLLNLIMAGCALGVVSERRERAATRRVKVNRRCE-----FGREGLWLPAMIEDVSVN  599

Query  614  GVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIF  673
            G R  VR+ G        E    I+F P     P    +V   IR++ +EG T+ VG  +
Sbjct  600  GAR--VRIHGKNAQGAVAEGQANIRFTPLSGGDPAALPVV---IRNSEKEGDTLAVGCQY  654

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                P   R  VA LIF  +  W   +++  R  G++ G    LW    +L +T R
Sbjct  655  VRSLPDHHR-LVADLIFANADQWTQFQKSRRRNPGVVIG---TLWFLRLALYQTWR  706


>TR:A0ABY1Y9B6 A0ABY1Y9B6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium cavarae OX=2528239 GN=bcsA PE=4 SV=1
Length=730

 Score = 581 bits (1498),  Expect = 0.0
 Identities = 329/729 (45%), Positives = 436/729 (60%), Gaps = 13/729 (2%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V+ F LW+ +     L+   PV+     +    ++ L+A +K    K   R + L   +
Sbjct  4    VIAFTLWLFVSACVLLIITLPVSLQTHLIATAISLALLATIKSLNGKGAWRLIGLGFGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  64   IVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKGRPGS  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            P  +PTVD+ VP+YNE A++L+ TLAAAKNM YPA   TV L DDGGT Q+  +P+   A
Sbjct  124  PGYVPTVDVFVPTYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGTVQKRNAPNGLEA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q A  R  ELQ+LC +LGV Y TRERN HAKAGN++  L+   GELV VFDADH P+RDF
Sbjct  184  QAATRRHAELQKLCADLGVNYLTRERNVHAKAGNLNNGLDHSTGELVTVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GA
Sbjct  244  LLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL E  GF+G +ITED ETAL +HSRGW SLY+D+ +IAGLQP TF S
Sbjct  304  FFCGSAAVLRREALKETDGFSGVSITEDCETALALHSRGWNSLYVDKPLIAGLQPATFTS  363
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Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILIFRQPLFRRGLSFPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ L
Sbjct  424  FDLQIFVASGGEFLAYTAAYMLVNLMIQNFLYGSFRWPWISELYEYVQTVHLLPAVVSVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              P    F VTAKDE++SE  +S I RP    F + +  ++  + R  A P    V LVV
Sbjct  484  FNPSKPTFKVTAKDESISEARLSEISRPFFVIFFVLVIAMIFAIYRIYAEPYKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN++  G AL  V+E+ ++ A+ R+ ++   E Q+   G   L ATV + S  G+
Sbjct  544  GGWNLLNIIFAGCALGVVSERGEKSASRRITVKRRCELQLQEDG-PWLPATVQNVSVHGM  602

Query  616  RLLV---RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
             + +    L  V    PA     +I+  P  P AP    M    +R+ +++G T  VG
Sbjct  603  LINIFEKDLDVVEKGRPA-----IIRVDPYSPGAP--SSMTIDIVRTVKQQGFT-SVGCT  654

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
            F   + I  R  +A LIF  S  W   + A     GL+ G    + +A     +    FM
Sbjct  655  FAPKENIEHR-LIADLIFANSEQWTEFQRARRGNPGLIRGTITFMGIALFQTQRGLFYFM  713

Query  733  DEPARRRRR  741
                 R R+
Sbjct  714  RSFRTRARQ  722


>TR:A0ABW9YTH2 A0ABW9YTH2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga arsenatis OX=2692265 GN=bcsA PE=4 SV=1
Length=715

 Score = 581 bits (1498),  Expect = 0.0
 Identities = 315/686 (46%), Positives = 424/686 (62%), Gaps = 10/686 (1%)

Query  32   LAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPP  91
            L   PV    Q  IA+  + ++A +K    +   R L  +  ++LV+RY +WR   TLP
Sbjct  10   LVLQPVGTETQWAIAMMCLAVMAAIKLLNLQGYWRHLFFTLGALLVLRYVYWRTTATLPD  69

Query  92   PALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNE  151
                  F+  + ++A E F + +  L+ F+ + P  RP    L   E PTVD+ VPSYNE
Sbjct  70   TNNLMDFVPGITIYAAEMFCVVMLGLSLFVISRPIQRPRAPRLSDVEAPTVDVFVPSYNE  129

Query  152  PADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRE  211
             A +L++TL+AAK M YP    TV L DDGGTDQ+  S +P +A  A  RR ELQ LCRE
Sbjct  130  DAALLAMTLSAAKAMDYPRDKLTVYLLDDGGTDQKVQSANPAIADAALRRREELQVLCRE  189

Query  212  LGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFL  271
            LGV Y TR RN +AKAGN+S  L   KG+LVVVFDADH P+RDFL  TVG+F  DP LFL
Sbjct  190  LGVEYLTRSRNVNAKAGNLSNGLLHSKGDLVVVFDADHAPARDFLVETVGFFTRDPKLFL  249

Query  272  VQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDE  331
            VQTPHFFINPDP++RNL+  DR P ENEMFYG I +GLD+W  +FFCGSAAVLRR AL++
Sbjct  250  VQTPHFFINPDPVERNLSTFDRMPSENEMFYGMIQKGLDKWNASFFCGSAAVLRRSALEQ  309

Query  332  AGGFAGETITEDAETALEIHSRGWKSLYIDRAIAGLQPETFASFIQQRGRWATGMMQML  391
            AGGFAG +ITED ETALE+H+ GW+SLY+D+ +IAGLQPETFA+FI QR RW TGMMQ+
Sbjct  310  AGGFAGTSITEDCETALELHATGWRSLYVDKPLIAGLQPETFAAFIGQRTRWCTGMMQIF  369

Query  392  LLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAY  451
            L KNPL +RGL +AQR CYL+S  FW FPL R+ F+ APL+Y+FF ++++ AT  E  AY
Sbjct  370  LTKNPLLKRGLTLAQRACYLSSCMFWLFPLPRITFIFAPLLYIFFNLKVYNATVGEFGAY  429

Query  452  MPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDET  511
               YLA + L+Q+  + R RWP VSE+YE  Q+ YL  AI++ +  PR   F VTAK  +
Sbjct  430  TCAYLAAAILLQSYAYGRFRWPWVSELYEYVQSVYLLPAILSVIKNPRRPTFNVTAKGGS  489
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Query  512  LSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALR  571
              E+ +S +  P    F +  +G +  + R    P    +LL+ G W + N+ + G AL
Sbjct  490  AGEDRLSSLAWPYFLIFGILFAGAVTVIYRLQHEPESTGILLIAGLWNLFNLFMAGLALG  549

Query  572  AVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPAL  631
             V+E+++RR   RV  +     QI      SLTA +LD S  G  +L+RLPG       L
Sbjct  550  VVSERRERRQMHRVPTQGRGMLQIDGI---SLTAQILDVSQGG--MLIRLPGTS----PL  600

Query  632  EAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFG  691
                  +     P+  ++  ++  R+ + R E  + +VG+ F   QP   R T++ L+FG
Sbjct  601  RMQSQARLAVASPNGREVSSVLPIRLANVRFEKDSQLVGLGFGELQPSHYR-TISELMFG  659

Query  692  ESAHWRTMREATMRPIGLLHGMARIL  717
            +    R  R A  R   +L   A ++
Sbjct  660  DLRLLRNARMARQRTRSILAATAEVM  685


>TR:A0ABS7VQH4 A0ABS7VQH4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga puerhi OX=2876078 GN=bcsA PE=4 SV=1
Length=736

 Score = 581 bits (1497),  Expect = 0.0
 Identities = 321/715 (45%), Positives = 432/715 (60%), Gaps = 16/715 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L    W        LL A P+      +  L  V  + +LK F  + + R + L+  + +
Sbjct  5    LFVAFWAVAATLILLLVALPINLQTHLIAGLVVVACMIVLKFFRLQGIWRLIALALGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR   TLPP     +++ A+LL+  E +S+ + FL+ F+ + P     P  +
Sbjct  65   VLRYVFWRTTSTLPPITDLVNYIPAILLYVAEMYSVLMLFLSLFVVSSPLPSRRPPKIGE  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             ELP+VD+ VPSYNE A +L+ TLAAAK M YPA   TV L DDGGTDQ+C S D   A+
Sbjct  125  AELPSVDVFVPSYNESASLLASTLAAAKAMNYPADKLTVWLLDDGGTDQKCQSTDKLQAE  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR ELQ LC  L V Y TR +N HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  185  EAKARRAELQALCAALDVTYLTRAKNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF  + +LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLDRW  AF
Sbjct  245  EETVGYFSTEKNLFLVQTPHFFINPDPLERNLGTFDTMPSENEMFYGIIQRGLDRWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRR AL E  GF+G +ITED ETALE+HSRGWKS+Y+D+ +IAGLQP+TFASF
Sbjct  305  FCGSAALLRREALQETNGFSGISITEDCETALELHSRGWKSIYVDKPLIAGLQPDTFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ++  + P  +RGL +AQRLCY++S  FWFFP  R  FL++PL YLFF
Sbjct  365  IGQRSRWAQGMMQIMRYRFPPLKRGLTLAQRLCYMSSTLFWFFPFTRFCFLISPLCYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  AI++ +
Sbjct  425  SLEIFTASGGEFLAYTSTYMMVNFMMQNYLYGRYRWPWISDLYEFIQTVYLLPAILSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+E ++ + +S +  P    F L L GV+AT VR  A P    V LV G
Sbjct  485  NPSKPTFKVTAKNEAMNLSRVSELGAPFYIIFGLLLLGVIATAVRVWAEPYKADVTLVTG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W  LN+++ G AL  V+E+  RR + RV+            G++ + A +LD S  G
Sbjct  545  AWNFLNLIIAGCALGVVSERGTRRQSHRVRTMRQGRF---IMGDKVVDAVILDVSVGGAN  601

Query  617  LLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            L +    +    P L+ G  G ++F P +   P  +  + R  S   +G  V++G  F
Sbjct  602  LRLTQSAL----PGLKKGALGTLEFSP-YSKLPINQLPMEVRKMSMDEKG--VLMGCRFL  654

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
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               P   R  +A L+F  +  W   ++   + IG+L G    LW  + ++ +T R
Sbjct  655  TDTPEHYR-LIADLVFANADQWSEFQKRRHQDIGILRG---TLWFFSVAVYQTGR  705


>TR:A0A917A2D5 A0A917A2D5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aureimonas endophytica OX=2027858 GN=GCM10011390_48490
PE=4 SV=1
Length=733

 Score = 581 bits (1497),  Expect = 0.0
 Identities = 319/699 (46%), Positives = 431/699 (62%), Gaps = 14/699 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            +W    +   LL   P++   Q  +AL+A+VL  L+  F  +   R   L  A  +V+RY
Sbjct  1    MWSLPAIAALLLIFQPLSVETQLAVALTAIVLSGLIYVFRLQGAWRHCFLVFAVAVVLRY  60

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLP  +   SF+ A++L+A E + I+  F++ F++ADP +R        E+LP
Sbjct  61   AYWRTTATLPSSSDLVSFVPAIILYAAEMYCIAFLFISLFVAADPLERKRAPQTADEDLP  120

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
             VD+ VPSYNE AD+LS+TL+AAK + YPA    V L DDGGTDQ+  S D   A +AQ
Sbjct  121  NVDVFVPSYNESADILSLTLSAAKALDYPAERLKVFLLDDGGTDQKRNSRDLRAAAEAQR  180

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            R  ELQ+LCR LGV Y TR +NEHAKAGN++  L    GELVVVFDADH P+++FL  TV
Sbjct  181  RHVELQELCRTLGVTYLTRAKNEHAKAGNLNNGLAHSTGELVVVFDADHAPAKEFLRETV  240

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            G+F ED  LFLVQTPHFF NPDP++RNL   DR P ENEMFY  I +GLD+W   FFCGS
Sbjct  241  GHFGEDDKLFLVQTPHFFSNPDPLERNLGTFDRMPSENEMFYNSIQKGLDKWNATFFCGS  300

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRRRAL++ GGFAG TITED ETALE+HSRGW S Y++R M+ GLQPET +SFI QR
Sbjct  301  AAVLRRRALEQVGGFAGVTITEDCETALELHSRGWTSRYVERPMVTGLQPETLSSFIGQR  360

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RW  GM+Q+ LLKNPL RR L ++Q+ CYL+S   WFFPL RM+FL++PL+++FF ++I
Sbjct  361  SRWCRGMIQIFLLKNPLLRRNLSLSQKTCYLSSCMCWFFPLPRMVFLLSPLLFIFFDLKI  420

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            F  + +E  AY   YLA++ L++N L+   RWP VSE+YE  Q+ YL RA+ + ++ PR
Sbjct  421  FDVSAQEFFAYTVTYLAINSLIRNYLYGSVRWPFVSELYEYVQSVYLFRAVFSVIVNPRR  480

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VTAK ETL E+ +SP+  P    F + L  ++ ++ R+   P    +LLVV  W
Sbjct  481  PTFNVTAKGETLQEDRLSPLAVPYFVIFAVLLGAMVYSVYRYETEPQVGGILLVVAAWNA  540

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LNVL+ G AL  V E+++RR  PR+     A   + +     +   V D S  G + +V
Sbjct  541  LNVLIAGAALGVVTERRERRQTPRIS---AARNAVLSVAGALIPVEVKDTSLGGAK-VVP  596

Query  621  LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA--GQP  678
            L  +    PAL      +      ++      +   IR       TV +G+ +EA  G
Sbjct  597  LAAL----PALAGQDRAEIIVVDGESGAERGRLPVTIRQVTSWSDTVTLGLRYEATSGDY  652

Query  679  IAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL  717
             A+ E    L+ G+ +  R  REA  RP G+L G   +L
Sbjct  653  AAIAE----LMTGDLSAVREEREARRRPRGMLRGSLTLL  687


>TR:A0A7X3SQF8 A0A7X3SQF8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Microvirga makkahensis OX=1128670 GN=bcsA PE=4 SV=1
Length=731

 Score = 580 bits (1496),  Expect = 0.0
 Identities = 319/714 (45%), Positives = 435/714 (61%), Gaps = 16/714 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
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              L  LW    +   LL A P++     +  L  V  + +LK F  + V R + L+  + +V
Sbjct  6     LVALWAVAAMLIVLLVALPISLQTHLVAGLVVVACMIVLKFFRAQGVWRVIALALGTAIV  65

Query  78    MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
             +RY FWR   T+PP     +F+ A+LL+  E +S+ + FL+ F+ + P     P  + P
Sbjct  66    LRYVFWRTTSTIPPYTELTNFIPAILLYIAEMYSVMMLFLSLFVVSSPMPSRKPPKIDPN  125

Query  138   ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
              LPTVD+ VPSYNE A +L+ TLAAAK M YPA   TV L DDGGTD++C S +   A+
Sbjct  126   NLPTVDVFVPSYNEDASLLATTLAAAKAMSYPAEKFTVWLLDDGGTDEKCNSDNVHAAEA  185

Query  198   AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
             A+ RR ELQ LC  L V Y TR RN HAKAGN++  LE   G+LV VFDADH P+R FL
Sbjct  186   ARARRTELQALCSALDVRYLTRARNLHAKAGNLNNGLEHSTGDLVAVFDADHAPARSFLE  245

Query  258   RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
              TVG+F  D +LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  AFF
Sbjct  246   ETVGFFSADKNLFLVQTPHFFINPDPLERNLGTFQTMPSENEMFYGVIQRGLDKWDAAFF  305

Query  318   CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
             CGSAAVLRR AL E  GF+G +ITED ETAL++H+RGW S+Y+D+ +IAGLQP+TFASFI
Sbjct  306   CGSAAVLRREALQETNGFSGLSITEDCETALDLHARGWSSVYVDKPLIAGLQPDTFASFI  365

Query  378   QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
              QR RWA GM+Q++    PL +RGL + QRL Y++S  FW FP  R++FL++PL YLFF
Sbjct  366   GQRTRWAQGMLQIMRFSFPLLKRGLRLPQRLAYMSSTLFWLFPFSRLVFLLSPLCYLFFS  425

Query  438   IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
             +EIF A+  E LAY   Y+ V+F++QN L+ R RWP +S++YE  Q  YL  A+++ +
Sbjct  426   LEIFTASGGEFLAYTFTYMMVNFMMQNYLYGRYRWPWISDLYEYIQTIYLLPALLSVMAN  485

Query  498   PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
             P+   F VT+K E++ E+ +S +  P    F + L GV+AT VR    P    + LV G
Sbjct  486   PKRPTFKVTSKGESMLESRVSELGTPYFIIFGVLLLGVVATGVRVWLEPYKADLTLVTGA  545

Query  558   WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
             W VLN+++ G AL  V+E+  RR + RV+++         FG+  + A+V D S  G RL
Sbjct  546   WNVLNLIIAGCALGVVSERASRRMSHRVRIDRTCRF---LFGDEIIEASVRDISVGGARL  602

Query  618   LVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
              V         P+L+ G  G ++F P + + P     V   IR  R +   +++G  F
Sbjct  603   HV----APSNEPSLKKGALGTLEFMP-YAELPSQHMPV--EIRKIRMDDKGLLLGCRFLI  655

Query  676   GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
               P    + VA L+F  +  W T ++   + IG+L G    LW    SL +T R
Sbjct  656   ESP-EHHKLVADLVFANADQWSTFQKRRHQDIGVLRG---TLWFLMVSLYQTGR  705


>TR:A0A939FY48 A0A939FY48_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Jiella flava OX=2816857 GN=bcsA PE=4 SV=1
Length=753

 Score = 580 bits (1495),  Expect = 0.0
 Identities = 320/719 (45%), Positives = 449/719 (62%), Gaps = 17/719 (2%)

Query  12    RVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
             +++  ++ + W+  L+  G+  A PV  ++Q LIA + V  + +L     +   R LLL
Sbjct  3     KIISSMVPVAWLLSLLGLGIAVAQPVGTNSQVLIAATLVAGMLVLWMSGPRSNERRLLLM  62

Query  72    AASMLVM-RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRP-  129
             A ++  + RY +WR   TLP  +   A+F+  + L+AVE F++ I  L+ F+   P  RP
Sbjct  63    ALALAAIGRYAYWRTVSTLPDSSDLANFIPGVALYAVEMFAMVILLLSLFVVLKPKSRPA  122

Query  130   ---FPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQR  186
                   P      LPTVD+ VP+YNE A++L+VTLAAA +M YPA   TV L DDGGTD++
Sbjct  123   RATMAGPASDAALPTVDVFVPTYNESAELLTVTLAAAISMDYPADKLTVYLLDDGGTDEK  182

Query  187   CMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFD  246
              +S DP +A +A  R+R L +LC ELG VY  RE+N  AKAGN++AAL R  G+L+ VFD
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Sbjct  183  RLSADPVVAHEANLRQRMLTKLCDELGAVYLAREKNVSAKAGNLNAALPRTSGDLIAVFD  242

Query  247  ADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIH  306
            ADH P RDFL +TV +F ED  LFLVQTPHFF+NPDPI++NL L  R P ENEMFYG +
Sbjct  243  ADHAPVRDFLRKTVHHFAEDAKLFLVQTPHFFLNPDPIEKNLGLFKRMPSENEMFYGVVQ  302

Query  307  RGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIA  366
            RGLD WG A+FCGSAAVLRR AL+  GGF+G +ITED ETAL +H RGW+S Y+D+ +IA
Sbjct  303  RGLDSWGAAYFCGSAAVLRRTALETVGGFSGTSITEDCETALTLHGRGWRSRYVDQPLIA  362

Query  367  GLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMF  426
            GLQPETF SFI QR RW  GM+Q++LLKNPLF RGL +AQR+CYL+S  FW FP +R+ F
Sbjct  363  GLQPETFGSFIGQRSRWCQGMLQIMLLKNPLFVRGLTMAQRICYLSSGLFWLFPFMRLTF  422

Query  427  LVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPY  486
            +VAPL+++FF + I+ A+ +E LAY   Y+  + ++QN L+   RWP +SE+YE  Q+ Y
Sbjct  423  MVAPLLFIFFDLRIYQASLQEFLAYTCTYMLANVMLQNYLYGDVRWPWISELYEYVQSIY  482

Query  487  LARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFP  546
            L RAI   +  PRS  FAVTAK   + ++ +S + RP L  F + L   L    RW   P
Sbjct  483  LIRAIAAVIRNPRSPIFAVTAKGALIEQDRLSTLARPYLMFFCVLLVATLWCAARWYLEP  542

Query  547  GDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTAT  606
              R +LL +GGW VLN+++ G AL  V E+ +RR   R+ +       I   G  ++
Sbjct  543  TSRDLLLALGGWNVLNLVVAGLALGVVTERAERRRNQRLSISRKGALNI---GETAIDVV  599

Query  607  VLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGT  666
            V D S+SGVR  +R  G+ +     +A  +            L  +VR RI  AR
Sbjct  600  VEDVSSSGVR--IRPLGL-ETAKLPKAASIGTLTLDGSRQAGLAVVVRRRIPDAR----G  652

Query  667  VMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL-WMAAASL  724
            + +G+ F A  P  +R TVA L++ +++   + RE+  + +G++ G   ++ W   +S+
Sbjct  653  ICLGLEFMALAPSQMR-TVADLMYADASALSSFRESRRKSVGVVGGSLNVIRWSIESSV  710


>TR:A0AAE3U1M6 A0AAE3U1M6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ferirhizobium litorale OX=2927786 GN=bcsA PE=4 SV=1
Length=728

 Score = 579 bits (1493),  Expect = 0.0
 Identities = 322/714 (45%), Positives = 432/714 (61%), Gaps = 17/714 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            + L+W A  V    +   P+    Q ++ L AV ++ ++K    +   R + L+  + +V
Sbjct  6    IVLIWAAFSVGLIAMVMIPINLQTQLILGLLAVTVMGVIKILKAEGNWRLVALAFGTAIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            MRY +WR F TLPP     +F+ A+LL+  E +S+ +  L+ F+ + P   P P P  PE
Sbjct  66   MRYVYWRTFNTLPPANQPENFIPAILLYLAEMYSVMMLALSLFVVSRPLP-PRPSPTPPE  124

Query  138  -ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             + P VD+ VP+YNE   +L+ TLAAAK M YPA    V L DDGGT Q+  S     AQ
Sbjct  125  GKFPRVDVFVPTYNEDPALLANTLAAAKGMDYPADRLEVWLLDDGGTAQKRNSDKLLEAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A  R RELQ LC +L V Y TR+RNEHAKAGN++  ++  K EL+ VFDADH P+RDFL
Sbjct  185  AATMRHRELQTLCADLDVHYLTRDRNEHAKAGNLNNGMKHSKSELIAVFDADHAPARDFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF EDP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AF
Sbjct  245  KETVGYFSEDPKLFLVQTPHFFLNPDPVERNLQTFEKMPSENEMFYGIIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL+ A GF+G +ITED ETA+E+HSRGW S+Y+D+ +IAGLQP TFASF
Sbjct  305  FCGSAAVLRREALESANGFSGISITEDCETAVELHSRGWSSVYVDKPLIAGLQPATFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ++  + PLF+RGL I QRLCY++S  FW FP  R  FLVAPL YLFF
Sbjct  365  IGQRSRWAQGMMQIMRFRFPLFKRGLSIPQRLCYMSSTLFWLFPFARATFLVAPLFYLFF  424
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Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IF+A+  E L Y   YL V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ ++
Sbjct  425  DLQIFMASGGEFLGYTLSYLLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVIV  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VTAKDE++  N +S I RP    F + L  ++ T+ R+   P    V LVVG
Sbjct  485  NPRKPTFKVTAKDESVLVNRLSEISRPFFVIFAVLLVALIVTVYRFQTDPFKADVTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GW +LN++L G AL  V+E+ +     RV++    E      G R   AT+ D S +G R
Sbjct  545  GWNLLNLILAGCALGVVSERAEHSPTRRVRVTRRCEF---GLGGRWFPATIEDVSVNGAR  601

Query  617  LLVRLPGVGD-PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            + V     GD       A   I+F+P    +   E ++   +R+   EG    +G  +
Sbjct  602  VQV----YGDLGEMPTSARAEIRFKPY---SSATEEILPVEVRNRETEGNLTAIGCRY-L  653

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             +       VA LIF  S  W   ++A  R  GL+ G A   W    S+ +T R
Sbjct  654  PEIARHHSLVADLIFANSTQWSQFQQARRRNPGLIRGTA---WFIGLSIFQTYR  704


>TR:A0ABU0UFU5 A0ABU0UFU5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium larrymoorei OX=160699 GN=QE408_000943
PE=4 SV=1
Length=730

 Score = 578 bits (1490),  Expect = 0.0
 Identities = 320/705 (45%), Positives = 428/705 (61%), Gaps = 7/705 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V+ F LW+ +     L+   PV+     +    ++ L+A +K    +   R + L   +
Sbjct  4    VITFTLWLFVSACVLLIITLPVSLQTHLIATAISLALLATIKFLNGRGAWRLIGLGFGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  64   IVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPGS  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            P  +PTVD+ VP+YNE A++L+ TLAAAKNM YPA   TV L DDGGT Q+  +P+   A
Sbjct  124  PGYVPTVDVFVPTYNEDAELLANTLAAAKNMDYPADKFTVWLLDDGGTVQKRNAPNGLEA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q A  R  ELQ+LC +LGV Y TR+RN HAKAGN++  L+   GELV VFDADH P+RDF
Sbjct  184  QAAIRRHAELQKLCADLGVNYLTRDRNVHAKAGNLNNGLDHSTGELVTVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GA
Sbjct  244  LLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL E  GF+G +ITED ETAL +HSRGW SLY+D+ +IAGLQP TF S
Sbjct  304  FFCGSAAVLRRTALKETDGFSGVSITEDCETALALHSRGWNSLYVDKPLIAGLQPATFTS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ L
Sbjct  424  FDLQIFVASGGEFLAYTAAYMLVNLMIQNFLYGSFRWPWISELYEYVQTVHLLPAVVSVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              P    F VTAKDE++SE  +S I RP    F + +  ++  + R  A P    V LVV
Sbjct  484  FNPSKPTFKVTAKDESISEARLSEISRPFFVIFFILIIAMVFAIYRIYAEPYKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN++  G AL  V+E+ ++ A+ R+ ++   E Q+   G   L ATV + S  G+
Sbjct  544  GGWNLLNIIFAGCALGVVSERGEKSASRRITVKRRCELQLQEDG-PWLPATVQNVSVHGM  602
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Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
             + +    +        A  +I+  P  P AP    M    +RS +++ G + VG  F
Sbjct  603  LIHIFEKDLDSVENGRSA--IIRVDPYSPGAP--SSMTINIVRSVKQQ-GFISVGCTFAP  657

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             + I  R  +A LIF  S  W   + A     GL+ G    + +A
Sbjct  658  KETIEHR-LIADLIFANSDQWTDFQRARRGNPGLIRGTITFMGIA  701


>TR:A0A2S9QI37 A0A2S9QI37_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Labrys okinawensis OX=346911 GN=bcsA PE=4 SV=1
Length=732

 Score = 578 bits (1490),  Expect = 0.0
 Identities = 314/717 (44%), Positives = 447/717 (62%), Gaps = 20/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+ L W+   +   +L   P++     +   + V+ +ALLK      V R + L+  + +
Sbjct  5    LVVLFWLLTSLFVLVLVTLPISQQTHLIAGTTVVIAMALLKAVKPTGVWRLIALALGTSI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP     +F+  L+++  E + +++  L+ F+ A P        L+
Sbjct  65   VLRYVYWRTTSTLPPINQPENFIVGLIVYLAEMYCVAMLALSLFVVATPLPSRVAPRLRD  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            +ELP+VD+ +PSYNE A++L+ TLAAA  M YP     V L DDGGT+Q+  S D + A
Sbjct  125  DELPSVDVFIPSYNEGAELLAGTLAAALGMDYPPDKLHVYLLDDGGTEQKRNSKDLQAAM  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +AQ+R  +L++LC ELG  Y TR RNEHAKAGN++  L     ++VVVFDADH P+RDFL
Sbjct  185  EAQQRHAQLKRLCEELGANYLTRARNEHAKAGNLNNGLAHSSSDIVVVFDADHAPARDFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVG+F +DP LF+VQTPHFF+NPDPI+RNL    + P ENEMFYG I RGLD+W  +F
Sbjct  245  HSTVGFFRDDPSLFMVQTPHFFLNPDPIERNLRTFQKMPSENEMFYGIIQRGLDKWNSSF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA LRR AL+   GF G +ITED ETA+E+H+RGW S+Y+D+ +IAGLQP TFASF
Sbjct  305  FCGSAAALRRSALEATEGFKGRSITEDCETAMELHARGWHSIYVDKPLIAGLQPATFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GM+Q+LL + P  +RGL I+QRLCY++S+ FWFFPL R++FLVAPL YLFF
Sbjct  365  IGQRSRWAQGMVQILLFQRPFMKRGLKISQRLCYMSSILFWFFPLARLVFLVAPLFYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             +EIFVA+ +E L+Y   Y+ V+ ++QN L+   RWP +SE+YE AQ  YL  A+ + ++
Sbjct  425  NLEIFVASGQEFLSYTLSYMLVNLMMQNYLYGSYRWPWISELYEYAQTLYLLPALASVIM  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAKD+++ E+ +S I  PL   F + ++G+  T+ R +  P    V LVVG
Sbjct  485  HPTKPTFRVTAKDDSVQESRLSEIAWPLFAFFCVLIAGMGMTVFRLIEQPYKADVTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LNVLL G AL  V+E+ +R+++ RV+ +   E      G+  + A + + ST+G
Sbjct  545  MWNLLNVLLAGCALGVVSERGERQSSQRVRADRRCEL---ILGDTVIPAMIENVSTNGAG  601

Query  617  LLVRLPGVGDPHPALEAGGL--IQFQP--KFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            + +    VG     LE    L  I+F P  +    P+L  +VR R+ +     G+  +GV
Sbjct  602  ISI----VG-AVKGLERESLLRIRFTPLSRLDGRPELPVVVR-RVSAG---AGSTTIGVR  652

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F+   PI  R  VA L++  S  W   + A     G+L G    +W  A +L +T R
Sbjct  653  FQTSDPIHFR-LVADLLYATSDRWTAFQAARRYNPGILRG---TIWFYALALKQTVR  705


>TR:A0ABQ6CKF8 A0ABQ6CKF8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Labrys miyagiensis OX=346912 GN=celA PE=4 SV=1
Length=732
```

```
 Score = 578 bits (1489),  Expect = 0.0
 Identities = 313/719 (44%), Positives = 447/719 (62%), Gaps = 22/719 (3%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V + LLW    V   +L   P++  A  +   + V+ +A LK F    + R + L+  +
Sbjct  4    VFVALLWALASVFVLILVTLPISQQAHLIAGTAVVIAMAFLKVFKPSGIWRPVALALGTS  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+  L ++  E + + +  L+ F+ + P        L+
Sbjct  64   IVLRYVYWRTTSTLPPINQPENFIVGLTVYLAEMYCVCMLALSLFVVSSPLPSRVAPRLK  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             EELP+VD+ VPSYNE +++L+ TLAAAK M YP     V L DDGGT+Q+  + + E A
Sbjct  124  DEELPSVDVFVPSYNEGSELLARTLAAAKGMDYPPDKLHVYLLDDGGTEQKRNAQNIESA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +AQ+R  EL+ LC  LGV Y TR RNEHAKAGN++  L     E+VVVFDADH P+RDF
Sbjct  184  TEAQQRHAELKSLCAGLGVHYLTRARNEHAKAGNLNNGLAHSSSEIVVVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  T+G+F + P LF+VQTPHFF+NPDP++RNL    + P ENEMFYG I RGLD+W  +
Sbjct  244  LHCTIGFFKDHPKLFMVQTPHFFLNPDPVERNLRTFLKMPSENEMFYGIIQRGLDKWNAS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA L R AL E GGF G +ITED ETA+E+H+RGW S+Y+D+ +IAGLQP TFAS
Sbjct  304  FFCGSAAALSRAALAETGGFKGRSITEDCETAMELHARGWHSIYVDKPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GM+Q+ L + P  +RGL I+QR+CY++S+ FWFFP+ R++FL+AP+ YLF
Sbjct  364  FIGQRSRWAQGMVQIFLFQRPFMKRGLSISQRICYMSSILFWFFPVARLIFLIAPMFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIFV++ +E L+Y   Y+ V+ ++QN L+   RWP VSE+YE AQ  YL  A+++ L
Sbjct  424  FNLEIFVSSGQEFLSYTLSYMLVNLMMQNYLYGSYRWPWVSELYEYAQTLYLLPALISVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            + P    F VTAKD++++E+ +S I  PL   F + L+G+  T+ R++  P    V +VV
Sbjct  484  MHPTKPTFRVTAKDDSVAESRLSEIAWPLFAFFCVMLAGIAMTIFRFIEQPYKADVTVVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAST--S  613
            G W +LNVLL G AL  V E+ +R++  RV+ +   E     FG  +++A + + S   +
Sbjct  544  GLWNILNVLLAGCALGVVCERGERQSTQRVKADRRCEL---TFGETTVSAMIENVSAYGA  600

Query  614  GVRLLVRLPGVG-DPHPALEAGGLIQFQP--KFPDAPQLERMVRGRIRSARREGGTVMVG  670
            G+RL+  + G+  D H        I+F P  K    P+L  +VR RI S     GT  VG
Sbjct  601  GIRLVGPVKGLSRDSHLR------IRFTPLTKLDGDPELPVVVR-RIDS---NAGTTTVG  650

Query  671  VIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            V +   +P+  R  +A L++  S  W   +       GL+ G    +W  A +L +T R
Sbjct  651  VRYVTTEPVHYR-LIADLLYANSDRWTAFQAGRRYNPGLVRG---TIWFYALALKQTIR  705


>TR:G4RFY7 G4RFY7_PELHB Cellulose synthase catalytic subunit [UDP-forming]
OS=Pelagibacterium halotolerans (strain DSM 22347 / JCM 15775
/ CGMCC 1.7692 / B2) OX=1082931 GN=KKY_995 PE=4 SV=1
Length=727

 Score = 577 bits (1488),  Expect = 0.0
 Identities = 320/714 (45%), Positives = 445/714 (62%), Gaps = 13/714 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            + FL W  +     +    PV+     + A+  + ++ ++K      V R LLL+  + +
Sbjct  4    ITFLFWALVATGTVIAITLPVSLQVHLITAVLFLGVMLVIKTLRLGGVWRLLLLALGTAI  63

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP    A F+  LLL+  E + I +  L+ F+ ++P      R L+P
Sbjct  64   VLRYAYWRTTSTLPPVEQWADFIPGLLLYLGEMYCILMLALSLFVISNPVPSRPSRSLKP  123
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Query  137  -EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             E +P+VD+ VP+YNE  ++L+ TLAAAK + YPA   T+ L DDGGT Q+   PDPE A
Sbjct  124  GEPVPSVDVFVPTYNEDYELLAGTLAAAKALDYPAEKLTIWLLDDGGTVQKRNDPDPEKA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            ++A ER   L++LC +LGV Y TRERNEHAKAGN++  L    G+LV VFDADH P+RDF
Sbjct  184  EEALERHTSLEKLCSDLGVNYLTRERNEHAKAGNLNNGLAHSTGDLVAVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TV YF +D  LFLVQTPHFF+NPDP++RNL   +R P ENEMFY  + RGLD W  +
Sbjct  244  LQETVPYFGDDEKLFLVQTPHFFLNPDPLERNLRTFERMPSENEMFYSILQRGLDSWNAS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRR ALD A GF+G +ITED ETAL++HS+ W S+YIDR +IAGLQP TF+S
Sbjct  304  FFCGSAALLRREALDIANGFSGRSITEDCETALDLHSKKWNSIYIDRPLIAGLQPATFSS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GM Q++L   PLF+RGL +AQRLCY++SM FW FP  R++FL+AP  YLF
Sbjct  364  FIGQRTRWAQGMTQIMLFNFPLFKRGLSMAQRLCYMSSMMFWLFPFTRIIFLIAPFFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IF A+  E  AY   YL V+ ++QN+L+ R RWP +SE+YE  Q+ +L  AI++ +
Sbjct  424  FNLQIFTASGGEFAAYTMTYLVVNLVMQNSLYGRWRWPWISELYEYIQSVHLLPAILSVI  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              P    F VTAKDE++ E+ +S + RP  F FLL L GV  T  R  A P    + LVV
Sbjct  484  RNPTKPTFKVTAKDESIDESRLSELARPFYFIFLLLLVGVAFTGYRLWAEPYRAEITLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW + N++L G AL  V+E+++ RA+ RV +E     +I +     +  T+L+ S+ GV
Sbjct  544  GGWNLFNLILAGCALGVVSERREVRASRRVPIE--RRCEIRSVDGTWVRGTILNVSSGGV  601

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
             + V     G    A +    I+FQ   P  P  E  +   +R+    G + MVG  F A
Sbjct  602  AIQV---ADGKTRLAKDQATAIRFQTLSP-VPDNEMGI--FVRNVSNAGKSSMVGCRFMA  655

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             +P   R  +A L++  S  W+  +E+    IG++ G  + L   + S+ +TAR
Sbjct  656  EKPSDYR-LIADLLYANSKLWKERQESRQVNIGIILGTLQFL---SISIYQTAR  705


>TR:A0A2U1SUW3 A0A2U1SUW3_METSR Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylosinus sporium OX=428 GN=bcsA PE=4 SV=1
Length=762

 Score = 577 bits (1486),  Expect = 0.0
 Identities = 319/732 (44%), Positives = 441/732 (60%), Gaps = 18/732 (2%)

Query  17   LLFLLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L FLL  A+ V    LA  PV+  AQ    +LS + L+A L  FA     R L ++ A  +
Sbjct  7    LSFLLLGAVAVA---LATQPVSVQAQLATSLSVIFLLAFLWRFARGAEARQLFIALALFV  63

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR+  TLPP +    F    +L A E + +++  L    ++A+P  R     ++
Sbjct  64   VLRYVYWRVTSTLPPLSDPVGFTCGSILLAAELYCVAMLLLTLVVNAEPLKREPAPQIED  123

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            E LP VD+LVPSY+E A +L+ TLAAAK+M YPA    V L DDGGT+Q+C  PDPE+A+
Sbjct  124  EALPAVDVLVPSYDESASILATTLAAAKSMDYPADRLNVFLLDDGGTEQKCAHPDPEIAE  183

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A+ RR  LQ+LC  LG  Y TRE NE AKAGN++ALE + G++VVV DADH P R FL
Sbjct  184  RARARRASLQELCAALGCYYLTREHNERAKAGNLNAALEHIDGDIVVVLDADHAPFRSFL  243

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              T+GYF ED  LFLVQTPH F+NPDPI++NL      P ENEMFYG   RGLD+W  AF
Sbjct  244  RETIGYFFEDDRLFLVQTPHVFLNPDPIEQNLRTFRHMPSENEMFYGVTQRGLDKWNAAF  303

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
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            FCGSAA+LRR ALD+AGGF+G ++TED ETALE+H++GW S+Y+D+ ++AGLQP+TFA+F
Sbjct  304  FCGSAALLRRAALDDAGGFSGVSVTEDCETALELHAQGWTSVYVDKPLVAGLQPQTFAAF  363

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GM+Q+LLL+NPL +RGL   QRL YL+SMSFWFFP  R++F++APL ++ F
Sbjct  364  IGQRVRWCQGMLQILLLRNPLLKRGLEPLQRLGYLSSMSFWFFPFPRLVFMLAPLAFILF  423

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFV+  EE +AY   Y+ V+ ++QN LF R RWP VSE+YE  Q  +L++AI++ LL
Sbjct  424  DVKIFVSNIEEAIAYTATYVVVNAMLQNYLFGRVRWPWVSELYEYCQGVFLSKAILSVLL  483

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            RP S  F VT K  T +++ +S +  P    + L   G +  + R VA PG R +++ VG
Sbjct  484  RPHSPSFRVTEKGATRAQDRLSELAWPFFAIYGLLAIGAVVAVYRCVAEPGVRQLIVFVG  543

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W   N++  G AL AVAE+++R   P + +E         A G   +   + + S  G R
Sbjct  544  LWNFFNLVTAGVALGAVAERRRREKHPSLPVE---RRGALALGEEHVRVAIEEVSAGGCR  600

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDA---PQLERMVRGRIRSARREGGTVMVGVIF  673
            L        +   A +      F     DA   P L   + G     RR        ++F
Sbjct  601  LRAATEADAEALAAAKQTEGRLFIDSVVDAARRPSLSARIVGVAADGRRH-------LVF  653

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMD  733
               QP      +A L++G++      + A  +  G++ G A+ LW  A   P  A  ++
Sbjct  654  ALTQP-QDHLALADLMYGDATALERFQAARRKHKGIVAGTAQFLWWGAIE-PLRAFAYLR  711

Query  734  EPARRRRRHEEP  745
              A    R E P
Sbjct  712  PRAGEAARSEPP  723


>TR:A0AAW4FTY5 A0AAW4FTY5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ensifer canadensis OX=555315 GN=bcsA PE=4 SV=1
Length=726

 Score = 576 bits (1484),  Expect = 0.0
 Identities = 314/685 (46%), Positives = 423/685 (62%), Gaps = 8/685 (1%)

Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
            PV    Q ++++  V  +A+LK    +   R + L+  + + +V+RY +WR   TLPP
Sbjct  24   PVNLQTQLIVSVLVVTFMAILKLIKAEGRWRLIALAFGTAIVLRYVYWRTTSTLPPLNQL  83

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
             +F+   LL+  E +S+ +  L+ F+ A P      + + P   P VD+ VPSYNE A +
Sbjct  84   ENFIPGFLLYLAEMYSVMMLSLSLFVVAMPLPPRKAKAISPGAFPKVDVFVPSYNEDAGL  143

Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAAK M YPA    V L DDGGT Q+  S +   AQ+A  R  ELQ LC +LGV
Sbjct  144  LANTLAAAKGMDYPADKLQVWLLDDGGTQQKRYSMNLVEAQRASARHMELQALCDDLGVR  203

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TRERNEHAKAGN++  +    GEL+ VFDADH P+RDFL  TVGYF  DP LFLVQTP
Sbjct  204  YLTRERNEHAKAGNLNNGMLHSDGELIAVFDADHAPARDFLLETVGYFESDPKLFLVQTP  263

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AFFCGSAAVLRR+ALD+  GF
Sbjct  264  HFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAAFFCGSAAVLRRKALDDTDGF  323

Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
            +G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFASFI QR RWA GMMQ+LL +
Sbjct  324  SGMSITEDCETALALHGRGWNSIYVDRPLIAGLQPATFASFIGQRSRWAQGMMQILLFRF  383

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PLF+RGL I QRLCY++S  FW FP+ R +FL APL YLFF +EIF A+  E LAY   Y
Sbjct  384  PLFKRGLSIPQRLCYMSSTLFWLFPVSRTIFLFAPLFYLFFDLEIFTASGGEFLAYTLAY  443

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            + V+ ++QN L+   RWP +SE+YE AQ  +L  A+++ L+RP    F VTAKDE++ E+
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Sbjct  444  MLVNLMMQNYLYGAFRWPWISELYEYAQTVHLLPAVISVLMRPSRPTFKVTAKDESILES  503

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
             +S I RP    F +    +L T+ R    P    V LVVGGW +LN+++ G AL  V+E
Sbjct  504  RLSEISRPFFVIFAVLFIALLMTVYRVYTEPYKADVTLVVGGWNLLNLIMAGCALGVVSE  563

Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            + ++ ++ RV++    E  +    ++   AT+ D S +G R  +++ GV      ++  G
Sbjct  564  RGEKASSRRVKVSRRCEFGV---ADQWYPATIEDVSANGAR--IQVYGVDAATLPVDTDG  618

Query  636  LIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAH  695
            LI+F+P   D       V   I++    G    +G  +   Q       VA LIF  S
Sbjct  619  LIRFEPYSGDGTSETLPV--AIKNKESAGDITTIGCRY-LPQVARHHSLVADLIFANSQQ  675

Query  696  WRTMREATMRPIGLLHGMARILWMA  720
            W   ++A     GL+ G A  LW+A
Sbjct  676  WSEFQKARRGNPGLVAGTAWFLWLA  700


>TR:A0A931I4R4 A0A931I4R4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobrevis albus OX=2793297 GN=bcsA PE=4 SV=1
Length=730

 Score = 575 bits (1483),  Expect = 0.0
 Identities = 321/704 (46%), Positives = 433/704 (62%), Gaps = 15/704 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            +W+ + V    +   P+   AQ +   + +  + LLK      V R + L+  + +V+RY
Sbjct  9    IWLVMSVAVMAVVTLPINLQAQLIAGAAVLFSMMLLKMVRPDGVWRLIALALGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRP---LQPE  137
             +WR   TLPP      F+   LL+  E +S+ +  L+ F+ A+P     PRP   L
Sbjct  69   VYWRTTSTLPPINQPEDFIVGFLLYLAEIYSVFMLALSLFVVANPLK---PRPAVKLVET  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            +LPTVD+ +P+YNE   +L+ T+AAAK M YPA   TV L DDGGT Q+  S   E A
Sbjct  126  DLPTVDVFIPTYNEDLPLLANTMAAAKGMDYPAEKVTVWLLDDGGTWQKRGSDRVEEALA  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A+ R  +LQ+LC +LGV Y TR+RN HAKAGN++  LE   GELVVVFDADH P+RDFL
Sbjct  186  AERRHADLQRLCADLGVRYLTRDRNLHAKAGNLNNGLEHSTGELVVVFDADHAPARDFLK  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVGYF EDP +FLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +FF
Sbjct  246  ETVGYFREDPRIFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNASFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR+AL+E  GF+G +ITED ETA+E+HSRGW S+Y+DR +IAGLQP TFASFI
Sbjct  306  CGSAAVLRRKALEETNGFSGVSITEDCETAIELHSRGWHSVYVDRPLIAGLQPATFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P F+RGL  AQRLCY++S  FW FP  R +FLV+PL YLFF
Sbjct  366  GQRSRWAQGMMQILRFRFPPFKRGLSPAQRLCYMSSTLFWLFPFARTIFLVSPLFYLFFD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EIF A+  E +AY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +L
Sbjct  426  LEIFTASGGEFMAYTLTYMVVNLMMQNYLYGAFRWPWISELYEYVQTVHLLPAVVSVILN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR   F VTAKDE++  + +S I  P    F +  +GVL T+ R +  P    V LVVG
Sbjct  486  PRKPTFKVTAKDESIDRSRLSEIGTPFFVIFAILCAGVLMTIYRVITEPYKADVTLVVGA  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN+LL G AL  V+E+ + +++ RVQ+    E      G   L AT+ D S +G R+
Sbjct  546  WNLLNLLLAGCALGVVSERGEPQSSRRVQVRRRCEF---LSGGEWLPATIEDVSVNGARV  602

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
            +V      D     E    I+F+P   + P  E  V  R   A ++G  + +G  ++
Sbjct  603  IVHGRIAEDVRVLHET--RIRFRP-HSEIPTNELPVTVRNLQASQQG--MAIGCQYDPKG  657
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Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
            P   R  V+ LIF  SA W   + +     GL+ G    LW+AA
Sbjct  658  PDHHR-LVSDLIFANSAQWTAFQLSRRVNPGLVRGTLWFLWLAA  700


>TR:A0ABS5R834 A0ABS5R834_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter radicis OX=2836179 GN=bcsA PE=4 SV=1
Length=735

 Score = 575 bits (1483),  Expect = 0.0
 Identities = 316/697 (45%), Positives = 428/697 (61%), Gaps = 16/697 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM-VPRFLLLSAASMLVMR  79
            LW    +    L   P++  A  +     V+ + LLK F   + + R + L+  + +V+R
Sbjct  9    LWAISSIIVVFLITLPISLQAHLIAGCIVVLAMILLKTFGPPVGIFRMIALALGTAIVLR  68

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP +    F+   +L+  E +S+ + FL+ F+ + P        + P E
Sbjct  69   YVYWRTTSTLPPISQIEDFIPGFMLYIAEMYSVFMLFLSLFVVSSPMPSRVSPAIPPGEE  128

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PT+D+ +P+YNE   +L+ T++AA ++ YP    TV L DDGGTDQ+C   D   A +AQ
Sbjct  129  PTIDVFIPTYNEDPHLLASTVSAALSLDYPQDKFTVWLLDDGGTDQKCEQDDSTKALEAQ  188

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +RR ELQ +C  LG  Y TR RNEHAKAGN++  L+   GELVVVFDADH P+RDFL  T
Sbjct  189  QRRAELQAMCEGLGCRYLTRARNEHAKAGNLNNGLKHSTGELVVVFDADHAPTRDFLKET  248

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VG+F++D +LFLVQTPHFFINPDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  249  VGFFLQDENLFLVQTPHFFINPDPLERNLNTFEFMPSENEMFYGIIQRGLDKWDAAFFCG  308

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            S AV+ RRAL E  GF G TITEDAETALE+HSRGW S+Y+DR +IAGLQPETFASFI Q
Sbjct  309  SGAVINRRALAETNGFQGITITEDAETALELHSRGWHSIYVDRPLIAGLQPETFASFIGQ  368

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L    P  +RGL + QRLCY +S  FW FP  R+MFL++PL YLFF +E
Sbjct  369  RSRWAQGMMQILRFHFPPGKRGLSLPQRLCYCSSTLFWLFPYPRLMFLISPLFYLFFSLE  428

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E  AY   Y+ V+ L+QN L+ R RWP +SE+YE  QA YL  A+V+ +L P
Sbjct  429  IFNASGAEFFAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQAIYLFPALVSVILNPH  488

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAK ETL E ++S I RP    F + + G+L T+ R    P +  V++VVG W
Sbjct  489  KPTFNVTAKGETLDEGHVSEIGRPFFIIFGVLILGLLVTIWRLFTEPFNADVIVVVGAWN  548

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQI--PAFGNRSLTATVLDASTSGVRL  617
            VLN+++ G AL  V+E++ RR A RV +    E  I   A+G     A + D S  G R+
Sbjct  549  VLNIIIAGCALGVVSERRNRRRAHRVDLLRRGELIIDGTAYG-----AMIDDGSLGGARI  603

Query  618  LVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
                P      P L  G   +++F+P   +   ++ +    IR+  R+   V++G  F
Sbjct  604  ---RPNANVTLPDLTRGQAAVLRFKPVASNI-AIDSLPM-TIRNVERDPDGVLIGAEFAP  658

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHG  712
             +P+  R  +A LIF  S  W+  +E+  R  G+L G
Sbjct  659  TEPMHHR-LIADLIFANSDQWKKFQESRRRNPGVLRG  694


>TR:A0A1G4T8G7 A0A1G4T8G7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter rudongensis OX=177413 GN=SAMN05660859_2721
PE=4 SV=1
Length=716

 Score = 575 bits (1483),  Expect = 0.0
 Identities = 312/685 (46%), Positives = 419/685 (61%), Gaps = 9/685 (1%)
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Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
            PV   AQ +     ++L+  LK FA + VPR + L+    +V RY +WR   TLPP    
Sbjct  9    PVNLQAQLVTGCIVILLIVFLKMFAPEGVPRMVALALGVAMVSRYVYWRTTSTLPPMEEL  68

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
            A+F+ A+LL+  E +S+++  L+ F+ + P        + P   PTVDI VPSYNE A +
Sbjct  69   ANFIPAMLLYCAEMYSVALMALSLFVVSSPQPPRTAPVIAPGREPTVDIFVPSYNEDAGL  128

Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAA  + YP    TV L DDGGTDQ+C   D   A++AQ RR  L +LCRELGV 
Sbjct  129  LATTLAAASAIDYPRDRFTVWLLDDGGTDQKCEQHDLAAAREAQMRRETLTELCRELGVN  188

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TR RNEHAKAGN++  L    GEL+VVFDADH P+R FL  T+GYF EDP LFLVQTP
Sbjct  189  YLTRPRNEHAKAGNLNHGLAHSSGELIVVFDADHAPARPFLRETIGYFNEDPRLFLVQTP  248

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFFINPDP++R+L    R P ENEMFYG I RGLDRWGGAFFCGSAAVLRR AL E  GF
Sbjct  249  HFFINPDPVERSLDTWRRMPSENEMFYGVIQRGLDRWGGAFFCGSAAVLRREALKETDGF  308

Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
            A  +ITED ETAL +H+RGW S+Y+D  +IAGLQPETFASFI QR RWA GM Q+L    
Sbjct  309  AHSSITEDCETALTLHARGWHSVYVDTPLIAGLQPETFASFIGQRSRWAQGMYQILRFHF  368

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PLFR GL +AQR+CY++S+ FWFFP+ R +FLV+P  YLFF +EIF  +  E +AY   Y
Sbjct  369  PLFRSGLTVAQRICYMSSILFWFFPISRAIFLVSPFFYLFFSLEIFNGSGAEFVAYTAVY  428

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            L ++  +Q+ L+ + RWP  SE+YE  Q  YL  A+++ ++ P+   F VT+K ET+ EN
Sbjct  429  LLINLFIQSYLYGKYRWPWFSELYEYIQTVYLLPALLSVMINPKKPTFKVTSKGETIDEN  488

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
             IS I  P    F++ ++ V  T  R    P    + +VVG W +LN+++ G AL  V+E
Sbjct  489  RISEIGIPFFVIFVIQIAAVFVTFWRIATEPYAADITIVVGMWNLLNLIISGCALGVVSE  548

Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            K  +R + R+ +       I       + A + D S  GVR+   LP        + A  
Sbjct  549  KAAKRHSQRMAITRRCSLLIDGV---EVPAIIDDVSMGGVRVRTELPSEATARVGMHA--  603

Query  636  LIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAH  695
            +++  P  PD   +   +   +R+  R+ G V++G  F A +  A  + +A LIF  +  
Sbjct  604  VVRITP--PD-DCISDTLPVLVRNVARDDGVVVLGTQFNA-KTAAHYQLIADLIFANADE  659

Query  696  WRTMREATMRPIGLLHGMARILWMA  720
            W+  +    +  G+L G    + MA
Sbjct  660  WKKFQAGRRKNPGVLRGTVMFVMMA  684


>TR:A0A1Q9A6T2 A0A1Q9A6T2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Allorhizobium taibaishanense OX=887144 GN=BJF91_13270
PE=4 SV=1
Length=729

 Score = 575 bits (1483),  Expect = 0.0
 Identities = 323/717 (45%), Positives = 443/717 (62%), Gaps = 23/717 (3%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            FLLW+       LLA  P+    Q +     +++VA +K    +   R + LS AS +V+
Sbjct  7    FLLWLTCASAMLLLAFLPIDTRTQLVTTFIILIIVAAMKMMRVEGRGRVVFLSLASAIVL  66

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTD--RPFPRPLQP  136
            RY +WR   TLPP     +F+  LLL+  E +S+ + FL+ F+ + P    +PF R L  
Sbjct  67   RYVYWRTSSTLPPVNQLENFIPGLLLYLAEMYSVMMLFLSLFVVSTPLPPRKPF-RTLSY  125

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            +ELP VDI VPSYNE   +L+ TLAAA+N+ YPA   TV L DDG T+Q+  S D   A+
Sbjct  126  DELPIVDIFVPSYNEEESLLANTLAAARNLDYPADKFTVWLLDDGSTEQKRQSTDLLAAK  185
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Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A++R + LQ LC +LGV Y TRERNEHAKAGN++  L    GELV VFDADH P+R FL
Sbjct  186  FAEQRHQSLQTLCSQLGVRYLTRERNEHAKAGNLNNGLNHSTGELVAVFDADHAPARSFL  245

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF +DP LFLVQTPHFFINPDPI+RNL   ++ P ENEMFYG I RGLD+W  AF
Sbjct  246  KETVGYFNDDPRLFLVQTPHFFINPDPIERNLNTFNKMPSENEMFYGIIQRGLDKWNAAF  305

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL+EA GF+G +ITED ETAL++HSRGW S+++D  +IAGLQP TFASF
Sbjct  306  FCGSAAVLRREALNEANGFSGLSITEDCETALDLHSRGWNSIFVDMPLIAGLQPATFASF  365

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ++  + PLF+RGL + QRLCY++S  FW FP  R +FL+APL YLFF
Sbjct  366  IGQRSRWAQGMMQIMRFRFPLFKRGLSLGQRLCYMSSTMFWLFPFPRAIFLLAPLFYLFF  425

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IF+ +  E +AY   Y+ V+ +VQN L+   RWP +SE+YE  Q+ +L  AI++ +
Sbjct  426  NLQIFMGSGGEFMAYTLSYMLVNLMVQNYLYGSFRWPWISELYEYVQSVHLLPAILSVMW  485

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VTAKDE+++EN +S I RP    FL+ L     T+ R  + P    V LVVG
Sbjct  486  DPRRPTFKVTAKDESVTENRLSEISRPFFLIFLILLIAFGVTIYRLYSDPYKFDVTLVVG  545

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GW ++N+++ G AL  V+E+ +R+++ RVQ+    E  +   G++   A + D S +G
Sbjct  546  GWNLVNLIMAGCALGVVSERGERQSSRRVQVSRRCEFSL---GDKLYPAMIDDVSVNGAS  602

Query  617  LLVRLPGVGDPHPALEAGGLIQFQP----KFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            L +      D     +  G + FQP    ++ + P         IR ++  G  + +G
Sbjct  603  LQI-FTRDRDIFKR-DVLGAVTFQPHGSTEWAELPV-------TIRHSQFSGDIISIGCR  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +   + +   E +A LIF  +  W   + +  R  GL+ G    L +   SL +T R
Sbjct  654  Y-LPETVRHHELIADLIFANAQQWSLFQHSRRRNPGLIGGAFMFLRL---SLTQTLR  706


>TR:A0ABY1IR28 A0ABY1IR28_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aureimonas altamirensis DSM 21988 OX=1121026 GN=SAMN02745911_3869
PE=4 SV=1
Length=729

 Score = 575 bits (1482),  Expect = 0.0
 Identities = 319/733 (44%), Positives = 436/733 (59%), Gaps = 13/733 (2%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            FLLW         L   PV+   Q +     +V +A++K        R + L+  + +V+
Sbjct  6    FLLWALTAALSISLITLPVSVETQLISVALILVAMAVIKGLKLSGNWRLVALALGTAVVL  65

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ-PE  137
            RY +WR   TLPP     +F+  LL++  E +S+ + FL+ F+ A P     PRP + PE
Sbjct  66   RYVYWRTTSTLPPINQPENFVPGLLVYLAEMYSVFMLFLSLFVVASPIPPRPPRPAEKPE  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            +LP VD+ VP+YNE A +L+ TLAA   + YPA    V L DDGGT Q+  + DPE AQ
Sbjct  126  DLPFVDVFVPTYNEDAGLLANTLAACLAIDYPADKLKVWLLDDGGTVQKRNADDPESAQG  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A+ R +ELQ LC  LG +Y TRERNEHAKAGN++  +    GEL+VVFDADH P+RDFL
Sbjct  186  AERRYKELQALCASLGAIYLTRERNEHAKAGNLNNGMAFSTGELIVVFDADHAPARDFLR  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVGYF EDP LFLVQTPHFF+NPDP++RNL      P ENEMFYG I RGLD+W  AFF
Sbjct  246  ETVGYFREDPKLFLVQTPHFFLNPDPVERNLRTFTHMPSENEMFYGIIQRGLDKWNAAFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVL R+AL   GGF+G +ITED ETA+E+HSRGW S+Y+D+ +IAGLQP TFASFI
Sbjct  306  CGSAAVLSRKALQTTGGFSGVSITEDCETAIELHSRGWNSVYVDKPLIAGLQPATFASFI  365
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Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P  +RGL + QRLCY++S  FW FP  R MFLVAPL YLF  
Sbjct  366  GQRSRWAQGMMQILRYRFPPLKRGLSLPQRLCYMSSTLFWLFPFPRAMFLVAPLFYLFLD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EIF A+  E LAY   Y+AV+ ++QN ++   RWP +SE+YE  Q  +L  A+++ +L 
Sbjct  426  LEIFTASGGEFLAYTLTYMAVNLMMQNYMYGYFRWPWISELYEYVQTVHLLPAVISVMLN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            P    F VTAKDE+++E+ +S I  P    F + L+ V  T+ R    P    + LVVGG
Sbjct  486  PSKPTFKVTAKDESIAESRLSEIALPFFVIFFVLLAAVGVTIWRIYTEPYRADLTLVVGG  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN+L+ G AL  V+E+  +R   RV+++   E ++     + L  T+ D S SG R 
Sbjct  546  WNLLNLLIAGCALGVVSERSSKRQTQRVRIKRRCEIEV---DGQVLPGTIEDVSVSGAR-  601

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
             +R+ G            +++F+   P  P     +   IR+  R G    +G  F    
Sbjct  602  -IRVFGTLPADLGQHVDAILRFK---PSRPMRSEALAIDIRNVERVGNGAAIGCQFAPAT  657

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPAR  737
             +     ++ L+F  S  W  ++++  R  G++ G    L +A     +T R       +
Sbjct  658  ALQY-SLISDLVFANSDQWSAIQQSRRRNPGVIRGTLYFLQIAVF---QTQRGLFYMFRQ  713

Query  738  RRRRHEEPKEKQA  750
            R  R E+P   QA
Sbjct  714  RFGRAEKPATVQA  726


>TR:A0A9X2PE93 A0A9X2PE93_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter mangrovi OX=2972472 GN=bcsA PE=4 SV=1
Length=736

 Score = 575 bits (1481),  Expect = 0.0
 Identities = 318/701 (45%), Positives = 436/701 (62%), Gaps = 16/701 (2%)

Query  24   ALLVPFGLLAAAPVAPSAQGLIALSAVVL-VALLKPFADKM-VPRFLLLSAASMLVMRYW  81
            +L+V F  L   P++  A  LIA S VVL + LLK F   + V R + L+  + +V+RY 
Sbjct  14   SLIVVF--LITLPISLQAH-LIAGSIVVLTMILLKTFGPPVGVFRMIALALGTAIVLRYV  70

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   T+PP +    F+   +L+  E +S+ + FL+ F+ + P  +    P+  ++ PT
Sbjct  71   YWRTTSTIPPISQIEDFIPGFMLYIAEMYSVFMLFLSLFVVSSPVPKRPTPPIPADQTPT  130

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VDI VPSYNE +D+L+ T++AA  + YPA   TV L DDGGTDQ+C   D   A++A+ R
Sbjct  131  VDIFVPSYNESSDLLASTISAALGIDYPADKFTVWLLDDGGTDQKCEQDDSVAAEEARSR  190

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
            R ELQ+LC  LG  Y TR RNEHAKAGN++  LE   G+L+VV DADH P+RDFL  TVG
Sbjct  191  RAELQRLCEGLGARYLTRARNEHAKAGNLNNGLENSTGDLIVVLDADHAPTRDFLQETVG  250

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            +F+++ +LFLVQTPHFFI+PDP++RNL   D  P ENEMFYG I RGLD+W  AFFCGSA
Sbjct  251  FFLQEENLFLVQTPHFFISPDPLERNLDTFDYMPSENEMFYGIIQRGLDKWDAAFFCGSA  310

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVL RRAL E  GF+G TITED E+ALE+HSRGW S+Y+++ MIAGLQP++FASFI QR 
Sbjct  311  AVLNRRALKETNGFSGITITEDCESALELHSRGWHSIYVEKPMIAGLQPDSFASFITQRS  370

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RWA GMMQ+L    P  +RGL +AQRL Y +S  FW F   R+MFL++PL YLFF ++IF
Sbjct  371  RWAQGMMQILRFHFPPLKRGLTLAQRLGYCSSSLFWLFSYPRLMFLISPLFYLFFSLQIF  430

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A   E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  Q+ YL  A+V+ +  P   
Sbjct  431  TAAGAEFLAYTTTYMLVNLLMQNYLYGRYRWPWISELYEYIQSVYLFPAVVSVIANPSKP  490
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Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAK ETL E ++S I RP    F + + G+  T+ R +  P +  VL+VVG W VL
Sbjct  491  TFKVTAKGETLEEGHVSQIGRPFFIIFAILVVGLFVTIYRLLTEPFNADVLIVVGAWNVL  550

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N+++ G AL  V+E++ RR + RV++    E  +   G  +   ++ D S  G RL
Sbjct  551  NIIIAGCALGVVSERRNRRRSHRVELMRRGELLV---GGATYPVSIEDGSLGGTRL---R  604

Query  622  PGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            P      P +  G   L++F+    + P     +   IR+   +G  V++G  F   QP+
Sbjct  605  PNANVVLPEINRGDMALLRFKTLANNIP--IDTIPLAIRNIENDGEGVLLGCQFMPDQPL  662

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              R  +A LIF  S  W   + +     G+L G  R L M+
Sbjct  663  HHR-LIADLIFANSDEWHKFQHSRRNNPGVLIGTIRFLRMS  702


>TR:A0A3Q8XQ71 A0A3Q8XQ71_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Georhizobium profundi OX=2341112 GN=bcsA PE=4 SV=1
Length=729

 Score = 575 bits (1481),  Expect = 0.0
 Identities = 319/717 (44%), Positives = 435/717 (61%), Gaps = 20/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L   +W+        + + P+      +     ++++ LLK F  +   R + L+  + +
Sbjct  5    LFAFVWLIAAACIVFIVSLPINLQTHLIAGTIVLLIMILLKLFKSEGTWRLVALAFGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP     SF+  LLL+  E +S+ + FL+ F+ A P      +P+
Sbjct  65   VLRYVYWRTTSTLPPVNQLESFIPGLLLYLAEMYSVFMLFLSLFIVARPLPSRPSQPVDE  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            ++LP+VD+ +PSYNE   +L+ T+AAA  + YPA   TV L DDGGTDQ+  S +    Q
Sbjct  125  DDLPSVDVFIPSYNEDPVLLADTIAAAMALDYPADRLTVWLLDDGGTDQKRNSDNVIEGQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A+ RR  LQ+LC ELG  Y TR RNEHAKAGN++  L+   G+LV VFDADH P+R FL
Sbjct  185  IAEARRANLQKLCAELGARYLTRARNEHAKAGNLNNGLDHSTGDLVAVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF ED  LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AF
Sbjct  245  RETVGYFNEDKRLFLVQTPHFFLNPDPLERNLKTFEKMPSENEMFYGVIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E+ GF+G +ITED ETA+E+HSRGW S+Y+D+ +IAGLQP TF+SF
Sbjct  305  FCGSAAVLRREALQESNGFSGISITEDCETAIELHSRGWNSVYVDKPLIAGLQPATFSSF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  + PL +RGL   QRLCY++S  FW FP  R +FL APL YLF
Sbjct  365  IGQRSRWAQGMMQILRFRFPLLKRGLSFPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFL  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IF A+  E LAY   Y+AV+ ++QN L+   RWP +SE+YE  Q  +L  A+++  L
Sbjct  425  DLQIFTASGGEFLAYTLSYMAVNLMMQNYLYGSFRWPWISELYEYIQTVHLLPAVISVAL  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VTAKDET++ + +S + RP    F + L GV  T+ R  A P    V LVVG
Sbjct  485  NPRKPTFKVTAKDETITTSRLSELSRPFFVIFGVLLIGVFVTVWRIYAEPYKADVTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN+++ G AL  VAE+++R A  RVQ+    E  +   G+  + AT+ D S +G R
Sbjct  545  AWNLLNLVMAGAALGVVAERRERAATRRVQINRRCEFGV---GDIWVPATIEDVSVNGAR  601

Query  617  LLVRLPGVGDPHPALEA----GGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            L V        H AL A       I+F P +   P++  +    IR+  REG  V +G
Sbjct  602  LRV------SGHSALAAVDTGQASIRFTPHWSTEPEILPVT---IRNKDREGDAVAIGCS  652

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
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            F   + +  R  VA LIF  ++ W   + +  R  G+L G A   W    +L +T R
Sbjct  653  FVRMKTVHHR-MVADLIFANASQWTHFQASRRRNPGVLLGTA---WFLRLALYQTIR  705


>TR:A0A9X3E3R7 A0A9X3E3R7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Kaistia nematophila OX=2994654 GN=bcsA PE=4 SV=1
Length=734

 Score = 574 bits (1480),  Expect = 0.0
 Identities = 324/715 (45%), Positives = 443/715 (62%), Gaps = 21/715 (3%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            LLW    +    L   P++  A  +   + + ++ +LK F    V R + L+  + LV+R
Sbjct  8    LLWAIAALATAFLITLPISLQAHLIAGTAVLGVMMVLKTFTSGGVWRQIALALGTSLVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ----  135
            Y +WR   TLPP     +F+   L++  E +SI + FL+ F+   P     PR L+
Sbjct  68   YAYWRTTSTLPPINELQNFIPGFLVYICEMYSIFMLFLSLFVVMLPHP---PRNLKISSS  124

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              +LPTVD+ VP+YNE  ++L+ TLAAAK M YPA   TV L DDGGT Q+  + + + A
Sbjct  125  DPDLPTVDVFVPTYNEEPELLATTLAAAKAMDYPAEKLTVWLLDDGGTVQKRNAENMQAA  184

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q+A+ER   LQ+L  +LG  Y TRERNEHAKAGNM+  L+  KGELVVVFDADH P+RDF
Sbjct  185  QEAEERFITLQKLAEDLGCRYLTRERNEHAKAGNMNNGLQFAKGELVVVFDADHAPARDF  244

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQ+PHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  +
Sbjct  245  LLYTVGYFKQDPKLFLVQSPHFFLNPDPVERNLRTFETMPSENEMFYGIIQRGLDKWDAS  304

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR ALD+ GGF+G +ITEDAETALE+H+ GW S+Y+DR +IAGLQP TFAS
Sbjct  305  FFCGSAAVLRREALDQTGGFSGVSITEDAETALELHASGWHSVYVDRPLIAGLQPATFAS  364

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GM Q+L  + P  +RGL I QRLCY++S  FWFFPL R +FL+APL YLF
Sbjct  365  FIGQRSRWAQGMYQILRFRFPPGKRGLSIPQRLCYMSSTLFWFFPLTRWIFLLAPLCYLF  424

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF A+  E +AY   Y+ V+ ++QN L+ R RWP +SE+YE  Q+ YL  A+ + +
Sbjct  425  FNLEIFTASAGEFVAYSSSYMIVNLMMQNYLYGRFRWPWISELYEYVQSVYLLPALFSVI  484

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VT+K E+L    +S + RP    F + +  VL T  R +  P    V  VV
Sbjct  485  LNPSKPTFKVTSKSESLDVARVSELSRPFFIIFAVLVFAVLMTAWRIINEPWKADVAFVV  544

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+++ G AL  V+E+Q+ RA+ RV ++   E  +   G++ + AT+ DAS  G
Sbjct  545  GGWNLLNLIIAGCALGVVSERQENRASRRVDVKRRCEILV---GDKVIPATIEDASVGGA  601

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDA-PQLERMVRGRIRSARREGGTVMVGVIFE  674
            R  + L  V  P  A +    ++F+     A P +   +R  IR  + EG  VM+GV +E
Sbjct  602  R--INLGNVKVPEIARDLYCDVRFKTNVEIATPSMPISIRSMIR--KPEG--VMLGVRYE  655

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                   R  ++ L+F  S  W   + +    IG+L G    +W  + S+ +T R
Sbjct  656  PSVADHYR-LISDLVFASSDLWTKFQWSRRTNIGILRG---TVWFLSLSVYQTGR  706


>TR:A0ABU0DG47 A0ABU0DG47_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter vacuolatus OX=223389 GN=J2S76_001788
PE=4 SV=1
Length=716

 Score = 574 bits (1480),  Expect = 0.0
 Identities = 312/685 (46%), Positives = 419/685 (61%), Gaps = 9/685 (1%)

Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
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            PV   AQ +     ++L+  LK FA + VPR + L+    +V RY +WR   TLPP
Sbjct  9    PVNLQAQLVTGCIVILLIVFLKMFASEGVPRMVALALGVAMVFRYVYWRTTSTLPPMEEL  68

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
            A+F+ A+LL++ E +S+++  L+ F+ + P        + P + PTVDI VPSYNE A +
Sbjct  69   ANFIPAVLLYSAEMYSVALMALSLFVVSSPQPPRIAPVIAPGKEPTVDIFVPSYNEDAGL  128

Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAA  + YP    TV L DDGGTDQ+C   D   A++AQ RR  L +LCRELGV
Sbjct  129  LATTLAAASALDYPRDRLTVWLLDDGGTDQKCEQHDLAAAREAQMRRETLTELCRELGVN  188

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TR RNEHAKAGN++  L    GEL+VVFDADH P+R FL  T+GYF EDP LFLVQTP
Sbjct  189  YLTRPRNEHAKAGNLNHGLAHSSGELIVVFDADHAPARPFLRETIGYFNEDPRLFLVQTP  248

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFFINPDP++R+L    R P ENEMFYG I RGLDRWGGAFFCGSAAVLRR AL E  GF
Sbjct  249  HFFINPDPVERSLDTWRRMPSENEMFYGVIQRGLDRWGGAFFCGSAAVLRREALKETNGF  308

Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
            A  +ITED ETAL +H+RGW S+Y+D  +IAGLQPETFASFI QR RWA GM Q+L
Sbjct  309  AHSSITEDCETALTLHARGWHSVYVDTPLIAGLQPETFASFIGQRSRWAQGMYQILRFHF  368

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PLFR GL IAQR+CY++S+ FWFFP+ R +FLV+P  YLFF +EIF  +  E  AY   Y
Sbjct  369  PLFRSGLTIAQRICYMSSILFWFFPISRAIFLVSPFFYLFFSLEIFNGSGAEFAAYTAVY  428

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            L ++  +Q+ L+ + RWP  SE+YE  Q  YL  A+++ ++ P+   F VT+K ET+ EN
Sbjct  429  LLINLFIQSYLYGKYRWPWFSELYEYIQTVYLLPALLSVMINPKKPTFKVTSKGETIDEN  488

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
             IS I  P    F++ +  V  T  R    P    + +VVG W +LN+++ G AL  V+E
Sbjct  489  RISEIGIPFFVIFVIQIVAVFVTFWRIATEPYSADITIVVGMWNLLNLIISGCALGVVSE  548

Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            K  +R + R+ +       I       + A + D S  G+R+   LP        + A
Sbjct  549  KAAKRHSQRIAITRRCSLLIAGV---EVPAIIDDVSMGGLRVRTELPPEATARVGMHA--  603

Query  636  LIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAH  695
            +++  P  PDA  +   +   +R+   + G V++G  F A +  A  + +A LIF  +
Sbjct  604  VVRVTP--PDA-CINDTLPVLVRNVALDEGVVVLGTQFNA-KTAAHYQLIADLIFANADE  659

Query  696  WRTMREATMRPIGLLHGMARILWMA  720
            W+  +    +  G+L G    + MA
Sbjct  660  WKKFQAGRRKNPGVLRGTVMFVVMA  684


>TR:A0A512J5T0 A0A512J5T0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium oxalidis OX=944322 GN=celA PE=4 SV=1
Length=784

 Score = 574 bits (1480),  Expect = 0.0
 Identities = 292/592 (49%), Positives = 395/592 (67%), Gaps = 5/592 (1%)

Query  31   LLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLP  90
            +L + PV    Q  ++L+A++ + +L  F D    RF+ L+  S++V+RY  WR+ +TLP
Sbjct  9    VLLSQPVGTQNQLAMSLAAMMAMVVLWLFFDGPRTRFVFLAMGSLVVLRYILWRVTDTLP  68

Query  91   PPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYN  150
             P    SF F LLL   E + + I F++  ++A+P  R  P P + E LPTVD+ VPSYN
Sbjct  69   SPGDPVSFGFGLLLLVGELYCVFILFVSLIINAEPLRRRPPPPQRAEALPTVDVFVPSYN  128

Query  151  EPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCR  210
            E A +L++TLAAA+ M YP    TV L DDGGTDQ+C   DP  A  A+ RR ELQ LC
Sbjct  129  EDASILAMTLAAARQMNYPPDKLTVWLLDDGGTDQKCADADPGKAAAARRRRTELQALCA  188

Query  211  ELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLF  270
            ELG  Y TRERN HAKAGN++  L +  G++VVVFDADHVP R FL  TVGYF+EDP LF
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Sbjct  189  ELGARYLTRERNLHAKAGNLNNGLAQATGDIVVVFDADHVPFRSFLRETVGYFLEDPRLF  248

Query  271  LVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALD  330
            LVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W G+FFCGSAA+LRR ALD
Sbjct  249  LVQTPHAFLNPDPIERNLRTFERMPSENEMFYAVTQRGLDKWNGSFFCGSAALLRRTALD  308

Query  331  EAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQM  390
            EAGGF+G TITED ETA E+H+RGW S Y+DR +IAGLQP+T A FI QR RW  GM Q+
Sbjct  309  EAGGFSGITITEDCETAFELHARGWTSAYVDRPLIAGLQPDTLADFIGQRSRWCQGMFQI  368

Query  391  LLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLA  450
            LLLKNP F+ GL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF ++IFVA+ +E +A
Sbjct  369  LLLKNPAFKAGLKPIQKVAYLSSMTFWFFPVPRLIFMFAPLLHIFFDLKIFVASVDESIA  428

Query  451  YMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDE  510
            Y   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AI + ++ PR   F VT+K
Sbjct  429  YTATYIVINLMMQNYVYGKFRWPFVSELYEYIQGLYLSKAIASVIVSPRKPTFNVTSKGA  488

Query  511  TLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFAL  570
            TL  +++SP+  P    + L L+G L    R++  PG  +++LVVG W   N+L  G AL
Sbjct  489  TLDHDHLSPLALPFFAVYALLLTGCLVAGWRYLFEPGVTNLMLVVGLWNFFNLLTAGAAL  548

Query  571  RAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLP  622
               AE++Q    P + +   A   + + G R++   +   S  G  L  RLP
Sbjct  549  GVCAERRQTERMPSLPI---ARRGVLSLGGRAVDVAIERVSAEGCTL--RLP  595


>TR:A0A1M5ALH3 A0A1M5ALH3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Kaistia soli DSM 19436 OX=1122133 GN=SAMN02745157_2174
PE=4 SV=1
Length=730

 Score = 574 bits (1479),  Expect = 0.0
 Identities = 329/737 (45%), Positives = 449/737 (61%), Gaps = 21/737 (3%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            L+W    V   +L   P+   A  +     V ++ LLK F   + V R + L+  + +V+R
Sbjct  8    LVWALAAVVMTILITLPINLQAHLVGGALVVGVMVLLKLFTRQGVWRQIALALGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE-  138
            Y +WR   TLPP       F+  LL++  E +SI + FL+ F+   P      PR L+
Sbjct  68   YAYWRTTSTLPPVNQPEDFIPGLLVYLAEMYSIFMLFLSLFVVMRPMA---PRTLKVSSS  124

Query  139  ---LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
               LPTVD+ VP+YNE A +L+ TLA+AK M YPA   TV L DDGG+ Q+  S + E A
Sbjct  125  DPGLPTVDVFVPTYNEDAALLATTLASAKAMDYPADKLTVWLLDDGGSVQKRNSDNIEAA  184

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q+A+ER   LQ+L  +LG  Y TRERNEHAKAGNM+  L+   G+L+ VFDADH P+RDF
Sbjct  185  QEAEERFVALQKLAADLGCRYLTRERNEHAKAGNMNNGLQYSTGDLIAVFDADHAPARDF  244

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF + P LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  +
Sbjct  245  LTYTVGYFQQTPKLFLVQTPHFFLNPDPVERNLRTFETMPSENEMFYGIIQRGLDKWDAS  304

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL++ GGF+G +ITEDAETALE+H+ GW S+Y+DR +IAGLQP TF S
Sbjct  305  FFCGSAAVLRREALEQTGGFSGVSITEDAETALELHATGWSSVYVDRPLIAGLQPATFTS  364

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L  + P  +RGL I QRLCY++S  FW FP+ R +FL+APL YLF
Sbjct  365  FIGQRSRWAQGMMQILRFRFPPGKRGLSIPQRLCYMSSTLFWLFPITRWIFLLAPLCYLF  424

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF A+  E +AY   Y+ V+ ++QN L+ R RWP +SE+YE  QA YL  A+++ +
Sbjct  425  FDLEIFTASGGEFVAYTSSYMLVNLMMQNYLYGRFRWPWISELYEFVQAVYLLPALISVI  484

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VTAK+E+L +  IS + RP    F + L GV+ T+ R  A P    V LVV
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Sbjct  485  LNPSKPTFKVTAKNESLDKARISELSRPFYIIFFVLLFGVVMTVWRIYAEPYKADVALVV  544

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+L+ G AL  ++E+Q+ R + R+++    E  I   G+R + ATV DAS  G
Sbjct  545  GGWNLLNILIAGCALGVISERQENRQSRRIEVRRRCEFII---GDRVVPATVEDASVGGA  601

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            R+ V      D    + A   I+F+    + P  +  +  R  +   +G  +M+G  +E
Sbjct  602  RINVSGLSQKDVERGMTAA--IRFKTSV-EIPTRDLPITLRTIAPGSKG--IMLGCRYEP  656

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR--DFMD  733
                  R  ++ LIF  S  W   + +    IG+L G    +W    S+ +T R   ++
Sbjct  657  HVADHYR-LISDLIFSSSDQWSKFQWSRRVNIGILRG---TIWFIGLSVYQTGRGLGYLV  712

Query  734  EPARRRRRHEEPKEKQA  750
            +  RR R    P EK+A
Sbjct  713  QSFRRERPATTPAEKRA  729


>TR:A0ABQ4SYI0 A0ABQ4SYI0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium jeotgali OX=381630 GN=AOPFMNJM_3491
PE=4 SV=1
Length=799

 Score = 574 bits (1479),  Expect = 0.0
 Identities = 317/723 (44%), Positives = 434/723 (60%), Gaps = 10/723 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L +L W+   +   +L + PV    Q  ++L+A+  + +L  F D    RF+ L+  S++
Sbjct  3    LRWLAWIGTTLAGLVLLSQPVGTQNQLAMSLAAMAAMIVLWLFLDGPRTRFVFLALGSLV  62

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY  WRL ETLP P    SF F LLL   E + + I F++  ++ADP  RP P
Sbjct  63   VLRYILWRLTETLPSPGDPVSFGFGLLLLVGELYCVFILFVSLVINADPLRRPPPPAAPA  122

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             ELP+VD+ VPSYNE A +L++TLAAA+ M YP    TV L DDGGTDQ+C   DPE A+
Sbjct  123  AELPSVDVFVPSYNEDAAILAMTLAAARQMNYPPEKLTVWLLDDGGTDQKCADSDPEKAR  182

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             AQ RR ELQ LC +LGV Y TR RN HAKAGN++  L    G+LV V DADHVP R FL
Sbjct  183  AAQARRVELQALCADLGVRYLTRPRNLHAKAGNLNNGLAHATGDLVAVLDADHVPFRSFL  242

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
            A TVGYF +DP LFLVQTPH F+NPDPI+RNL    R P ENEMFY     GLD+W G+F
Sbjct  243  AETVGYFAQDPKLFLVQTPHAFLNPDPIERNLRTFARMPSENEMFYAVTQAGLDKWNGSF  302

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRR ALDEAGGF+G TITED ETA E+H+RGW S Y+D+ +IAGLQPET  +F
Sbjct  303  FCGSAALLRRTALDEAGGFSGITITEDCETAFELHARGWTSAYVDKPLIAGLQPETLTAF  362

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GM Q+LLLKNP F++GL   Q+L YL+SM+FWFFP+ R++F+ APL+++FF
Sbjct  363  IGQRSRWCQGMFQILLLKNPAFQKGLKPIQKLAYLSSMTFWFFPVPRLIFMFAPLLHIFF  422

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ +
Sbjct  423  DLKIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIVSVIW  482

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VT K  +L  ++IS    P    + L L+G      R++  PG  +++LVVG
Sbjct  483  SPRKPTFNVTDKGVSLDHDHISSAALPFFVVYGLLLAGCAVAAWRYLFEPGVTNLMLVVG  542

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTSG  614
             W + N+L  G AL   AE++Q    P + +   A   +   G R++   V  + A
Sbjct  543  LWNLFNLLTAGAALGVCAERRQLERTPSLAVRRRA---LMTLGGRAVDVAVERVSAEACT  599

Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            VRL   +   G    AL     +      P A  L       + S  R G   +  ++F
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Sbjct  600  VRLPAAMLAPGAGQRALPGALTVVPVEGAPPAGPLP----VALESVERAGDEAVCRLVFG  655

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDE  734
              +P      +A L++G++   R  +    R   +L G A+ +W   +   +  R  +
Sbjct  656  RLRP-QDYTALAGLMYGDAEAMRRFQLRRRRHKDILTGTAQFVWWGFSEPVRALRVLLAG  714

Query  735  PAR  737
             AR
Sbjct  715  DAR  717


>TR:A0A1L3LXG1 A0A1L3LXG1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Sinorhizobium americanum OX=194963 GN=celA PE=4 SV=1
Length=723

 Score = 573 bits (1478),  Expect = 0.0
 Identities = 317/699 (45%), Positives = 424/699 (61%), Gaps = 8/699 (1%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            WV + +    L   PV    Q + ++  V  +AL+K        R + L+  S +V+RY
Sbjct  10   WVVISLCLVTLITLPVNMQTQLVASVLVVTFMALIKLLDAGGKWRLVALAFGSAMVLRYV  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R   P + P
Sbjct  70   YWRTTSTLPPVNQPENFIPGFLLYLAEMYSVVMLGLSLFVVAMPLPPRPSRSATPGKYPK  129

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VPSYNE AD+L+ TLAAAK M YPA   TV L DDG T Q+  S +   AQ+A  R
Sbjct  130  VDVFVPSYNEDADLLANTLAAAKGMDYPAEKLTVWLLDDGATLQKRNSTNLVDAQRAAAR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
             RELQ+LC +LGV Y TR+RNEHAKAGN++  +    GEL+ VFDADH P+RDFL  TVG
Sbjct  190  HRELQKLCEDLGVRYLTRDRNEHAKAGNLNNGMLNSNGELIAVFDADHAPARDFLFETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            YF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AFFCGSA
Sbjct  250  YFEDDPRLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAAFFCGSA  309

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVLRR+AL++  GF+G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFASFI QR
Sbjct  310  AVLRRKALEDTSGFSGLSITEDCETALALHGRGWNSVYVDRPLIAGLQPATFASFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RWA GMMQ+L+ + PL + GL I QRLCY++S  FW FP  R +FL APL YLFF ++IF
Sbjct  370  RWAQGMMQILMFRFPLLKGGLSIPQRLCYMSSTLFWLFPFSRTIFLFAPLFYLFFDLQIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A+  E LAY   Y+ V+  +QN L+   RWP +SE+YE AQ  +L  A+V+ LL PR
Sbjct  430  TASGGEFLAYTLVYMLVNLTMQNYLYGAFRWPWISELYEYAQTVHLLPAVVSVLLNPRKP  489

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAKDE++ E+ +S I RP    F + L      + R    P    + LVVGGW +L
Sbjct  490  TFKVTAKDESVLESRLSEISRPFFVIFAVLLIATALAIYRVYTEPYKADITLVVGGWNLL  549

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N+++ G AL  V+E+ ++ A+ RV++    E    +FG ++  AT+ + S  G R  V++
Sbjct  550  NLIMAGCALGVVSERGEKAASRRVKVSRRCEF---SFGEQTYPATIENVSAHGAR--VQV  604

Query  622  PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAV  681
             G+      ++  G I+FQP   D       V  +IR+   EG   +VG  +   +
Sbjct  605  YGLPTDELLIDVKGKIRFQPYSGDGTFETLPV--KIRNVETEGDLTIVGCRY-LPEVARH  661

Query  682  RETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
               VA LIF  S  W   +       GL+ G    LW+A
Sbjct  662  HSLVADLIFANSQQWSEFQRMRRGNPGLVRGTLWFLWLA  700


>TR:A0A1Q9AQZ1 A0A1Q9AQZ1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Xaviernesmea oryzae OX=464029 GN=BJF93_13335 PE=4
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SV=1
Length=730

 Score = 573 bits (1477),  Expect = 0.0
 Identities = 317/702 (45%), Positives = 431/702 (61%), Gaps = 12/702 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            +W+ + +    L   PV+ S   + A   + L+A+LK    +   R + L   + +V+RY
Sbjct  9    IWMLVSLFVLTLVTLPVSLSTHLVAAFCCMALLAVLKVCKAEGNWRLIGLGFGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLPP     +F+   LL+ VE +S+++  L+ FL + P      R       P
Sbjct  69   VYWRTTNTLPPVNQLENFIPGFLLYLVEMYSVAMLALSLFLVSMPLPEKKKRTANTAYQP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
             VD+ VP+YNE A +L+ TLAAAKNM YPA   T+ L DDGGT Q+    D   A+ A+
Sbjct  129  HVDVFVPTYNEDAQLLANTLAAAKNMDYPAEKLTIWLLDDGGTVQKRSVSDVPSAKAAER  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            R  EL +L  +LGV Y TRERNEHAKAGN++  L+  KGELVVVFDADH P+RDFL  TV
Sbjct  189  RYAELSKLAADLGVNYLTRERNEHAKAGNLNNGLKHSKGELVVVFDADHAPARDFLQETV  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF EDP LFLVQTPHFF+NPDPI+RNL      P ENEMFYG I RGLD+W  +FFCGS
Sbjct  249  GYFEEDPRLFLVQTPHFFLNPDPIERNLNTFGHMPSENEMFYGLIQRGLDKWNASFFCGS  308

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AA+LRR+AL+E  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  309  AAILRRQALEETDGFSGISITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ+L+ + P+F+ GL +AQRLCY++S  FW FP  RMMFL+APL YLFF +EI
Sbjct  369  SRWAQGMMQILIFRLPIFKSGLTLAQRLCYMSSTLFWLFPFPRMMFLIAPLFYLFFDLEI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FV +  E  AY   Y+ V+ L+QN L+ R RWP +SE+YE A   +L  A+++ LL P
Sbjct  429  FVGSGGEFFAYTMTYMLVNLLMQNYLYGRYRWPWISELYEYAHTIHLLPAVISVLLNPSK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VTAKDE+++E+ +S I  P    F + ++ ++  + R+ A P    V LVVGGW +
Sbjct  489  PTFKVTAKDESIAESRLSEIALPFFIIFAVLIAAMVMVVYRYYAEPAKADVTLVVGGWNL  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LN++  G AL AV E+  + AA RV+++   E Q+   G     A + + S +G+ + V
Sbjct  549  LNLIFAGCALGAVTERGDKSAARRVKVKRRCEFQV---GETWYPAVIENVSVNGMLVHV-  604

Query  621  LPGVGDPHPALEAGGL--IQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQP  678
                      L  GGL  I+  P     P  + M    +RS++ EG ++ +G  F A Q
Sbjct  605  ---YDKTLKPLATGGLEKIRVIPYSEGVP--DTMSVNIVRSSKGEGESISLGCTF-APQS  658

Query  679  IAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
                  +A L+F  S+ W   +    +  GL+ G    L +A
Sbjct  659  AMDHRLIADLMFVNSSQWSEFQMGRRKNPGLIRGTISFLGIA  700


>TR:A0A7Y6UQB5 A0A7Y6UQB5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ensifer oleiphilus OX=2742698 GN=bcsA PE=4 SV=1
Length=725

 Score = 573 bits (1476),  Expect = 0.0
 Identities = 313/685 (46%), Positives = 423/685 (62%), Gaps = 8/685 (1%)

Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
            PV    Q ++++  V  +A+LK    +   R + L+  + +V+RY +WR   TLPP
Sbjct  24   PVNLQTQLIVSVLVVTFMAILKLIKAEGRWRLIALAFGTAIVLRYVYWRTTSTLPPLNQL  83

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
             +F+   LL+  E +S+ +  L+ F+ A P      + + P   P VD+ VPSYNE A +
Sbjct  84   ENFIPGFLLYLAEMYSVMMLSLSLFVVAMPLPPRKAKAVSPGAFPKVDVFVPSYNEDAGL  143
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Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAAK M YPA   TV L DDGGT Q+  S +   AQ+A  R  ELQ LC +LGV
Sbjct  144  LANTLAAAKGMDYPADKLTVWLLDDGGTQQKRYSMNLVEAQRASARHVELQALCDDLGVR  203

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TRERNEHAKAGN++  +    GEL+ VFDADH P+RDFL  TVGYF  DP LFLVQTP
Sbjct  204  YLTRERNEHAKAGNLNNGMLHSDGELIAVFDADHAPARDFLLETVGYFESDPKLFLVQTP  263

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AFFCGSAAVLRR+AL++  GF
Sbjct  264  HFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAAFFCGSAAVLRRKALEDTEGF  323

Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
            +G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFASFI QR RWA GMMQ+LL +
Sbjct  324  SGMSITEDCETALALHGRGWNSIYVDRPLIAGLQPATFASFIGQRSRWAQGMMQILLFRF  383

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PLF+RGL I QRLCY++S  FW FP+ R +FL APL YLFF +EIF A+  E LAY   Y
Sbjct  384  PLFKRGLSIPQRLCYMSSTLFWLFPVSRTIFLFAPLFYLFFDLEIFTASGGEFLAYTLAY  443

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            + V+ ++QN L+   RWP +SE+YE AQ  +L  A+++ L+RP    F VTAKDE++ E+
Sbjct  444  MMVNLMMQNYLYGAFRWPWISELYEYAQTVHLLPAVISVLMRPSRPTFKVTAKDESIQES  503

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
             +S I RP    F +    +L T+ R    P    V LVVGGW +LN+++ G AL  V+E
Sbjct  504  RLSEISRPFFVIFAVLFVALLMTVYRVYTEPYKADVTLVVGGWNLLNLIMAGCALGVVSE  563

Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            + ++ A+ RV++    E  +    ++    AT+ D S +G R  V++ GV      ++  G
Sbjct  564  RGEKAASRRVKVSRRCEFGV---ADQWYPATIEDVSANGAR--VQVYGVDAATLPVDTDG  618

Query  636  LIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAH  695
            LI+F+P   D       V   +++    G    +G  +   +       VA LIF  S
Sbjct  619  LIRFEPYSGDGTSETLPV--AVKNKEIAGDITTLGCRY-LPEVARHHSLVADLIFANSQQ  675

Query  696  WRTMREATMRPIGLLHGMARILWMA  720
            W   ++A     GL+ G    LW+A
Sbjct  676  WSEFQKARRGNPGLVGGTVWFLWLA  700


>TR:A0ACC5SVE7 A0ACC5SVE7_ENSAD Cellulose synthase (UDP-forming) OS=Ensifer
adhaerens OX=106592 GN=J2Z19_002575 PE=4 SV=1
Length=725

 Score = 573 bits (1476),  Expect = 0.0
 Identities = 313/685 (46%), Positives = 423/685 (62%), Gaps = 8/685 (1%)

Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
            PV    Q ++++  V  +A+LK    +   R + L+  + +V+RY +WR   TLPP
Sbjct  24   PVNLQTQLIVSVLVVTFMAILKLIKAEGRWRLIALAFGTAIVLRYVYWRTTSTLPPLNQL  83

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
             +F+   LL+  E +S+ +  L+ F+ A P      + + P   P VD+ VPSYNE A +
Sbjct  84   ENFIPGFLLYLAEMYSVMMLSLSLFVVAMPLPPRKAKAVSPGAFPKVDVFVPSYNEDAGL  143

Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAAK M YPA   TV L DDGGT Q+  S +   AQ+A  R  ELQ LC +LGV
Sbjct  144  LANTLAAAKGMDYPADKLTVWLLDDGGTQQKRYSMNLVEAQRASARHVELQALCDDLGVR  203

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TRERNEHAKAGN++  +    GEL+ VFDADH P+RDFL  TVGYF  DP LFLVQTP
Sbjct  204  YLTRERNEHAKAGNLNNGMLHSDGELIAVFDADHAPARDFLLETVGYFESDPKLFLVQTP  263

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AFFCGSAAVLRR+AL++  GF
Sbjct  264  HFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAAFFCGSAAVLRRKALEDTEGF  323
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Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
            +G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFASFI QR RWA GMMQ+LL +
Sbjct  324  SGMSITEDCETALALHGRGWNSIYVDRPLIAGLQPATFASFIGQRSRWAQGMMQILLFRF  383

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PLF+RGL I QRLCY++S  FW FP+ R +FL APL YLFF +EIF A+  E LAY   Y
Sbjct  384  PLFKRGLSIPQRLCYMSSTLFWLFPVSRTIFLFAPLFYLFFDLEIFTASGGEFLAYTLAY  443

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            + V+ ++QN L+   RWP +SE+YE AQ  +L  A+++ L+RP    F VTAKDE++ E+
Sbjct  444  MMVNLMMQNYLYGAFRWPWISELYEYAQTVHLLPAVISVLMRPSRPTFKVTAKDESIQES  503

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
             +S I RP    F +    +L T+ R    P    V LVVGGW +LN+++ G AL  V+E
Sbjct  504  RLSEISRPFFVIFAVLFVALLMTVYRVYTEPYKADVTLVVGGWNLLNLIMAGCALGVVSE  563

Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            + ++ A+ RV++    E  +    ++   AT+ D S +G R  V++ GV      ++  G
Sbjct  564  RGEKAASRRVKVSRRCEFGV---ADQWYPATIEDVSANGAR--VQVYGVDAATLPVDTDG  618

Query  636  LIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAH  695
            LI+F+P   D       V   +++    G    +G  +   +       VA LIF  S
Sbjct  619  LIRFEPYSGDGTSETLPV--AVKNKEIAGDITTLGCRY-LPEVARHHSLVADLIFANSQQ  675

Query  696  WRTMREATMRPIGLLHGMARILWMA  720
            W   ++A     GL+ G    LW+A
Sbjct  676  WSEFQKARRGNPGLVGGTVWFLWLA  700


>TR:A0A2R4WRB4 A0A2R4WRB4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium currus OX=2051553 GN=bcsA PE=4 SV=1
Length=837

 Score = 573 bits (1476),  Expect = 0.0
 Identities = 303/642 (47%), Positives = 402/642 (63%), Gaps = 27/642 (4%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            VV  L +L W+        L + PV    Q  ++L+A+  +A L    D    RF+ L+
Sbjct  4    VVRALRWLAWIGTTAAGLALLSQPVGTQNQLAMSLAAMAAMAGLWLVFDGPRTRFVFLAM  63

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             S++V+RY  WR+ +TLP P    SF F LLL   E + + I F++  ++A+P  RP P
Sbjct  64   GSLVVLRYILWRVTDTLPSPGDPVSFGFGLLLLLCELYCVFILFVSLVINAEPLRRPPPA  123

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
                 +LP+VD+ VPSYNE A++L++TLAAA+ M YP    TV L DDGGTDQ+C  P+P
Sbjct  124  AAPAADLPSVDVFVPSYNEDAEILAMTLAAARQMNYPPEKLTVWLLDDGGTDQKCADPNP  183

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
            E AQ AQ RRRELQ LC ELG  Y TR RNEHAKAGN++  L    G+LV+V DADHVP
Sbjct  184  EKAQGAQARRRELQALCEELGARYLTRARNEHAKAGNLNNGLAAATGDLVLVLDADHVPF  243

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            R  LA TVGYF EDP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY     GLD+W
Sbjct  244  RSLLAETVGYFAEDPRLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYAVTQAGLDKW  303

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
             G+FFCGSAA+LRR ALDEAGGFAG TITED ETA E+HSRGW S Y+D+ +IAGLQP+T
Sbjct  304  NGSFFCGSAALLRRAALDEAGGFAGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPDT  363

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
             A F+ QR RW  GM Q+L+LKNP  +RGL   Q+L YL+SM+FWFFP+ R++F+ APL+
Sbjct  364  LADFVGQRSRWCQGMFQILILKNPALQRGLKPIQKLAYLSSMTFWFFPVPRLVFMFAPLL  423

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            ++FF ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV
Sbjct  424  HIFFDLKIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIV  483

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
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            + +  PR   F VT K  TL  +++S +  P    + L L+G L    R++  PG  +++
Sbjct  484  SVIWSPRKPTFNVTNKGATLDHDHLSALSLPFFAVYGLLLTGCLVAAWRYLFEPGVTNLM  543

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAP----------------------RVQME--  588
            LVVG W + N+L  G AL   AE++Q    P                      RV  E
Sbjct  544  LVVGLWNLFNLLTAGAALGVCAERRQIERTPSLPVSRRGQLTLGGRAVDVAIERVSAEAC  603

Query  589  ---VPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDP  627
               +PA    P  G+R +  T+     +G R    LP V  P
Sbjct  604  TVRMPAAFLAPGAGHRPVPGTLTVVPMAGSRPAGALPVVLGP  645


>TR:A0ABU3SD64 A0ABU3SD64_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Bosea rubneri OX=3075434 GN=bcsA PE=4 SV=1
Length=727

 Score = 572 bits (1475),  Expect = 0.0
 Identities = 307/708 (43%), Positives = 430/708 (61%), Gaps = 23/708 (3%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQ---GLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            ++W         L A P++  A    G I + A++L+ LL+P     V R + L   + +
Sbjct  8    IVWAVTAALVTALIALPISLQAHLIAGTILVGAMILLKLLRPLG---VWRLIALGLGTAV  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP      F+  ++L+  E ++I + FL+ F+ A P  R    P+
Sbjct  65   VLRYVYWRTTSTLPPVNQLEDFIPGVILYVAELYNIGMLFLSLFVVAMPLPRRATPPIDL  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
               PTVD+ VPSYNE AD+L+ TL+AA  M YP     V L DDGGTD++C S +   A
Sbjct  125  ANAPTVDVFVPSYNEDADLLATTLSAALAMDYPTGKLQVYLLDDGGTDEKCASDNFAAAH  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A+ERR  LQ+LC  LGV Y TRERN +AKAGN++  +   +GEL+VVFDADH P+R FL
Sbjct  185  AAKERRATLQKLCEGLGVTYLTRERNLNAKAGNLNNGIAHSQGELIVVFDADHAPARSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVG+F  DP LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  +F
Sbjct  245  TETVGFFARDPKLFLVQTPHFFINPDPLERNLKTFKEMPSENEMFYGIIQRGLDKWNSSF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVL R+AL    GF+G +ITEDAETA+ +H+ GW S+Y+D+ +IAGLQP TF SF
Sbjct  305  FCGSAAVLSRKALLTTNGFSGRSITEDAETAITLHAAGWNSVYVDKPLIAGLQPATFTSF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L+   PL +RGL + QRLCY ++  FW FP  RM+FL++PL YLFF
Sbjct  365  IGQRSRWAQGMMQILIYHRPLLKRGLSLPQRLCYTSTALFWLFPFARMIFLISPLFYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G++IFVAT  E +AY+ GY+ V+ ++QN L+ R RWP +SE+YE  Q+ YL  A+++ +L
Sbjct  425  GLQIFVATGGEFIAYILGYMVVNLMMQNYLYGRYRWPWISELYEFIQSIYLLPAVISVML  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAK+E+L    +S +  P L  F++   GV+A   R +A P +    LVVG
Sbjct  485  NPSKPTFKVTAKNESLETRRVSELGMPFLIIFIVLTLGVVAQYWRTIAEPYNADTTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W ++N+L+ G AL  V+E+ + RAA R  ++   E         ++     +AS  G+
Sbjct  545  LWNMMNLLMAGCALGVVSERPEGRAARRFAVKRRGEM---VLNGDAMPMVTENASVDGIA  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRG----RIRSARREGGTVMVGVI  672
            + +  PG     PA+    LI F+           M RG    R++   ++   +M+G
Sbjct  602  IRI-APGTA-AKPAIGDQALISFETTL-------AMPRGTLPIRVKRIEQDPQGLMLGCR  652

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            +E  +P+  R  +A L F ++  W   ++A    IG++ G  R L +A
Sbjct  653  YEPSEPLHSR-MIADLAFSDAERWSRFQKARRNNIGVVRGTTRFLRIA  699


>TR:A0A2C9DCN8 A0A2C9DCN8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
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OS=Hartmannibacter diazotrophicus OX=1482074 GN=bcsA
PE=4 SV=1
Length=747

 Score = 572 bits (1475),  Expect = 0.0
 Identities = 328/744 (44%), Positives = 431/744 (58%), Gaps = 32/744 (4%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            +L   W A    F  L A P+    Q ++ ++ +  +  L     +   R +++  A  +
Sbjct  1    MLKFAWFAAASMFLFLVAQPIGSEGQVIVGVTLIAAMLGLWLTGRRGTTRTVVIMLALAV  60

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRP-FPRPLQ  135
            V RY +WR   TLP P    +F+   LL+ VE FS+ + F++ F+ ADP DRP
Sbjct  61   VCRYVYWRTTSTLPDPGDLVNFIPGALLYGVEMFSVLMLFISLFVVADPKDRPAVVVDDN  120

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              +LPTVD+ +P+YNE  ++L+ T+AAA  M YPA   TV L DDGG+DQ+C S DP  A
Sbjct  121  DHDLPTVDVFIPTYNEDPELLATTVAAAVAMDYPAGHLTVYLLDDGGSDQKCNSEDPVAA  180

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              A ERRREL QLC  LG VY TR RN  AKAGNM+AAL R  G+LV VFDADH P R F
Sbjct  181  HAAIERRRELTQLCEGLGAVYMTRARNVSAKAGNMNAALPRTHGDLVAVFDADHAPVRSF  240

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L +TVG+F+EDP LFLVQTPHFF+NPDPI++NL+L    P ENEMFYG I +GLDRW  A
Sbjct  241  LKKTVGHFLEDPRLFLVQTPHFFLNPDPIEKNLSLFKSMPSENEMFYGVIQKGLDRWNAA  300

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRR AL+EAGGF G TITED ETAL +HSRGW S YID  +IAGLQPETF+S
Sbjct  301  FFCGSAALLRRTALEEAGGFDGVTITEDCETALTLHSRGWNSRYIDTPLIAGLQPETFSS  360

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RW  GMMQ+LLLKNP+FR+GL  AQR+CYL+S  FW F L R+ F+ APL+++F
Sbjct  361  FIGQRSRWCQGMMQILLLKNPVFRKGLSFAQRVCYLSSSLFWLFSLTRLTFVFAPLLHIF  420

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EI+ A+ +E  AY   Y+  + ++QN LF R RWP +SE+YE  Q+ YL +AI
Sbjct  421  FSMEIYQASLQEFFAYTTVYMVANMMLQNYLFGRVRWPWMSELYEYVQSVYLIQAIAKVF  480

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR   F VTAK  T+  + +S I  P    F + L+      +RW   P  R +L VV
Sbjct  481  LNPRKPTFNVTAKGVTIDRDQLSEIALPYFVIFGMLLTAAGVDALRWWNEPASRDMLAVV  540

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W  LN+++ G +L AV+E+ +RR + R+ +   A   +      +    V D S+ GV
Sbjct  541  GLWNGLNLIIAGLSLGAVSERAERRRSQRLAV---ARKGVMELDGNAFQVLVEDVSSGGV  597

Query  616  RL-----LVRLPGVGDPHPAL-----EAGGLIQFQPKFPDAPQLERMVRGRIRSARREGG  665
            R+       R    G     L     + GG IQ          L   VR  I   R
Sbjct  598  RVRPLGARPRFNRAGSRTGTLAIRRNDPGGTIQ---------TLNVAVRRNISDER----  644

Query  666  TVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL-WMAA---  721
             + +G+ F     +A   T+A L++ +S      R+     +G++ G  R L W  A
Sbjct  645  GLSLGLEF-VDLSLAQYRTIADLMYADSRPLEEFRDGRRTSMGIVRGSMRFLGWSMAYIM  703

Query  722  ASLPKTARDFMDEPARRRRRHEEP  745
              L    R     P R      EP
Sbjct  704  RGLSLAGRHGKAAPLRSELARSEP  727


>TR:A0A1Q9ADB1 A0A1Q9ADB1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Xaviernesmea rhizosphaerae OX=1672749 GN=BJF92_17815
PE=4 SV=1
Length=731

 Score = 572 bits (1475),  Expect = 0.0
 Identities = 319/705 (45%), Positives = 430/705 (61%), Gaps = 12/705 (2%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
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            FL+W+ + +    L   P++     + A   + L+A+LK    +   R + L   + +V+
Sbjct  7    FLIWMLVSLFVLTLVTLPISLQTHLVAAFLCMALLAILKVMKAEGNWRLIGLGFGTAIVL  66

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY +WR   TLPP     +F+   LL+ VE +S+++  L+ FL + P      RP
Sbjct  67   RYVYWRTTSTLPPLNQLENFIPGFLLYLVEMYSVAMLALSLFLVSMPLEKKKRPGTTAY  126

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
             PTVD+ VP+YNE A +L+ TLAAAKNM YPA   TV L DDGGT Q+  + D   A+ A
Sbjct  127  RPTVDVFVPTYNEDAQLLANTLAAAKNMDYPADKLTVWLLDDGGTVQKRSATDIPSARAA  186

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            + R  EL +L  +L V Y TRERNEHAKAGN++  L++ +GELVVVFDADH P+RDFL
Sbjct  187  ERRHAELSRLAADLDVKYLTRERNEHAKAGNLNNGLKQSEGELVVVFDADHAPARDFLLE  246

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF EDP LFLVQTPHFF+NPDPI+RNL      P ENEMFYG I RGLD+W  +FFC
Sbjct  247  TVGYFEEDPKLFLVQTPHFFLNPDPIERNLNTFGHMPSENEMFYGLIQRGLDKWNASFFC  306

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAAVLRR AL +  GF+G +ITED ETAL +H RGW S+Y+D+ +IAGLQP TFASFI
Sbjct  307  GSAAVLRREALQDTDGFSGVSITEDCETALALHGRGWNSVYVDKPLIAGLQPATFASFIG  366

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RWA GMMQ+L+ + PLF+ GL  AQRLCY++S  FW FP  R MFL+APL YLFF +
Sbjct  367  QRSRWAQGMMQILIFRQPLFKGGLTFAQRLCYMSSTLFWLFPFPRTMFLIAPLFYLFFDL  426

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            EIFV +  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  Q  +L  A+++ +L P
Sbjct  427  EIFVGSGGEFLAYTMTYMLVNLLMQNYLYGRFRWPWISELYEYVQTVHLLPAVISVMLNP  486

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
                F VTAKDE+++++ +S I  P    F + ++ +   + R    P    V LVVGGW
Sbjct  487  SKPTFKVTAKDESITQSRLSEISAPFFIIFAILIAAMGMVVYRLYVEPTKADVTLVVGGW  546

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             +LN++  G AL AV E+  + AA RV ++   E ++   G+    A + + S  G  LL
Sbjct  547  NLLNLIFAGCALGAVTERGDKSAARRVTVKRRCEFKV---GDAWYPAVIDNVSVDG--LL  601

Query  619  VRLPGVGDPHPALEAGGL--IQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            V +         L+AG +  I+ +P     P  + M    +RS++ EG  + VG  F A
Sbjct  602  VHV--YDQSLAPLKAGNIEAIRVKPYSEGIP--DTMAVNVVRSSKGEGEAISVGCTF-AP  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
            Q       +A L+F  SA W   +    R  GL+ G    L +AA
Sbjct  657  QRALDHRLIADLMFANSAQWSEFQMGRRRNPGLIRGTLSFLGIAA  701


>TR:A0A175RMM7 A0A175RMM7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aureimonas ureilytica OX=401562 GN=NS365_14755 PE=4
SV=1
Length=730

 Score = 572 bits (1474),  Expect = 0.0
 Identities = 322/711 (45%), Positives = 433/711 (61%), Gaps = 13/711 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            LLW+   +    +   PV+  AQ    L  + ++ +LK      V R + L+  + +V+R
Sbjct  8    LLWILASILAIAVITLPVSLQAQLFAVLFVLGVMVILKTLDLGGVWRLVALALGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP-EE  138
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R L P  +
Sbjct  68   YVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVFMLALSLFVVAAPVPPRPSRTLTPGRQ  127

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
             P+VD+ VP+YNEP  +L+ TLA+A  M YPA   TV L DDGGTDQ+  S D   A+ A
Sbjct  128  PPSVDVFVPTYNEPTKLLANTLASALAMNYPADRFTVWLLDDGGTDQKRQSDDMVSAESA  187

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
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            + R  EL  LC  LG  Y TR RN  AKAGN++  + +  GEL+ VFDADH P+RDFLA
Sbjct  188  ERRHAELNALCEALGARYLTRARNTSAKAGNLNHGMTQSTGELIAVFDADHAPARDFLAE  247

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF +DP LFLVQTPHFF+NPDP++RNL   D+ P ENEMFYG I RGLD+W  AFFC
Sbjct  248  TVGYFEDDPRLFLVQTPHFFLNPDPLERNLRTFDKMPSENEMFYGIIQRGLDKWNAAFFC  307

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR AL E  GF+G +ITED ETA+E+HSRGW SLY+D+ +IAGLQP TFASFI
Sbjct  308  GSAALLRREALMETSGFSGISITEDCETAVELHSRGWSSLYLDKPLIAGLQPATFASFIG  367

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RWA GMMQ+LLL+ PLF+RGL   QRLCY +S  FW FP  R+MFLVAPL YLFFG+
Sbjct  368  QRSRWAQGMMQILLLRAPLFKRGLSFPQRLCYTSSTLFWLFPFPRLMFLVAPLFYLFFGL  427

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IF A+  E +AY   Y+AV+ ++QN+++   RWP +SE+YE  Q+ +L  A+V+T+L P
Sbjct  428  QIFTASSGEFVAYTLTYMAVNLMMQNSMYGSFRWPWISELYEYVQSVHLLPAVVSTMLHP  487

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VTAKDE+++E+ +S I  P    F + L G++AT+ R +  P    + +VVG W
Sbjct  488  RKPTFNVTAKDESIAESRVSEIGLPFYVIFAVLLLGLVATVWRVIDEPYRADLTMVVGAW  547

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             VLN+++ G AL  V+E     A  R+ ++   + QI       L  T+ D S SGV
Sbjct  548  NVLNLVIAGCALGVVSELGTPTANRRIAVKRRCDIQIE---GTLLAGTIEDVSVSGVS--  602

Query  619  VRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQP  678
            VR+ G   P          ++ + +         +V  RI+  R EG TV+ G  F A
Sbjct  603  VRVTGALPPEVERGTSATLRVRTELESGRDTIPLVFKRIQ--RGEGSTVL-GCAFAADSA  659

Query  679  IAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
               R  +A LIF +S  W+ ++ A  R  G+L G     W     L +T R
Sbjct  660  HHNR-LIADLIFADSGQWQQLQRARRRNPGILRGS---FWFFGVCLYQTFR  706


>TR:A0A916YG50 A0A916YG50_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aureimonas glaciei OX=1776957 GN=GCM10011335_53370
PE=4 SV=1
Length=732

 Score = 572 bits (1473),  Expect = 0.0
 Identities = 325/723 (45%), Positives = 435/723 (60%), Gaps = 17/723 (2%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKM--VPRFLLL  70
            ++ +LL L+W  +      +   P++   Q LIA +A VL A++     K+    R + L
Sbjct  1    MLKLLLGLVWACVAAVSLAVITLPISLQTQ-LIA-TATVLAAMVAIKVTKLGGTWRLVAL  58

Query  71   SAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPT-DRP  129
            +  + +V+RY FWR   TLPP     +F+    L++  E +S+ + FL+ F+ A P   RP
Sbjct  59   ALGTTVVLRYVFWRTTSTLPPINQIENFIPGFLVYLAEMYSVLMLFLSLFVVAAPLPSRP  118

Query  130  FPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMS  189
                   + LPTVD+ +PSYNE   +L+ TLAAA  M YP+    V L DDG T Q+  S
Sbjct  119  ARVNWDGDNLPTVDVFIPSYNEGTTLLANTLAAALTMDYPSDRLKVWLLDDGSTLQKRSS  178

Query  190  PDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADH  249
             +   +Q A++R  EL+QLC +LG  Y  RERNEHAKAGN++  L   +G L+ VFDADH
Sbjct  179  ENAGESQTAEKRHAELKQLCADLGATYLARERNEHAKAGNLNNGLLHSEGSLIAVFDADH  238

Query  250  VPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGL  309
             P+R+FL  TVG+F EDP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGL
Sbjct  239  APAREFLLDTVGHFEEDPRLFLVQTPHFFVNPDPLERNLGTFEKMPSENEMFYGIIQRGL  298

Query  310  DRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQ  369
            D+W  AFFCGSAAVLRR AL+EAGGF+G +ITED ETAL++H RGW S+Y+D  MIAGLQ
Sbjct  299  DKWNAAFFCGSAAVLRREALNEAGGFSGVSITEDCETALDLHGRGWNSVYVDTPMIAGLQ  358

Query  370  PETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVA  429
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            P TFASFI QR RWA GMMQ+L  + PLF+RGL + QR+CY++S  FW FP  R MFLVA
Sbjct  359  PATFASFIGQRSRWAQGMMQILRFRMPLFKRGLSLPQRICYMSSTLFWLFPFSRAMFLVA  418

Query  430  PLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLAR  489
            PL YLFFG++IF A+  E LAY   Y  V+ ++QN LF   RWP +S++YE  Q  +L
Sbjct  419  PLFYLFFGLQIFTASGGEFLAYTATYFVVNLMMQNYLFGSYRWPWISDLYEYVQTVHLLP  478

Query  490  AIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDR  549
            A+V+ +L PRS  F VTAKDE++  + +S I RP    F + L GV  T  R +  P
Sbjct  479  AVVSVILNPRSPTFKVTAKDESILHDRLSEISRPFFIIFAILLVGVGVTAYRVITEPYRA  538

Query  550  SVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLD  609
             + LVVGGW +LN+LL G AL  V+E+    A+ RV +    +  I   G+R   AT+ +
Sbjct  539  DLTLVVGGWNLLNLLLAGCALGVVSERGTPSASRRVAVRRRCDLLI---GDRVFPATIDN  595

Query  610  ASTSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMV  669
             S  G RL V     G     L AGG I  + + P +      +   +R+ R E     +
Sbjct  596  VSVDGARLRV----YGSVPADLVAGGAISMRFR-PHSKSGTASLPAVVRNVRPEPDGASI  650

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            G  +   Q  A    VA L+F  S  WR  + A     GL+ G    +W     L +T R
Sbjct  651  GCSYVTSQ-AADHFLVADLVFANSEQWRAFQLARRNDPGLVRG---TVWFFGLCLAQTCR  706

Query  730  DFM  732
             F+
Sbjct  707  GFV  709


>TR:A0ABU0HB47 A0ABU0HB47_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Kaistia dalseonensis OX=410840 GN=QO014_003940 PE=4
SV=1
Length=732

 Score = 571 bits (1472),  Expect = 0.0
 Identities = 321/718 (45%), Positives = 441/718 (61%), Gaps = 19/718 (3%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            + + +LW    +   +L   P+   A  +   + V ++ LLK F  + V R + L+  +
Sbjct  4    IAIAVLWGISALAVIILITLPINLQAHLVAGATVVGVMILLKLFTREGVWRQIALALGTS  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+  +L++  E +SI + FL+ F+   P     PR L+
Sbjct  64   IVLRYAYWRTTSTLPPINEPENFIPGVLVYIAEMYSIFMLFLSLFVVMRPMA---PRSLK  120

Query  136  PE----ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
             E    +LP+VD+ VP+YNE A++L+ TLAAAK M YPA   TV L DDGGT Q+  S +
Sbjct  121  VESNAPDLPSVDVFVPTYNEEAELLATTLAAAKAMDYPADKLTVWLLDDGGTIQKRHSDN  180

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
             + A +A+ER   LQ+L  +L   Y TRERNEHAKAGNM+  L   KG+L+ VFDADH P
Sbjct  181  LQTAHEAEERYVALQKLAADLDCRYLTRERNEHAKAGNMNNGLGVSKGDLIAVFDADHAP  240

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            +RDFL  TVGYF +DP LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+
Sbjct  241  ARDFLNYTVGYFAQDPKLFLVQTPHFFLNPDPVERNLRTFETMPSENEMFYGIIQRGLDK  300

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            W  +FFCGSAAVLRR ALD+ GGF+G +ITEDAETALE+H+ GW S+Y+DR +IAGLQP
Sbjct  301  WDASFFCGSAAVLRREALDQTGGFSGVSITEDAETALELHATGWHSVYVDRPLIAGLQPA  360

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TF SFI QR RWA GMMQ+L  + P  +RGL I QRLCY++S  FWFFPL R +FL+APL
Sbjct  361  TFTSFIGQRSRWAQGMMQILRFRFPPLKRGLSIPQRLCYMSSTLFWFFPLTRWVFLLAPL  420

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLFF +EIF A+  E LAY   Y+ V+ ++QN L+ R RWP +SE+YE  Q+ YL  A+
Sbjct  421  CYLFFNLEIFTASGAEFLAYTSSYMLVNLMMQNYLYGRFRWPWISELYEYVQSVYLLPAL  480

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
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            ++ +L P    F VTAK+E+L E  IS + RP    F L ++G++ T+ R  + P    V
Sbjct  481  ISVILNPSKPTFKVTAKNESLDEARISELARPFYIIFFLLVAGLIMTVWRIYSEPYKTDV  540

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
             LVVGGW +LN+L+ G AL  V+E+Q+ R + RV ++   +  I   G+R   AT+ DAS
Sbjct  541  ALVVGGWNLLNLLIAGCALGVVSERQESRQSRRVSVKRRCDLLI---GDRVFPATIEDAS  597

Query  612  TSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
              G R+        D H      G+I       + P L   +   +R+     G +M+G
Sbjct  598  VGGARINATGLTAQDVH-----RGMICAIRYKTNVPILRNELPISVRTVAGGTGGLMLGC  652

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             ++       R  ++ L+F  S  W     +    IG+L G    +W    +L +T R
Sbjct  653  RYDPTIADHYR-LISDLVFSSSDLWYKFLWSRRVNIGILRG---TIWFVGLALYQTGR  706


>TR:A0AAE5RXX0 A0AAE5RXX0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium rosae OX=1972867 GN=bcsA PE=4 SV=1
Length=731

 Score = 571 bits (1472),  Expect = 0.0
 Identities = 315/701 (45%), Positives = 427/701 (61%), Gaps = 7/701 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            ++WV +     ++   PV+     +    ++VL+A +K    K   R + L   + +V+R
Sbjct  8    IVWVLVSACVLVIITLPVSLQTHLIATAISLVLLATIKSLNGKGAWRLIALGFGTAIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P  +
Sbjct  68   YVYWRTTSTLPPINQPENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPGSPGYV  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVDI VP+YNE + +L+ TL+AAKN+ YPA   TV L DDG T Q+  + +   AQ A
Sbjct  128  PTVDIFVPTYNEDSTLLANTLSAAKNIDYPADKFTVWLLDDGSTVQKRNATNVPDAQAAA  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +R  ELQ+LC +LGV Y TRERN HAKAGN++  LE   GEL+ VFDADH P+RDFL  T
Sbjct  188  KRHEELQKLCADLGVKYLTRERNVHAKAGNLNNGLEYSTGELITVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF ED  LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCG
Sbjct  248  VGYFEEDEKLFLVQTPHFFLNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL E  GF+G +ITED ETAL +HSRGW SLY+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRSALKETDGFSGVSITEDCETALALHSRGWNSLYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLFF ++
Sbjct  368  RSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQ  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  428  IFVASGGEFLAYTAAYMLVNLMMQNFLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPS  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKD+++SE  +S I RP    F + +  ++  + R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDDSISEARLSEISRPFFVIFAVLVVAMIFAIYRVYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN++  G AL  V+E+ ++ A+ R+ ++   E Q+    +  + ATV + S  G+ + +
Sbjct  548  LLNIIFAGCALGVVSERGEKSASRRITVKRRCELQV-GDNDTWMPATVENVSVHGMLINI  606

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
              PG+        A   I+ +P    AP    M    +RS +++ G V VG  F   Q +
Sbjct  607  FEPGLAPVEKG--APTTIRIKPYSEGAP--TTMSINIVRSVKQD-GFVQVGCTFAPKQAV  661

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              R  +A LIF  S  W   +    +  GL+ G A  L +A
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Sbjct  662  DHR-LIADLIFANSEQWSEFQRVRRKNPGLIKGTATFLAIA  701


>TR:A0A509EB28 A0A509EB28_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium symbioticum OX=2584084 GN=bcsA PE=4
SV=1
Length=813

 Score = 571 bits (1471),  Expect = 0.0
 Identities = 309/704 (44%), Positives = 432/704 (61%), Gaps = 9/704 (1%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+  +W++  +   LL A P+   AQ  ++L A+VL+ALL  F    V R + L+  S++
Sbjct  5    LVRTIWLSSAIVVLLLLAQPIGTPAQLELSLGAIVLMALLWVFGRGRVARSMFLAVGSLV  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL-Q  135
            V+RY +WRL  TLPP +    F   L+L A E +   I  ++  ++ADP  R  P P
Sbjct  65   VLRYLYWRLSSTLPPMSDPFGFGAGLILLAAELYCFYILAVSLVVNADPLVR-VPAPAGD  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             E+LPTVDI VPSYNE   +L+ TLAAA+ + YPA   TV L DDGGTDQ+C   D   A
Sbjct  124  DEDLPTVDIFVPSYNEDRHILATTLAAARAIDYPADKLTVWLLDDGGTDQKCSDTDSAKA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +A+ RR+ LQ LC +LGV Y TR RN HAKAGN++  L    GE+VVV DADHVP R F
Sbjct  184  AEARARRQVLQALCDDLGVSYLTRPRNVHAKAGNLNNGLRHATGEIVVVLDADHVPFRSF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  T+G+F  DP LFLVQTPH F+NPDP++RNL   DR P ENEMFY     GLD+W G+
Sbjct  244  LRETIGHFARDPKLFLVQTPHAFLNPDPLERNLQTFDRMPSENEMFYAISQCGLDKWNGS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRR AL+EAGGF+G TITED ETA E+HSRGW S+Y+D+ +IAGLQPET +
Sbjct  304  FFCGSAALLRRAALEEAGGFSGVTITEDCETAFELHSRGWTSVYVDKPLIAGLQPETLSD  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RW  GM+Q++LLKNPLF+ GL   QRLCY++SM+FWFFPL R++F+VAPL+Y+F
Sbjct  364  FIGQRSRWCQGMLQIMLLKNPLFKSGLKPIQRLCYMSSMTFWFFPLPRLIFMVAPLLYIF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++I VA  +E +AY   Y+AV+ ++QN L+ R RWP VSE+YE  Q  +L +A    +
Sbjct  424  FDMKIVVANVDEAIAYTATYIAVNLMMQNYLYGRVRWPFVSELYEYVQGLFLIKATAAVI  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR  +F VTAK+ +L  + +SP+  P +  + + L+G++    R++  PG  +++LVV
Sbjct  484  LSPRKPQFKVTAKNVSLDHDQLSPLALPYILVYAVLLAGMVVATYRYLFEPGITNLMLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W +  +L  G AL   AE++Q   +P + ++  A   I       +   V     S
Sbjct  544  GLWNLFGLLTAGAALGVAAERRQTEKSPSLAVDRKAVLTI-----NGMAIDVAVDRISSA  598

Query  616  RLLVRLPGVGDPHPALEA-GGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            R  VR+  V     + ++  G +  +P +         +  R+      G   +  + FE
Sbjct  599  RCRVRMDAVLPVRRSDDSFSGTLSVRPHWAMPTDEISAIPVRVAGVTAAGEESVCDLAFE  658

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILW  718
            A  P A    +A L++G++      ++       LL G  + +W
Sbjct  659  ALPPQAY-FALADLMYGDAGAMTRFQQRRRTHKDLLTGTLQFIW  701


>TR:A0A7W6HG51 A0A7W6HG51_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aurantimonas endophytica OX=1522175 GN=GGR03_003699
PE=4 SV=1
Length=732

 Score = 571 bits (1471),  Expect = 0.0
 Identities = 323/722 (45%), Positives = 437/722 (61%), Gaps = 21/722 (3%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVV-LVALLKPFADKMVPRFLLLS  71
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            ++ +LL   W+        +   P++  AQ L+A++ V+ ++ LLK        R + L+
Sbjct  1    MLKILLSFAWILAAALALFVITLPISLQAQ-LVAVTLVLGVMMLLKVLKLGGTWRLIALA  59

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
              + +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P
Sbjct  60   LGTTIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVFMLALSLFVVAAPLPPRSG  119

Query  132  RPL-QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
            R     +  P+VD+ VPSYNE   +L+ TLAAA  M YP+    V L DDGGT+Q+  +
Sbjct  120  RDTPNSDRFPSVDVFVPSYNEDYTLLANTLAAALKMDYPSDRMKVWLLDDGGTNQKRFAE  179

Query  191  DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
                +Q A++R   L+QLC +LG +Y TRERNEHAKAGN++  +     EL+ VFDADH
Sbjct  180  HAGTSQAAEKRNTSLKQLCADLGAIYLTRERNEHAKAGNLNNGMLHSDAELIAVFDADHA  239

Query  251  PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            P+RDFL +TV YF +DP LFLVQTPHFFINPDP++RNL   ++ P ENEMFYG I RGLD
Sbjct  240  PARDFLLQTVNYFEQDPRLFLVQTPHFFINPDPVERNLRTFEKMPSENEMFYGIIQRGLD  299

Query  311  RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            +W  AFFCGSAAVLRR ALDEAGGF+G +ITED ETAL++HSRGW SLY+D  +IAGLQP
Sbjct  300  KWNAAFFCGSAAVLRREALDEAGGFSGVSITEDCETALDLHSRGWNSLYVDIPLIAGLQP  359

Query  371  ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
             TFASFIQQR RWA GMMQ++L + PLF+RGL   QRLCY++S  FW FP  R MFLVAP
Sbjct  360  ATFASFIQQRSRWAQGMMQIMLFRFPLFKRGLSFPQRLCYMSSTLFWLFPFPRAMFLVAP  419

Query  431  LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L YLFFG+EIF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A
Sbjct  420  LFYLFFGLEIFNASGGEFLAYTSTYIIVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPA  479

Query  491  IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
            +++ L+ PR   F VTAKDE++  + +S I  P    F + L GV AT  R V  P
Sbjct  480  VISVLINPRKPTFNVTAKDESILTSRLSEISLPFFVIFFVLLLGVAATAWRVVTEPAQAD  539

Query  551  VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDA  610
            + LVVGGW VLN+L+ G AL  V+E+  R A+ R+ +    E  +   G++   AT+ D
Sbjct  540  LTLVVGGWNVLNLLIAGCALGVVSERGARSASRRIGVARRCEMLV---GDQVFPATINDV  596

Query  611  STSGVRLLVRLPGVGD-PHPALEAG-GLIQFQPKFPDAPQLERMVRG-RIRSARREGGTV  667
            S  G R+ V     GD P    + G G ++F+P        E    G +IR+A++E
Sbjct  597  SVGGARIQV----FGDAPLQTFKNGPGTLRFRPH----SSSETAALGLQIRNAQKESDGA  648

Query  668  MVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKT  727
             +G  +           +A LIF  S  WR+ + +  R  GLL G     W       +T
Sbjct  649  SIGCSYVVND-ATDHFLIADLIFANSEQWRSFQLSRRRNPGLLRGTG---WFIGLCFYQT  704

Query  728  AR  729
            +R
Sbjct  705  SR  706


>TR:A0A4R2D499 A0A4R2D499_SHIGR Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella granuli OX=323621 GN=EV665_101250 PE=4 SV=1
Length=723

 Score = 570 bits (1470),  Expect = 0.0
 Identities = 320/715 (45%), Positives = 436/715 (61%), Gaps = 17/715 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V  +A++K    + + R + L+  + +V+R
Sbjct  8    ILWALVSALVILVITLPINLQTQLVASIAVVTFMAVIKVLRAEGIWRLIALAFGTAVVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R  +   L
Sbjct  68   YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPPRKSRLAEEGRL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE   +L+ TLAAAK M YPA   TV L DDGGT+Q+  +     AQ A+
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Sbjct  128  PSVDVFVPSYNEDIGLLANTLAAAKAMDYPADKLTVWLLDDGGTEQKRNAAAVIEAQVAE  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R RELQ LCR+LGV Y TR RNEHAKAGNM+  ++   GEL+ VFDADH P+RDFL +T
Sbjct  188  ARHRELQALCRDLGVNYLTRARNEHAKAGNMNNGMQHSTGELIAVFDADHAPARDFLRQT  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFADDPKLFLVQTPHFFLNPDPLERNLRTFETMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRTALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL + QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKRGLSVPQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428  IFTASGGEFLGYTLAYMFVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++ E+ +S I RP    F +     L ++ R+ + P    V  VVGGW
Sbjct  488  KPTFKVTAKDESIRESRLSEISRPFFVIFAVLFVAFLMSIYRFYSEPYKADVTFVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+++ G AL  V+E+ +R A+ RV   V       A G R   +T+ + S +G R  V
Sbjct  548  LLNLIIAGCALGVVSERSERAASRRV--TVKRRCTFIADG-REYPSTLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+ +P  A +A   ++F P        E ++   +R+    G  V VG  F    P
Sbjct  603  QVFGL-EPDLATDARCALRFTPY---GAAHEEVLPVDVRNVENLGSVVAVGCRF---MPE  655

Query  680  AVR--ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
              R    VA LIF  S  W   + +     GL  G    LW    +L +T+R  +
Sbjct  656  VARHHSLVADLIFANSNQWSDFQVSRRYNPGLFRGS---LWFLGIALYQTSRGLL  707


>TR:A0A9X1SZ89 A0A9X1SZ89_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium quercicola OX=2901226 GN=bcsA PE=4 SV=1
Length=731

 Score = 570 bits (1470),  Expect = 0.0
 Identities = 308/700 (44%), Positives = 429/700 (61%), Gaps = 9/700 (1%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +V  L+ + W+ + +    +   PV+     + A   + L+A+LK    +   R + L
Sbjct  1    MVKALIVIAWICMSIVIVAITTLPVSLQTHLVAAFLCMALLAVLKVLKAEGNWRLIGLGF  60

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             + +V+RY +WR   TLPP     +F+   LL+  E +S+++  L+ F+ + P     PR
Sbjct  61   GTAIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVAMLALSLFIVSMPLPPNRPR  120

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
            P   +  PTVD+ +P+YNE ADML+ TLAAAKNM YP    TV L DDGGT Q+  +
Sbjct  121  PGSADYAPTVDVFIPTYNEDADMLANTLAAAKNMDYPPEKLTVWLLDDGGTLQKRNAASI  180

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
              AQ AQ R  EL++LCR L   Y TR+RNEHAKAGN++  + + +G+L+ VFDADH P+
Sbjct  181  PDAQVAQRRHEELKELCRNLDANYLTRDRNEHAKAGNLNNGMRQSQGDLITVFDADHAPA  240

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            RDFL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   ++ P ENEMFYG I RGLD+W
Sbjct  241  RDFLRETVGYFEEDPRLFLVQTPHFFLNPDPIERNLKTFNKMPSENEMFYGIIQRGLDKW  300

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
              AFFCGSAAVL RRAL++  GF+G +ITED ETAL +H+RGW S+Y+D+ +IAGLQP T
Sbjct  301  NAAFFCGSAAVLNRRALEDTNGFSGISITEDCETALALHARGWNSVYVDKPLIAGLQPAT  360
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Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
            FASFI QR RWA GMMQ+L+ + PLF+RGL + QRLCY++S  FW FP  R +FL APL
Sbjct  361  FASFIGQRSRWAQGMMQILMFRMPLFKRGLSMPQRLCYMSSTLFWLFPFPRTVFLFAPLF  420

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            Y+FF +EIFV +  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  Q  +L  A++
Sbjct  421  YIFFDLEIFVGSGGEFLAYTTTYMLVNLLMQNYLYGRFRWPWISELYEYVQTVHLLPAVI  480

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +  P    F VTAKDE++S+N +S I RP    F + L     +  +  A P    V
Sbjct  481  SVIFNPSKPTFKVTAKDESISDNRLSEISRPFFVIFGVLLIATAMSFYKIYAEPYKSDVT  540

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAST  612
            LVV GW +LN+L  G AL  V+E++++ ++ RV ++   E ++   G++     + + S
Sbjct  541  LVVAGWNLLNLLFAGCALGVVSERREKSSSRRVNVKRRCEFRV---GDQWFPGVIENVSV  597

Query  613  SGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            +G  LLV +         + A   I+ +   P AP     +  +I  + R  G V+VG
Sbjct  598  NG--LLVHVYDRSMQPLTVGAMEEIRVETFSPGAPS---SIPVKIVRSGRGDGFVLVGCT  652

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHG  712
            F   +P   R  +A +IF  SA W   +    R  GL+ G
Sbjct  653  FAPREP-QERRLLADIIFANSAQWTEFQMGRRRNPGLIRG  691


>TR:A0ACD4NPT0 A0ACD4NPT0_9HYPH UDP-forming cellulose synthase catalytic subunit
OS=Antarcticirhabdus aurantiaca OX=2606717 GN=bcsA PE=4
SV=1
Length=733

 Score = 570 bits (1470),  Expect = 0.0
 Identities = 318/716 (44%), Positives = 436/716 (61%), Gaps = 19/716 (3%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L +LW+   +    +   PV+  AQ    L  + ++ +LK F    V R + L+  + +V
Sbjct  6    LTVLWIVASIVAIAVITLPVSLQAQLFAVLFVLGVMVVLKVFDLGGVWRLVALALGTSIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPT----DRPFPRP  133
            +RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R  P
Sbjct  66   LRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVFMLALSLFVVAAPVPPRPSRGLPAD  125

Query  134  LQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPE  193
            L+P   PTVD+ +PSYNEP  +L+ T+A+A  M YPA   TV L DDG TDQ+  S D
Sbjct  126  LRP---PTVDVFIPSYNEPPKLLANTIASALAMNYPADRFTVWLLDDGSTDQKRTSEDAA  182

Query  194  LAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSR  253
             A  A+ R  EL++LC ++G  Y TR RNEHAKAGN++  +    GEL+ VFDADH P+
Sbjct  183  AAMVAEARHAELKRLCEDMGARYLTRARNEHAKAGNLNNGMLHSTGELIAVFDADHAPAH  242

Query  254  DFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWG  313
            DFLA TVGYF +DP LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W
Sbjct  243  DFLAETVGYFEDDPRLFLVQTPHFFLNPDPLERNLRTFETMPSENEMFYGIIQRGLDKWN  302

Query  314  GAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETF  373
             +FFCGSAA+LRR AL+E  GF+G +ITED ETA+E+HSRGW SLY+D+ +IAGLQP TF
Sbjct  303  ASFFCGSAALLRREALNETSGFSGISITEDCETAIELHSRGWNSLYVDKPLIAGLQPATF  362

Query  374  ASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIY  433
            ASFI QR RWA GMMQ+L L+ PL +RGL + QRLCY++S  FW FP  R+MFL+APL Y
Sbjct  363  ASFIGQRSRWAQGMMQILFLRVPLLKRGLSLPQRLCYMSSTLFWLFPFPRLMFLIAPLFY  422

Query  434  LFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVT  493
            LFFG++IF A+  E +AY   Y+AV+ ++QN ++   RWP +SE+YE  Q+ +L  A+V+
Sbjct  423  LFFGLQIFTASSGEFVAYTLTYMAVNLMMQNYMYGAYRWPWISELYEYVQSVHLLPAVVS  482

Query  494  TLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLL  553
            T+L P+    F VTAKDE++  + IS I  P    F + L+GV AT+ R +  P    + L
Sbjct  483  TILHPKKPTFNVTAKDESIVISRISEIGLPFYLIFAVLLAGVGATVWRVIYEPYRADLTL  542
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Query  554   VVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTS  613
             VVG W VLN+L+ G AL  V+E+    A+ RV +    +  I   G+  LT T+ D S S
Sbjct  543   VVGAWNVLNLLIAGCALGVVSERGTPSASRRVSVRRRCDVVI---GDTVLTGTIEDVSVS  599

Query  614   GVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIF  673
             G R  +R+ G        +   L++ +       Q E  +  RIR   R    V++G  +
Sbjct  600   GAR--IRVAGALPFETERDGPALLRLR---TFRNQEEDTIPLRIRRIERGTADVVLGCAY  654

Query  674   EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                +       +A LIF  S  W  ++++  R  GLL G A   W  A  + +T R
Sbjct  655   -VTETARHHRVIADLIFANSGQWDAIQKSRRRNPGLLRGSA---WFFAICIYQTFR  706


>TR:A0ABU0GBS2 A0ABU0GBS2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Peteryoungia aggregata LMG 23059 OX=1368425 GN=J2045_003844
PE=4 SV=1
Length=743

 Score = 570 bits (1469),  Expect = 0.0
 Identities = 290/603 (48%), Positives = 398/603 (66%), Gaps = 3/603 (0%)

Query  16    VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
             ++ +  W+A+++   LL A PV  SA+  +++  +V++A +         R + L+ AS+
Sbjct  4     IVRYAAWLAIVIAMFLLVAQPVGHSARFNLSVIVIVILAAIMLLKLDGFWRHVFLALASV  63

Query  76    LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
             ++++Y +WR   TLPP     SF+  ++L+A E + I +  ++ F+ ADP DRP    L
Sbjct  64    VILQYAYWRTTSTLPPVEDLYSFIPGIILYAAEMYCILMLGISLFVVADPIDRPRAPQLD  123

Query  136   PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              +E P VD+ +P+YNE  ++L++T+AAAK M YPA   TV L DDGGTDQ+  S DP  A
Sbjct  124   DDESPNVDVFIPTYNEDREILALTVAAAKAMDYPADKFTVYLLDDGGTDQKRNSDDPVAA  183

Query  196   QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              KA ER   L+ LC +LG VY TR  N HAKAGN++AAL R   +LVVVFDADH P R+F
Sbjct  184   AKATERATILKDLCSDLGAVYMTRAENVHAKAGNLNAALWRTHADLVVVFDADHAPERNF  243

Query  256   LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
             L  TVG+F+ED  LFLVQTPHFF NPDPI+RNL    R P ENEMFYGKI +GLDRW  +
Sbjct  244   LRETVGHFLEDERLFLVQTPHFFSNPDPIERNLGTFGRMPSENEMFYGKIQKGLDRWNAS  303

Query  316   FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
             FFCGSAAVLRR AL+E GGF+G TITED ETALE+H+RGW SLY+++ +I+GLQPETFAS
Sbjct  304   FFCGSAAVLRREALEEVGGFSGITITEDCETALELHARGWNSLYVEKPLISGLQPETFAS  363

Query  376   FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
             F+ QR RW  GM+Q+L+LKNPLF+RGL + QRL Y++S  FWFFP VR +F VAPL+++
Sbjct  364   FVGQRSRWCQGMVQILMLKNPLFKRGLSLPQRLSYISSSLFWFFPFVRAVFFVAPLLFIL  423

Query  436   FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
             F ++IFVA+FE+  AY   YL V  +V+  L+   RWP +SE+YE  Q+ YL +AIV+ L
Sbjct  424   FDMKIFVASFEDFFAYTIMYLIVGEMVRTYLYGSVRWPWISEIYEYVQSVYLFQAIVSVL  483

Query  496   LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
             ++PRS  F VTAK  +L  + +S +  P    F +    +     R+   P   S+LL+V
Sbjct  484   MKPRSPTFKVTAKGVSLKHDRLSELSLPYFIIFGILSFTLFVAAYRYNTEPEISSLLLIV  543

Query  556   GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
             G W  +N+++ G AL  V E+ Q  +   + +    E Q   FG   L   V +AS  G
Sbjct  544   GAWNWMNLMIAGCALGVVTERSQDLSGVELPLRTTVELQ---FGETVLRGAVTEASAQGA  600

Query  616   RLL  618
             +L+
Sbjct  601   KLI  603


>TR:A0AA43ZDJ7 A0AA43ZDJ7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ferranicluibacter rubi OX=2715133 GN=bcsA PE=4 SV=1
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Length=731

 Score = 570 bits (1469),  Expect = 0.0
 Identities = 309/700 (44%), Positives = 431/700 (62%), Gaps = 9/700 (1%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +V  L+ + W+ + +    +   PV+     + A   + L+A+LK    +   R + L
Sbjct  1    MVKALIVIAWICMSIVIVAITTLPVSLQTHLVAAFLCMALLAVLKVLKAEGNWRLIGLGF  60

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             + +V+RY +WR   TLPP     +F+   LL+  E +S+++  L+ F+ + P     PR
Sbjct  61   GTAIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVAMLALSLFIVSMPLPPNRPR  120

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
            P   +  P+VD+ +P+YNE ADML+ TLAAAKNM YP    TV L DDGGT Q+  +
Sbjct  121  PGSADYAPSVDVFIPTYNEDADMLANTLAAAKNMDYPPEKLTVWLLDDGGTLQKRNAASI  180

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
              AQ AQ R  EL++LCR L   Y TR+RNEHAKAGN++  + + +G+L+ VFDADH P+
Sbjct  181  PDAQAAQRRHEELKELCRNLDANYLTRDRNEHAKAGNLNNGMRQSQGDLITVFDADHAPA  240

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            RDFL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   ++ P ENEMFYG I RGLD+W
Sbjct  241  RDFLRETVGYFEEDPRLFLVQTPHFFLNPDPIERNLKTFNKMPSENEMFYGIIQRGLDKW  300

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
              AFFCGSAAVL RRAL++  GF+G +ITED ETAL +H+RGW S+Y+D+ +IAGLQP T
Sbjct  301  NAAFFCGSAAVLNRRALEDTNGFSGISITEDCETALALHARGWNSVYVDKPLIAGLQPAT  360

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
            FASFI QR RWA GMMQ+L+ + PLF+RGL + QRLCY++S  FW FP  R +FL APL
Sbjct  361  FASFIGQRSRWAQGMMQILMFRMPLFKRGLSMPQRLCYMSSTLFWLFPFPRTVFLFAPLF  420

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            Y+FF +EIFV +  E LAY   Y+ V+ L+QN L+ R RWP +SE+YE  Q  +L  A++
Sbjct  421  YIFFDLEIFVGSGGEFLAYTTTYMLVNLLMQNYLYGRFRWPWISELYEYVQTVHLLPAVI  480

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +  P    F VTAKDE++S+N +S I RP    F + L   + +  +  A P    V
Sbjct  481  SVIFNPSKPTFKVTAKDESISDNRLSEISRPFFVIFGVLLIATVMSFYKIYAEPYKSDVT  540

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAST  612
            LVV GW +LN+L  G AL  V+E++++ ++ RV ++   E ++   G++     + + S
Sbjct  541  LVVAGWNLLNLLFAGCALGVVSERREKSSSRRVNVKRRCEFRV---GDQWFPGVIENVSV  597

Query  613  SGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            +G  LLV +         + A   I+ +   P AP    M    +RS R + G V+VG
Sbjct  598  NG--LLVHVYDRSMQPLTVGAMEEIRVETFSPGAP--SSMPVKIVRSGRGD-GFVLVGCT  652

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHG  712
            F   +P   R  +A +IF  SA W   +    R  GL+ G
Sbjct  653  FAPREP-QERRLLADIIFANSAQWTEFQMGRRRNPGLIRG  691


>TR:Q0FZX8 Q0FZX8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Fulvimarina pelagi HTCC2506 OX=314231 GN=FP2506_04521
PE=4 SV=1
Length=741

 Score = 570 bits (1468),  Expect = 0.0
 Identities = 297/605 (49%), Positives = 400/605 (66%), Gaps = 7/605 (1%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            W      F ++   P++  AQ LIAL+A+ +  L+         R++ ++A S++V+RY
Sbjct  10   WFISAAAFLIMVQQPISVDAQWLIALTALGIAGLIYILKLDGAWRYVFMAAVSIVVLRYA  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR  ETLPP    ASF+ A+ L+  E + + +  ++ F+ +DP +R        E LPT
Sbjct  70   YWRTTETLPPADELASFITAICLYGAEMYCLFMLAISLFVVSDPLERRRAPQFDDESLPT  129
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Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VPS+NE +D+LS+TL+AAK M YP     V L DDGGTD++ +S DP ++  A+ R
Sbjct  130  VDVFVPSFNEASDILSLTLSAAKAMDYPHEKLKVYLLDDGGTDEKRLSSDPRISTAAKRR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
            + ELQ++CR+LGV+Y TR  N HAKAGN++  L   +GELVVV DADH P+R+FL  TVG
Sbjct  190  QSELQEVCRKLGVIYLTRPANIHAKAGNLNNGLAHSQGELVVVLDADHAPAREFLRETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            +F  DP LFLVQTPHFF NPDP+++NL   +R P ENEMFYG+I +GLD+W  AFFCGSA
Sbjct  250  HFKTDPKLFLVQTPHFFANPDPLEKNLNTFERMPSENEMFYGQIQKGLDKWNAAFFCGSA  309

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVLRR+AL E  GF+G +ITED ETALE+H+ GW SLY+DR M+ GLQPET ASFI QR
Sbjct  310  AVLRRQALLEVEGFSGVSITEDCETALELHANGWNSLYVDRPMVVGLQPETVASFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RW  GM+Q++LLKNP+FR GL +AQRLCYL+SM FWFFP +R +FLVAPL+++ F ++IF
Sbjct  370  RWCRGMIQIMLLKNPMFRSGLTLAQRLCYLSSMMFWFFPFIRTVFLVAPLLFILFDMKIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
            VA+ +E +AY   YL    L++N L+ R RWP VS++YE  Q+ YL RAIV+ L+ PR
Sbjct  430  VASVDEFVAYSLTYLVAGELLRNYLYGRVRWPWVSDLYEYVQSVYLLRAIVSVLINPRRP  489

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAK ETL  + +S +  P    F   L      L R+   P    +LLVVG W +L
Sbjct  490  TFNVTAKGETLDRDQLSQLAWPYFAIFGTLLVAAGICLYRYQTEPEISGMLLVVGAWNLL  549

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVL--DASTSG--VRL  617
            N+ + G AL  V E+++RR +PR+      E     F N +  A V   DAS  G  V +
Sbjct  550  NLCVAGAALGVVTERRERRRSPRLSSMRRGEL---VFSNGAEIAPVAIDDASLVGAHVTI  606

Query  618  LVRLP  622
            L R P
Sbjct  607  LDRAP  611


>TR:A0ABU7T5L8 A0ABU7T5L8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium radiotolerans OX=31998 GN=bcsA PE=4
SV=1
Length=803

 Score = 570 bits (1468),  Expect = 0.0
 Identities = 324/745 (43%), Positives = 445/745 (60%), Gaps = 22/745 (3%)

Query  15   PVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAAS  74
            P L   +W+A      LL + P+  + Q  +++ A+V++ LL  FA     R   L+  S
Sbjct  3    PFLARTIWLASAALTLLLLSQPLGTTVQLEMSIGAIVVMVLLWLFAKGRAGRLTFLAIGS  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
            ++V+RY +WRL  TLPP     +F   ++L A E +   I  ++  ++A P  R  P
Sbjct  63   LVVLRYIYWRLSSTLPPVDDPINFGAGVILIAAELYCFYILAISLVINAAPLYREPPPQE  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
              E+LPTVDI VPSYNE   +L+ TLAAAK++ YPA   TV L DDGGTDQ+C   DP
Sbjct  123  DDEDLPTVDIFVPSYNEDRHILATTLAAAKSLDYPADKVTVWLLDDGGTDQKCADADPRK  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A++A+ RRR LQ LC +LGV Y TR RN HAKAGN++  L+   GE+VVV DADHVP R
Sbjct  183  AEEARARRRVLQALCADLGVSYLTRRRNLHAKAGNLNNGLQNSVGEIVVVLDADHVPFRS  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  T+G+F  DP LFLVQTPH F+NPDPI+RNL   DR P ENEMFY     GLD+W G
Sbjct  243  FLRDTIGHFSTDPKLFLVQTPHAFLNPDPIERNLKTFDRMPSENEMFYAVGQCGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            +FFCGSAA+LRRRALDEAGGF+G TITED ETA E+HSRGW SLY+D+ +IAGLQPET +
Sbjct  303  SFFCGSAALLRRRALDEAGGFSGITITEDCETAFELHSRGWTSLYVDKPLIAGLQPETLS  362
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Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
             FI QR RW  GM+Q++LLKNP+ + GL   QRLCYL+SM+FWFFPL R++F+ APL+Y+
Sbjct  363  DFIGQRSRWCQGMLQIMLLKNPVLKSGLKPIQRLCYLSSMTFWFFPLPRLVFMAAPLLYI  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++I VA  +E +AY   Y+ V+ ++QN L+ R RWP VSE+YE  Q  +L +A  +
Sbjct  423  FFNMKIVVANVDEAIAYTATYIIVNLMMQNYLYGRVRWPFVSELYEYVQGLFLIKATASV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            ++ PR   F VTAK+ +L  + +SP+  P    F L   G + +  R+   PG  +++LV
Sbjct  483  IVSPRKPTFKVTAKNVSLDHDQLSPLALPYFLVFALLSCGAVVSAYRYAFEPGVTNLMLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VG W + N++  G AL   AE++Q   AP + ++ PA   +      +L  TV   S++
Sbjct  543  VGLWNLFNLITAGAALGVAAERRQTEKAPSLVVDRPAVLNL---NGMALDVTVERISSAQ  599

Query  615  VRLLVRLPGVGDPHPALEAG-GLIQFQPKFPDA--PQLE--RMVRGRIRSARREGGTVMV  669
             R  +RL  V    P   AG G +      P A  P L   R +  R+      G   +
Sbjct  600  CR--IRLDAV---LPMRRAGDGSVGTLSALPQANLPLLSHARTIPVRLAGVTAAGEESVC  654

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMAR-ILW-------MAA  721
             + FE   P      +A L++G++      ++       ++ G  + I W         A
Sbjct  655  DLAFETMTP-GSYFALADLMYGDADAMVRFQQRRRAHKDIVSGTLQFIRWGITGPIRAFA  713

Query  722  ASLPKTARDFMDEPARRRRRHEEPK  746
              +  TAR  ++EPA R R  E  +
Sbjct  714  CLMTPTARPEVEEPAARPRAAERQR  738


>TR:A0A7W8MDM3 A0A7W8MDM3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium rosettiformans OX=1368430 GN=HNR26_003368
PE=4 SV=1
Length=743

 Score = 570 bits (1468),  Expect = 0.0
 Identities = 290/603 (48%), Positives = 398/603 (66%), Gaps = 3/603 (0%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V  +  W+A++V   LL A PV  SA+  +++  + ++A +         R + L+ AS+
Sbjct  4    VFRYAAWLAIVVAMFLLIAQPVGHSARFNLSVIVIAILAAIMLLKLDGFWRHVFLALASV  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            ++++Y +WR   TLPP     SF+  ++L+A E + I +  ++ F+ ADP +RP    L+
Sbjct  64   VILQYAYWRTTSTLPPVEDLYSFIPGIILYAAEMYCILMLGISLFVVADPIERPRAPELE  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             +E P VD+ +P+YNE  ++L++T+AAAK M YP+   TV L DDGGTDQ+  S DP  A
Sbjct  124  EDECPEVDVFIPTYNEDREILALTVAAAKAMDYPSDKFTVYLLDDGGTDQKRNSDDPVAA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             KA+ER   L+ LC +LG VY TR  N HAKAGN++AAL R   +LVVVFDADH P R+F
Sbjct  184  AKAKERAAILKDLCSDLGAVYLTRAENVHAKAGNLNAALWRTHADLVVVFDADHAPERNF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF+ED  LFLVQTPHFF NPDPI+RNL    R P ENEMFYGKI +GLDRW  +
Sbjct  244  LRETVGYFLEDERLFLVQTPHFFSNPDPIERNLGTFGRMPSENEMFYGKIQKGLDRWNAS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL+E GGF+G TITED ETALE+H+RGW SLY+D+ +I+GLQPETFAS
Sbjct  304  FFCGSAAVLRREALEEVGGFSGITITEDCETALELHARGWNSLYVDKPLISGLQPETFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            F+ QR RW  GM+Q+L+LKNPLF+RGL   QRL Y++S  FWFFP VR +F VAPL+++
Sbjct  364  FVGQRSRWCQGMVQILMLKNPLFKRGLSFPQRLSYISSSLFWFFPFVRSVFFVAPLLFIL  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IFVA+FE+  AY   YL V  +V+  L+   RWP +SE+YE  Q+ YL +AI++ L
Sbjct  424  FDMKIFVASFEDFFAYTVMYLIVGEMVRTYLYGSVRWPWISELYEYVQSVYLFQAIISVL  483
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Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            ++P+S  F VTAK  +L  + +S +  P    F +    +     R+   P   S+LL+V
Sbjct  484  MKPKSPTFKVTAKGVSLKHDSLSELSLPYFIIFGILSFTLFVAAYRYNTEPEISSLLLIV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W  +N+++ G AL  V E+ Q  A   + +    E Q   FG   L   V++AS  G
Sbjct  544  GAWNWMNLMIAGCALGVVTERSQDLAGVELPLRTNVELQ---FGETVLRGAVIEASAQGA  600

Query  616  RLL  618
            +L+
Sbjct  601  KLI  603


>TR:A0A5B0DR25 A0A5B0DR25_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aureimonas fodinaquatilis OX=2565783 GN=bcsA PE=4
SV=1
Length=729

 Score = 569 bits (1467),  Expect = 0.0
 Identities = 307/706 (43%), Positives = 430/706 (61%), Gaps = 10/706 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V  F+LWV        +   PV+   Q +     + ++A++K        R + L+  +
Sbjct  3    VAAFILWVISAFLALTIVTLPVSVETQLIAVAVVLTIMAVIKALKLHGGWRLVALALGTS  62

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+  LL++  E +S+ + FL+ F+ + P     PR  +
Sbjct  63   VVLRYVYWRTTSTLPPVNQLENFIPGLLVYLAEMYSVFMLFLSLFVVSVPLPPRPPRQAE  122

Query  136  PEEL-PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
            P EL PTVD+ VP+YNE A++L+ TLA+   M YP    TV L DDGGT Q+  S DPE
Sbjct  123  PAELLPTVDVYVPTYNEDAELLANTLASCLAMDYPPEKMTVWLLDDGGTLQKRNSDDPET  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            +Q A+ R   LQ+LC +LG  Y TRERN+HAKAGN++  +   +G+L+VVFDADH P+RD
Sbjct  183  SQIAEARYVRLQKLCADLGARYLTRERNQHAKAGNLNNGMAHSEGQLIVVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W
Sbjct  243  FLKETVGYFREDPKLFLVQTPHFFLNPDPIERNLRTFNHMPSENEMFYGVIQRGLDKWNA  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL+  GGF+G +ITED ETA+E+H+RGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRRAALETTGGFSGVSITEDCETAVELHARGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L  + P  +RGL + QRLCY +S  FW FP  R +FL+APL YL
Sbjct  363  SFIGQRSRWAQGMMQILRYRFPPLKRGLSLPQRLCYTSSTLFWLFPFPRAIFLIAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IF A+  E LAY   Y+AV+ ++QN ++ R RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFTASGGEFLAYTLTYMAVNLVMQNYMYGRYRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +L P    F VTAKDE+++ + +S I  P    F + L  V  T+ R  A P    + LV
Sbjct  483  VLNPSKPTFKVTAKDESINNSRLSEIGLPFFIIFFILLIAVGVTIYRVYAEPYRADLTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN+++ G AL  V+E+  +R   R+ ++   +     F  ++L  T+ D S SG
Sbjct  543  VGGWNLLNLIIAGCALGVVSERSSKRQTQRINVKRRCDVD---FAGKTLPGTIEDVSVSG  599

Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
             R  VRL G      +  +  ++ F+P        E  +   +R+  + G  V++G +FE
Sbjct  600  AR--VRLFGQLPAGASTTSDAILHFKPARDIG---EPALPISVRNIEQAGNNVIIGCLFE  654

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              +       +A L+F  S  W  ++       G++ G    L +A
Sbjct  655  P-KHATDHNLIADLVFASSDQWARLQAERRTNPGVIRGTFHFLKIA  699
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>TR:A0A4R1IA37 A0A4R1IA37_ANCAQ Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter aquaticus OX=100 GN=EV667_1218 PE=4 SV=1
Length=730

 Score = 569 bits (1467),  Expect = 0.0
 Identities = 311/700 (44%), Positives = 421/700 (60%), Gaps = 9/700 (1%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            +WV L+     +   PV   AQ +     ++L+  LK FA + VPR + L+  + +V RY
Sbjct  9    VWVLLIALVAFIITLPVNLQAQLVTGCIVILLIVFLKMFAPEGVPRMVALALGTAMVFRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLPP    A+F+ ALLL+  E +S+++  L+ F+ + P        +     P
Sbjct  69   VYWRTTSTLPPMEELANFIPALLLYGAEMYSVALMGLSLFVVSSPQPPRTAPVIASGREP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVDI VPSYNE A +L+ TLAAA  + YP    TV L DDGGTDQ+C   D   A++AQ
Sbjct  129  TVDIFVPSYNEDAGLLATTLAAASAIDYPRDRFTVWLLDDGGTDQKCEQHDLPAAREAQM  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            RR  L +LCRELGV Y TR RNE+AKAGN++  L    GEL+VVFDADH P+R FL  T+
Sbjct  189  RRETLTELCRELGVNYLTRPRNEYAKAGNLNHGLAHSSGELIVVFDADHAPARSFLRETI  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF EDP LFLVQTPHFFINPDP++R+L    R P ENEMFYG I RGLDRWGGAFFCGS
Sbjct  249  GYFNEDPRLFLVQTPHFFINPDPVERSLDTWRRMPSENEMFYGVIQRGLDRWGGAFFCGS  308

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR AL E  GFA  +ITED ETAL +H+RGW S+Y+D  +IAGLQPETFASFI QR
Sbjct  309  AAVLRREALRETDGFAHSSITEDCETALTLHARGWHSVYVDTPLIAGLQPETFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GM Q+L    PLFR GL +AQR+CY++S+ FWFFP+ R +FLV+P  YLFF +EI
Sbjct  369  SRWAQGMYQILRFHFPLFRSGLTMAQRICYMSSILFWFFPISRAIFLVSPFFYLFFSLEI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            F  +  E +AY   YL ++  +Q+ L+ + RWP  SE+YE  Q  YL  A+++ ++ P+
Sbjct  429  FNGSGAEFVAYTAVYLLINLFIQSYLYGKYRWPWFSELYEYIQTVYLLPALLSVMINPKK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VT+K ET+ EN IS I  P    F++ +  V  T  R    P    + +VVG W +
Sbjct  489  PTFKVTSKGETIDENRISEIGLPFFVIFVIQIIAVFVTFWRIATEPYSADITIVVGMWNL  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LN+++ G AL  V+E+  +R + R+ +       I       + A + + S  GVR+
Sbjct  549  LNLIISGCALGVVSERAAKRHSQRMAITRRCSLLIDGV---EVPAVIENVSMGGVRIRTE  605

Query  621  LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
            LP        + A  +++  P  PDA  +   +   +R      G V++G  F A +  A
Sbjct  606  LPADAKARVGMHA--VVRVTP--PDA-CISDTLPILVRKVALSEGAVVLGAQFNA-KCAA  659

Query  681  VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              + +A LIF  +  W+  +       G+L G    + +A
Sbjct  660  HYQLIADLIFANADEWKKFQAGRRNNPGVLRGTVMFVMIA  699


>TR:A0ABV6AKD8 A0ABV6AKD8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium puerariae OX=1585791 GN=bcsA PE=4 SV=1
Length=724

 Score = 569 bits (1466),  Expect = 0.0
 Identities = 317/716 (44%), Positives = 432/716 (60%), Gaps = 16/716 (2%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            VL  + W    V   LL   P+    Q + +L  V ++ ++K    +   R + L+  +
Sbjct  4    VLSAITWALASVLIILLVTLPINTRTQLIASLLVVAVMVVIKLLKAEGKWRLVALAFGTA  63
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Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP +   +F+  LL++  E +S+ +  L+ F+ + P     P   +
Sbjct  64   MVLRYVYWRTTSTLPPMSQLENFIPGLLVYLAEMYSVLMLALSLFVVSMPLPPRPPYKRR  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              ELPTVD+ VPSYNE  D+L+ TLAAA+NM YP    TV L DDGGT Q+  S +   A
Sbjct  124  GGELPTVDVFVPSYNEDVDLLANTLAAARNMDYPPEKLTVWLLDDGGTVQKRKSANIMEA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              A+ R + LQ+LC ELGV Y TRERNEHAKAGN++  L+   G L+ VFDADH P RDF
Sbjct  184  HMAELRHKVLQELCEELGVRYLTRERNEHAKAGNLNNGLQHSTGSLIAVFDADHAPGRDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF E+P LFLVQTPHFF+NPDP++RNL   +R P ENEMFYG I RGLD+W  A
Sbjct  244  LLETVGYFDENPKLFLVQTPHFFLNPDPVERNLRTFERMPSENEMFYGIIQRGLDKWNAA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVL R+AL+ + GF+G +ITED ETAL++H  GW S+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLNRKALEVSNGFSGVSITEDCETALDLHGLGWHSIYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L  + P  +RGL +AQRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILRFRFPPLKRGLSLAQRLCYMSSTLFWLFPFPRTIFLFAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF ++   E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ +
Sbjct  424  FDLEIFTSSGGEFLVYSLAYMVVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVISVI  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR   F VTAKDE++S + +S I RP    F + L      ++ R  A P    V LVV
Sbjct  484  LNPRKPTFKVTAKDESVSVSRLSEISRPFFVIFFVLLVAFGISVYRIYAEPYKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN++L G AL  V+E+ +R+A+ RV++    +  I     R  TAT+ + S  G
Sbjct  544  GGWNLLNIILAGCALGVVSERGERQASRRVKVSRRCQFGI---DGRWFTATIENVSVHGA  600

Query  616  RLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIF  673
             + V   G  D    +E G  G ++FQP   D P  +  +   IR+    G    +G  +
Sbjct  601  SVQVHTEGFRD----IEIGKMGALRFQP-HSDLPVSDLPI--EIRNFNAVGDVTSIGCRY  653

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
               Q       +A LIF  SA W   + +  R  G++ G    LW    ++ +TAR
Sbjct  654  -MPQESTDHRLIADLIFANSAQWTQFQTSRRRNPGIIGG---TLWFLGLAMYQTAR  705


>TR:A0A849VWR4 A0A849VWR4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Phyllobacterium pellucidum OX=2740464 GN=bcsA PE=4
SV=1
Length=726

 Score = 569 bits (1466),  Expect = 0.0
 Identities = 316/715 (44%), Positives = 430/715 (60%), Gaps = 12/715 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+ L+W+   +   LL   PV    Q +   S + L+ +LK      + R + L+  + +
Sbjct  5    LIILMWLVTSISVLLLVTLPVNLQTQLIAGASVLFLMMVLKTLNAGGIWRLIALAFGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            VMRY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ + P      RP
Sbjct  65   VMRYVYWRTTSTLPPVNQLENFVPGFLLYLAEIYSVMMLALSLFVVSMPLPHRTTRPATK  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             ELP+VD+ +P+YNE  ++L+ T+AAAK M YPA   TV + DDGGT Q+  +     +
Sbjct  125  GELPSVDVFIPTYNEDIELLANTMAAAKAMDYPADKLTVWILDDGGTLQKRNADKIVESH  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A++R ++L +LC  LGV Y TRE+N HAKAGN++  LE   GEL+ VFDADH P+RDFL
Sbjct  185  IAEKRFKDLSELCEALGVHYLTREKNVHAKAGNLNNGLEHSTGELIAVFDADHAPTRDFL  244
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Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
             TVGYF ED  LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  AF
Sbjct  245  LETVGYFDEDEKLFLVQTPHFFLNPDPLERNLRTFEEMPSENEMFYGIIQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL+  GGF+G +ITED ETA+ +HS+GW S+Y+D+ +IAGLQP TFASF
Sbjct  305  FCGSAAVLRREALNVTGGFSGISITEDCETAIALHSKGWNSVYLDKPLIAGLQPATFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L  + PLF  GL I QRLCYL+S  FW FP  R +FLVAPL YLFF
Sbjct  365  IGQRSRWAQGMMQILRFRFPLFNGGLTIPQRLCYLSSTLFWLFPFPRAIFLVAPLFYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
            G+EIF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+  L
Sbjct  425  GLEIFTASGGEFLAYTLIYMVVNLMMQNYLYGAFRWPWISELYEYVQTVHLLPAVVSVAL  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VTAKDE +  + +S +  P    FL+ L GV  T+ R    P    V LVVG
Sbjct  485  NPRKPTFKVTAKDERIDRSRLSELSTPFFVIFLVLLVGVGVTIYRIYTEPYKADVTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W +LN++  G AL  V+E+  +R + RV++    E ++   G R L  T+ D S +G+R
Sbjct  545  AWNLLNLVFAGCALGVVSERGDKRPSRRVKVSRRCEFRV---GERWLQGTIDDVSVNGLR  601

Query  617  LLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAG  676
            + V    +GD   A+  G L   + K      L  +   ++R+ R++ G   VG +F
Sbjct  602  VQV----LGDVAEAVSVGMLTDVRFKTFATGDLGDLPL-QVRNVRKQAGETSVGCMFMPD  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF  731
            QP +    +A LIF  SA W   +       GL  G    +W    ++ +T R F
Sbjct  657  QP-SDHSLIADLIFANSAQWTKFQLDRRGNPGLFKG---TIWFFGVAIFQTYRGF  707


>TR:A0ABU9Z8K4 A0ABU9Z8K4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylorubrum rhodesianum OX=29427 GN=bcsA PE=4 SV=1
Length=835

 Score = 568 bits (1465),  Expect = 0.0
 Identities = 306/675 (45%), Positives = 417/675 (62%), Gaps = 17/675 (3%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            V+  L +L W+   V   +L + PV    Q  ++L+A+  + LL  F D    RF+ L+
Sbjct  4    VIRALRWLAWMGTTVAGLVLLSQPVGTQNQLAMSLAAMAAMILLWLFLDGPRTRFVFLAL  63

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             S++V+RY  WR+ +TLP P    SF F LLL   E + + I F++  ++ADP  R  P
Sbjct  64   GSLVVLRYILWRVTDTLPSPGDPVSFGFGLLLLLGELYCVFILFVSLIINADPLKRRPPP  123

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
                  ELPTVD+ VPSYNE A +L++TLAAA+ M YP    TV L DDGG+DQ+C  P+P
Sbjct  124  AASAAELPTVDVFVPSYNEDAAILAMTLAAARQMNYPPDKLTVWLLDDGGSDQKCADPNP  183

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
            E A+ A+ERRREL  L   LG  Y TR RNEHAKAGN++  L    GE+VVV DADHVP
Sbjct  184  EKAKAARERRRELTALAEALGCRYLTRARNEHAKAGNLNNGLAFATGEIVVVLDADHVPF  243

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            R FL+ TVGYF EDP LFLVQTPH F+NPDPI+RNL   DR P ENEMFY    RGLD+W
Sbjct  244  RSFLSETVGYFAEDPKLFLVQTPHAFLNPDPIERNLKTFDRMPSENEMFYAVTQRGLDKW  303

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
             G+FFCGSAA+LRR ALDEAGGF+G TITED ETA E+HSRGW S Y+D+ +IAGLQPET
Sbjct  304  NGSFFCGSAALLRRTALDEAGGFSGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPET  363

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
             ++FI QR RW  GM Q+LLLKNP+ ++GL   Q++ YL+SM+FWFFP+ R++F+ APL+
Sbjct  364  LSAFIGQRSRWCQGMFQILLLKNPVLQKGLKPIQKIAYLSSMTFWFFPVPRLIFMFAPLL  423

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
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             ++FF ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV
Sbjct  424  HIFFDLKIFVASVDESIAYTATYIVINLMMQNYVYVGKFRWPFVSELYEFVQGLYLSKAIV  483

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +  PR   F VT K  +L  N++S    P    + L   G      R++  PG  +++
Sbjct  484  SVIWSPRKPTFNVTDKGISLDHNHLSSASLPFFAVYGLLAVGCAVAAWRYLFEPGVTNLM  543

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDA  610
            LVVG W + N+L  G AL   AE++Q    P   + +    QI   G R++  ++  + A
Sbjct  544  LVVGLWNLFNLLTAGAALGVCAERRQLERTP--SLAISRRGQI-TLGGRAIDVSIERVSA  600

Query  611  STSGVRLLVRL--PGVGD----------PHPALEAGGLIQFQPKFPDAPQLERMVRGRIR  658
                VRL   L   G+G           P P   A G +    +  D  + E   R
Sbjct  601  EACTVRLPAALLPAGIGHRTMTGALTVVPMPGARAAGALPVTLEGIDRAKDEAFARLSFG  660

Query  659  SARREGGTVMVGVIF  673
              R +    + G+++
Sbjct  661  RLRPQDYVALAGLMY  675


>TR:A0A135P1E1 A0A135P1E1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium bohemicum OX=2052828 GN=ATO67_08435
PE=4 SV=1
Length=731

 Score = 568 bits (1465),  Expect = 0.0
 Identities = 315/701 (45%), Positives = 421/701 (60%), Gaps = 7/701 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            ++W  + V   ++   PV+     +    ++VL+A +K    K   R + L   + +V+R
Sbjct  8    VVWAFVSVCVLVIVTLPVSLQTHLIATAISLVLLATIKSLNGKGAWRLIALGFGTAIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+    LL+  E +S+ +  L+  + + P      RP  P  +
Sbjct  68   YVYWRTTSTLPPINQPENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPGSPGYV  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVDI VP+YNE   +L+ TL+AAKN+ YP    TV L DDG T Q+  +     AQ A
Sbjct  128  PTVDIFVPTYNEDTTLLANTLSAAKNIDYPTDKFTVWLLDDGSTVQKRNASSVPDAQAAA  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            +R  ELQ+LC +LGV Y TRERN HAKAGN++  LE   GEL+ VFDADH P+RDFL  T
Sbjct  188  KRHEELQKLCADLGVNYLTRERNVHAKAGNLNNGLEHSTGELITVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF ED  LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCG
Sbjct  248  VGYFEEDEKLFLVQTPHFFLNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL E  GF+G +ITED ETAL +HSRGW SLY+D+ +IAGLQP TF SFI Q
Sbjct  308  SAAVLRRAALKETDGFSGVSITEDCETALALHSRGWNSLYVDKPLIAGLQPATFTSFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLFF ++
Sbjct  368  RSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQ  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  428  IFVASGGEFLAYTAAYMLVNLMMQNFLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPS  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKD+++SE  +S I RP    F + +  ++  + R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDDSISEARLSEISRPFFVIFAVLIIAMIFAIYRIYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN++  G AL  V+E+ ++ A+ R+ +    E QI         ATV + S +G+ + +
Sbjct  548  LLNIIFAGCALGVVSERGEKSASRRITVNRRCELQI-GDSEAWSPATVENVSVNGMLINI  606

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
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               G+G     +E G     + K   A     M    +RS +++G T  VG  F   Q I
Sbjct  607  FEQGLG----TVEKGSAATIRVKPHSAGAPTTMSIDIVRSVKKDGFT-QVGCTFAPKQAI  661

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              R  +A LIF  S  W   + A +   GL+ G A  L +A
Sbjct  662  DHR-LIADLIFANSEQWSEFQRARRKNPGLIKGTATFLAIA  701


>TR:A0A2U8WTS2 A0A2U8WTS2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium terrae OX=2202827 GN=bcsA PE=4 SV=1
Length=848

 Score = 568 bits (1464),  Expect = 0.0
 Identities = 320/729 (44%), Positives = 433/729 (59%), Gaps = 14/729 (2%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +V  L +L W+        L + PV    Q  ++L+A+  +A L    D    RF+ L+
Sbjct  1    MVRALRWLAWMGTTAAGLALLSQPVGTQNQLAMSLAAMAAMAGLWLLVDGPRARFVFLAM  60

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             S++V+RY  WR+ +TLP P    SF F LLL   E + + I F++  ++A+P  R  P
Sbjct  61   GSLVVLRYILWRVTDTLPSPGDPVSFGFGLLLLFCELYCVFILFVSLIINAEPLRRRPPV  120

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
                 +LPTVD+ VPSYNE A++L++TLAAA+ M YPA   TV L DDGGTDQ+C   DP
Sbjct  121  AAPAADLPTVDVFVPSYNEDAEILAMTLAAARQMNYPADKLTVWLLDDGGTDQKCTDSDP  180

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
            E A  A+ RR ELQ LC  LG  Y TRERNEHAKAGN++  L    G+LV+V DADHVP
Sbjct  181  EKAAAARARRAELQALCGALGARYLTRERNEHAKAGNLNNGLSAATGDLVLVLDADHVPF  240

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            R  LA TVGYF EDP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY     GLD+W
Sbjct  241  RSLLAETVGYFAEDPKLFLVQTPHAFLNPDPIERNLKTFERMPSENEMFYAVTQAGLDKW  300

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
             G+FFCGSAA+LRR+ALDEAGGFAG TITED ETA E+HSRGW S Y+DR +IAGLQP+T
Sbjct  301  NGSFFCGSAALLRRQALDEAGGFAGITITEDCETAFELHSRGWTSAYVDRPLIAGLQPDT  360

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
             A FI QR RW  GM Q+LLLKNP  ++GL   Q+L YL+SM+FWFFP+ R+ F+ APL+
Sbjct  361  LADFIGQRSRWCQGMFQILLLKNPALQKGLKPIQKLAYLSSMTFWFFPIPRLAFMFAPLL  420

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            ++FF ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV
Sbjct  421  HIFFDLKIFVASVDESIAYTATYIVINLMMQNYVVGKFRWPFVSELYEYVQGLYLSKAIV  480

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +  PR   F VT K  TL  +++S +  P    + L L G L    R++  PG  +++
Sbjct  481  SVIWSPRKPTFNVTNKGATLDHDHLSSLSLPFFAVYGLLLVGCLVAGWRYLFEPGVTNLM  540

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDA  610
            LVVG W   N+L  G AL   AE++Q    P + +   A       G R++   +  + A
Sbjct  541  LVVGLWNFFNLLTAGAALGVCAERRQLERTPSLAV---ARRGRLTLGGRAVDVAIERVSA  597

Query  611  STSGVRLLVRL--PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVM  668
                VR+   L  PG G  HP     G +  +P    AP     V   +    R G   +
Sbjct  598  EACTVRMPASLLAPGAGH-HP---VPGTLAVEPVAGAAPAGALPV--ILGPVTRSGADAV  651

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
              + F  G  +     +A L++G++   R  +    R   L  G  + +W   A   +
Sbjct  652  CRLAF-GGLRVQDYVALAGLMYGDAEAMRRFQLRRRRHKDLFTGTLQFIWWGLAEPVRAL  710

Query  729  RDFMDEPAR  737
            R  +   AR
Sbjct  711  RYALAGDAR  719


>TR:A0A840AL96 A0A840AL96_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
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OS=Kaistia hirudinis OX=1293440 GN=GGR25_001003 PE=4
SV=1
Length=729

 Score = 568 bits (1464),  Expect = 0.0
 Identities = 323/715 (45%), Positives = 434/715 (61%), Gaps = 21/715 (3%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            L+W  + +    L   P+   A  +     V L+ +LK F  + V R + L+  + +V+R
Sbjct  8    LVWGLVTLVVIALITLPINLQAHLVAGAMVVGLMIILKLFTRQGVWRQIALALGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE--  137
            Y +WR   TLPP      F+  LL++  E +SI + F++ F+   P     PR L+
Sbjct  68   YAYWRTTSTLPPINQPEDFIPGLLVYLAEMYSIFMLFISLFVVMRPMA---PRTLKVSSS  124

Query  138  --ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              +LPTVD+ VP+YNE A +L+ TLA+A+ M YP    TV L DDGGT Q+  S + E A
Sbjct  125  DPDLPTVDVFVPTYNEDAALLATTLASARAMDYPPEKLTVWLLDDGGTVQKRNSDNLEAA  184

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
             +A+ R  ELQ+L  +L   Y TRERNEHAKAGNM+ AL+   GELV VFDADH P+RDF
Sbjct  185  HEAEARHVELQKLAADLDCRYLTRERNEHAKAGNMNNALQHATGELVAVFDADHAPARDF  244

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF E P LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  +
Sbjct  245  LNYTVGYFRETPKLFLVQTPHFFLNPDPVERNLRTFETMPSENEMFYGIIQRGLDKWDAS  304

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR ALD+  GF+G +ITEDAETALE+H+ GW S+Y+DR +IAGLQP TF S
Sbjct  305  FFCGSAAVLRRAALDQTHGFSGISITEDAETALELHASGWSSVYVDRPLIAGLQPATFTS  364

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L  + P  +RGL  AQRLCY++S  FW FP+ R +FL+APL YLF
Sbjct  365  FIGQRSRWAQGMMQILRFRFPPGKRGLSFAQRLCYMSSTLFWLFPITRWIFLLAPLCYLF  424

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF A+  E LAY   Y+ V+ ++QN L+ R RWP +SE+YE  Q  YL  A+++ +
Sbjct  425  FNLEIFTASGAEFLAYTSSYMLVNLMMQNYLYGRFRWPWISELYEFVQGVYLLPALISVI  484

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VTAK+E+L E+ IS + RP    F + L+GV  T+ R    P    V LVV
Sbjct  485  LNPSKPTFKVTAKNESLDESRISELARPFYIIFFVLLAGVFMTVWRIYTEPYKADVALVV  544

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+L+ G AL  V+E+Q+ R + RV ++   E  I   G+R++ AT+ DAS  G
Sbjct  545  GGWNLLNILIAGCALGVVSERQESRQSRRVDVKRRCELII---GDRAVPATIEDASVGGA  601

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFP-DAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            R  V L G        +   +++F+       P L   +R    S +     + +G  +E
Sbjct  602  R--VNLVGFKAQDLERDMRCVLRFKTSVEVSDPSLPINIRSVFASPK----GIAIGCRYE  655

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
               P   R  +A L+F  S  W   + +    IG+L G    +W    SL +T R
Sbjct  656  PSLPDHFR-MIADLVFVSSDQWAKFQWSRRVNIGILRG---TIWFIGLSLYQTGR  706


>TR:A0A1Q8ZMB1 A0A1Q8ZMB1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium oryziradicis OX=1867956 GN=BJF95_14050 PE=4
SV=1
Length=730

 Score = 568 bits (1464),  Expect = 0.0
 Identities = 312/707 (44%), Positives = 427/707 (60%), Gaps = 14/707 (2%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            FL W  +   F +L + P++     +  L AVV++A LK    K   R + L+  + +V+
Sbjct  7    FLAWALVSAGFLILISLPISLQTHLIATLLAVVVLATLKTLEIKGPWRMVGLACGTAVVL  66

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
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            RY +WR   TLPP     +F+  ++L+  E +S+ +  L+  + + P      +    +
Sbjct  67   RYVYWRTTSTLPPVNQLENFIPGIVLYIAEMYSVVMLALSLVIVSSPLRSSVGKRGSADY  126

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
             PTVDI +P+YNE   ML+ TL A +N+ YPA   TV L DDGGT Q+  S D   A  A
Sbjct  127  KPTVDIFIPTYNEDPQMLANTLGATRNLDYPADKITVWLLDDGGTLQKRSSNDIPQAHAA  186

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            + R  ELQ LCRE+GV Y TR+RNEHAKAGN++  ++   GEL+VVFDADH P++DFL
Sbjct  187  ERRHEELQTLCREMGVRYLTRDRNEHAKAGNLNNGMQHSTGELIVVFDADHAPAQDFLLE  246

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF +DP LFLVQTPHFF+NPDPI+RNL   ++ P ENEMFYG I RGLD+W G+FFC
Sbjct  247  TVGYFEDDPKLFLVQTPHFFLNPDPIERNLNTFEKMPGENEMFYGIIQRGLDKWNGSFFC  306

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAAVLRRRALDEAGGF+G +ITED ETAL +HS GW S+Y+D+++IAGLQP TFASFI
Sbjct  307  GSAAVLRRRALDEAGGFSGISITEDCETALALHSSGWNSVYVDKSLIAGLQPATFASFIG  366

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RWA GMMQ+L+ + P+FRRGL +AQRLCY++S  FW FP+ R +FL+APL Y+FF +
Sbjct  367  QRSRWAQGMMQILIFRQPMFRRGLSLAQRLCYMSSTLFWLFPIPRTIFLIAPLFYIFFDL  426

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVA+    LAY   Y+  + L+QN L+ R RWP +SE+YE  Q  +L  AI++ +L P
Sbjct  427  QIFVASGGTFLAYTATYMLANLLIQNYLYGRFRWPWISELYEYVQTIHLLPAIISVMLHP  486

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
                F VTAKDE++ ++ +S I  P    F +     +    R  A P    V LVVGGW
Sbjct  487  TKPTFKVTAKDESIKQSRLSEIGLPFFIIFGVLAVATVVAAYRIYAEPYKADVTLVVGGW  546

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             +LN++  G AL  V+EK  + ++ RV +E   E  +    N    A V + S  G+ +
Sbjct  547  NLLNLIFAGCALGVVSEKGDKSSSRRVTVERRCEFML---ANEWHQARVENVSVHGMLIH  603

Query  619  V---RLPGVGDPHPALEAGGLIQFQPKFPDAPQL--ERMVRGRIRSARREGGTVMVGVIF  673
            V             A E  G I+ +P    AP      +VR  +       G V +G  F
Sbjct  604  VFCKDSDAASMQAAAQETAGTIRIKPFCDGAPSTMPVNIVRSHVGD-----GYVGIGCTF  658

Query  674  EAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
               Q +  R  +A L+F  S+ W   ++   +  GL+ G    L +A
Sbjct  659  SPQQTLDHR-LIADLMFANSSQWSEFQKRRHKNPGLIRGTINFLGIA  704


>TR:A0A4D7E1C1 A0A4D7E1C1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium larrymoorei OX=160699 GN=bcsA PE=4 SV=1
Length=730

 Score = 568 bits (1464),  Expect = 0.0
 Identities = 320/707 (45%), Positives = 425/707 (60%), Gaps = 11/707 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            + F++W+ +     ++    PV+     +    ++ L+A +K    K   R + L   + +
Sbjct  5    ITFIIWLFISACVLVIITLPVSLQTHLIATAISLALLATIKSLNGKGAWRLIGLGFGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP     +F+   L++  E +S+ +  L+  + + P      RP  P
Sbjct  65   VLRYVYWRTTSTLPPVNQLENFIPGFLVYLAEMYSVLMLGLSLVIVSMPLPSRKGRPGSP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
               PTVDI VP+YNE  ++L+ TLAAAKNM YP    TV L DDGGT Q+  +P+   AQ
Sbjct  125  GYRPTVDIFVPTYNEDFELLANTLAAAKNMDYPEDKFTVWLLDDGGTVQKRNAPNGLDAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A  R  ELQQLC +LGV Y TRERN HAKAGN++  LE   GELV VFDADH P+RDFL
Sbjct  185  AATRRYNELQQLCADLGVNYLTRERNVHAKAGNLNNGLEHSTGELVTVFDADHAPARDFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF ED  LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAF
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Sbjct  245  LETVGYFEEDERLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL E  GF+G +ITED ETAL +HSRGW SLY+D+ +IAGLQP TFASF
Sbjct  305  FCGSAAVLRRTALTETDGFSGVSITEDCETALALHSRGWNSLYVDKPLIAGLQPATFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLFF
Sbjct  365  IGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ L
Sbjct  425  DLQIFVASGGEFLAYTAAYMLVNLMMQNFLYGSFRWPWISELYEYVQTVHLLPAVVSVLF  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAKDE++SE  +S I RP    F + +  ++  + R  A P    V LVVG
Sbjct  485  NPSKPTFKVTAKDESISEARLSEISRPFFVIFAVLILAMIFAIYRIYAEPYKADVTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GW +LN++  G AL  V+E+ +R A+ R+ ++   E Q+   G   L ATV + S  G+
Sbjct  545  GWNLLNIIFAGCALGVVSERGERSASRRITVKRRCELQMDEDG-PWLPATVENVSVHGML  603

Query  617  LLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            + +          A+E G    I+     P  P    M    +R+ +++ G + +G  F
Sbjct  604  INI----FDKDLVAIEKGKTATIRVATHSPGVP--PTMTINVVRTVKQQ-GFMSIGCTFA  656

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAA  721
                I  R  +A LIF  S  W   +    +  GL+ G A  L +AA
Sbjct  657  PKAAIEHR-LIADLIFANSEQWTEFQRVRRKNPGLIKGTATFLAIAA  702


>TR:A0ABW0H9R0 A0ABW0H9R0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Bosea vestrisii OX=151416 GN=bcsA PE=4 SV=1
Length=727

 Score = 568 bits (1463),  Expect = 0.0
 Identities = 318/705 (45%), Positives = 427/705 (61%), Gaps = 12/705 (2%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V+ + +  A++V    L  +  A    G I + A++L+  L+P+    V R + L   +
Sbjct  7    VIFWAIATAIVVALISLPISLQAHLIAGTIVVGAMILLKFLRPYG---VWRLIALGLGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP      F+  L+L+  E ++I + FL+ F+ A P  R    P
Sbjct  64   IVLRYVYWRTTSTLPPVNQLEDFIPGLILYLAELYNIGMLFLSLFVVAMPLPRRKSAPPI  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            P + PTVD+ VPSYNE  ++L+ TL+AA  M YPA   +V L DDGGTD++C   +   A
Sbjct  124  PADAPTVDVFVPSYNEEPELLATTLSAALAMDYPAGRLSVYLLDDGGTDEKCNVDNFVAA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              A+ERR  LQ LC  LGV Y TRERN  AKAGN++  L    G+LVVVFDADH P+R+F
Sbjct  184  SAARERRAALQTLCEGLGVTYLTRERNISAKAGNLNNGLANSSGDLVVVFDADHAPARNF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF  DP LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  +
Sbjct  244  LTETVGYFDRDPKLFLVQTPHFFINPDPLERNLKTFKAMPSENEMFYGIIQRGLDKWNAS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR AL    GF+G +ITEDAETA+ +H+ GW S+Y+D+ +IAGLQP TFAS
Sbjct  304  FFCGSAAVLRRTALQTTNGFSGRSITEDAETAITLHATGWNSIYVDKPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+LL   P+ + GL + QRLCY +S  FW FP VR+ FLVAPL YLF
Sbjct  364  FIGQRSRWAQGMMQILLYHRPMLKSGLSLPQRLCYSSSALFWLFPFVRLTFLVAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+EIF A+  E +AY+  Y+AV+ ++QN L+ R RWP +SE+YE  Q+ YL  A+V+ L
Sbjct  424  FGLEIFTASGAEFIAYVFSYMAVNLMMQNYLYGRYRWPWISELYEFIQSVYLLPAVVSVL  483
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Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VTAK E L    IS +  P    F +   GV+AT  R +A P +    LVV
Sbjct  484  LNPGKPTFKVTAKSEELGTRRISELGLPFFIIFAVLALGVVATYWRTIAQPYNADTTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W +LN+L+ G AL  V+E+ + R A R  ++   E  I        TA ++  + S
Sbjct  544  GLWNILNLLMAGCALGVVSERPEGRGARRFPVKRRGEISID-----GRTAPIVTENVSVD  598

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
             + VR+   G     L + G I FQ      P     VR  +R A  E G V+ G  +E
Sbjct  599  GVAVRVLSKGFDTLPLNSKGEIAFQTSIA-MPSGALPVR-IVRQASDEKGLVL-GCRYEP  655

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             +P+  R  +A L F ++  W   ++A  + +G+++G  R L +A
Sbjct  656  SEPLHSR-IIADLCFSDAGIWSDFQKARRQNMGVVYGTLRFLRIA  699


>TR:A0ABR5D522 A0ABR5D522_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium arsenijevicii OX=1585697 GN=RP75_17775
PE=4 SV=1
Length=729

 Score = 568 bits (1463),  Expect = 0.0
 Identities = 326/717 (45%), Positives = 438/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  VL+A +K F  +   R + L   +
Sbjct  5    ITIIVW--LLVSLCVLAIVTMPVSLQTHLVATAISLVLLATIKGFNGQGAWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P+  PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPDYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIIE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSSGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL ++ GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRREALQDSDGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L L  +   + R  A P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFALLLVAMAFAIWRIYAEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+ ++ A+ R+ ++   E ++    +  + A++ + S  G
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGEKSASRRITVKRRCEVKLEG-SDAWVPASIDNVSVHG  601

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
              LL+ L    D   A+E     +++ +P     P  E M    +R+ R E G V +G
Sbjct  602  --LLINL---FDSITAIEKNTTAIVRVKPHSEGVP--ETMPINVVRTVRGE-GFVSIGCT  653
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Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + I  R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  654  FSPQRAIDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706


>TR:A0A4Z0NI22 A0A4Z0NI22_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium nonmethylotrophicum OX=1141884 GN=bcsA
PE=4 SV=1
Length=932

 Score = 567 bits (1462),  Expect = 0.0
 Identities = 323/716 (45%), Positives = 436/716 (61%), Gaps = 30/716 (4%)

Query  17   LLFLLW-VALLVPFGLLAAAPVAPSAQ-GLIALSAVVLVALLKPFADKMVPRFLLLSAAS  74
            L + +W ++  V  GLLA  PV P AQ  L   +   ++AL      + +PR   L+  +
Sbjct  16   LRWTIWGLSAAVTIGLLAQ-PVGPEAQLWLCGAACAGMLALWLLAPRRGLPRLAFLALGT  74

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDR---PFP  131
            ++V+RY +WRL  TLP         F ++L   E + + I  ++  ++ADP  R   PFP
Sbjct  75   LVVIRYVYWRLTGTLPSLDDPVGLGFGMMLLGAELYCVLILAVSLVVTADPLVRETVPFP  134

Query  132  RPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
                  +LP VD+L+PSYNEP ++L+VTLAAA N+ YPA   TV L DDGGTDQ+C  P+
Sbjct  135  ADA---DLPAVDVLIPSYNEPTEILAVTLAAALNLDYPADKLTVWLLDDGGTDQKCADPN  191

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            P  A  AQERR ELQ LC  LG  Y TR RNEHAKAGN++  L   + E+V+V DADH P
Sbjct  192  PAKAAAAQERRAELQALCAALGACYLTRARNEHAKAGNLNNGLTASRAEIVLVLDADHAP  251

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
             R FL  TVG F EDP+LFLVQTPH F+NPDP++RNL    R P ENEMFYG    GLD+
Sbjct  252  FRSFLRETVGLFSEDPNLFLVQTPHVFLNPDPVERNLRTFARMPSENEMFYGVTQAGLDK  311

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            W G+FFCGSAA+LRRRALD  GGF+G TITED ETAL++H RGW S Y+ + +IAGLQPE
Sbjct  312  WNGSFFCGSAALLRRRALDAVGGFSGITITEDCETALDLHGRGWTSAYVGKPLIAGLQPE  371

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            + A FI QR RW  GM+Q+L+LKNPL + GL   QRL YL+SM+FWFFPL R++F++APL
Sbjct  372  SLADFIGQRARWCQGMIQILMLKNPLMKPGLRPIQRLAYLSSMTFWFFPLPRLVFMLAPL  431

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
            +++FF ++IFV++ +E +AY   Y+  + ++QN L+   RWP VSE+YE  Q  YLAR+I
Sbjct  432  LHIFFDVKIFVSSVDEAIAYTATYIVANLMIQNYLYGHVRWPFVSELYEYVQGVYLARSI  491

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
             + ++ PR   F+VTAK   L+ +++SP+  P    F    +G      R++  PG  S+
Sbjct  492  ASVIVSPRRPSFSVTAKGAGLAHDHLSPLAWPFFAIFAALAAGCGMAAWRYLYEPGVTSL  551

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
            +LVVG W   N+++ G AL AVAE++Q    P + +  PA   + A G+  +  TV   S
Sbjct  552  MLVVGLWCGFNLVIAGVALGAVAERRQEETTPSLPVGRPA---LAAIGDERVPVTVERMS  608

Query  612  TSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
                 L +R    G P PA+  GGL+Q        P L    R  +R+A      V+
Sbjct  609  AEAATLRLRRAD-GAPFPAMPQGGLLQ----AGTGPAL----RFTLRAAPAPDLRVV---  656

Query  672  IFEAGQPIAVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARIL-WMAAASL  724
               A  P+A  E  TVA L++G++A  R       R   L+ G  R L W  A  L
Sbjct  657  ---AFAPLAPAEYRTVAGLMYGDAAALRGFLAGRRRHRDLVTGTLRFLAWGVAEPL  709


>TR:A0ABU0C508 A0ABU0C508_9BRAD Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhodopseudomonas julia OX=200617 GN=J2R99_000021 PE=4
SV=1
Length=823

 Score = 567 bits (1462),  Expect = 0.0
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 Identities = 291/621 (47%), Positives = 410/621 (66%), Gaps = 8/621 (1%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            L +LW+       LL   P++  AQ ++ ++AV  +A +  F+ + V R + L+ A+ +V
Sbjct  7    LAMLWLLATTATLLLIMQPISIEAQFVMGVAAVGGMAAVWMFSKEGVWRQVFLALATAVV  66

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY +WR   TLPP +   +F+   L++ +E FS+ + F++ F++ADP +R   R L+
Sbjct  67   LRYVYWRTTSTLPPISEPINFVPGFLVYLMEMFSVLMLFISLFITADPLERKRARQLRDA  126

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            ELPTVDI +P+YNE   +L+ T+AAA  M YP   R V L DDGGT+Q+  +PDP ++
Sbjct  127  ELPTVDIFIPTYNEDKSLLATTIAAALAMDYPLEKRQVWLLDDGGTEQKVNNPDPNVSVP  186

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A+ RR ELQ+LC +LG  Y TRERNEHAKAGN++  L     +L+VVFDADH P R FL
Sbjct  187  AKRRRAELQRLCAQLGAHYLTRERNEHAKAGNLNNGLACSTADLIVVFDADHGPVRSFLR  246

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVG+F +DP LFLVQTPHFF+NPDP++RNL+  +R P ENEMFY  I RGLD+W  AFF
Sbjct  247  ETVGHFADDPRLFLVQTPHFFLNPDPVERNLSTFERMPSENEMFYSMIQRGLDKWNAAFF  306

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR AL+E GGF+G +ITED ETALE+HSRGW S Y+D  +IAGLQPE F SFI
Sbjct  307  CGSAAVLRRAALEETGGFSGVSITEDCETALELHSRGWNSRYVDIPLIAGLQPENFVSFI  366

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RW  GM+Q+L+LKNPLF+RGL   QR+ YL+S  FW FPL R+ F++APL+Y+ F
Sbjct  367  GQRSRWCRGMVQILMLKNPLFKRGLRFEQRIAYLSSSLFWLFPLTRLTFMLAPLLYIIFS  426

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            ++I+ A+F E + Y   Y+ V+ ++Q+ L+ R RWP VSE+YE  Q+ YL RAI++ ++
Sbjct  427  LQIYEASFREFVGYTVAYMTVNIMLQSYLYGRLRWPWVSELYEYVQSVYLGRAILSVVVN  486

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTF-LLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            PR+  F VTAK +T  +  +S +  P    F +L ++G+ A   R+   P    +L++ G
Sbjct  487  PRAPTFNVTAKGQTSDKEQLSALAGPYFAIFGVLAVTGIYAGW-RYFTEPAGNDLLMICG  545

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W  +N+++ G AL  V+E  +RR A R  + V   A +   G   +  +V D STSG
Sbjct  546  VWNAINLVIAGVALGVVSEMPERRRAQR--LAVVRRAVLEIVGVGEIAVSVEDVSTSG--  601

Query  617  LLVRLPGVGDPHPALEAGGLI  637
              +R+  + D  P ++AG  I
Sbjct  602  --IRVRPLEDALPPMKAGATI  620


>TR:A0ABQ5ZQ31 A0ABQ5ZQ31_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella yambaruensis OX=415996 GN=GCM10007923_54120
PE=4 SV=1
Length=723

 Score = 567 bits (1462),  Expect = 0.0
 Identities = 315/715 (44%), Positives = 434/715 (61%), Gaps = 17/715 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V  +A++K    + + R + L+  + +V+R
Sbjct  8    ILWALVSALVILVITLPINLQTQLIASIAVVTFMAVIKVLRAEGIWRLIALAFGTAVVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R  +   L
Sbjct  68   YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPPRKSRVAEEGRL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVD+ VPSYNE   +L+ TLAAAK M YPA   TV L DDGGT+Q+  +     AQ A+
Sbjct  128  PTVDVFVPSYNEDTGLLANTLAAAKAMDYPADKLTVWLLDDGGTEQKRNAAAVIEAQVAE  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R RELQ LCR+LGV Y TR RNEHAKAGNM+  ++   GEL+ VFDADH P+RDFL  T
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Sbjct  188  ARHRELQALCRDLGVNYLTRARNEHAKAGNMNNGMQHSTGELIAVFDADHAPARDFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +D  LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFADDQKLFLVQTPHFFLNPDPLERNLRTFETMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRTALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL + QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKRGLSLPQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428  IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++ E+ +S I RP    F +     L ++ R+ + P    V  VVGGW
Sbjct  488  KPTFKVTAKDESIRESRLSEISRPFFVIFAVLFVAFLMSIYRFYSEPYKADVTFVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+++ G AL  V+E+ +R A+ RV ++      +     R   +T+ + S +G R  V
Sbjct  548  LLNLIIAGCALGVVSERSERAASRRVTVKRRCTFIV---DGREYPSTLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+ +P  A +A   ++F P        E ++   +R+    G  + VG  F    P
Sbjct  603  QVFGL-EPDLAKDARCALRFTPY---GAGQEEVLPVDVRNVENLGSVIAVGCRF---MPE  655

Query  680  AVR--ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
              R    VA LIF  S  W   + +     GL  G    LW    ++ +T+R  +
Sbjct  656  VARHHSLVADLIFANSNQWSDFQVSRRYNPGLFRGS---LWFLGIAVYQTSRGLL  707


>TR:A0A564FVQ6 A0A564FVQ6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium dankookense OX=560405 GN=bcsA_1 PE=4
SV=1
Length=886

 Score = 567 bits (1462),  Expect = 0.0
 Identities = 331/727 (46%), Positives = 431/727 (59%), Gaps = 31/727 (4%)

Query  5    AKARSPLRVVPVLLFLLWVALLVPFGLLAAA-------PVAPSAQGLIALSAVV-LVALL  56
            A A SP       + LLW+A    +GL AAA       PV P AQ  +   AV  ++AL
Sbjct  3    APASSPASPSRPAMALLWLA----WGLAAAAALAFLTQPVGPEAQAALCGGAVAGMLALW  58

Query  57   KPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFF  116
                 + +PR   L+  S + +RY +WRL  TLP      SF   L+L A E + + I
Sbjct  59   LACPRRGLPRAAFLALGSFVAIRYVYWRLTATLPAIDDPLSFGLGLVLLAAELYCVLILA  118

Query  117  LNGFLSADPTDR-PFPRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTV  175
            ++  ++A+P +R P P P  P E P+VDILVPSYNE AD+L VTLAAA N+ YPA   TV
Sbjct  119  VSLVVNAEPLERGPVPVP-DPAEAPSVDILVPSYNEGADILGVTLAAACNLDYPADRFTV  177

Query  176  VLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALE  235
             L DDGGTDQ+C  PDPE A  A+ RR ELQ LC  LG  Y TR RN HAKAGN++A L
Sbjct  178  WLLDDGGTDQKCADPDPEKAAAARARRAELQALCAGLGARYLTRARNAHAKAGNLNAGLR  237

Query  236  RLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCP  295
               G+LV+V DADH P R FL  TVG F +DP LFLVQTPH F NPDP++RNL   +R P
Sbjct  238  AGSGDLVLVLDADHAPFRSFLKETVGLFGQDPKLFLVQTPHIFHNPDPLERNLRTFERMP  297

Query  296  PENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGW  355
             ENEMFY     GLD+W G+FFCGSAA+LRR ALD  GGFAG TITED ETALE+H+RGW
Sbjct  298  SENEMFYAATQAGLDKWNGSFFCGSAALLRRSALDTVGGFAGITITEDCETALELHARGW  357

Query  356  KSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMS  415
             S ++DR +I+GLQPETF++F+ QR RW  GM+Q+LLLKNPLF+RGL   QRL YL+SM
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  Sbjct  358  ASAFVDRPLISGLQPETFSAFVGQRARWCQGMLQILLLKNPLFKRGLKPIQRLAYLSSML  417

  Query  416  FWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLV  475
              FWFFPL R++F++APL+++FF ++IFV++ +E LAY   Y+ V+ L+Q+ L+   RWP V
  Sbjct  418  FWFFPLSRLVFMLAPLLHIFFDVKIFVSSIDETLAYTATYVGVNMLMQSYLYGHLRWPWV  477

  Query  476  SEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGV  535
              SE+YE     +LAR+IV+ ++ PR   F VT K  +L  +++S +  P    F L  +G
  Sbjct  478  SELYEYVLGIFLARSIVSVVVSPRKPGFNVTDKGVSLESDHLSALAWPFFLVFGLLAAGC  537

  Query  536  LATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQI  595
                   R++  PG   ++LVVG W   N+++ G AL  VAE++    AP +   +PA
  Sbjct  538  ATAAWRYLCEPGVTGLMLVVGLWCAFNLVIAGAALGVVAERRTLERAPSLPTALPARL--  595

  Query  596  PAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEA-----GGLIQFQPKFPDAPQLE  650
                 G  SL   V  AS +   +L R  G   P  A E        L+   P  P  P L
  Sbjct  596  -GLGGASLPVRVERASIAEC-VLRRADGGAWPKVAFEGAIEGEAALLGPDPAGPAFPPLR  653

  Query  651  RMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLL  710
                +   +    R       G       P A R TVA L++G++   R       R  GLL
  Sbjct  654  LTLGPVLADGTRRAAYAETG-------PEAFR-TVARLMYGDAGPLRAFLAGRRRHRGLL  705

  Query  711  HGMARIL  717
               G   +L
  Sbjct  706  SGSLGVL  712


  >TR:C5AXY6 C5AXY6_METEA Cellulose synthase catalytic subunit [UDP-forming]
  OS=Methylorubrum extorquens (strain ATCC 14718 / DSM 1338
  / JCM 2805 / NCIMB 9133 / AM1) OX=272630 GN=celA PE=4 SV=1
  Length=834

   Score = 566 bits (1460),  Expect = 0.0
   Identities = 295/621 (48%), Positives = 401/621 (65%), Gaps = 5/621 (1%)

  Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
              V+  L +L W+   V   +L + PV    Q  ++L+A+  + +L  F D    RF+ L+
  Sbjct  4    VIRALRWLAWMGTTVAGLILLSQPVGTQNQLAMSLAAMAAMIVLWLFLDGPRTRFVFLAL  63

  Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
               S++V+RY  WR+ +TLP P    SF F LLL   E + + I F++  ++ADP  R  P
  Sbjct  64   GSLVVLRYILWRVTDTLPSPGDPVSFGFGLLLLVGELYCVFILFVSLIINADPLKRAPPP  123

  Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
                +  ELPTVD+ VPSYNE A +L++TLAAA+ M YP    TV L DDGG+DQ+C  P+P
  Sbjct  124  VARAAELPTVDVFVPSYNEDAAILAMTLAAARQMNYPPDKLTVWLLDDGGSDQKCADPNP  183

  Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
              E A+ A++RRREL  L  ELG  Y TR RNEHAKAGN++  L    GE+VVV DADHVP
  Sbjct  184  EKAKAARDRRRELTTLAEELGCRYLTRARNEHAKAGNLNNGLAFASGEIVVVLDADHVPF  243

  Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
              R FL+ TVGYF EDP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W
  Sbjct  244  RSFLSETVGYFAEDPKLFLVQTPHAFLNPDPIERNLKTFERMPSENEMFYAVTQRGLDKW  303

  Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
               G+FFCGSAA+LRR ALDEAGGF+G TITED ETA E+HSRGW S Y+D+ +IAGLQPET
  Sbjct  304  NGSFFCGSAALLRRTALDEAGGFSGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPET  363

  Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
               ++FI QR RW  GM Q+LLLKNP  ++GL   Q++ YL+SM+FWFFP+ R++F+ APL+
  Sbjct  364  LSAFIGQRSRWCQGMFQILLLKNPALQKGLKPIQKIAYLSSMTFWFFPVPRLIFMFAPLL  423

  Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
              ++FF ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV
  Sbjct  424  HIFFDLKIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIV  483

  Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
              + +  PR   F VT K  +L  +++S    P    + L  +G      R++  PG  +++
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Sbjct  484  SVIWSPRKPTFNVTDKGISLDHDHLSSASLPFFAVYGLLAAGCAVATWRYLFEPGVTNLM  543

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDA  610
            LVVG W   N+L  G AL   AE++Q    P   + +    QI   G R++  ++  + A
Sbjct  544  LVVGLWNFFNLLTAGAALGVCAERRQLERTP--SLAINRRGQI-TLGGRAIDVSIERVSA  600

Query  611  STSGVRLLVRLPGVGDPHPAL  631
                VRL   L   G  H  L
Sbjct  601  EACTVRLPAALLPTGGGHRKL  621


>TR:A0ABQ4UMR6 A0ABQ4UMR6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylorubrum suomiense OX=144191 GN=mdoH_1 PE=4 SV=1
Length=804

 Score = 566 bits (1460),  Expect = 0.0
 Identities = 291/603 (48%), Positives = 393/603 (65%), Gaps = 3/603 (0%)

Query  15   PVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAAS  74
            P L    W+       LL + P++ + Q  +++ A+VL+ALL   A     R   L+  S
Sbjct  3    PFLTRATWLISAALTLLLLSQPLSTTVQLEMSIGAIVLMALLWLVAKGQTGRLTFLAIGS  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
            ++V+RY +WRL  TLPP +   +F   LLL   E +   I  ++  ++A P  R  P
Sbjct  63   LVVLRYIYWRLSSTLPPLSDPINFGAGLLLVGAELYCFYILAVSLVINAAPLYRAPPPQD  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
            + ++LPTVDI VPSYNE   +L+ TLAAAK++ YPA   TV L DDGGTDQ+C  PDP
Sbjct  123  EDDDLPTVDIFVPSYNEDRHILATTLAAAKSIDYPAGKFTVWLLDDGGTDQKCADPDPRK  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A++A+ RR+ LQ LC +LGV Y TR RN HAKAGN++  L+   GE+VVV DADHVP R
Sbjct  183  AEEARARRKVLQALCADLGVSYLTRRRNLHAKAGNLNNGLQNSVGEIVVVLDADHVPFRS  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  T+G+F  DP LFLVQTPH F+NPDPI+RNL   DR P ENEMFY     GLD+W G
Sbjct  243  FLRDTIGHFAVDPRLFLVQTPHAFLNPDPIERNLKTFDRMPSENEMFYAVGQCGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            +FFCGSAA+LRRRALDEAGGF+G TITED ETA E+HSRGW S+Y+D+ +IAGLQPET +
Sbjct  303  SFFCGSAALLRRRALDEAGGFSGITITEDCETAFELHSRGWTSIYVDKPLIAGLQPETLS  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
             FI QR RW  GM+Q++LLKNP+ + GL   QRLCYL+SM+FWFFPL R++F+ APL+Y+
Sbjct  363  DFIGQRSRWCQGMLQIMLLKNPVLKSGLKPIQRLCYLSSMTFWFFPLPRLVFMAAPLLYI  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++I VA  +E +AY   Y+ V+ ++QN L+ R RWP VSE+YE  Q  +L +A  +
Sbjct  423  FFDMKIVVANVDEAIAYTATYIVVNLMMQNYLYGRVRWPFVSELYEYVQGLFLIKATASV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            ++ PR   F VTAK+  L  + +SP+  P    F +   G L +  R+   PG  +++LV
Sbjct  483  IISPRKPTFKVTAKNVNLDHDQLSPLALPYFLVFAILSIGALVSAYRYTFEPGVTNLMLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VG W + N++  G AL   AE++Q   AP + ++ PA   +      +L  TV   S +G
Sbjct  543  VGLWNLFNLITAGAALGVAAERRQTEKAPSLAVDRPAVLNL---NGMALDVTVERISGAG  599

Query  615  VRL  617
             R+
Sbjct  600  CRI  602


>TR:A0A6L9MGI7 A0A6L9MGI7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aurantimonas aggregata OX=2047720 GN=bcsA PE=4 SV=1
Length=732

 Score = 566 bits (1460),  Expect = 0.0
 Identities = 323/744 (43%), Positives = 447/744 (60%), Gaps = 21/744 (3%)
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Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVV-LVALLKPFADKMVPRFLLLS  71
            ++ +L  + W+       L+   P++  AQ L+A++ V+ ++ LLK        R + L+
Sbjct  1    MLKILFAIAWLLAAALALLVITLPISLQAQ-LVAVALVLGVMMLLKVLKLGGTWRLIALA  59

Query  72   AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
              + +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P
Sbjct  60   LGTTIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVFMLALSLFVVAAPLPPRSG  119

Query  132  RPL-QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
            R     + LP+VD+ VPSYNE   +L+ TLAAA  M YP+    V L DDG T Q+  +
Sbjct  120  RDTPHSDRLPSVDVFVPSYNEDYTLLANTLAAALKMNYPSDRMKVWLLDDGATSQKRSAE  179

Query  191  DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
                AQ A++R   L+QLC +LG  Y TRERNEHAKAGN++  +     EL+ VFDADH
Sbjct  180  HAGTAQAAEKRHVILKQLCLDLGATYLTRERNEHAKAGNLNNGMLHSDAELIAVFDADHA  239

Query  251  PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            P+RDFL +TV YF +DP LFLVQTPHFFINPDP++RNL+  ++ P ENEMFYG I RGLD
Sbjct  240  PARDFLLQTVSYFEQDPRLFLVQTPHFFINPDPVERNLSTFEKMPSENEMFYGIIQRGLD  299

Query  311  RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            +W  AFFCGSAAVLRR ALDEAGGF+G +ITED ETAL++HSRGW SLY+D  +IAGLQP
Sbjct  300  KWNAAFFCGSAAVLRREALDEAGGFSGVSITEDCETALDLHSRGWNSLYVDIPLIAGLQP  359

Query  371  ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
             TFASFIQQR RWA GMMQ++L + PLF+RGL   QRLCY++S  FW FP  R MFLVAP
Sbjct  360  ATFASFIQQRSRWAQGMMQIMLFRFPLFKRGLSFPQRLCYMSSTLFWLFPFPRTMFLVAP  419

Query  431  LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L YLFFG+EIF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A
Sbjct  420  LFYLFFGLEIFNASGGEFLAYTSTYIIVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPA  479

Query  491  IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
            +V+ L+ PR   F VTAKDE++  + +S I  P    F + L GV AT+ R +  P
Sbjct  480  VVSVLINPRRPTFNVTAKDESILTSRLSEISLPFFVIFFVLLLGVAATVWRVINEPAQAD  539

Query  551  VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDA  610
            + LVVGGW VLN+L+ G AL  V+E+  R ++ R+ +    E  +   G+++  AT+ D
Sbjct  540  LTLVVGGWNVLNLLIAGCALGVVSERGARSSSRRIGVARRCELLV---GDQAFPATINDV  596

Query  611  STSGVRLLVRLPGVGD-PHPALEAG-GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVM  668
            S  G R+ V     GD P    + G   ++FQP   +      +   +IR+ ++E
Sbjct  597  SVGGARVQV----FGDSPLQTFKNGPATLRFQPHSSEETATLSL---QIRNCQKESDGAS  649

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            +G  +           +A LIF  S  WR+ + +  R  GL+ G     W       +T+
Sbjct  650  IGCSYIV-HAATDHFLIADLIFANSEQWRSFQLSRRRNPGLIRGTG---WFIGLCFYQTS  705

Query  729  R--DFMDEPARRRRRHEEPKEKQA  750
            R   ++   A   ++   P +K+A
Sbjct  706  RGLSYLARRAMGPKKSASPAQKRA  729


>TR:A0A7W6BWD3 A0A7W6BWD3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Aureimonas phyllosphaerae OX=1166078 GN=GGR05_003732
PE=4 SV=1
Length=741

 Score = 566 bits (1460),  Expect = 0.0
 Identities = 316/723 (44%), Positives = 438/723 (61%), Gaps = 16/723 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            +L LLW+        L + PV+  AQ  +A  A+ + A +     +   RF+ L+  + +
Sbjct  5    VLGLLWLLTACSGLFLISQPVSVDAQLTVASIAIAVGAAIYVLRLQGPWRFVFLAITTAV  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLP P   A+F+ A++L+  E F I +  +N F+ +DP +R      +
Sbjct  65   VLRYAYWRTTATLPSPDDLANFVPAVILYLAEMFYIVLLGMNLFVVSDPLERAAAPEVDD  124
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Query  137   EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
               LP VD+ VPSYNE   +L++TL++A  M YPA    V L DDGGTD++  + DP  A
Sbjct  125   AALPHVDVFVPSYNESKAILALTLSSALAMDYPAGKLRVFLLDDGGTDEKRNARDPMKAA  184

Query  197   KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             +A+ R  +LQ LCR+LGV Y TR RN HAKAGN++A L    GELVVVFDADH P+R+FL
Sbjct  185   EARHRHEDLQALCRDLGVTYVTRARNTHAKAGNLNAGLAASNGELVVVFDADHAPAREFL  244

Query  257   ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              +TVGY V DP  FLVQTPHFF NPDPI++NL+  +R P ENEMFYG I +GLD+W  AF
Sbjct  245   RQTVGYMVADPKTFLVQTPHFFSNPDPIEKNLSTFERMPSENEMFYGTIQKGLDKWNAAF  304

Query  317   FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
             FCGSAA+LRR AL E GGF+G TITED ETAL++HSRGWKS+Y+DR M+ GLQPET +SF
Sbjct  305   FCGSAALLRRSALMEVGGFSGITITEDCETALDLHSRGWKSVYVDRPMVTGLQPETLSSF  364

Query  377   IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
             I QR RW  GM+Q+L LKN     GL +AQR+CYL+S   WFFP+VR++FL+APL+++FF
Sbjct  365   IGQRSRWCRGMLQILFLKNAALVPGLSLAQRICYLSSALIWFFPIVRVVFLIAPLLFIFF  424

Query  437   GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
              ++I+  + +E +AY   YL +S L++N L+ R RWP +SE+YE  Q+ YL RA+++ ++
Sbjct  425   DMKIYDVSAQEFVAYTLTYLVISSLIRNYLYGRVRWPWISELYEYVQSVYLFRAVLSVIV  484

Query  497   RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
              PR   F VTAK +TL+E+ +S +  P    F + L  +   + R+   P    +LLVVG
Sbjct  485   NPRRPTFNVTAKGDTLAEDRLSELAWPYFAIFAVLLGAMGYAVYRYQTEPLVGGILLVVG  544

Query  557   GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
              W +LN+++   AL  V E+++RR  PR+  E  AE    AF    +   V+D S+SG +
Sbjct  545   AWNLLNLVIAAAALGVVTERRERRGMPRIVTERMAEL---AFAETVVPVVVVDISSSGAK  601

Query  617   L--LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
             L  L  LP VG    A         +    D   +  +    +RS   EGG  ++GV +
Sbjct  602   LRPLAGLPFVGTEQRA-------DLKVSRTDGSPVGTL-PVVVRSTGEEGGRPVLGVHYR  653

Query  675   AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARIL-WMAAASLPKTARDFMD  733
                       +A L+ G+ A  R  R    R  GL+   A I+ W     L        D
Sbjct  654   T--ETCDYPLIAELMMGDMASVRAQRAGRQRRRGLVLSSASIIGWALGTPLRAFRHLVFD  711

Query  734   EPA  736
              PA
Sbjct  712   RPA  714


>TR:A0A1G5NVG9 A0A1G5NVG9_AFIMA Cellulose synthase catalytic subunit [UDP-forming]
OS=Afifella marina DSM 2698 OX=1120955 GN=SAMN03080610_02753
PE=4 SV=1
Length=823

 Score = 566 bits (1460),  Expect = 0.0
 Identities = 292/621 (47%), Positives = 411/621 (66%), Gaps = 8/621 (1%)

Query  18    LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
             L +LW+       LL   P++  AQ ++ ++AV  +A +  F+ + V R + L+ A+ +V
Sbjct  7     LAVLWLLATTATLLLIMQPISIEAQFVMGVAAVGGMAAVWMFSKEGVWRQVFLALATAVV  66

Query  78    MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
             +RY +WR   TLPP +   +F+   L++ +E FS+ + F++ F++ADP +R   R L+
Sbjct  67    LRYVYWRTTSTLPPISEPINFVPGFLVYLMEMFSVLMLFISLFITADPLERKRARQLRDA  126

Query  138   ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
             ELPTVDI +P+YNE   +L+ T+AAA  M YP   R V L DDGGT+Q+  +PDP ++
Sbjct  127   ELPTVDIFIPTYNEDKSLLATTIAAALAMDYPHEKRQVWLLDDGGTEQKVNNPDPNVSVP  186

Query  198   AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
             A+ RR ELQ+LC +LG  Y TRERNEHAKAGN++  L+    +L+VVFDADH P R FL
Sbjct  187   AKRRRAELQRLCAQLGAHYLTRERNEHAKAGNLNNGLDCSTADLIVVFDADHGPVRSFLR  246
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Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVG+F +DP LFLVQTPHFF+NPDP++RNL+  +R P ENEMFY  I +GLD+W  AFF
Sbjct  247  ETVGHFADDPRLFLVQTPHFFLNPDPLERNLSTFERMPSENEMFYSVIQKGLDKWNAAFF  306

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR AL+E GGF+G +ITED ETALE+HSRGW S Y+D  +IAGLQPE F SFI
Sbjct  307  CGSAAVLRRAALEETGGFSGVSITEDCETALELHSRGWNSRYVDIPLIAGLQPENFVSFI  366

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RW  GM+Q+L+LKNPLF+RGL + QR+ YL+S  FW FPL R+ F+VAPL+Y+ F
Sbjct  367  GQRSRWCRGMVQILMLKNPLFKRGLRLEQRIAYLSSSLFWLFPLTRLTFMVAPLLYIIFS  426

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            ++I+ A+F E + Y   Y+AV+ ++Q+ L+ R RWP VSE+YE  Q+ YL RAI++ ++
Sbjct  427  LQIYEASFREFVGYTVAYMAVNIMLQSYLYGRLRWPWVSELYEYVQSVYLGRAILSVVVN  486

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTF-LLCLSGVLATLVRWVAFPGDRSVLLVVG  556
            PR+  F VTAK +T  +  +S +  P    F +L ++G  A   R+   P    +L++ G
Sbjct  487  PRAPTFNVTAKGQTSDKEQLSALAGPYFAIFGVLAVAGAYAAW-RYFTEPTGNDLLMICG  545

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
             W  +N+++ G AL  V+E  +RR A R  + V   A +   G   +  +V D ST G
Sbjct  546  VWNAINLVIAGVALGVVSEMPERRRAQR--LAVVRRAVLEIVGVGEIAVSVEDVSTCG--  601

Query  617  LLVRLPGVGDPHPALEAGGLI  637
              VR+  + D  P ++AG  I
Sbjct  602  --VRVRPLEDALPPMKAGATI  620


>TR:A0A7W6C4A4 A0A7W6C4A4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium skierniewicense OX=984260 GN=GGQ73_000484
PE=4 SV=1
Length=731

 Score = 566 bits (1460),  Expect = 0.0
 Identities = 317/701 (45%), Positives = 426/701 (61%), Gaps = 7/701 (1%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            ++WV + V   ++   PV+     +    ++VL+A +K    K   R + L   + +V+R
Sbjct  8    IVWVLVSVCVLVIVTLPVSLQTHLIATAISLVLLATIKSLNGKGAWRLIGLGFGTAIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P  L
Sbjct  68   YVYWRTTSTLPPINQLENFIPGFLLYLAEMYSVLMLALSLVIVSMPLPSRKSRPGSPGYL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVDI VP+YNE A +L+ TLAAAKN+ YPA   TV L DDGGT Q+  + +   AQ A
Sbjct  128  PTVDIFVPTYNEDAVLLANTLAAAKNIDYPADKFTVWLLDDGGTVQKRNASNVLEAQAAA  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  EL+QLC +LGV Y TR RN HAKAGN++  LE   GEL+ VFDADH P+RDFL  T
Sbjct  188  RRHEELKQLCADLGVNYLTRGRNAHAKAGNLNNGLEHSTGELITVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF ED  LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCG
Sbjct  248  VGYFEEDDRLFLVQTPHFFLNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL E  GF+G +ITED ETAL +HSRGW SLY+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRLALKETNGFSGVSITEDCETALALHSRGWHSLYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLFF ++
Sbjct  368  RSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQ  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  428  IFVASGGEFLAYTAAYMLVNLMMQNFLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPS  487
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Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++SE  +S I RP    F + +  ++  + R  A P    V LVVGGW 
Sbjct  488  KPTFKVTAKDESISEARLSEISRPFFVIFGVLVIAMIFAIYRIYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN++  G AL  V+E+ ++ A+ RV ++   E Q+    +  L ATV + S  G+ + +
Sbjct  548  LLNIIFAGCALGVVSERSEKSASRRVTVKRRCELQV-GDSDAWLPATVENVSVHGMLIHI  606

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
               G+        A   I+ +P     P  E M    +RS +++ G + VG  F   + +
Sbjct  607  FDSGLVPVEKGTTA--TIRVKPHSEGVP--ETMGINIVRSVKQD-GFISVGSTFSPQKAV  661

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              R  +A LIF  S  W  ++    +  GL+ G    + +A
Sbjct  662  DHR-LIADLIFANSEQWSEIQRVRRKNPGLIKGTVTFMVIA  701


>TR:A0A4R3R4N4 A0A4R3R4N4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium azibense OX=1136135 GN=EV129_114126 PE=4
SV=1
Length=729

 Score = 566 bits (1460),  Expect = 0.0
 Identities = 318/708 (45%), Positives = 432/708 (61%), Gaps = 12/708 (2%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            W  + +   +L   PV    Q + +++ V ++A++K    +   R + L+  + +V+RY 
Sbjct  10   WAIVSLCVIVLITLPVNLQTQLIASITVVTIMAVIKVLKGEGTWRLIALAFGTAVVLRYA  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   TLPP      F+  LLL+  E +SI++  L+ F+ A P      RP++ E+ P 
Sbjct  70   YWRTTNTLPPVNQLENFIPGLLLYLAEMYSIAMLALSLFIVATPLPPRRSRPVKQEDFPH  129

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VP+YNE A +L  TLAAAK M YP     V L DDGGT Q+  S     AQ A  R
Sbjct  130  VDVFVPTYNEDAHLLGNTLAAAKAMDYPTDKLQVWLLDDGGTLQKRNSNKLLEAQAAIAR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
              EL+QLC+ L V Y TR+RNEHAKAGN++  ++   GEL+ VFDADH P+RDFL  TVG
Sbjct  190  HNELRQLCQALSVNYLTRDRNEHAKAGNLNNGMQHSTGELIAVFDADHAPARDFLRETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            YF +DP LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCGSA
Sbjct  250  YFDDDPKLFLVQTPHFFINPDPLERNLRTFDSMPSENEMFYGIIQRGLDKWNAAFFCGSA  309

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVL RRAL    GF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI QR 
Sbjct  310  AVLSRRALQSTNGFSGISITEDCETALALHGAGWNSIYVDKPLIAGLQPATFASFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RWA GMMQ+L  + PLF+RGL I QRLCY++S  FW FP  R +FL APL YLFF +EIF
Sbjct  370  RWAQGMMQILRFRFPLFKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLEIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ ++ PR 
Sbjct  430  TASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVMINPRKP  489

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAKDE++S + +S I RP    F + +  +  T+ R  A P    V LVVGGW ++
Sbjct  490  TFKVTAKDESISVSRLSEISRPFFVIFAVQIIALAITIYRIYAEPYKADVTLVVGGWNLI  549

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N+++ G AL  V+E+ +R A+ RV++    E  +      +  TA++ D S  G RL V 
Sbjct  550  NLIMAGCALGVVSERGERAASRRVRVNRRCEFGV---NGKWHTASIEDVSVHGARLHVFN  606

Query  622  PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAV  681
              + DP   + A G I+F+P       LE +    +R+  R+G  + VG  +     +  
Sbjct  607  KQL-DP-MTIGAEGEIRFRPY--SGANLETLPL-IVRNMERDGDIMAVGCQYIPKSALDH  661
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Query  682  RETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            R  +A LIF  S  W   +E+  R  GL+ G    +W    SL +T+R
Sbjct  662  R-LIADLIFANSDQWAQFQESRRRNPGLIRG---TIWFLGLSLYQTSR  705


>TR:A0ABX4TET6 A0ABX4TET6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Sinorhizobium medicae OX=110321 GN=BMJ33_27205 PE=4
SV=1
Length=726

 Score = 566 bits (1459),  Expect = 0.0
 Identities = 309/705 (44%), Positives = 427/705 (61%), Gaps = 8/705 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V +  +W  + +    +   PV    Q + +L  V L+A++K        R + L+  +
Sbjct  4    VFVLAVWAFISLCVVAIITLPVNLQTQLIASLLIVTLMAIIKLVDAGGRWRLIALAFGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R
Sbjct  64   VVLRYVYWRTTGTLPPINQPENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPPRPSRAAT  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            P + P VD+ VPSYNE A +L+ TLAAAK M YPA    V L DDGGT Q+  S +   A
Sbjct  124  PGDYPKVDVFVPSYNEDASLLANTLAAAKGMDYPAEKLRVWLLDDGGTLQKRNSTNLVEA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q+A  R  ELQ+LC +LGV Y TR+RNEHAKAGN++  +    G+L+ VFDADH P+RDF
Sbjct  184  QRATARNLELQKLCTDLGVRYLTRDRNEHAKAGNLNNGMSHSDGDLIAVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  A
Sbjct  244  LLETVGYFEDDPRLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR+AL++  GF+G++ITED ETAL +H RGW S+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLRRKALEDTSGFSGKSITEDCETALALHGRGWNSVYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L+ + PLF+ GL I QRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILMFRFPLFKGGLTIPQRLCYMSSTLFWLFPFPRTIFLFAPLCYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IF A+  E + Y   YL V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +
Sbjct  424  FDLQIFTASGGEFMGYTLAYLVVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVV  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR   F VTAKDE++ E+ +S I RP    F++    +L T  R    P    + +VV
Sbjct  484  LNPRKPTFKVTAKDESIQESRLSEIGRPFFVVFIVLFIALLVTAYRVYTEPYKADITMVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+++ G AL  V+E+ ++ A+ RV++    E    + G R   AT+ D S +GV
Sbjct  544  GGWNLLNLIMAGCALGVVSERGEKAASRRVKVSRRCEF---STGERWYPATIEDVSANGV  600

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            R  +++ G+     ++EA   I+F+P   D      ++   +R+    G    VG  F
Sbjct  601  R--IQVYGLAKDDLSVEARTEIRFEPFAGDG--AIEILPMAVRNVEVTGDITAVGCRF-L  655

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             +       VA L+F  S  W   +       GL+ G    LW+A
Sbjct  656  PEVARHHSLVADLLFANSRQWSEFQHKRRGNPGLVRGTVWFLWLA  700


>TR:A0ABU7T6U9 A0ABU7T6U9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium radiotolerans OX=31998 GN=bcsA PE=4
SV=1
Length=825

 Score = 566 bits (1459),  Expect = 0.0
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 Identities = 296/617 (48%), Positives = 397/617 (64%), Gaps = 7/617 (1%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            V+  L +L W+   V   +L + PV    Q  ++L+A+  + +L  F D    RF+ L+ 
Sbjct  4    VIRALRWLAWMGTTVAGLILLSQPVGTQNQLAMSLAAMAAMIVLWLFLDGPRTRFVFLAL  63

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             S++V+RY  WR+ +TLP P    SF F LLL   E + + I F++  ++ADP  R  P 
Sbjct  64   GSLVVLRYILWRVTDTLPSPGDPVSFGFGLLLLVGELYCVFILFVSLIINADPLKRRPPP  123

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
                  LPTVDI VPSYNE A +L++TLAAA+ + YP    TV L DDGGTDQ+C   +P
Sbjct  124  AANAAALPTVDIFVPSYNEDAAILAMTLAAARQINYPPDKLTVWLLDDGGTDQKCADTNP  183

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
            + A+ AQERRR+LQ LC ELG  Y TR RNEHAKAGN++  L    G++V V DADHVP 
Sbjct  184  DKARAAQERRRDLQALCDELGCRYLTRARNEHAKAGNLNNGLAHATGDIVAVLDADHVPF  243

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            R FL+ TVGYF EDP LFLVQTPH F+NPDPI+RNL   DR P ENEMFY    RGLD+W
Sbjct  244  RSFLSETVGYFAEDPKLFLVQTPHAFLNPDPIERNLETFDRMPSENEMFYAVTQRGLDKW  303

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
             G+FFCGSAA+LRR ALDEAGGF+G TITED ETA E+HSRGW S Y+D+ +IAGLQPET
Sbjct  304  NGSFFCGSAALLRRTALDEAGGFSGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPET  363

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
              +FI QR RW  GM Q+LLLKNP  ++GL   Q++ YL+SM+FWFFP+ R++F+ APL+
Sbjct  364  LTAFIGQRSRWCQGMFQILLLKNPALQKGLKPIQKIAYLSSMTFWFFPVPRLIFMFAPLL  423

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            ++FF ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV
Sbjct  424  HIFFDLKIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIV  483

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +  PR   F VT K  +L  N++S    P    + L   G      R++  PG  +++
Sbjct  484  SVIWSPRKPTFNVTDKGISLDHNHLSSASLPFFAVYGLLAIGCAVAAWRYMFEPGVTNLM  543

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAST  612
            LVVG W   N+L  G AL   AE++Q    P + +       +   G R++  ++   S 
Sbjct  544  LVVGLWNFFNLLTAGAALGVCAERRQLERTPSLAINRRGGLTL---GGRAVDVSIERVSA  600

Query  613  SG--VRLLVRL--PGVG  625
             G  VRL   L  PGVG
Sbjct  601  EGCSVRLPAALAPPGVG  617


>TR:A0A3S2VGV2 A0A3S2VGV2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium oryzihabitans OX=2499852 GN=bcsA
PE=4 SV=1
Length=837

 Score = 566 bits (1458),  Expect = 0.0
 Identities = 313/715 (44%), Positives = 428/715 (60%), Gaps = 26/715 (4%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            L WV       +L A PV+   Q  +++ A + +  L  F      RF+ L+  S++V+R
Sbjct  8    LSWVLAAAMLVVLLAQPVSTQVQLAMSVGAGLCMTALWLFFRGPTTRFVFLALGSLVVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WRL  TLPP      F F +LL   E + + I F++  ++ADP DR  P     +EL
Sbjct  68   YLYWRLTSTLPPVQDPVGFGFGVLLLIAELYCVFILFVSLIINADPLDRAPPYQAPEDEL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VDI VPSYNE A +L  TLAAA+ + YPA   TV L DDGGTDQ+C  PDP  A+ A+
Sbjct  128  PSVDIFVPSYNEDASILIPTLAAARALDYPADKVTVWLLDDGGTDQKCNDPDPLKAEAAR  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
            ERR  LQ+L  ELG  Y TR RN HAKAGN++  L+    ELVVV DADH P R FL  T
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Sbjct  188  ERRASLQRLAAELGCRYLTRARNLHAKAGNLNNGLQNSTAELVVVLDADHAPFRTFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF EDP LFLVQTPH F+NPDPI+RNL   ++ P ENEMFYG   RGLD+W G+FFCG
Sbjct  248  VGYFAEDPRLFLVQTPHAFLNPDPIERNLRTFEKMPSENEMFYGITQRGLDKWNGSFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR ALDEAGGF+G TITED ETA E+H+RGW S+Y+ + +IAGLQPET  SFI Q
Sbjct  308  SAAVLRRAALDEAGGFSGITITEDCETAFELHARGWTSVYVAKPLIAGLQPETLDSFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RW  GM+Q+++LKNP   RGL + QRL YL+SM+FWF+P+ R++F+ APL+++FF ++
Sbjct  368  RSRWCQGMIQIMILKNPALVRGLHMIQRLAYLSSMTFWFYPVPRLIFMFAPLLHIFFDMK  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            +FVA  +E +AY   Y+ ++ ++QN L+ R RWP +SE+YE  Q  +L +AI   +  PR
Sbjct  428  VFVANVQESIAYTATYIVINLMMQNYLYGRVRWPFMSELYEYVQGLFLIKAIAKVIASPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAK  +L ++++SP+  P    + L  +G    L R++  PG  S++LVVG W
Sbjct  488  KPTFNVTAKGASLDQDHLSPLALPFFLVYGLLAAGCATALYRYLYEPGVTSLMLVVGLWT  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV---R  616
              N++  G AL  VAE++Q  A P     +P   +    G  +L    +D +   V   R
Sbjct  548  FYNLITAGAALGVVAERRQTEANP----SLPVRRE----GTLTLGGVAVDVAVERVSVDR  599

Query  617  LLVRLPGVGDPHP--ALEAGGLIQFQPKF-----PDAPQLERMVRGRIRSARREGGTVMV  669
              VR+  +  P      E  G++   P       P+   +  +V GR  SA   G   +
Sbjct  600  CTVRMTAMLPPRAPGETEQRGVLAVTPMARTDGRPEVRAVLPVVLGRTTSA---GEVSVC  656

Query  670  GVIFEAGQPIAVRETVAY--LIFGESAHWRTMREATMRPIGLLHGMARILWMAAA  722
             ++F+    I  RE  A+  L++G+    +           L  G A+ +W   A
Sbjct  657  ELVFDG---IGAREAAAHVELMYGDPGAMQRFLGRRHAHKDLFTGTAQFVWWGLA  708


>TR:A0ABU0BCK4 A0ABU0BCK4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Ancylobacter polymorphus OX=223390 GN=J2S75_001795
PE=4 SV=1
Length=705

 Score = 566 bits (1458),  Expect = 0.0
 Identities = 308/680 (45%), Positives = 416/680 (61%), Gaps = 9/680 (1%)

Query  41   AQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALDASFLF  100
            AQ +     ++L+  L+ FA + VPR + L+    +V RY +WR   TLPP    A+F+
Sbjct  3    AQLVTGCIVILLIVFLRMFAPEGVPRMVALALGVAMVSRYVYWRTTSTLPPVEELANFIP  62

Query  101  ALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADMLSVTL  160
            A+LL+  E +S+++  L+ F+ + P        ++P   PTVDI VPSYNE A +L+ TL
Sbjct  63   AVLLYVAEMYSVALMALSLFVVSAPQPARVAPAIEPGSEPTVDIFVPSYNEDAGLLATTL  122

Query  161  AAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVVYSTRE  220
            AAA  + YP    TV L DDGGTDQ+C   D   A++AQERR  L QLC ELGV Y TR
Sbjct  123  AAAMAIDYPRDRFTVWLLDDGGTDQKCEQHDLAAAREAQERRATLTQLCEELGVNYLTRP  182

Query  221  RNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTPHFFIN  280
            RNE AKAGN++  L    GELVVVFDADH P+R FL  TVGYF +DP LFLVQTPHFFIN
Sbjct  183  RNEFAKAGNLNHGLAHSHGELVVVFDADHAPARSFLRETVGYFHQDPRLFLVQTPHFFIN  242

Query  281  PDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGFAGETI  340
            PDP++R+L    R P ENEMFYG I RGLDRWGGAFFCGSAAVLRR AL E  GFA  +I
Sbjct  243  PDPVERSLGTWRRMPSENEMFYGVIQRGLDRWGGAFFCGSAAVLRREALLETDGFAHSSI  302

Query  341  TEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKNPLFRR  400
            TED ETAL +H+RGW S+Y+D  +IAGLQPETFA+FI QR RWA GM Q+L    PLFR
Sbjct  303  TEDCETALSLHARGWHSVYVDTPLIAGLQPETFANFIGQRSRWAQGMYQILRFHFPLFRS  362

Query  401  GLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGYLAVSF  460
            GL +AQR+CY++S+ FWFFP+ R +FL++P  YLFF +EIF  +  E +AY   YL  +
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Sbjct  363  GLTVAQRICYMSSILFWFFPISRAIFLISPFCYLFFSLEIFNGSGAEFIAYTAVYLLTNL  422

Query  461  LVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSENYISPI  520
             +Q+ LF + RWP  SE+YE  Q  YL  A+++ ++ P+   F VT+K ET+ EN IS I
Sbjct  423  FIQSYLFGKYRWPWFSELYEYIQTVYLLPALLSVMIDPKKPTFRVTSKGETIDENRISEI  482

Query  521  YRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAEKQQRR  580
              P    F++ +  V  T  R    P    + LVVG W +LN+++ G AL  V+EK  +R
Sbjct  483  GIPFFIIFVIQIVAVFVTFWRIATEPYSADITLVVGIWNLLNLIISGCALGVVSEKAVKR  542

Query  581  AAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGGLIQFQ  640
             + R+ +       I       + A + D S  G+R+   LP        + A  +++
Sbjct  543  HSQRMAISRRCNLLIDGV---EVPAVIDDVSMGGLRVRTELPPEAQARLGMHA--VVRLT  597

Query  641  PKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAHWRTMR  700
            P  PD   +   +   +R+   + G +++G  F A +  A  + +A LIF ++  W+  +
Sbjct  598  P--PD-ECISDTLPVLVRNIAHDDGVIVLGTQFNA-KCAAHYQLIADLIFADADEWKKFQ  653

Query  701  EATMRPIGLLHGMARILWMA  720
            E   R  G+L G    + +A
Sbjct  654  EGRRRNPGVLRGTVMFVLIA  673


>TR:A0ABV1QJ74 A0ABV1QJ74_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylorubrum podarium OX=200476 GN=bcsA PE=4 SV=1
Length=815

 Score = 566 bits (1458),  Expect = 0.0
 Identities = 307/719 (43%), Positives = 442/719 (61%), Gaps = 31/719 (4%)

Query  14    VPVLLFLL--WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLS  71
            +P+ L  L  +V   +  GLL   PV  + Q  ++L A+ ++  L  F       ++ L
Sbjct  1     MPIFLTRLSWFVTAALVIGLLLQ-PVGTAVQLEMSLGAIAVMTALWLFTRGRTAHYIFLG  59

Query  72    AASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFP  131
              S++V++Y++WR+  TLP  A   S    L+L A E + + I FL+ F++ADP  RP P
Sbjct  60    IGSLVVIKYFYWRITRTLPWSADPISLTAGLILLAAELYYLYILFLSLFINADPLKRP-P  118

Query  132   RPLQPE-ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
             P+  E +LPTVDI VPSYNE A +L+ TLAAA+++ YPA+  TV L DDGGTDQ+C  P
Sbjct  119   APIGNEADLPTVDIFVPSYNEDASILATTLAAARSLDYPAQKLTVWLLDDGGTDQKCADP  178

Query  191   DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
            D   + +A+ RR  L++LC ELGV Y TR RN HAKAGN++  L+   GE+VVV DADHV
Sbjct  179   DARKSAEARARRVGLERLCEELGVRYLTRRRNVHAKAGNLNNGLKHATGEIVVVLDADHV  238

Query  251   PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            P R FL  T+G+F +DP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY     GLD
Sbjct  239   PFRSFLKETIGHFAQDPRLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYAISQPGLD  298

Query  311   RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            +W G+FFCGSAA+LRR ALDEAGGF+G TITED ETA E+HSRGW S+Y+D+ +IAGLQP
Sbjct  299   KWNGSFFCGSAALLRRTALDEAGGFSGITITEDCETAFELHSRGWTSIYVDKPLIAGLQP  358

Query  371   ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
            +T   FI QR RW  GM+Q+L+LKNP+F+RGL + QRLCY+++M++WFFP+  ++F+ AP
Sbjct  359   DTLRDFIGQRSRWCQGMLQILILKNPVFKRGLNMIQRLCYMSNMTYWFFPVPCLVFMFAP  418

Query  431   LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L+Y+FF ++I VA  +E +AY   Y+ V+ ++QN L+ R RWP VSE+YE  Q  +L +A
Sbjct  419   LLYIFFDMKIVVANVDEAIAYTATYIIVNLMMQNYLYGRVRWPFVSELYEYVQGLFLIKA  478

Query  491   IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
                +L PR   F VTAK+ TL ++++SP+  P    +L+ L+G L    R+   PG  +
Sbjct  479   TAAVILSPRKPTFNVTAKNVTLDQDHLSPLALPFFVVYLILLAGSLLAAYRYAFEPGITN  538

Query  551   VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDA  610
            ++LVVG W ++NV+  G AL   AE++Q    P + ++  A   +       L   V
Sbjct  539   LMLVVGLWNLVNVIKAGAALGVTAERRQTETTPSLTVDRQAVLTL-----NGLAIDVRVE  593
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Query  611  STSGVRLLVRLPGVGDPHPALEAG-GLIQFQPK--------FPDAPQLERMVRGRIRSAR  661
              S  R  +R+  +     + ++  G +   P+        +P  P         + S+
Sbjct  594  RVSAQRCRIRMDTIAPTRRSEDSSTGTLAIVPQQVGSSVGTWPSMPVT-------LTSSA  646

Query  662  REGGTVMVGVIFEAGQPIAVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARILW  718
              G   +  + FE   P   R+   +A L++G++      ++A  R   L  G+A+ +W
Sbjct  647  LSGEETVCELQFERLSP---RDYFALADLMYGDAEAMTRFQQARRRHKTLFAGIAQFVW  702


>TR:A0A922T9K3 A0A922T9K3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudorhizobium pelagicum OX=1509405 GN=GV68_19455
PE=4 SV=1
Length=726

 Score = 566 bits (1458),  Expect = 0.0
 Identities = 312/703 (44%), Positives = 430/703 (61%), Gaps = 15/703 (2%)

Query  21   LWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            LW  + +    L   PV+  AQ +  +S V L+  +K    +   R + L+  + +V+RY
Sbjct  9    LWAIVAILEIALITLPVSLQAQLIAGISVVTLMGTIKILNAQGTWRLVSLALGTGIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR  ETLPP      F+  ++L+  E +++ +  L+ F+ A P      R    E+LP
Sbjct  69   VYWRTTETLPPIDQIQDFVPGMILYLAEMYNVLMLALSLFIVAMPLPPRPSRTDATEDLP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
             VD+ +P+YNE A++L+ TLAAAK M YPA    + L DDGGT Q+  S D   A+ A+E
Sbjct  129  DVDVFIPTYNEDANLLANTLAAAKAMDYPAEKLHIWLLDDGGTVQKRSSADVASAEAARE  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            R  +L QLC+ LG  Y TRERNEHAKAGN++  L    GELV VFDADH P+RDFL  TV
Sbjct  189  RHHQLAQLCQILGANYLTRERNEHAKAGNLNNGLAHSSGELVAVFDADHAPARDFLRETV  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF EDP LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCGS
Sbjct  249  GYFAEDPKLFLVQTPHFFINPDPLERNLRTFDTMPSENEMFYGVIQRGLDKWNAAFFCGS  308

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVL RRAL++ GGF+G +ITED ETAL +HS GW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  309  AAVLSRRALEQTGGFSGLSITEDCETALALHSAGWNSVYVDKPLIAGLQPATFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ+L  + PLF+RGL + QRLCY++S  FW FP  R  FL APL YL F ++I
Sbjct  369  SRWAQGMMQILHFRFPLFKRGLTLPQRLCYMSSTLFWLFPFTRATFLFAPLFYLLFDLQI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FVA+  + LAY   YL V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ ++ PR
Sbjct  429  FVASGGDFLAYTLSYLIVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVISVMINPRK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VTAKDE+++ + +S I RP    F + +      + R    P    + LVV GW +
Sbjct  489  PTFKVTAKDESIAVSRLSEISRPFFVIFAILVIVTGFGIYRIYTEPYKADITLVVTGWNI  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV-  619
            LN++L G AL  VAE+ +R A+ RV+++   E  +    +R L A++ D S  G ++ +
Sbjct  549  LNLILAGCALGVVAERGERAASRRVRLQRRCEVMV---DDRPLAASIEDVSVGGAQVHIF  605

Query  620  --RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
              ++ G+     A     L++FQP       ++E +    IRS    G   ++GV ++
Sbjct  606  SRQVHGLSRGKTA-----LLRFQPH--GMTRMETLPI-TIRSFEPSGDLTVIGVQYQPAG  657

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            P+  R  +A LIF  S  W   +E+  +  G++ G    L MA
Sbjct  658  PLDHR-WIADLIFANSRQWSQFQESRRKNPGIVKGSLMFLSMA  699


>TR:C3KKQ1 C3KKQ1_SINFN Cellulose synthase catalytic subunit [UDP-forming]
OS=Sinorhizobium fredii (strain NBRC 101917 / NGR234) OX=394
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GN=celA PE=4 SV=1
Length=731

 Score = 566 bits (1458),  Expect = 0.0
 Identities = 316/705 (45%), Positives = 426/705 (60%), Gaps = 15/705 (2%)

Query  23   VALLVPFGLLAAA-------PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            VA L  +G+++         PV    Q + ++  V  +AL+K        R + L+  S
Sbjct  12   VATLAAWGIISLCLVALITLPVNLQTQLIASVLVVTFMALIKLLDAGGKWRPIALAFGSA  71

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R
Sbjct  72   MVLRYVYWRTTSTLPPVNQPENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPPRASRSAT  131

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
            P + P VD+ VPSYNE AD+L+ TLAAAK M YP    TV L DDGGT Q+  S +   A
Sbjct  132  PGKYPKVDVFVPSYNEDADLLANTLAAAKGMDYPVDKLTVWLLDDGGTLQKRNSTNLVDA  191

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q+A  R R+LQ+LC +LGV Y +R+RNEHAKAGN++  +    GEL+ VFDADH P+RDF
Sbjct  192  QRATGRHRDLQKLCEDLGVRYLSRDRNEHAKAGNLNNGMLHSNGELIAVFDADHAPARDF  251

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  A
Sbjct  252  LLETVGYFEDDPRLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAA  311

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR+AL++  GF+G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFAS
Sbjct  312  FFCGSAAVLRRKALEDTSGFSGLSITEDCETALALHGRGWNSVYVDRPLIAGLQPATFAS  371

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L+ + PL + GL I QRLCY++S  FW FP  R +FL APL YLF
Sbjct  372  FIGQRSRWAQGMMQILMFRFPLLKGGLSIPQRLCYMSSTLFWLFPFSRTIFLFAPLFYLF  431

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IF A+  E LAY   Y+ V+  +QN L+   RWP +SE+YE AQ  +L  A+V+ L
Sbjct  432  FDLQIFTASGGEFLAYTLVYMLVNLTMQNYLYGSFRWPWISELYEYAQTVHLLPAVVSVL  491

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR   F VTAKDE++ E+ +S I RP    F + L      + R    P    + LVV
Sbjct  492  LNPRKPTFKVTAKDESVLESRLSEISRPFFVIFAILLIATALAIYRVYTEPYKADITLVV  551

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+++ G AL  V+E+ ++ A+ RV++    E    +FG ++  AT+ + S  G
Sbjct  552  GGWNLLNLIMAGCALGVVSERGEKAASRRVKVSRRCEF---SFGEQTYPATIENVSAHGA  608

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            R  V++ G+      ++  G I+FQP   D       V   IR+   EG   +VG  +
Sbjct  609  R--VQVYGLPTDELLVDVRGQIRFQPYSGDGTFETLPV--SIRNIETEGDLTIVGCRY-L  663

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             +       VA LIF  S  W   +       GL+ G    LW+A
Sbjct  664  PEIAHHHSLVADLIFANSQQWSEFQRKRRGNPGLVRGTLWFLWLA  708


>TR:A0ABS3EMR3 A0ABS3EMR3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium burrii OX=2815339 GN=bcsA PE=4 SV=1
Length=729

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 323/709 (46%), Positives = 433/709 (61%), Gaps = 13/709 (2%)

Query  23   VALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            V LLV   +LA   +  S Q  +  +A+  VL+A +K F  +   R + L   + +V+RY
Sbjct  9    VWLLVSLCVLAIVTMPVSLQTHLVATAISLVLLATIKGFNGQGAWRLVALGFGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P+  P
Sbjct  69   VYWRTTSTLPPINQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPGSPDYRP  128
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Query  141   TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
             TVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +   AQ AQ
Sbjct  129   TVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVEAQAAQR  188

Query  201   RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
             R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RDFL  TV
Sbjct  189   RHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARDFLLETV  248

Query  261   GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
             GYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCGS
Sbjct  249   GYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCGS  308

Query  321   AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
             AAVLRR AL ++ GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  309   AAVLRREALQDSDGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFASFIGQR  368

Query  381   GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
              RWA GMMQ+L+ + PLF+RGL   QRLCY++S  FW FP  R +FL APL YLFF ++I
Sbjct  369   SRWAQGMMQILIFRQPLFKRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQI  428

Query  441   FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
             FVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  429   FVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPGK  488

Query  501   ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
               F VTAKDE+++E  +S I RP    F L L  +   + R  + P    V LVVGGW +
Sbjct  489   PTFKVTAKDESIAEARLSEISRPFFVIFALLLVAMAFAIWRIYSEPYKADVTLVVGGWNL  548

Query  561   LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
             LN++  G AL  V+E+  + A+ R+ ++   E ++    +  L A++ + S  G  LL+
Sbjct  549   LNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SDAWLPASIDNVSVHG--LLIN  605

Query  621   LPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIA  680
             L   G    A +   +++ +P     P  + M    +R+ R E G V +G  F   + I
Sbjct  606   LFD-GATAVAKDTTAIVRVKPHSEGVP--DTMPVNVVRTVRGE-GLVSIGCTFSPQRAID  661

Query  681   VRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
              R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  662   HR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706


>TR:A0A2W4CQ29 A0A2W4CQ29_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium tubonense OX=484088 GN=bcsA PE=4 SV=1
Length=731

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 311/710 (44%), Positives = 431/710 (61%), Gaps = 12/710 (2%)

Query  20    LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
             ++W+ +      L   P+    Q + +++ V ++A++K    +   R + L+  S +++R
Sbjct  8     IIWIIVTACVCTLITLPINLQTQLIASVTVVAIMAVIKFMKGEGKWRLVALAFGSSIILR  67

Query  80    YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
             Y FWR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R     +
Sbjct  68    YVFWRTTSTLPPLNQPENFIPGFLLYLAEMYSVMMGALSLFVVAMPLPPRPSRAATETKF  127

Query  140   PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
             P VD+ VPSYNE A +L+ TLAAAK+M YPA    V L DDG T Q+  +P+   AQ A
Sbjct  128   PRVDVFVPSYNEDAALLANTLAAAKSMDYPADRVDVWLLDDGSTLQKRNAPNLLEAQAAT  187

Query  200   ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
              R  +LQQLC EL   Y TR+RNEHAKAGN++  ++  KGEL+ VFDADH P+RDFL  T
Sbjct  188   ARHEQLQQLCEELDAHYLTRDRNEHAKAGNLNNGMKASKGELIAVFDADHAPARDFLLET  247

Query  260   VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
             VGYF +DP LFLVQTPHFF+NPDPI+RNL   D+ P ENEMFYG I RGLD+W  AFFCG
Sbjct  248   VGYFDDDPRLFLVQTPHFFLNPDPIERNLQTFDKMPSENEMFYGIIQRGLDKWNAAFFCG  307
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Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR ALDE  GF+G +ITED ETA+ +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRTALDETNGFSGISITEDCETAIALHSRGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PL +RGL I QRLCY++S  FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLLKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFNLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF ++  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ +L PR
Sbjct  428  IFTSSGGEFLAYTLAYMVVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVISVILNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++S + +S I RP    F + L       + R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDESISVSRLSEISRPFFVIFAVLLVAFGMAIYRVYAEPYKADVTLVVGGWT  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+++ G AL  V+E+ +R ++ RV++    E  +    ++   A++ D S  G RL V
Sbjct  548  LLNLIMAGCALGVVSERGERSSSRRVRVNRRCEFGV---DDKWYPASIEDVSVHGARLHV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
                  DP   ++A G+I+F+P    +   E  +   +R+    G    +G ++     +
Sbjct  605  -FSKTFDP-LEMDARGIIKFRPY---SGAQEETLSVAVRNTHGAGDITSIGCLYLPTSAL  659

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
              R  +A LIF  S  W   + +  R  GL+ G    +W    +L +T+R
Sbjct  660  DHR-LIADLIFANSDQWTKFQLSRRRNPGLIRG---TIWFVGMALYQTSR  705


>TR:A0ABT1C838 A0ABT1C838_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Mesorhizobium liriopis OX=2953882 GN=bcsA PE=4 SV=1
Length=734

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 324/711 (46%), Positives = 430/711 (60%), Gaps = 21/711 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L+ L+W  +      L    P+    Q +  +S V+ + LLK    + V R + L+  + +
Sbjct  5    LILLVWAMIAAFVIALITLPINIQGQLITGVSIVLCMMLLKLLRPEGVFRLISLAFGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P     PRP +
Sbjct  65   VLRYVYWRTTSTLPPFNQPENFIPGFLLYLAEMYSVLMLALSLFVVAAPLP---PRPSRS  121

Query  137  ------EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
                  ++LPTVD+ VP+YNE A++L+ TLAAAK M YPA   TV L DDGGT Q+  +
Sbjct  122  ANIGPRDQLPTVDVFVPTYNEDAELLANTLAAAKAMDYPADKFTVWLLDDGGTAQKRNAD  181

Query  191  DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
                A +A+ R  ELQQL  +L   Y TRERNEHAKAGNM+ AL +  GEL+VVFDADH
Sbjct  182  KVAEANRAERRHAELQQLAADLDCRYLTRERNEHAKAGNMNNALAQSTGELIVVFDADHA  241

Query  251  PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            P+RDFL  TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD
Sbjct  242  PARDFLTETVGYFKDDPKLFLVQTPHFFLNPDPVERNLQTFEKMPSENEMFYGVIQRGLD  301

Query  311  RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            +W  AFFCGSAAVLRR AL E GGF+G +ITED ETALE+H RGW SLY+D+ +IAGLQP
Sbjct  302  KWNAAFFCGSAAVLRRAALMETGGFSGISITEDCETALELHGRGWHSLYVDKPLIAGLQP  361

Query  371  ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
             TFASFI QR RWA GM+Q+L  + P  +RGL + QRLCY++S  FW FP  R +FLVAP
Sbjct  362  ATFASFIGQRSRWAQGMLQILRFRFPPLKRGLQLPQRLCYMSSTLFWLFPFPRAIFLVAP  421

Query  431  LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L YLFF +EIF A+  E +AY   Y+ V+ ++QN L+ + RWP +SE+YE  Q  +L  A
Sbjct  422  LFYLFFDLEIFTASGGEFMAYTLSYMLVNLIMQNYLYGQFRWPWISELYEYVQTIHLLPA  481

Query  491  IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
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            +++ +L PR   F VTAKDE+++++ +S I  P    F + L+ V  T  R    P
Sbjct  482  VISVILNPRKPTFKVTAKDESIAKSRLSEIAAPFFIIFFILLAAVFVTAWRVYHEPYKAD  541

Query  551  VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDA  610
            V LVVG W +LN+++ G AL  V+E+ +R A  RV++   A  QI   G +S  AT+ D
Sbjct  542  VTLVVGAWNLLNLVMAGCALGVVSERGERAATRRVKVSRRARFQI---GEQSFQATIEDV  598

Query  611  STSGVRLLVRLPGVGD-PHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMV  669
            S  G R+ V     G  P    +  G +QFQ     A + E  +   IR+  R      +
Sbjct  599  SVHGARVQV----FGQLPELTQDMMGELQFQ---TFAEKREGGLPILIRNFERTPDGGFI  651

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            G  +    P   R  VA LIF  S  W   + +     GLL G  R   MA
Sbjct  652  GCRYRPSIPDHHR-FVADLIFANSNQWTQFQLSRRGNPGLLMGTIRFFRMA  701


>TR:A0A366E0W3 A0A366E0W3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Pseudochrobactrum asaccharolyticum OX=354351 GN=DFR47_103512
PE=4 SV=1
Length=736

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 309/736 (42%), Positives = 444/736 (60%), Gaps = 18/736 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            +FL W+       LL   P+    Q  + +S ++++A+ K F  +   R ++L+  + +V
Sbjct  6    IFLCWLLSAACVLLLTFMPINLPTQLALGISLLIVLAVFKHFRIRGSWRLVVLAIGTSIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY +WR  +T+PP +   +F+  ++L+  E +S+ +  L+ F+ + P   P    L+ +
Sbjct  66   LRYVYWRTTQTIPPASQLQNFIPGIILYLAEMYSVMMLALSMFVVSFPRVSPAAVQLRED  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            E+P VD+ +P+YNE A +L+ TL AA NM YPA   T+ L DDGGTDQ+C S +   +++
Sbjct  126  EMPAVDVFIPTYNEDAKLLANTLGAAVNMDYPADRLTIWLLDDGGTDQKCNSANLLESRR  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A ERR ELQ LC + GV Y TR RNEHAKAGN++  L    G+LV VFDADH P+R+FL
Sbjct  186  ATERRAELQALCADFGVKYLTRARNEHAKAGNLNNGLAHSTGKLVAVFDADHAPARNFLT  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVGYF ++  LFLVQTPHFFINPDP++RNL   ++ P ENEMFYG I RGLD+W  AFF
Sbjct  246  ETVGYFRDNAKLFLVQTPHFFINPDPVERNLRTFNQMPSENEMFYGMIQRGLDKWNAAFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAA+L R AL    GF+G +ITED ETA+ +H++GW S+YIDR +IAGLQP TFASFI
Sbjct  306  CGSAALLSRDALATTDGFSGVSITEDCETAVNLHAQGWDSIYIDRPLIAGLQPATFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P    GL + QRLCY++S  FW FP  RM FLVAPL YLFF
Sbjct  366  GQRSRWAQGMMQILRFRFPPLMAGLSLPQRLCYMSSTLFWLFPFARMTFLVAPLFYLFFD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            ++IFVA+  E LAY   YL V+ ++QN L+   RWP +SE+YE  Q+ +L  AI++ +L
Sbjct  426  LQIFVASGGEFLAYTLIYLCVNLMLQNYLYGSYRWPWISELYEYVQSVHLLPAIISVILN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR   F VTAKDE++    +S I RP    F++ +  +L    R    P    VLLVVGG
Sbjct  486  PRKPTFNVTAKDESILVARLSEIARPFFIIFIVLVLALLLAAYRIYTEPYKADVLLVVGG  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN+++ G AL  V+E+ ++ ++ RV++    E  +    +   T T+ D S +G+ L
Sbjct  546  WTLLNLIMAGCALGVVSERGEKSSSVRVKVTRRCEVLVDGQWH---TGTIDDVSANGMHL  602

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
            ++    +     +L  G  +  +     A +    +   IR+  REG  + VG +++  Q
Sbjct  603  MIYAGDI----TSLTIGSEVSAR-FITHAGEQSSDLPVEIRNVSREGDLISVGCLYKP-Q  656

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR------DF  731
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              A    VA LIF  S  W  +++      G+L      LW  + SL +T R
Sbjct  657  QAAHHRLVADLIFANSGRWAEIQQERRTNPGVLRA---TLWFFSLSLYQTGRGLAYFLGL  713

Query  732  MDEPARRRRRHEEPKE  747
                A+R+ + E+P +
Sbjct  714  KQYSAKRKEKAEKPAQ  729


>TR:A0ABR6IQ28 A0ABR6IQ28_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium mongolense OX=57676 GN=GGD56_003751 PE=4
SV=1
Length=729

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 318/708 (45%), Positives = 430/708 (61%), Gaps = 12/708 (2%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            W  + +   +L   PV    Q + +++ V ++A++K    +   R + L+  + +V+RY
Sbjct  10   WAIVSLCVFVLITLPVNLQTQLIASITVVTIMAMIKILKGEGTWRLIALAFGTAVVLRYA  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   TLPP     +F+  LLL+  E +SI++  L+ F+ A P      RP++ E  P
Sbjct  70   YWRTTSTLPPVNQLENFIPGLLLYLAEMYSIAMLALSLFIVATPLPPRRSRPVKEERFPH  129

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VP+YNE A +L  TLAAAK M YPA    V L DDGGT Q+  S     AQ A  R
Sbjct  130  VDVFVPTYNEDAHLLGNTLAAAKAMDYPADKLHVWLLDDGGTLQKRNSNKLLEAQAAIAR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
              EL+QLC  L V Y TRERNEHAKAGN++  ++   GEL+ VFDADH P+RDFL  TVG
Sbjct  190  HNELRQLCEALSVNYLTRERNEHAKAGNLNNGMQHSTGELIAVFDADHAPARDFLRETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            YF +DP LFLVQTPHFFINPDP++RNL   DR P ENEMFYG I RGLD+W  AFFCGSA
Sbjct  250  YFDDDPKLFLVQTPHFFINPDPLERNLRTFDRMPSENEMFYGIIQRGLDKWNAAFFCGSA  309

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVL RRAL    GF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  310  AVLSRRALQSTNGFSGISITEDCETALALHGAGWNSIYVDKPLIAGLQPATFASFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RWA GMMQ+L  + PL +RGL I QRLCY++S  FW FP  R +FL APL YLFF +EIF
Sbjct  370  RWAQGMMQILRFRFPLLKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLEIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ ++ PR
Sbjct  430  TASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVISVMINPRKP  489

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAKDE++S + +S I RP    F + +  +  T+ R  A P    V LVVGGW +
Sbjct  490  TFKVTAKDESISVSRLSEISRPFFVIFAVQIIALAITIYRIYAEPYKADVTLVVGGWNLF  549

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N+++ G AL  V+E+ +R A+ RV++    E  +     +  TA++ D S  G RL V
Sbjct  550  NLIMAGCALGVVSERGERAASRRVRVNRRCEFGV---NGKWHTASIEDVSVHGARLHVFN  606

Query  622  PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAV  681
              + DP   + A G I+F+P       LE +    +R+  ++G  + VG  +     +
Sbjct  607  KQL-DP-MTIGAEGEIRFRPY--SGADLETLPL-IVRNMEQDGDIMAVGCQYIPKSALDH  661

Query  682  RETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            R  +A LIF  S  W   +E+  R  GL+ G    +W    SL +T+R
Sbjct  662  R-LIADLIFANSDQWAQFQESRRRNPGLIRG---TIWFLGLSLYQTSR  705


>TR:A0A1W2DEM9 A0A1W2DEM9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Fulvimarina manganoxydans OX=937218 GN=SAMN06297251_11495
PE=4 SV=1
Length=741
```

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 Score = 565 bits (1457),  Expect = 0.0
 Identities = 280/601 (47%), Positives = 401/601 (67%), Gaps = 3/601 (0%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            W+A    F LL   P++ +AQ +IA++A+ + A +         RF+ L+AAS++++RY 
Sbjct  10   WLACAAAFLLLIQQPISVNAQWVIAMTALGVAAAIYALRLGGTWRFIFLAAASVVILRYA  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   TLP      +F+ A++L+  E + + +  ++ F++ADP +R         +LP+
Sbjct  70   YWRTTATLPSTEDLINFVPAIILYGAEMYCLLMLAMSLFVAADPLERSRAPQYPDNDLPS  129

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VPSYNE +D+L++TL+AAK M YPA    V L DDGGTD++ +S +P +A  A  R
Sbjct  130  VDVFVPSYNESSDILALTLSAAKGMDYPADRLRVHLLDDGGTDEKRLSRNPAIATAALRR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
              EL+ LCR+L V Y TR  N HAKAGN++  L R  G+L+VVFDADH P+R+FL  TVG
Sbjct  190  HEELKDLCRDLEVTYHTRVANVHAKAGNLNNGLSRSSGKLIVVFDADHAPAREFLRETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            +F+ DP LFLVQTPHFF NPDP+++NL+   R P ENEMFYG I +GLD+W  AFFCGSA
Sbjct  250  FFLTDPKLFLVQTPHFFANPDPLEKNLSTFKRMPSENEMFYGPIQKGLDKWNAAFFCGSA  309

Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVLRR AL + GGF+G +ITED ETAL++HSRGW SLY+DR M+ GLQPET +SFI QR 
Sbjct  310  AVLRREALAQVGGFSGISITEDCETALDLHSRGWNSLYVDRPMVTGLQPETVSSFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RW  GM+Q+LLLKNP FRRGL + QR+CYL+SM FWFFP +R++FL++PL+++ F ++IF
Sbjct  370  RWCRGMVQILLLKNPAFRRGLSLPQRICYLSSMMFWFFPFIRLIFLISPLLFILFDLKIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
              A+ +E ++Y    YL    L++N L+ R RWP VS++YE  Q+ YLARA+++ L+ PR  
Sbjct  430  DASVDEFISYSITYLCAGELIRNYLYGRVRWPWVSDLYEYVQSVYLARAVISVLINPRRP  489

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAK +T  + ++S +  P    F + L  +   + R+   P    +LLVVG W ++
Sbjct  490  TFNVTAKGQTTDKEHLSELAWPYFAIFGVLLFVMGVAIYRFQTEPAISGMLLVVGAWNLM  549

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N+++ G AL  V E+ +RR +PR+      +  I   G  ++   + D S  G ++L   
Sbjct  550  NLIVAGAALGVVTERMERRQSPRLLAMRKGDLCI---GGATVPVAIEDVSLGGAKVLALG  606

Query  622  P  622
            P
Sbjct  607  P  607


>TR:A0ABU4RS24 A0ABU4RS24_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Terrihabitans rhizophilus OX=3092662 GN=bcsA PE=4
SV=1
Length=729

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 324/733 (44%), Positives = 431/733 (59%), Gaps = 21/733 (3%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            + L L W+         L   P++  +  +     V ++ +LK      V R + L   +
Sbjct  5    IFLALTWLVCAAAVIFLITLPISLQSHLIAGTFVVAIMIVLKAVGAGGVWRIISLCLGTA  64

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP      F+  LLL+  E +S+ + FL+ F+ A P       P 
Sbjct  65   IVLRYAYWRTTSTLPPINELEDFIPGLLLYLAEMYSVFMLFLSLFVVARPLKEGQVAP-P  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
             +  P VD+ VP+YNE A +L+ TLAAA+ M YP     V L DDGG+DQ+C S + E +
Sbjct  124  TKTFPMVDVFVPTYNEEASLLTSTLAAAQAMDYPKDRFNVWLLDDGGSDQKCNSNNAEES  183
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Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            + A+ERR ELQ LC  +G  Y TR RN HAKAGN++  LE   GELV VFDADH P+RDF
Sbjct  184  EAARERRAELQALCENMGARYLTRARNVHAKAGNLNNGLENSTGELVAVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF  DP LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W  A
Sbjct  244  LKATVGYFEHDPKLFLVQTPHFFINPDPVERNLRTFQVMPSENEMFYGIIQRGLDKWNAA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVL R  L    GF+G +ITED ETALE+HSRG+ S+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLSRECLKVTNGFSGVSITEDCETALELHSRGYNSIYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+ + + P  +RGL IAQRLCY++S  FW FP+ RM+FLVAP  YLF
Sbjct  364  FIGQRTRWAQGMMQINMFRFPPLKRGLTIAQRLCYMSSTMFWLFPIARMIFLVAPFFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            FG+EIF A+  E +AY   Y+ V+ ++QN L+   RWP +SE+YE  Q+ YL  A+++ +
Sbjct  424  FGLEIFTASGPEFMAYTWTYILVNLMMQNYLYGYFRWPWISELYEFIQSVYLFPALISVM  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L PR   F VT+K+E L   +IS + RP    F L L GV  T+ R +A P +  V LVV
Sbjct  484  LNPRRPTFKVTSKNEDLQTAHISELGRPFYIIFALLLVGVGVTIWRVIAHPYEADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            G W +LN+++ G AL  V+E+   R + RV ++  AE     FG++ + AT+ D S  G
Sbjct  544  GAWNILNLIMAGCALGVVSERTDPRHSHRVNVQRRAEF---LFGDQVVPATIEDVSYGGA  600

Query  616  RL----LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
            ++      RL G+     A  A   I+FQ   P   +  + +  R+R+   E G V +G
Sbjct  601  KIRFGSAKRLQGL-----ASGAIATIRFQ---PHGQEEMKELPLRVRTMTHEDG-VFLGT  651

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF  731
             F  G     R  +A LIF  S  W   + +  R  G+L G     W    +  +T R
Sbjct  652  QFMPGTAEHHR-LIADLIFANSDQWTQFQRSRRRNPGILRG---TFWFLGTAFWQTGRGL  707

Query  732  MDEPARRRRRHEE  744
            +      R RH E
Sbjct  708  VYLVRAMRPRHAE  720


>TR:A9CEZ7 A9CEZ7_AGRFC Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299
GN=celA PE=4 SV=1
Length=729

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 318/702 (45%), Positives = 427/702 (61%), Gaps = 14/702 (2%)

Query  23   VALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            V LLV   +LA   +  S Q  +  +A+  +L+A +K F  +   R + L   + +V+RY
Sbjct  9    VWLLVSLCVLAIITMPVSLQTHLVATAISLILLATIKSFNGQGAWRLVALGFGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P+  P
Sbjct  69   VYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPGSPDYRP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +   AQ AQ
Sbjct  129  TVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNAANIVEAQAAQR  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RDFL  TV
Sbjct  189  RHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARDFLLETV  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCGS
Sbjct  249  GYFDEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCGS  308
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Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR AL ++ GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  309  AAVLRREALQDSDGFSGVSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ+L+ + PLF+RGL   QRLCY++S  FW FP  R +FL APL YLFF ++I
Sbjct  369  SRWAQGMMQILIFRQPLFKRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  429  FVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPGK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VTAKDE+++E  +S I RP    F L L  +   + R  + P    V LVVGGW +
Sbjct  489  PTFKVTAKDESIAEARLSEISRPFFVIFALLLVAMAFAVWRIYSEPYKADVTLVVGGWNL  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LN++  G AL  V+E+  + A+ R+ ++   E Q+        + T + AS   V +
Sbjct  549  LNLIFAGCALGVVSERGDKSASRRITVKRRCEVQLGG------SDTWVPASIDNVSVHGL  602

Query  621  LPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQP  678
            L  + D    +E G   +++ +P     P  E M    +R+ R E G V +G  F   +
Sbjct  603  LINIFDSATNIEKGATAIVKVKPHSEGVP--ETMPLNVVRTVRGE-GFVSIGCTFSPQRA  659

Query  679  IAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
            +  R  +A LIF  S  W   +    +  GL+ G A  L +A
Sbjct  660  VDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFLAIA  700


>TR:A0ABV1QU59 A0ABV1QU59_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
(Fragment) OS=Methylorubrum podarium OX=200476 GN=bcsA
PE=4 SV=1
Length=745

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 309/709 (44%), Positives = 429/709 (61%), Gaps = 10/709 (1%)

Query  31   LLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLP  90
            +L + PV    Q  ++L+A+  + +L  F D    RF+ L+  S++V+RY  WR+ +TLP
Sbjct  9    ILLSQPVGTQNQLAMSLAAMAAMIVLWLFLDGPRTRFVFLALGSLVVLRYILWRVTDTLP  68

Query  91   PPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYN  150
             P    SF F LLL   E + + I F++  ++ADP  RP P   +  +LPTVD+ VPSYN
Sbjct  69   SPGDPVSFGFGLLLLLGELYCVFILFVSLIINADPLRRPPPPAARAADLPTVDVFVPSYN  128

Query  151  EPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCR  210
            E A +L++TLAAA+ + YP    TV L DDGG+DQ+C  P+PE A+ A+ERRR+L  L
Sbjct  129  EDAAILAMTLAAARQINYPPDKLTVWLLDDGGSDQKCADPNPEKARAARERRRDLTALAE  188

Query  211  ELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLF  270
            +LG  Y TR RNEHAKAGN++  L    GE+VVV DADHVP R FL+ T+GYF +DP LF
Sbjct  189  QLGCRYLTRARNEHAKAGNLNNGLAFATGEIVVVLDADHVPFRSFLSETIGYFAQDPKLF  248

Query  271  LVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALD  330
            LVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W G+FFCGSAA+LRR ALD
Sbjct  249  LVQTPHAFLNPDPIERNLKTFERMPSENEMFYAVTQRGLDKWNGSFFCGSAALLRRTALD  308

Query  331  EAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQM  390
            EAGGF+G TITED ETA E+HSRGW S Y+D+ +IAGLQPET  +FI QR RW  GM Q+
Sbjct  309  EAGGFSGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPETLTAFIGQRSRWCQGMFQI  368

Query  391  LLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLA  450
            LLLKNP  +RGL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF ++IFVA+ +E +A
Sbjct  369  LLLKNPALQRGLKPIQKIAYLSSMTFWFFPVPRLIFMFAPLLHIFFDLKIFVASVDESIA  428

Query  451  YMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDE  510
            Y   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ +  PR   F VT K
Sbjct  429  YTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIVSVIWSPRKPTFNVTDKGV  488
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Query  511  TLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFAL  570
            +L  N++S    P    +LL  +G      R++  PG  +++LVVG W   N+L  G AL
Sbjct  489  SLDHNHLSSASLPFFAVYLLLAAGCAVATWRYLFEPGVTNLMLVVGLWNFFNLLTAGAAL  548

Query  571  RAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTSGVRLLVRLPGVGDPH  628
               AE++Q    P   + +    QI   G R++   +  + A    VRL   L   G  H
Sbjct  549  GVCAERRQLERTP--SLAIDRRGQI-TLGGRAIDVAIERVSAEACTVRLPAALLPAGVGH  605

Query  629  PALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYL  688
             AL   G +   P     P     V   +    R        + F   +P      +A L
Sbjct  606  RALT--GALTVVPVAGARPAGALPV--TLEGIERAKDEAFARLSFGRLRP-QDYVALAGL  660

Query  689  IFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPAR  737
            ++G++   R  +    R   +L G  + +W   +   + AR  +   AR
Sbjct  661  MYGDAEAMRRFQMRRRRHKDILAGTLQFIWWGLSEPVRAARYALTADAR  709


>TR:A0ABW1WXE1 A0ABW1WXE1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylorubrum zatmanii OX=29429 GN=bcsA PE=4 SV=1
Length=800

 Score = 565 bits (1457),  Expect = 0.0
 Identities = 290/597 (49%), Positives = 392/597 (66%), Gaps = 5/597 (1%)

Query  31   LLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLP  90
            +L + PV    Q  ++L+A+  + +L  F D    RF+ L+  S++V+RY  WR+ +TLP
Sbjct  9    VLLSQPVGTQNQLAMSLAAMAAMIVLWLFLDGPRTRFVFLALGSLVVLRYILWRVTDTLP  68

Query  91   PPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYN  150
             P    SF F LLL   E + + I F++  ++ADP  R  P      ELPTVD+ VPSYN
Sbjct  69   SPGDPVSFGFGLLLLVGELYCVFILFVSLIINADPLQRRAPPAAGAAELPTVDVFVPSYN  128

Query  151  EPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCR  210
            E A +L++TLAAA+ M YP    TV L DDGG+DQ+C  P+PE A+ A+ERRR+L  LC
Sbjct  129  EDAAILAMTLAAARQMNYPPDKLTVWLLDDGGSDQKCADPNPEKARAARERRRDLMALCA  188

Query  211  ELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLF  270
            ELG  Y TR RNEHAKAGN++  L    GE+VVV DADHVP R FL+ TVGYF EDP LF
Sbjct  189  ELGCRYLTRARNEHAKAGNLNNGLAFATGEIVVVLDADHVPFRSFLSETVGYFAEDPKLF  248

Query  271  LVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALD  330
            LVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W G+FFCGSAA+LRR ALD
Sbjct  249  LVQTPHAFLNPDPIERNLRTFERMPSENEMFYAVTQRGLDKWNGSFFCGSAALLRRTALD  308

Query  331  EAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQM  390
            EAGGF+G TITED ETA E+HSRGW S Y+D+ +IAGLQPET  +FI QR RW  GM Q+
Sbjct  309  EAGGFSGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPETLTAFIGQRSRWCQGMFQI  368

Query  391  LLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLA  450
            LLLKNP F++GL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF ++IFVA+ +E +A
Sbjct  369  LLLKNPAFQKGLKPIQKIAYLSSMTFWFFPVPRLIFMFAPLLHIFFDLKIFVASVDESIA  428

Query  451  YMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDE  510
            Y   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ +  PR   F VT K
Sbjct  429  YTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIVSVIWSPRKPTFNVTDKGI  488

Query  511  TLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFAL  570
            +L  N++S    P    + L  +G      R++  PG  +++LVVG W + N+L  G AL
Sbjct  489  SLDHNHLSSASLPFFAVYGLLATGCAVAAWRYLFEPGVTNLMLVVGLWNLFNLLTAGAAL  548

Query  571  RAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTSGVRLLVRLPGVG  625
               AE++Q    P + +       +   G+R++   +  + A T  VRL   L   G
Sbjct  549  GVCAERRQLERTPSLPVN---RRGLLTLGDRAVDVAITRVSAETCTVRLPAALLPAG  602


>TR:A0AA37MCD6 A0AA37MCD6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium gregans OX=374424 GN=NBEOAGPD_4365
PE=4 SV=1
Length=800
```

```
 Score = 565 bits (1456),  Expect = 0.0
 Identities = 293/620 (47%), Positives = 395/620 (64%), Gaps = 6/620 (1%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            +L W+ +     +L + PV    Q  ++L+A+  +  L  F D    RF+ L+  S++V+
Sbjct  6    WLAWMGVTAAGLVLLSQPVGTQNQLAMSLAAMAAMIALWLFLDGPRSRFIFLAMGSLVVL  65

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY  WR+ +TLP P    SF F LLL   E + + I F++  ++A+P  R  P      +
Sbjct  66   RYILWRVTDTLPSPGDPVSFGFGLLLLVGELYCVFILFVSLIINAEPLRRRPPPAAPAAD  125

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LP VD+ VPSYNE A +L++TLAAA+ M YP    TV L DDGGTDQ+C  PDPE A  A
Sbjct  126  LPGVDVFVPSYNEDAAILAMTLAAARQMNYPPGKLTVWLLDDGGTDQKCADPDPEKAVSA  185

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            + RR ELQ LC +LG  Y TR RNEHAKAGN++  L   +GE+VVV DADHVP R FL+
Sbjct  186  RARRAELQALCDDLGCRYLTRARNEHAKAGNLNNGLSHARGEIVVVLDADHVPFRSFLSE  245

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF EDP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W G+FFC
Sbjct  246  TVGYFAEDPKLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYSVTQRGLDKWNGSFFC  305

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR ALDEAGGF+G TITED ETA E+HSRGW S Y+D  +IAGLQP+T   FI
Sbjct  306  GSAALLRRTALDEAGGFSGITITEDCETAFELHSRGWTSAYVDTPLIAGLQPDTLTDFIG  365

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RW  GM Q+LLLKNP F+RGL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF +
Sbjct  366  QRSRWCQGMFQILLLKNPAFQRGLKPIQKIAYLSSMTFWFFPVPRLIFMFAPLLHIFFDL  425

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ +  P
Sbjct  426  KIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIVSVIWSP  485

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VT K  TL  +++S +  P    + L  +G       R++  PG  +++LVVG W
Sbjct  486  RKPTFNVTNKGATLEHDHLSSLAAPFFAVYALLATGCAVAAYRYLFEPGVTNLMLVVGLW  545

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTSGVR  616
               N+L  G AL   AE++Q    P + +       +   G R++   V  + A    VR
Sbjct  546  NFFNLLTAGAALGVCAERRQLERMPSLPISRRGHLTL---GGRAVDVAVERVSAEACTVR  602

Query  617  LLVRLPGVGDPHPALEAGGL  636
            +     G G  H  + AG L
Sbjct  603  MPAAALGAGAGHRPI-AGSL  621


>TR:A0A7W8XA59 A0A7W8XA59_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium giardinii OX=56731 GN=GGD55_004610 PE=4
SV=1
Length=728

 Score = 565 bits (1456),  Expect = 0.0
 Identities = 320/733 (44%), Positives = 439/733 (60%), Gaps = 21/733 (3%)

Query  11   LRVVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLL  70
            +R V ++LF  W+   +    L   P+    Q + +++ V  +A++K    +   R   L
Sbjct  1    MRKVAIILF--WIITSLGVIALVTLPINLQTQLIASIAVVTFMAVIKILRAEGTWRLTAL  58

Query  71   SAASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPF  130
            +  + +VMRY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ + P
Sbjct  59   AFGTAIVMRYVYWRTTSTLPPFNQLENFIPGFLLYLAEMYSVMMLGLSLFVVSMPLPPRP  118

Query  131  PRPLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSP  190
             R     + P+VD+ VPSYNE A++L+ TLAAAK M YPA   TV L DDGGT Q+  SP
Sbjct  119  SRAASEGKYPSVDVFVPSYNEDAELLANTLAAAKAMDYPAEKLTVWLLDDGGTLQKRTSP  178
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Query  191  DPELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHV  250
            +    Q A+ R +ELQ LC +L V Y TR+RNEHAKAGN++  ++   GEL+ VFDADH
Sbjct  179  NLLEDQMAKARHQELQILCNDLDVRYLTRDRNEHAKAGNLNNGMQHSTGELIAVFDADHA  238

Query  251  PSRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLD  310
            P+RDFL  TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD
Sbjct  239  PTRDFLLETVGYFEDDPKLFLVQTPHFFLNPDPVERNLRTFEKMPSENEMFYGIIQRGLD  298

Query  311  RWGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQP  370
            +W  +FFCGSAAVLRR+ALD+ GGF+G +ITED ETA+ +H+ GW S+Y+DR +IAGLQP
Sbjct  299  KWNASFFCGSAAVLRRQALDQTGGFSGLSITEDCETAIALHASGWNSVYVDRPLIAGLQP  358

Query  371  ETFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAP  430
             TFASFI QR RWA GMMQ+L  + PL +RGL I QRLCY++S  FW FP  R +FL AP
Sbjct  359  ATFASFIGQRSRWAQGMMQILRFRFPLLKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAP  418

Query  431  LIYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARA  490
            L YLFF +EIF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A
Sbjct  419  LFYLFFDLEIFTASGSEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTIHLLPA  478

Query  491  IVTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRS  550
            +V+ ++ PR   F VTAKDE++  + +S I RP    F + L  VL T  R    P
Sbjct  479  VVSAIVNPRKPSFKVTAKDESVLVSRLSEISRPFFVIFAVLLLAVLVTAYRVYTEPYKAD  538

Query  551  VLLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDA  610
            V LVVGGW +LN+LL G AL  V+E+ +  A  RV++    E        +   AT+ +
Sbjct  539  VTLVVGGWNLLNLLLAGCALGVVSERGELTATRRVKVARRCEF---GLDEQWYPATIDNV  595

Query  611  STSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVG  670
            S +G R+ V    +G     L+  GLI+F P    +   E ++   +R+ +  G  V VG
Sbjct  596  SVNGARVNVYAKNLGT--LPLDKRGLIRFTPY---SSGHEEILPVAVRNTQVAGDIVTVG  650

Query  671  VIFEAGQPIAVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
             ++    P A R+   +A LIF  S  W   + +     GLL G    +W    +L +T+
Sbjct  651  CLY---LPEAARDHSLIADLIFANSQQWTQFQMSRRGNPGLLRG---TIWFLGLALYQTS  704

Query  729  RD---FMDEPARR  738
            R    F   P  R
Sbjct  705  RGIIYFFSSPGAR  717


>TR:A0ABV7LEU7 A0ABV7LEU7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Camelimonas abortus OX=1017184 GN=bcsA PE=4 SV=1
Length=757

 Score = 565 bits (1456),  Expect = 0.0
 Identities = 282/572 (49%), Positives = 377/572 (66%), Gaps = 3/572 (1%)

Query  20   LLWVALLVPFGL---LAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L W+A +V  GL       PV    Q ++ L+ +V +  +  F    + R + L+  ++L
Sbjct  5    LRWLAWMVLGGLTFVFLTLPVGVPIQLVLGLAVIVTMIAVWLFTKGFLSRQIFLALGTLL  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY FWR+  TLPPPA    F+  + L   E + +    +   ++ADP  RP PR +
Sbjct  65   VIRYAFWRITNTLPPPADLPGFIAGVTLLLGELYCVFFLAMTLLINADPLKRPRPRRVPD  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            EELPTVD+ VPSYNE   ML++TL+AA+ M YP    TV L DDGGTDQ+C   DPE A
Sbjct  125  EELPTVDVFVPSYNEDPSMLALTLSAARAMDYPRDKLTVWLLDDGGTDQKCSDRDPEKAA  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
            +A++RR  LQ LC E+G  Y TR RNE AKAGNM+  L+   GELV+V DADHVP R+FL
Sbjct  185  QARQRRATLQALCAEIGARYLTRARNERAKAGNMNNGLQHSSGELVLVLDADHVPFREFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYFV+DP LFLVQTPH F+NPDP+++NL      P ENEMFY    RGLD+W  AF
Sbjct  245  RETVGYFVDDPKLFLVQTPHVFLNPDPVEKNLDTFRFMPSENEMFYSVTQRGLDKWNAAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
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            FCGSAAVLRR AL+ AGGF G TITED ETA E+HSRGW S+Y+D+ M+AGLQPETF+SF
Sbjct  305  FCGSAAVLRRAALETAGGFHGVTITEDCETAFELHSRGWHSIYVDKPMVAGLQPETFSSF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GM Q+L+LKNP F+RGL   QR+ YL+SMSFWFFP+ R++F+  PL+Y+FF
Sbjct  365  IGQRTRWCQGMFQILILKNPAFKRGLSFMQRISYLSSMSFWFFPVPRLIFIFVPLVYIFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             + IFVAT +E +A+   Y+  S ++QN L+ R RWP VSE+YE  Q  +L RAI    +
Sbjct  425  DLRIFVATVDESIAFTFTYMIASLMLQNYLYGRVRWPWVSEMYETLQGMFLVRAIGAVAV  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VT+K++ + E+++S +  P  F F L    ++  + R+   PG  + +++VG
Sbjct  485  NPRKPSFNVTSKNDVMEEDHLSELAWPFFFLFGLLALAMVVVIYRFFTEPGVSAAMIIVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQME  588
             W  LN+++ G  L AVAE++     P + +E
Sbjct  545  LWNALNLMIAGACLGAVAERRTPERPPSLDIE  576


>TR:S3HPC9 S3HPC9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium grahamii CCGE 502 OX=990285 GN=RGCCGE502_00250
PE=4 SV=1
Length=729

 Score = 565 bits (1456),  Expect = 0.0
 Identities = 318/731 (44%), Positives = 438/731 (60%), Gaps = 16/731 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            + W  + +    L   PV    Q + ++  V ++A++K    +   R + L+  + +V+R
Sbjct  8    ITWAIVSLCVIALITLPVNLQTQLIASIVVVAVMAIIKGLKAEGTWRLIALAFGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+  LLL+  E +S+++  L+ F+ A P      R  + E
Sbjct  68   YVYWRTTNTLPPINQPENFIPGLLLYLAEMYSVAMLALSLFIVATPLPPRPSRASKEERF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VD+ VPSYNE + +L+ TLAAAK M YPA    V L DDGGT Q+  S     AQ A
Sbjct  128  PHVDVFVPSYNEDSHLLANTLAAAKAMDYPAERLHVWLLDDGGTLQKRNSNKLLEAQAAM  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  EL++LC +L V Y TR+RNEHAKAGN++  ++   GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHNELRKLCDDLDVRYLTRDRNEHAKAGNLNNGMKHSSGELIAVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFFINPDP++RNL   +R P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFDDDPKLFLVQTPHFFINPDPLERNLRTFERMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL+  GGF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRRALESQGGFSGISITEDCETALALHGSGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PL +RGL + QRLCY++S  FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLLKRGLTVPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +L PR
Sbjct  428  IFTASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVMLNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE+++ + +S I RP    F + L  +  T  R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDESIAVSRLSEISRPFFVIFAVQLVALAVTFYRIYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            ++N+++ G AL  V+E+ +R A+ RV++    E  +   G +  TA++ D S  G RL V
Sbjct  548  IINLIMAGCALGVVSERGERAASRRVRVNRRCEFGV---GGKWYTASIEDVSVHGARLHV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
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                 + DP   + + G I+FQP    + +   ++   +R+ +  G  + VG  +     +
Sbjct  605  FNKQL-DP-MVIGSEGEIRFQPHSGASIETLPLI---VRNIQPSGEILAVGCQYVPKNAL  659

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARD----FMDEP  735
              R  +A LIF  S  W   ++A     GL+ G    +W    SL +T+R     F
Sbjct  660  DHR-LIADLIFANSDQWTQFQQARRHNPGLIRG---TIWFLGLSLYQTSRGLVYLFRSMR  715

Query  736  ARRRRRHEEPK  746
              R R+H+  K
Sbjct  716  PERERQHQAAK  726


>TR:A0A5D4GQK2 A0A5D4GQK2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Neoaquamicrobium microcysteis OX=2682781 GN=bcsA PE=4
SV=1
Length=730

 Score = 565 bits (1455),  Expect = 0.0
 Identities = 321/718 (45%), Positives = 437/718 (61%), Gaps = 20/718 (3%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVAL--LKPFADKMVPRFLLLSAA  73
            +L+ LLW A  V   L+ + P+  + Q  +   AVVL A+  LK        R + L+
Sbjct  4    LLIVLLWAAAAVMVLLIVSLPI--NLQTHLIAGAVVLTAMMTLKLVGAGGTWRLIALALG  61

Query  74   SMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRP  133
            + +VMRY +WR   TLPP +   +F+  LLL+  E +S+ +  L+ F+ A P
Sbjct  62   TAIVMRYVYWRTTSTLPPVSQLENFIPGLLLYLAEMYSVFMLALSLFIVAKPLPSRPSIS  121

Query  134  LQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPE  193
            +  E+LPTVD+ +P+YNE   +L+ T+AAA+ M YP    TV L DDGGT Q+  + +
Sbjct  122  VAEEDLPTVDVFIPTYNEEPSLLADTIAAAQAMDYPKDRFTVWLLDDGGTVQKRNADNVV  181

Query  194  LAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSR  253
             AQ+A+ER  ELQ+LC +LG  Y TRERNEHAKAGN++  L    G L+ VFDADH P+R
Sbjct  182  AAQEAEERHAELQKLCADLGANYLTRERNEHAKAGNLNNGLAHSTGALIAVFDADHAPAR  241

Query  254  DFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWG  313
             FL  TVGYF EDP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W
Sbjct  242  SFLRETVGYFNEDPKLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWN  301

Query  314  GAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETF  373
             +FFCGSAAVL R+AL+E  GF+G +ITED ETA+E+HSRGW S+Y+D+ +IAGLQP TF
Sbjct  302  ASFFCGSAAVLNRKALEETQGFSGISITEDCETAVELHSRGWNSVYVDKPLIAGLQPTTF  361

Query  374  ASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIY  433
            ASFI QR RWA GMMQ+L  + P  +RGL + QRLCY++S  FW FP  R +FL APL Y
Sbjct  362  ASFIGQRSRWAQGMMQILRFRFPPLKRGLSLPQRLCYMSSTLFWLFPFPRTIFLFAPLFY  421

Query  434  LFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVT  493
            LFF ++IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+
Sbjct  422  LFFDLQIFTASGGEFLAYTLSYMVVNLMMQNYLYGNFRWPWISELYEYIQSVHLLPAVVS  481

Query  494  TLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLL  553
             +L PR   F VTAKDE++S + +S + RP    F + L GV  T  R  A P    V L
Sbjct  482  VMLNPRKPTFKVTAKDESVSTSRLSELSRPFFVIFAVLLVGVAVTAWRVYAEPWKADVTL  541

Query  554  VVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFG--NRSLTATVLDAS  611
            VVGGW +LN++L G AL  V+E+++  A  RV++    E     FG   + L AT+ D S
Sbjct  542  VVGGWNLLNLILAGCALGVVSERREWTATRRVKVNRRCE-----FGQDGQWLPATIEDVS  596

Query  612  TSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
             +G R  VR+ G        +    ++F    P +     M+   IR++ ++G  VM+G
Sbjct  597  VNGAR--VRVYGKNVQPLIAQGHANLRF---IPQSGGERAMLPIDIRNSEKDGEGVMIGC  651

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             +    P   R  VA LIF  +  W   +    R  G+L G    +W    S  +T R
Sbjct  652  RYIRSAPEHHR-LVADLIFANAEQWTQFQHTRRRNPGVLLG---TVWFLRLSFFQTWR  705
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>TR:A0ABW4M9L3 A0ABW4M9L3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium helianthi OX=1132695 GN=bcsA PE=4 SV=1
Length=720

 Score = 565 bits (1455),  Expect = 0.0
 Identities = 315/715 (44%), Positives = 432/715 (60%), Gaps = 15/715 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LWVA+ +    L   PV    Q +++++ V ++ALLK        R + L+    +V R
Sbjct  8    VLWVAMAICVIGLITLPVNLQTQLILSVTVVTIMALLKILGIGGRWRLVALAFGMAIVWR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR  ETLPP    A+F+  LLL+  E +S+ +  L+ F+ A P      R    +
Sbjct  68   YVYWRTTETLPPINQPANFIPGLLLYLAEIYSVMMLALSLFIVAMPLPSRPSRAAAQKTF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVD+ +P+YNE A +LS TLAAAK M YPA   TV L DDGGT Q+  + D   +  A
Sbjct  128  PTVDVFIPTYNEDAVLLSNTLAAAKAMDYPADRLTVWLLDDGGTVQKRNATDVRESAAAV  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R ++L +LC+ LGV Y TRERNEHAKAGN++  L    GELV VFDADH P+RDFL  T
Sbjct  188  ARHKQLTELCQALGVNYLTRERNEHAKAGNLNNGLRHSTGELVAVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF EDP LFLVQTPHFF+NPDP++RNL   +R P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFEEDPKLFLVQTPHFFLNPDPLERNLRTFERMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL R+AL+   GF+G +ITED ETALE+HS GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRKALETTKGFSGLSITEDCETALELHSAGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL + QR CY++S  FW FP  R +FL+APL YLFF +E
Sbjct  368  RSRWAQGMMQILRYRMPLFKRGLSMPQRFCYMSSTLFWLFPFPRTIFLIAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ +L P+
Sbjct  428  IFTASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEFVQTIHLLPAVISVMLNPK  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++  + +S I RP    F + +  ++ T+ R    P    V LVVG W
Sbjct  488  KPTFKVTAKDESVFVSRLSEISRPFFIIFAIQIIALIVTVYRIYTEPYKADVTLVVGAWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            ++N++L G AL  V+E+ ++ ++ RV+++   E      G++   A++ D S  G  L V
Sbjct  548  LINLILAGCALGVVSERGEKSSSRRVRVQRRCEF---GTGDQWYAASIEDVSVGGAGLQV  604

Query  620  RLPGVGDPHPALEAGGLIQFQP--KFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
                +    P  +A   I+F+P     +   L  +VRG        G   ++G  +
Sbjct  605  FGRDLASLAPGTDAA--IRFRPHGSTDETVTLPLVVRG----ITNAGDVSLLGCQYRPRS  658

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
            P   R  +A LIF  SA W   ++      G+L G    +W    SL +T+R  +
Sbjct  659  PQDHR-WIADLIFANSAQWAEFQKGRRYNPGILRG---TIWFLGLSLYQTSRGLL  709


>TR:A0A125Q599 A0A125Q599_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium altiplani OX=1864509 GN=AS026_17135 PE=4
SV=1
Length=729

 Score = 565 bits (1455),  Expect = 0.0
 Identities = 319/731 (44%), Positives = 440/731 (60%), Gaps = 16/731 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            + W  + +   +L   PV    Q + +   V ++A++K    +   R + L+  + +V+R
Sbjct  8    ITWAFVSLCVIVLITLPVNLQTQLIASFVVVAVMAIIKGLKAEGTWRLIALAFGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
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            Y +WR   TLPP     +F+  LLL+  E +S+++  L+ F+ A P      R  + E
Sbjct  68   YVYWRTTNTLPPINQPENFIPGLLLYLAEMYSVAMLALSLFIVATPLPPRPSRASKEERF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VD+ VPSYNE + +L+ TLAAAK M YPA    V L DDGGT Q+  S     AQ A
Sbjct  128  PHVDVFVPSYNEDSHLLANTLAAAKAMDYPAERLHVWLLDDGGTLQKRNSNKLLEAQAAV  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  EL++LC +L V Y TR+RNEHAKAGN++  +++  GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHDELKKLCEDLDVRYLTRDRNEHAKAGNLNNGMKQSSGELIAVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFFINPDP++RNL   +R P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFDDDPKLFLVQTPHFFINPDPLERNLRTFERMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL+  GGF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRRALESQGGFSGISITEDCETALALHGSGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PL +RGL + QRLCY++S  FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLLKRGLTLPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +L PR
Sbjct  428  IFTASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVMLNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE+++ + +S I RP    F + L  +  T+ R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDESIAVSRLSEISRPFFVIFAVQLIALAVTIYRIYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            V+N+++ G AL  V+E+ +R A+ RV++    E  +   G +  TA++ D S  G RL V
Sbjct  548  VINLIMAGCALGVVSERGERAASRRVRVNRRCEFGV---GGKWYTASIEDVSVHGARLHV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
                + DP   +   G I+FQP    + +   ++   +R+ +  G  + VG  +   + +
Sbjct  605  FNKQL-DP-MVIGTEGEIRFQPHSGASMETLPLI---VRNIQPSGEILAVGCQYIPKRAL  659

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARD----FMDEP  735
              R  +A LIF  S  W   ++A     GL+ G    +W    SL +T+R     F
Sbjct  660  DHR-LIADLIFANSDQWTQFQQARRHNPGLIRG---TIWFLGLSLYQTSRGLVYLFRSTR  715

Query  736  ARRRRRHEEPK  746
            + R R H+  K
Sbjct  716  SERERPHQVAK  726


>TR:A0ABU7TZN9 A0ABU7TZN9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium oryzae OX=334852 GN=bcsA PE=4 SV=1
Length=804

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 311/735 (42%), Positives = 437/735 (59%), Gaps = 17/735 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L +L WV   V    L + PV   AQ  ++L+A+  + +L    D    RF+ ++  S++
Sbjct  13   LRWLAWVGATVASLALLSQPVGTQAQLAMSLAAMAAMIVLWAVFDGPRTRFVFMALGSLV  72

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY  WRL  TLP P    SF F L+L   E + + I F++  ++ADP  R  P
Sbjct  73   VLRYILWRLTNTLPSPGDPVSFGFGLILLVAELYCVFILFVSLIINADPLRRDPPPAAPA  132

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             +LP VD+ VPSYNE A +L++TLAAA+ + YP    TV L DDGGTDQ+C   DP  A
Sbjct  133  ADLPAVDVFVPSYNEDASILAMTLAAARQLNYPPDKLTVWLLDDGGTDQKCSDADPAKAA  192

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A+ RR ELQ LC ELG  Y TR RNEHAKAGN++  L   +G+LV V DADHVP R FL
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Sbjct  193  AARARRGELQALCDELGARYLTRARNEHAKAGNLNNGLAHARGDLVAVLDADHVPFRSFL  252

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF +DP LFLVQTPH F+NPDP++RNL   +R P ENEMFY    RGLD+W G+F
Sbjct  253  TETVGYFAQDPRLFLVQTPHAFLNPDPVERNLRTFERMPSENEMFYAVTQRGLDKWNGSF  312

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRR ALDEAGGF+G TITED ETA E+H+RGW S Y+D+ +IAGLQP+T   F
Sbjct  313  FCGSAALLRRTALDEAGGFSGITITEDCETAFELHARGWTSAYVDKPLIAGLQPDTLTDF  372

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GM Q+LLLKNP+F++GL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF
Sbjct  373  IGQRSRWCQGMFQILLLKNPVFQKGLKPIQKIAYLSSMTFWFFPIPRLIFMFAPLLHIFF  432

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YLA+AIV+ +
Sbjct  433  DLKIFVASVDESIAYTLTYIIINLMIQNYVYGKFRWPFVSELYEYIQGVYLAKAIVSVIA  492

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VT K  TL  ++IS +  P    +LL + G      R++  PG  +++LVVG
Sbjct  493  SPRKPTFNVTNKGATLDHDHISSLALPFFLIYLLLMLGCAVAAWRYLYEPGVTNLMLVVG  552

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTSG  614
             W   N+L  G +L   AE++Q    P + ++      +      S+  ++  + A
Sbjct  553  LWNFFNLLTAGASLGVCAERRQLERTPSLPID---RRGVLTLSGHSVDVSIERVSAEACT  609

Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            +R L      G   P L   G +  +P      +    +   +  A R+G  +++ V F
Sbjct  610  LRFLSGALDQGLTRPPLR--GTLGVEP--TAGARRTAPLPVHLDQATRDGQELVMRVTFG  665

Query  675  AGQPIAVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
            A   +AVR+   +A L++G++   R  +    R   +  G  +  W       +  R  +
Sbjct  666  A---LAVRDYPALAGLMYGDAEAMRRFQLRRRRHKDIPTGTLQFAWWGLVEPFRALRYLL  722

Query  733  DEPARRRRRHEEPKE  747
               A RR R  E +E
Sbjct  723  ---ASRRPRPVEIEE  734


>TR:A0A9X3KGF6 A0A9X3KGF6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium leguminum OX=2792015 GN=bcsA PE=4 SV=1
Length=729

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 323/717 (45%), Positives = 434/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            L  ++W  LLV   +LA   +  S Q  +  +A+  +L+A +K F  +   R + L   +
Sbjct  5    LTIIVW--LLVSLCVLAIVTMPVSLQTHLVATAISLILLATIKSFNGQGAWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P+  PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPDYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362
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Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L L  +     R  + P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFALLLVAMAFAAWRIYSEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++       + A++ + S  G
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SEAWVPASIDNVSVHG  601

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
              LL+ L    D    +E G   +++ +P     P  E M    +R+ + E G V +G
Sbjct  602  --LLINL---FDSATTIEKGATAIVKVKPHSEGVP--ETMPVNVVRTVKGE-GFVSIGCT  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + +  R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  654  FSPQRAVDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706


>TR:A0A1I5KM00 A0A1I5KM00_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Cohaesibacter marisflavi OX=655353 GN=SAMN04488056_11476
PE=4 SV=1
Length=734

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 307/717 (43%), Positives = 433/717 (60%), Gaps = 13/717 (2%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            + +F +WV  +V F ++   P+    Q + +L    L+A+LK        R + L+
Sbjct  6    IQVFFVWVLSVVAFLIITTMPINLQTQLICSLVVFTLMAILKLLKKNGSLRIISLTFGLS  65

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPT-DRPFPRPL  134
            ++ RY FWR  ET+P P    +F+  LLL+  E +++    L+ F+ + P   RP
Sbjct  66   IIARYVFWRTTETIPSPNQIENFIPGLLLYIAEMYNVLTLLLSLFVVSRPLPSRPSCELP  125

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
                LPTVD+ VPSYNEPAD+L  TLAAAK M YPA   TV L DDGGT ++  S D
Sbjct  126  SHNRLPTVDVFVPSYNEPADILGNTLAAAKAMDYPAEKVTVWLLDDGGTLEKRNSSDILK  185

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            A  A++R  +LQ+LC EL V Y TRERNEHAKAGN++  LE   G+LV +FDADH P+R+
Sbjct  186  ANAARKRHEDLQKLCAELDVRYLTRERNEHAKAGNLNYGLEHSTGDLVAIFDADHAPARE  245

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVG+F +D  LFLVQTPHFFINPDP++RNL      P ENEMFYG I RGLD+W
Sbjct  246  FLTETVGHFSKDSKLFLVQTPHFFINPDPLERNLKTFSFMPSENEMFYGIIQRGLDKWNA  305

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            +FFCGSAAVLRR AL+E GGF+G+TITED E+AL +H++GW S+YID+ +IAGLQP TFA
Sbjct  306  SFFCGSAAVLRREALEETGGFSGKTITEDCESALSLHAKGWNSVYIDKPLIAGLQPATFA  365

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GM+Q++    PLF+ GL + QRLCYL+SM FWFFP+ R +FL AP  Y+
Sbjct  366  SFIGQRSRWAQGMIQLMRYNFPLFKSGLSLPQRLCYLSSMMFWFFPISRTIFLFAPFCYI  425

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IF A+  + +AY   Y+ V+ ++QN L+   RWP +SE+YE +Q  +L  A+++
Sbjct  426  FFDLKIFEASGGDFMAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYSQTIHLLPAVLSA  485

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            ++ P    F VTAKDE+++ N +S I RP    F   L  V  ++ +  A P    V LV
Sbjct  486  IINPSKPSFNVTAKDESITSNRLSEINRPFFVVFFAILLAVAFSIYKIYAEPYKADVTLV  545
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Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW + N++L G AL  V+E+ +R+ A R+ +    E     +G+     ++ + S  G
Sbjct  546  VGGWNIFNLILAGCALGVVSERGERQGARRISVSRSCEF---LYGDSWHECSIDNVSIHG  602

Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
              L + P    P    +A G I+F        + +  +  ++R+ R+ G  +++G  F+
Sbjct  603  AALHIYEPDF--PEIKRDAIGKIRFT---KHDGENKASLSIKVRNVRQSGDRLILGSAFK  657

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDF  731
               P      +A L+F  S  W     +  +  G++ G    +W  A SL +T R F
Sbjct  658  PESP-KDYSAIADLVFANSRQWTDFMRSRRKNPGIVSG---TVWFLALSLRQTLRGF  710


>TR:A0A7L5BLW1 A0A7L5BLW1_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium oryzihabitans OX=2267833 GN=bcsA PE=4 SV=1
Length=729

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 324/717 (45%), Positives = 436/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  VL+A +K F  +   R + L   +
Sbjct  5    ITIIVW--LLVSLCVLAIITMPVSLQTHLVATAISLVLLATIKSFNGQGAWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P+  PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPDYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L +  +   + R  + P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFALLVVAMAFAIWRIYSEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++    +  + A++ + S  G
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SDAWVPASIENVSVHG  601

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
              LL+ L    D   A+E     +++ +P     P  E M    +R+ R E G V +G
Sbjct  602  --LLINL---FDNATAIEKNTTAIVKVKPHSEGVP--ETMPINVVRTVRGE-GFVSIGCT  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + I  R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  654  FSPQRAIDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706
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>TR:A0AA37H9T5 A0AA37H9T5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium frigidaeris OX=2038277 GN=MPEAHAMD_1812
PE=4 SV=1
Length=819

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 299/642 (47%), Positives = 399/642 (62%), Gaps = 27/642 (4%)

Query  13   VVPVLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +V  L +L W+        L + PV    Q  ++L+A+  +A L    D    RF+ L+
Sbjct  1    MVRALRWLAWMGTTAAGLALLSQPVGTQNQLAMSLAAMAAMAGLWLVFDGPRTRFVFLAM  60

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             S++V+RY  WR+ +TLP P    SF F LLL   E + + I F++  ++A+P  R  P
Sbjct  61   GSLVVLRYILWRVTDTLPSPGDPVSFGFGLLLLLCELYCVFILFVSLIINAEPLRRRPPA  120

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
             +   +LP VD+ VPSYNE A++L++TLAAA+ M YP    TV L DDGGTDQ+C  PDP
Sbjct  121  AVPAADLPHVDVFVPSYNEDAEILAMTLAAARQMNYPPEKLTVWLLDDGGTDQKCADPDP  180

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
            E A+ A+ RRRELQ LC +L   Y TR RNEHAKAGN++  L    G+LV+V DADHVP
Sbjct  181  EKAEGARARRRELQALCADLDARYLTRARNEHAKAGNLNNGLASATGDLVLVLDADHVPF  240

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            R  L  TVGYF EDP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY     GLD+W
Sbjct  241  RSLLTETVGYFAEDPKLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYAVTQAGLDKW  300

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
             G+FFCGSAA+LRR ALDEAGGFAG TITED ETA E+HSRGW S Y+D+ +IAGLQP+T
Sbjct  301  NGSFFCGSAALLRRTALDEAGGFAGITITEDCETAFELHSRGWTSAYVDKPLIAGLQPDT  360

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
             A FI QR RW  GM Q+LLLKNP  +RGL   Q+L YL+SM+FWFFP+ R++F+ APL+
Sbjct  361  LADFIGQRSRWCQGMFQILLLKNPALQRGLKPIQKLAYLSSMTFWFFPIPRLVFMFAPLL  420

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            ++FF ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV
Sbjct  421  HIFFDLKIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIV  480

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +  PR   F VT K  TL  +++S +  P    + L L+G L    R++  PG  +++
Sbjct  481  SVIWSPRKPTFNVTNKGATLDHDHLSALSLPFFAVYGLLLTGCLVAAWRYLFEPGVTNLM  540

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAP----------------------RVQME--  588
            LVVG W + N+L  G AL   AE++Q    P                      RV  E
Sbjct  541  LVVGLWNLFNLLTAGAALGVCAERRQLERTPSLAVNRRGQLTLGGRAVDVAIERVSAEAC  600

Query  589  ---VPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDP  627
               +PA    P  G+R +  T+     +G R    LP V  P
Sbjct  601  TVRMPAAFLAPGAGHRPVPGTLTVVPVAGARPAGALPVVLGP  642


>TR:A0ABT0CTE6 A0ABT0CTE6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella sedimenti OX=2919913 GN=bcsA PE=4 SV=1
Length=722

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 315/710 (44%), Positives = 429/710 (60%), Gaps = 13/710 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V  +A++K    + + R + L+  + +V+R
Sbjct  8    VLWACVSALVILVITLPINLQTQLVASIAVVTFMAVIKVLRAEGIWRLIALAFGTAIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P           E L
Sbjct  68   YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVALPLPSRKGSVTPLERL  127
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Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE   +L+ TLAAAK M YPA   T+ L DDGGT+Q+  +     AQ A
Sbjct  128  PSVDVFVPSYNEDIGLLANTLAAAKAMDYPADKMTIWLLDDGGTEQKRNAAAVVEAQVAT  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  ELQ LCR+LGV Y TR RNEHAKAGNM+  +   KGEL+ +FDADH P+RDFL  T
Sbjct  188  ARHAELQALCRDLGVNYLTRARNEHAKAGNMNNGMLHSKGELIAIFDADHAPARDFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +FFCG
Sbjct  248  VGYFADDPKLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNASFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRTALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+ GL + QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKSGLSLPQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428  IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE+++   +S I RP    F +     L ++ R+ A P    V  VVG W
Sbjct  488  KPTFKVTAKDESIAVARLSEISRPFFVIFAVLFVAFLMSIYRFYAEPYKADVTFVVGAWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E+ ++ A+ RV   V       + G R   AT+ + S +G R  V
Sbjct  548  LLNLLIAGCALGVVSERSEKAASRRV--TVKRRCTFLSDG-REYPATLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+ D H A  A G +QF+P   D    E  +   IR+    G  +++G  F   Q
Sbjct  603  QVFGLED-HIATGAEGALQFKPYGGDH---EEALPVEIRNTETAGNVMVIGCRF-TPQDA  657

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                 VA LIF  S  W   + +     G+  G     LW    +  +T+R
Sbjct  658  RHHSLVADLIFANSNQWSDFQVSRRYNPGIFRG---TLWFLGIAAYQTSR  704


>TR:A0A9W5B551 A0A9W5B551_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium genomosp. 2 str. CFBP 5494 OX=1183436
GN=AGR2A_Lc50046 PE=4 SV=1
Length=729

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 321/717 (45%), Positives = 434/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  +L+A +K F  + V R + L   +
Sbjct  5    ITIIVW--LLVSLCVLAIITMPVSLQTHLVATAISLILLATIKGFNGQGVWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P       RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P   PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPTYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNAANIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302
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Query  315   AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
             AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303   AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375   SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
             SFI QR RWA GMMQ+L+ + PLF+RGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363   SFIGQRSRWAQGMMQILIFRQPLFKRGLTFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435   FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
             FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423   FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495   LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
             +  P    F VTAKDE+++E  +S I RP    F L +  ++  + R  + P    V LV
Sbjct  483   IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFGLLVVAMIFAVWRIYSEPYKADVTLV  542

Query  555   VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
             VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++        + T + AS
Sbjct  543   VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG------SDTWVPASIDN  596

Query  615   VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
             V +   L  + D    +E G   +++ +P     P  E M    +R+ R E G + +G
Sbjct  597   VSVHGLLINLFDNATTVEKGETAIVRVKPHSEGVP--ETMPLNIVRTVRGE-GFISIGCT  653

Query  673   FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             F   + +  R  +A LIF  S  W   +    R  GL+ G A  L   A SL +T R
Sbjct  654   FSPQRAVDHR-LIADLIFANSEQWSEFQRVRRRNPGLIRGTATFL---AISLFQTQR  706


>TR:A0ABY9KA08 A0ABY9KA08_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella oryzae OX=2871820 GN=bcsA PE=4 SV=1
Length=722

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 314/710 (44%), Positives = 430/710 (61%), Gaps = 13/710 (2%)

Query  20    LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
             +LW  +     L+   P+    Q + +++ V  +A++K    + + R + L+  + +V+R
Sbjct  8     ILWACVSALVILVITLPINLQTQLVASIAVVTFMAVIKVLRAEGIWRLIALAFGTAIVLR  67

Query  80    YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
             Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P           E L
Sbjct  68    YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVALPLPSRKGSVTPLERL  127

Query  140   PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
             P+VD+ VPSYNE   +L+ TLAAAK M YPA   T+ L DDGGT+Q+  +     AQ A
Sbjct  128   PSVDVFVPSYNEDIGLLANTLAAAKAMDYPADKMTIWLLDDGGTEQKRNAAAVVEAQIAT  187

Query  200   ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
              R  ELQ LCR+LGV Y TR RNEHAKAGNM+  +   KGEL+ +FDADH P+RDFL  T
Sbjct  188   ARHAELQALCRDLGVNYLTRARNEHAKAGNMNNGMLHSKGELIAIFDADHAPARDFLRET  247

Query  260   VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
             VGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +FFCG
Sbjct  248   VGYFADDPKLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNASFFCG  307

Query  320   SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
             SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308   SAAVLRRTALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380   RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
             R RWA GMMQ+L  + PLF+RGL + QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368   RSRWAQGMMQILRFRFPLFKRGLSLPQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440   IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
             IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428   IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500   SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
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               F VTAKDE+++   +S I RP    F +     L ++ R+ A P    V  VVG W
Sbjct  488  KPTFKVTAKDESIAVARLSEISRPFFVIFAVLFIAFLMSIYRFYAEPYKADVTFVVGAWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E+ ++ A+ RV   V       + G R   AT+ + S +G R  V
Sbjct  548  LLNLLIAGCALGVVSERSEKAASRRV--TVKRRCTFLSEG-REYPATLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+ D H A  A G ++F+P      + E  +   IR+    G  +++G  F   Q
Sbjct  603  QVFGLED-HIATGAEGALRFKPY---GGEHEEALPVEIRNTETTGNVMVIGCRF-TPQDA  657

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                 VA LIF  S  W   + +     G+  G    LW    +  +T+R
Sbjct  658  RHHSLVADLIFANSNQWSDFQVSRRYNPGIFRG---TLWFLGIAAYQTSR  704


>TR:A0AA44IYU6 A0AA44IYU6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium pusense OX=648995 GN=bcsA PE=4 SV=1
Length=729

 Score = 564 bits (1454),  Expect = 0.0
 Identities = 321/717 (45%), Positives = 434/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  +L+A +K F  + V R + L   +
Sbjct  5    ITIIVW--LLVSLCVLAIITMPVSLQTHLVATAISLILLATIKGFNGQGVWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P   PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPTYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNAANIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLF+RGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFKRGLTFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L +  ++  + R  + P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFGLLVVAMIFAVWRIYSEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++        + T + AS
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG------SDTWVPASIDN  596

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            V +   L  + D    +E G   +++ +P     P  E M    +R+ R E G + +G
Sbjct  597  VSVHGLLINLFDNATTVEKGETAIVRVKPHSEGVP--ETMPLNIVRTVRGE-GFISIGCT  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + +  R  +A LIF  S  W   +    R  GL+ G A  L   A SL +T R
```

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Sbjct  654  FSPQRAVDHR-LIADLIFANSEQWSEFQRVRRRNPGLIRGTATFL---AISLFQTQR  706


>TR:A0ABY8RR92 A0ABY8RR92_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium cucumeris OX=2862866 GN=bcsA PE=4 SV=1
Length=729

 Score = 564 bits (1453),  Expect = 0.0
 Identities = 324/711 (46%), Positives = 432/711 (61%), Gaps = 17/711 (2%)

Query  23   VALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            V LLV   +LA   +  S Q  +  +A+  VL+A +K F  +   R + L   + +V+RY
Sbjct  9    VWLLVSLCVLAIVTMPVSLQTHLVATAISLVLLATIKGFNGQGAWRLVALGFGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P+  P
Sbjct  69   VYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPGSPDYRP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  S +   AQ AQ
Sbjct  129  TVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNSSNIVEAQAAQR  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            R  EL+QLC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RDFL  TV
Sbjct  189  RHEELKQLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARDFLLETV  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCGS
Sbjct  249  GYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCGS  308

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  309  AAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ+L+ + PLF+RGL   QRLCY++S  FW FP  R +FL APL YLFF ++I
Sbjct  369  SRWAQGMMQILIFRQPLFKRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  429  FVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPGK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
              F VTAKDE+++E  +S I RP    F L +  +   + R  + P    V LVVGGW +
Sbjct  489  PTFKVTAKDESIAEARLSEISRPFFVIFALLVVAMAFAIWRIYSEPYKADVTLVVGGWNL  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LN++  G AL  V+E+  + A+ R+ ++   E ++    +  + A++ + S  G  LL+
Sbjct  549  LNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SDAWVPASIDNVSVHG--LLIN  605

Query  621  LPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQP  678
            L    D    +E     +++ +P     P  E M    +R+ R E G V +G  F   +
Sbjct  606  L---FDSATTVEKNTTAIVKVKPHSEGVP--ETMPVKVVRTVRGE-GLVSIGCTFSPQRA  659

Query  679  IAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +  R  +A LIF  S  W   +    R  GL+ G A  L   A SL +T R
Sbjct  660  VDHR-LIADLIFANSEQWSEFQRVRRRNPGLIRGTAIFL---AISLFQTQR  706


>TR:A0A1S7U1W9 A0A1S7U1W9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium deltaense NCPPB 1641 OX=1183425 GN=AGR7A_Lc130049
PE=4 SV=1
Length=729

 Score = 564 bits (1453),  Expect = 0.0
 Identities = 322/717 (45%), Positives = 435/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  +L+A +K F  +   R + L   +
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Sbjct  5    ITIIVW--LLVSLCVLAIVTMPVSLQTHLVATAISLILLATIKSFNGQGAWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP 
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P+  PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +   
Sbjct  123  SPDYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ 
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L L  +     R  + P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFALLLVAMAFAAWRIYSEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++    +  + A++ + S  G
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SDAWVPASIDNVSVHG  601

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
              LL+ L    D    +E G   +++ +P     P  E M    +R+ + E G V +G 
Sbjct  602  --LLINL---FDSATTIEKGATAIVKVKPHSEGVP--ETMPVNVVRTVKGE-GFVSIGCT  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + +  R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  654  FSPQRAVDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706


>TR:A0A2U8W9W9 A0A2U8W9W9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium durans OX=2202825 GN=bcsA PE=4 SV=1
Length=795

 Score = 564 bits (1453),  Expect = 0.0
 Identities = 288/605 (48%), Positives = 393/605 (65%), Gaps = 5/605 (1%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            +L+W+        +L + PV    Q  ++L+A+  +  L  F D    RF+ L+  S++V+
Sbjct  6    WLVWMGTTAAGLVLLSQPVGTQNQLAMSLAAMAAMIGLWLFLDGPRTRFVFLAMGSLVVL  65

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY  WR+  TLP P    SF F LLL   E + + I F++  ++ADP  R  P P +  E
Sbjct  66   RYILWRVTNTLPSPGDPVSFGFGLLLLLGELYCVFILFVSLIINADPLRRRPPTPQRAAE  125

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LPTVD+ VPSYNE A +L++TLAAA+ M YP    TV L DDGGTDQ+C   D   A+ A
Sbjct  126  LPTVDVFVPSYNEDASILAMTLAAARQMNYPPEKLTVWLLDDGGTDQKCADADRGKAEAA  185

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            + RR +L+ LC ELG  Y TRERN HAKAGN++  L +  G++VVV DADHVP R FL  
Sbjct  186  RARRAQLKALCAELGARYLTRERNLHAKAGNLNNGLAQASGDIVVVLDADHVPFRSFLRE  245
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Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF EDP LFLVQTPH F+NPDP++RNL   +R P ENEMFY    RGLD+W G+FFC
Sbjct  246  TVGYFAEDPRLFLVQTPHAFLNPDPVERNLRTFERMPSENEMFYAVTQRGLDKWNGSFFC  305

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR ALDEAGGF+G TITED ETA E+H+RGW S Y+D+ +IAGLQP+T A FI 
Sbjct  306  GSAALLRRAALDEAGGFSGITITEDCETAFELHARGWTSAYVDKPLIAGLQPDTLADFIG  365

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RW  GM Q+LLLKNP  + GL   Q++ YL+SM+FWFFP+ R+ F+ APL+++FF +
Sbjct  366  QRSRWCQGMFQILLLKNPALKAGLKPIQKIAYLSSMTFWFFPMPRLAFMFAPLLHIFFDL  425

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVA+  E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AI + +L P
Sbjct  426  KIFVASVAESIAYTATYIIINLMMQNYVYGKFRWPFVSELYEYIQGLYLSKAIASVILSP  485

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VT+K  +L  +++SP+  P    + L L+G      R++  PG  +++LVVG W
Sbjct  486  RKPTFNVTSKGASLDHDHLSPLALPFFAVYALLLAGCAVAGWRYLFEPGVTNLMLVVGLW  545

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
               N+L  G AL   AE++Q    P + ++      + + G R++  +V   S  G  L 
Sbjct  546  NFFNLLTAGAALGVCAERRQLERMPSLPVD---RRGVLSLGGRAVDVSVTRVSAEGCTL-  601

Query  619  VRLPG  623
             RLPG
Sbjct  602  -RLPG  605


>TR:A0A6N6MVW7 A0A6N6MVW7_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium planeticum OX=2615211 GN=bcsA PE=4
SV=1
Length=795

 Score = 564 bits (1453),  Expect = 0.0
 Identities = 285/604 (47%), Positives = 390/604 (65%), Gaps = 5/604 (1%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            +L W+       LL + PV    Q  ++L+A+  + +L  F D    RF+ L+  S++V+
Sbjct  7    WLAWMGTTAAGLLLLSQPVGTGNQLAMSLAAMAAMIVLWLFLDGPRTRFVFLAMGSLVVL  66

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY  WR+  TLP PA   SF F LLL   E + + I F++  ++ADP  RP P      +
Sbjct  67   RYILWRVTSTLPSPADPVSFGFGLLLLVGELYCVFILFVSLIINADPLRRPPPPAAPAGD  126

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LP+VD+ VP+YNE A +L++TLAAA+ M YP    T+ L DDGGTDQ+C  PDP  A+ A
Sbjct  127  LPSVDVFVPTYNEDAAILAMTLAAARQMSYPPEKLTIWLLDDGGTDQKCADPDPRKAEAA  186

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            + RR  L  LC + G  Y TRERN HAKAGN++  L +  GE+VVVFDADHVP R FL  
Sbjct  187  RRRRAALTALCADHGARYLTRERNLHAKAGNLNNGLAQATGEIVVVFDADHVPFRSFLRE  246

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            T+GYF +DP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W G+FFC
Sbjct  247  TIGYFAQDPRLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYAVTQRGLDKWNGSFFC  306

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR ALDEAGGF+G TITED ETA E+H+RGW S Y+D+ +IAGLQP+T A FI 
Sbjct  307  GSAALLRREALDEAGGFSGITITEDCETAFELHARGWTSAYVDKPLIAGLQPDTLADFIG  366

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RW  GM Q+LLLKNP F+ GL   Q+L YL+SM+FWFFP+ R++F+ APL+++FF +
Sbjct  367  QRSRWCQGMFQILLLKNPAFQTGLKPIQKLAYLSSMTFWFFPVPRLIFMFAPLLHIFFDL  426

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ ++ P
Sbjct  427  KIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYIQGLYLSKAIVSVMVSP  486
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Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VT K   L  +++S +  P    + L  +G      R++  PG  +++LVVG W
Sbjct  487  RKPTFKVTNKGANLDHDHLSSLALPFFAVYALLFAGCAVAAWRYLFEPGVTNLMLVVGLW  546

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
               N+L  G AL   AE++QR   P + ++      +   G R++   +   S     L
Sbjct  547  NFFNLLTAGAALGVCAERRQRERTPSLPID---RRGVLTLGGRAVDVAIERVSAEACTL-  602

Query  619  VRLP  622
             RLP
Sbjct  603  -RLP  605


>TR:A0ABQ4SLE8 A0ABQ4SLE8_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium isbiliense OX=315478 GN=GMJLKIPL_4517
PE=4 SV=1
Length=810

 Score = 563 bits (1452),  Expect = 0.0
 Identities = 321/728 (44%), Positives = 433/728 (59%), Gaps = 25/728 (3%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            +L W+       LL + PV    Q  ++L+A+ ++  L  F D    RF+ L+  S++V+
Sbjct  7    WLAWMITTAAGLLLLSQPVGTLNQLAMSLAAMAVMIGLWLFLDGPRTRFVFLAMGSLVVL  66

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY  WR+  TLP P     F F LLL A E +   I FL+  ++A+P  R  P PL P +
Sbjct  67   RYMLWRVTSTLPSPGDPVDFGFGLLLLAGELYCAFILFLSLIINAEPLRRRTP-PLGPAQ  125

Query  139  -LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
             LP VD+ VPSYNE A +L++TLAAA+ + YPA   TV L DDGGTDQ+C  PDPE
Sbjct  126  ALPRVDVFVPSYNEDASILALTLAAARQLDYPADRLTVWLLDDGGTDQKCADPDPEKRAA  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            AQ RR +LQ+LC +LG  Y TR  N HAKAGN++  L    G+LV VFDADH P R FL
Sbjct  186  AQARRADLQRLCADLGARYLTRPTNRHAKAGNLNNGLAHATGDLVAVFDADHAPFRAFLR  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVGYF +DP LFLVQTPH F+NPDPI+RNL    R P ENEMFY     GLD+W G+FF
Sbjct  246  ETVGYFAQDPRLFLVQTPHAFLNPDPIERNLRTFARMPSENEMFYAVTQCGLDKWNGSFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAA+LRR ALDEAGGF+G TITED ETALE+H+RGW S+Y+D+ +IAGLQPET A  I
Sbjct  306  CGSAALLRRSALDEAGGFSGITITEDCETALELHARGWNSVYVDKPLIAGLQPETLADLI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RW  GM Q+LLLKNPL++RGL   QRL YL+SM+FWFFP+ R++F+ APL+++FF
Sbjct  366  GQRSRWCQGMFQILLLKNPLWQRGLTPIQRLAYLSSMTFWFFPVPRLIFMFAPLLHIFFD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            ++IFVA+ EE +AY   Y+ ++ ++QN ++ + RWPL+SE+YE  Q  YL RAIV+ L+
Sbjct  426  LKIFVASIEESIAYTATYIVINLMMQNYMYGKFRWPLISELYEYIQGLYLFRAIVSVLVS  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR+  F VT K  +L  +++S +  P    + L L G +    R++  PG   ++LVVG
Sbjct  486  PRTPTFNVTRKGVSLDHDHLSAVSAPFFAVYGLLLVGGVVAGWRYLFEPGVTDLMLVVGL  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG--V  615
            W + N+L  G AL   AE++Q   AP + +       + A   R L   +   S  G  +
Sbjct  546  WNLFNLLTAGAALGVCAERRQSEKAPSLPI---GRRGVLALEGRVLDVGIERVSAEGCTI  602

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAP------QLERMVRGRIRSARREGGTVMV  669
            RL   L   G  H  +   G +  +P     P       L ++ R R  + R    +
Sbjct  603  RLAAGLLAPGAGHRPM--AGELTVEPVEGARPGGSLPVTLVQVARSREDAVCR----LAF  656

Query  670  GVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            G +     P      +A L++G+S   R  +    R   LL G+    W       +  R
Sbjct  657  GALRSRDYP-----ALAGLMYGDSDAMRRFQLRRRRHKDLLSGLLHFAWWGLVEPLRAVR  711
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Query  730  D-FMDEPA  736
              F+ EPA
Sbjct  712  TLFLPEPA  719


>TR:A0ABV2NCP4 A0ABV2NCP4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium radiotolerans OX=31998 GN=ABIC20_001565
PE=4 SV=1
Length=648

 Score = 563 bits (1452),  Expect = 0.0
 Identities = 282/578 (49%), Positives = 379/578 (66%), Gaps = 0/578 (0%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            L +L WV   V    L + PV   AQ  ++L+A+ ++ +L    D    RF+ ++  S++
Sbjct  5    LRWLAWVGATVASLALLSQPVGTQAQLAMSLAAMAVMIVLWAVLDGPRTRFVFMALGSLV  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY  WRL  TLP P    SF F L+L   E + + I F++  ++ADP  R  P
Sbjct  65   VLRYILWRLTNTLPLPGDPVSFGFGLILLVAELYCVFILFVSLIINADPLRRDPPPAAPA  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
             +LPTVD+ VPSYNE   +L++TLAAA+ + YP    TV L DDGGTDQ+C   DP  A
Sbjct  125  ADLPTVDVFVPSYNEDTSILAMTLAAARQLNYPPDKLTVWLLDDGGTDQKCSDADPAKAA  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             A+ RR ELQ LC ELG  Y TR RNEHAKAGN++  L + +G+LV V DADHVP R FL
Sbjct  185  AARARRGELQALCDELGARYLTRARNEHAKAGNLNNGLAQARGDLVAVLDADHVPFRSFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF +DP LFLVQTPH F+NPDP++RNL   +R P ENEMFY    RGLD+W G+F
Sbjct  245  TETVGYFAQDPRLFLVQTPHAFLNPDPVERNLRTFERMPSENEMFYAVTQRGLDKWNGSF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAA+LRR ALDEAGGF+G TITED ETA E+HSR W S Y+D+ +IAGLQP+T A F
Sbjct  305  FCGSAALLRRTALDEAGGFSGITITEDCETAFELHSRNWTSAYVDKPLIAGLQPDTLADF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RW  GM Q+LLLKNP+F++GL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF
Sbjct  365  IGQRSRWCQGMFQILLLKNPVFQKGLKPIQKIAYLSSMTFWFFPIPRLIFMFAPLLHIFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YLA+AIV+ +
Sbjct  425  DLKIFVASVDESIAYTLTYIVINLMIQNYVYGKFRWPFVSELYEYIQGVYLAKAIVSVIA  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             PR   F VT K  TL  ++IS +  P    +LL + G      R++  PG  +++LVVG
Sbjct  485  SPRKPTFNVTNKGATLDHDHISSLALPFFLIYLLLMLGCAVAAWRYLYEPGVTNLMLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQ  594
             W   N+L  G +L   AE++Q    P +    P   Q
Sbjct  545  LWNFFNLLTAGASLGVCAERRQLERTPSLGDRSPRGPQ  582


>TR:W6RJE0 W6RJE0_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium favelukesii OX=348824 GN=celA PE=4 SV=1
Length=730

 Score = 563 bits (1452),  Expect = 0.0
 Identities = 313/710 (44%), Positives = 433/710 (61%), Gaps = 12/710 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            + W  + +    L   PV    Q + ++  V ++A++K    +   R + L+  + +V+R
Sbjct  8    ITWAFVSLCVIALITLPVNLQTQLIASIVVVAVMAIIKGLKAEGTWRLIALAFGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+  LLL+  E +S+++  L+ F+ A P      R  + E
Sbjct  68   YVYWRTTSTLPPINQPENFIPGLLLYLAEMYSVAMLALSLFIVATPLPPRPSRASKEERF  127
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Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VD+ VPSYNE + +L+ TLAAAK M YPA    V L DDGGT Q+  S     AQ A
Sbjct  128  PHVDVFVPSYNEDSHLLANTLAAAKAMDYPAERLHVWLLDDGGTLQKRNSNKLLEAQAAA  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  EL++LC +LGV Y TR+RNEHAKAGN++  ++   GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHNELKKLCEDLGVRYLTRDRNEHAKAGNLNNGMKHSSGELIAVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFFINPDP++RNL   +R P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFDDDPKLFLVQTPHFFINPDPLERNLRTFERMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL+  GGF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRRALESQGGFSGISITEDCETALALHGSGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PL +RGL + QRLCY++S  FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLLKRGLTLPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +L PR
Sbjct  428  IFTASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVMLNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE+++ + +S I RP    F + L  ++ T+ R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDESIAVSRLSEISRPFFVIFAVQLIALVVTIFRIYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            ++N+++ G AL  V+E+ +R A+ RV++    E  +     +  TA++ D S  G RL V
Sbjct  548  IINLIMAGCALGVVSERGERAASRRVRVNRRCEFGV---NGKWHTASIEDVSVHGARLHV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
                + DP   + A G I+FQP    + +   ++   +R+ +  G  + VG  +     +
Sbjct  605  FNKQL-DP-MVIGAEGEIRFQPHSGASIETLPLI---VRNIQPSGEILAVGCQYSPKNAL  659

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
              R  +A L+F  S  W   ++A     GL+ G    +W    SL +T+R
Sbjct  660  DHR-LIADLMFANSDQWTQFQQARRHNPGLIRG---TIWFLGLSLYQTSR  705


>TR:A0A0B4XAZ2 A0A0B4XAZ2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium gallicum bv. gallicum R602sp OX=1041138
GN=RGR602_PC01129 PE=4 SV=1
Length=729

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 316/708 (45%), Positives = 430/708 (61%), Gaps = 12/708 (2%)

Query  22   WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYW  81
            W  + +   +L   PV    Q + +++ V ++A++K    +   R + L+  + +V+RY
Sbjct  10   WAIVSLCVFVLITLPVNLQTQLIASITVVTIMAMIKILKGEGTWRLIALAFGTAVVLRYA  69

Query  82   FWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPT  141
            +WR   TLPP     +F+  LLL+  E +SI++  L+ F+ A P      RP++ E  P
Sbjct  70   YWRTTSTLPPVNQLENFIPGLLLYLAEMYSIAMLALSLFIVATPLPPRRSRPVKQERFPH  129

Query  142  VDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQER  201
            VD+ VP+YNE A +L  TLAAAK + YPA    V L DDGGT Q+  S     AQ A  R
Sbjct  130  VDVFVPTYNEDAHLLGNTLAAAKAIDYPADKLQVWLLDDGGTLQKRNSNKLLEAQAAIAR  189

Query  202  RRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVG  261
              EL+QLC  L V Y TR+RNEHAKAGN++  ++   GEL+ VFDADH P+RDFL  TVG
Sbjct  190  HNELRQLCEALSVNYLTRDRNEHAKAGNLNNGMQHSTGELIAVFDADHAPARDFLRETVG  249

Query  262  YFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSA  321
            YF +DP LFLVQTPHFFINPDP++RNL   DR P ENEMFYG I RGLD+W  AFFCGSA
Sbjct  250  YFDDDPKLFLVQTPHFFINPDPLERNLRTFDRMPSENEMFYGIIQRGLDKWNAAFFCGSA  309
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Query  322  AVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRG  381
            AVL RRAL    GF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  310  AVLSRRALQSTNGFSGLSITEDCETALALHGAGWNSIYVDKPLIAGLQPATFASFIGQRS  369

Query  382  RWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIF  441
            RWA GMMQ+L  + PL +RGL I QRLCY++S  FW FP  R +FL APL YLFF +EIF
Sbjct  370  RWAQGMMQILRFRFPLLKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLEIF  429

Query  442  VATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSA  501
             A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ ++ PR
Sbjct  430  TASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVISVMINPRKP  489

Query  502  RFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVL  561
             F VTAKDE++S + +S I RP    F + +  +  T+ R  A P    V LVVGGW +
Sbjct  490  TFKVTAKDESISVSRLSEISRPFFVIFAVQIIALAITIYRIYAEPYKADVTLVVGGWNLF  549

Query  562  NVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRL  621
            N+++ G AL  V+E+ +R A+ RV++    E  +     +  TA++ D S  G RL V
Sbjct  550  NLIMAGCALGVVSERGERAASRRVRVNRRCEFGV---NGKWHTASIEDVSVHGARLHVFN  606

Query  622  PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAV  681
              + DP   + A G I+F+P       LE +    +R+  ++G  + VG  +     +
Sbjct  607  KQL-DP-MTIGAEGEIRFRPY--SGADLETLPL-IVRNMEQDGDIMAVGCQYIPKSALDH  661

Query  682  RETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            R  +A LIF  S  W   +E+  R  GL+ G    +W    SL +T+R
Sbjct  662  R-LIADLIFANSDQWAQFQESRRRNPGLIRG---TIWFLGLSLYQTSR  705


>TR:A0A068T187 A0A068T187_NEOGA Cellulose synthase catalytic subunit [UDP-forming]
OS=Neorhizobium galegae bv. orientalis str. HAMBI 540
OX=1028800 GN=RG540_PA05640 PE=4 SV=1
Length=719

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 309/710 (44%), Positives = 427/710 (60%), Gaps = 11/710 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +      +   PV    Q +++++ V+++  LK        R + L+    +V+R
Sbjct  8    ILWTIMAACVVSVITLPVNLQTQLIVSVTVVIIMGGLKLLKSDGRWRLVALAFGVSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR  ETLPP     +F+  +LL+  E ++I + FL+ F+ A P      R  Q +
Sbjct  68   YAYWRTTETLPPINQPENFIPGMLLYLAEMYNILMLFLSLFIVAMPLASRPSRAGQQKTF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VD+ +PSYNE A +L+ T+AAAK M YPA    V L DDGGT Q+  S D   ++ A
Sbjct  128  PAVDVFIPSYNEDAMLLANTIAAAKAMDYPADRLRVWLLDDGGTLQKRNSADVRESETAV  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R   L  LCR+LG  Y TRERNEHAKAGN++  L   +G+L+ VFDADH P+RDFL  T
Sbjct  188  ARHALLSDLCRQLGANYLTRERNEHAKAGNLNNGLAHSQGQLIAVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF EDP LFLVQTPHFF+NPDP++RNL   +R P ENEMFYG I RGLD+W  +FFCG
Sbjct  248  VGYFEEDPKLFLVQTPHFFLNPDPLERNLRTFERMPSENEMFYGIIQRGLDKWNASFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL+   GF+G +ITED ETALE+HS GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRRALETTNGFSGMSITEDCETALELHSTGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + P  + GL I QR CY++S  FW FP  R +FL+APL Y+FF +E
Sbjct  368  RSRWAQGMMQILRFRMPFLKSGLSIPQRFCYMSSTLFWLFPFPRTIFLIAPLFYIFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ ++ PR
Sbjct  428  IFTASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEFVQTVHLLPAVVSVMVNPR  487
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Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++S N +S I RP    F + +  V+ T+ +    P    V LVVGGW
Sbjct  488  KPTFKVTAKDESVSVNRLSEISRPFFVIFAVQIVAVIMTIFKIYTEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            ++N++L G AL  V+E+ ++ ++ R+++    E  +         A++ D S  G  L V
Sbjct  548  IINLILAGCALGVVSERGEKSSSRRIRVRRRCEFGVE---GSWYPASIEDVSVGGAGLQV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
                +    P  EA  +++F+P   D  Q   ++   IR A+  G TV VG  +     +
Sbjct  605  FGKQLSSIRPGAEA--VLRFRPH--DEQQELALLPIVIRGAQSSGDTVQVGCQYRPRDAL  660

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
              R  +A L+F  SA W   + +  R  GL+ G    LW    SL +T+R
Sbjct  661  DHR-WIADLLFANSAQWAEFQTSRRRNPGLVRG---TLWFLGLSLYQTSR  706


>TR:A0ABU0MCJ3 A0ABU0MCJ3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Kaistia geumhonensis OX=410839 GN=QO015_004291 PE=4
SV=1
Length=730

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 324/741 (44%), Positives = 445/741 (60%), Gaps = 21/741 (3%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            ++  L+W    V   +L   P+   A  +     V  + LLK F  + V R + L+  +
Sbjct  4    IVYALVWALAAVVMTILITLPINLQAHLVAGAVVVGAMILLKLFTRQGVWRQIALALGTS  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP      F+  LL++  E +SI + FL+ F+   P     PR L+
Sbjct  64   IVLRYAYWRTTSTLPPINQPEDFIPGLLVYLAEMYSIFMLFLSLFVVMRPMA---PRTLK  120

Query  136  PE----ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
                  +LPTVD+ VP+YNE   +L+ TLA+AK M YPA   TV L DDGGT Q+  S +
Sbjct  121  VSSSDPDLPTVDVFVPTYNEEPALLATTLASAKAMDYPADKLTVWLLDDGGTVQKRNSEN  180

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
             E AQ+A++R  ELQ+L  +LG  Y TRE+NEHAKAGNM+  L+   G+L+ VFDADH P
Sbjct  181  IEAAQEAEDRYIELQKLAADLGCRYLTREKNEHAKAGNMNNGLKVSTGDLIAVFDADHAP  240

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
            +RDFL  TVGYF + P LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+
Sbjct  241  ARDFLTYTVGYFQQIPKLFLVQTPHFFLNPDPIERNLRTFETMPSENEMFYGIIQRGLDK  300

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            W  +FFCGSAAVL+R ALD+ GGF+G +ITEDAETALE+H+ GW S+Y+DR +IAGLQP
Sbjct  301  WDASFFCGSAAVLKREALDQTGGFSGISITEDAETALELHATGWSSVYVDRPLIAGLQPA  360

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            TF SFI QR RWA GMMQ+L  + P  +RGL I QRLCY++S  FW FP+ R +FL+APL
Sbjct  361  TFTSFIGQRSRWAQGMMQILRFRFPPGKRGLSIPQRLCYMSSTLFWLFPITRWIFLLAPL  420

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
             YLF  +EIF A+  E +AY   Y+ V+ ++QN L+ R RWP +SE+YE  Q  YL  A+
Sbjct  421  CYLFLDLEIFTASGGEFVAYTSSYMLVNLMMQNYLYGRFRWPWISELYEFVQGVYLLPAL  480

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
            ++ +L P    F VTAK+E+L +  +S + RP    F + L+GV  T+ R  A P    V
Sbjct  481  ISVILNPSKPTFKVTAKNESLDKARLSELARPFYIIFFVLLAGVFMTIWRIYAEPYKADV  540

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDAS  611
             LVVGGW +LN+L+ G AL  ++E+Q+ R + R+ +    E  I   G+R +  TV DAS
Sbjct  541  ALVVGGWNLLNILIAGCALGVISERQENRQSRRIDVRRRCELVI---GDRIVPGTVEDAS  597

Query  612  TSGVRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
              G RL +      D    + A   ++F+    D P  +  +  R  +   +G  V++G
Sbjct  598  VGGARLNITGLTPKDVERGMTAS--LRFKTSV-DIPTRDLPITMRTIAPGSKG--VILGC  652
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Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR--  729
             +E       R  ++ LIF  S  W   +      IG+L G    +W    S+ +T R
Sbjct  653  RYEPTVADHYR-LISDLIFSSSDQWSKFQWNRRVNIGILRG---TIWFVGLSVYQTGRGL  708

Query  730  DFMDEPARRRRRHEEPKEKQA  750
             ++ +  RR R      EK+A
Sbjct  709  GYLLQSLRRDRGAAVAAEKRA  729


>TR:A0A6L3T0K5 A0A6L3T0K5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium soli OX=553447 GN=bcsA PE=4 SV=1
Length=807

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 285/604 (47%), Positives = 393/604 (65%), Gaps = 5/604 (1%)

Query  19   FLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVM  78
            +L W+       +L + PV    Q  ++L+A+V + LL  F D    RF+ L+  S++V+
Sbjct  7    WLAWMGTTAAGLVLLSQPVGTQNQLAMSLAAMVAMILLWLFLDGPRTRFVFLAMGSLVVL  66

Query  79   RYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEE  138
            RY  WR+  TLP PA   SF F  LL   E + + I F++  ++ADP  RP P      +
Sbjct  67   RYILWRVTSTLPSPADPVSFGFGCLLLVGELYCVFILFVSLIINADPLRRPPPPVAAAAD  126

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
            LP VD+ VP+YNE A +L++TLAAA+ M YP    T+ L DDGGTDQ+C   DPE A+ A
Sbjct  127  LPKVDVFVPTYNEDASILAMTLAAARQMSYPPDKLTIWLLDDGGTDQKCADADPEKAEAA  186

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            + RR  LQ LC +LG  Y TRERN HAKAGN++  L    G++VVVFDADHVP R FL
Sbjct  187  RRRRVALQALCADLGARYLTRERNLHAKAGNLNNGLAHAAGDIVVVFDADHVPFRSFLRE  246

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF +DP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY    RGLD+W G+FFC
Sbjct  247  TVGYFAQDPRLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYAVTQRGLDKWNGSFFC  306

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAA+LRR+ALDEAGGF+G TITED ETA E+H+RGW S Y+D+ +IAGLQP+T   FI
Sbjct  307  GSAALLRRQALDEAGGFSGITITEDCETAFELHARGWTSAYVDKPLIAGLQPDTLTDFIG  366

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RW  GM Q+LLLKNP+ ++GL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF +
Sbjct  367  QRSRWCQGMFQILLLKNPVLQKGLKPIQKVAYLSSMTFWFFPVPRLIFMFAPLLHIFFDL  426

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            +IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ +L P
Sbjct  427  KIFVASVDESIAYTATYIVINLMMQNYVYGKFRWPFVSELYEYIQGLYLSKAIVSVILSP  486

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
            R   F VT K  TL  +++S +  P    + L  +G      R++  PG  +++LVVG W
Sbjct  487  RKPTFNVTNKGATLDHDHLSSLTLPFFAVYALLFAGCAVAAWRYLFEPGVTNLMLVVGLW  546

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             + N+L  G AL   AE++Q   +P + ++      +   G R++   V   S     L
Sbjct  547  NLFNLLTAGVALGVCAERRQLERSPSLPID---RRGVLTLGGRAVDVAVERVSAEACTL-  602

Query  619  VRLP  622
             R+P
Sbjct  603  -RMP  605


>TR:A0ABQ4TDV6 A0ABQ4TDV6_METOR Cellulose synthase catalytic subunit [UDP-forming]
OS=Methylobacterium organophilum OX=410 GN=bcsA PE=4
SV=1
Length=803

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 304/707 (43%), Positives = 428/707 (61%), Gaps = 13/707 (2%)
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Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V+ +L W+   +   +L + PV    Q  ++L+A+  + +L  F D    RF+ L+  S+
Sbjct  3    VIRWLAWMGTTIAGLILLSQPVGTQNQLFMSLAAMAAMTILWLFFDGPRTRFVFLALGSL  62

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY  WRL +TLP P    SF F LLL   E + + I F++  ++ADP  R  P
Sbjct  63   VVLRYILWRLTDTLPSPGDPVSFGFGLLLLLGELYCVFILFVSLIINADPLRRRPPPVAD  122

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
               LPTVD+ VPSYNE   +L++TLAAA+ M YP    TV L DDGGTDQ+C  P+PE A
Sbjct  123  AAALPTVDVFVPSYNEDTAILAMTLAAARQMNYPPEKLTVWLLDDGGTDQKCADPNPEKA  182

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
              A++RRR+LQ LC ELG  Y TR RNEHAKAGN++  L    GE+V+V DADHVP R
Sbjct  183  AAARDRRRDLQALCAELGARYLTRARNEHAKAGNLNNGLASASGEIVLVLDADHVPFRSL  242

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVG+F EDP LFL+QTPH F+NPDPI+RNL    R P ENEMFY     GLD+W G+
Sbjct  243  LTETVGHFAEDPRLFLIQTPHAFLNPDPIERNLRTFTRMPSENEMFYAVTQCGLDKWNGS  302

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAA+LRR ALDEA GF+G TITED ETALE+HSRGW S Y+D+ +IAGLQPE+ ++
Sbjct  303  FFCGSAALLRRTALDEANGFSGITITEDCETALELHSRGWTSAYVDKPLIAGLQPESLSA  362

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RW  GM Q+LLLKNPLF+RGL   Q++ YL+SM+FWFFP+ R+ F+ APL+++F
Sbjct  363  FIGQRSRWCQGMFQILLLKNPLFKRGLKPIQKIAYLSSMTFWFFPVPRLAFMFAPLLHIF  422

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL +AI + +
Sbjct  423  FDLKIFVASVDESIAYTATYIIINLMMQNYVYGKFRWPFVSELYEYIQGLYLFKAIASVI  482

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              P+   F VT K   L  N++S    P +  + +  +G      R++  PG  +++LVV
Sbjct  483  WSPKKPTFNVTDKGIALDHNHLSSAALPYVIVYGVLFAGCAVATWRYLFEPGVTNLMLVV  542

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATV--LDASTS  613
            G W   N+L  G AL   AE++Q  A P + +       +   G R++   V  + A
Sbjct  543  GLWNFFNLLTAGAALGVCAERRQSEATPSLAINRRGTLTL---GGRAVDVAVERVSAQAC  599

Query  614  GVRLLVRL--PGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGV  671
             +RL   L  PG G   P   + G++  +     +P+   ++   +    R G      +
Sbjct  600  SIRLPTALLAPGAGQ-KPMTGSLGVVPIK----GSPRPTGLLPVTLDEVERSGDEAFCRL  654

Query  672  IFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILW  718
             F   +P     T+A L++G++   R  +    R   +L G  + +W
Sbjct  655  TFGRLRPQDYM-TLAGLMYGDAEAMRRFQLRRRRHKDILTGTLQFIW  700


>TR:A0A561QSG9 A0A561QSG9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Neorhizobium alkalisoli OX=528178 GN=FHW37_104603
PE=4 SV=1
Length=723

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 314/728 (43%), Positives = 435/728 (60%), Gaps = 9/728 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V+   +W A      LL   P+    Q + ++  V++++++K    +   R + LS  ++
Sbjct  4    VISAAIWAAASAMIALLVTLPINTRTQLIASIMVVLVMSIIKLLNAEGKWRLVALSFGTV  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V RY +WR   TLPP     +F+  LL++  E +S+ +  L+ F+ A P
Sbjct  64   MVFRYVYWRTTNTLPPVNQLENFIPGLLVYLAEMYSVVMLGLSLFVVAMPLTPRKAGDRN  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              ELPTVD+ VPSYNE   +L+ TLAAA+NM YP    TV L DDGGT Q+  S +   A
Sbjct  124  KGELPTVDVFVPSYNEDEVLLANTLAAARNMDYPPEKLTVWLLDDGGTVQKRKSANVADA  183
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Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            + A+ R   L+QLC ELGV Y TRERNEHAKAGN++  L    G+L+ VFDADH P+RDF
Sbjct  184  RAAEARYNSLRQLCEELGVKYLTRERNEHAKAGNLNNGLAHSTGDLIAVFDADHAPTRDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TV +F ++P LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  A
Sbjct  244  LLETVHFFEKEPKLFLVQTPHFFLNPDPVERNLRTFEKMPSENEMFYGIIQRGLDKWNAA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVL R+AL+ + GF+G +ITED ETAL++H  GW S+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLNRKALEVSNGFSGVSITEDCETALDLHGLGWHSIYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L  + P  +RGL   QRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILRFRFPPLKRGLSFPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF ++  E L Y   Y+ V+ L+QN L+   RWP +SE+YE  Q  +L  A+V+ +
Sbjct  424  FDLEIFTSSGGEFLVYSLTYMVVNMLMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVM  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            L P    F VTAKDE++S + +S I RP    F + +   + ++ R    P    V LVV
Sbjct  484  LNPSKPTFKVTAKDESVSVSRLSEISRPFFVIFCVLVIAFIMSVYRVYTEPYKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+++ G AL  V+E+ +R+++ R+++    E  +    +R  TAT+ D S  G
Sbjct  544  GGWNLLNIIIAGCALGVVSERGERQSSRRIRVSRRCEFGV---DDRWFTATIEDVSVHGS  600

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
             + V   G  D   A+   GLI+FQP F D P  E  V   IR+    G    +G  +
Sbjct  601  AMQVYTEGFKD--LAVGKRGLIRFQP-FSDLPVSELPV--EIRNFESLGDVTTMGCRYTP  655

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEP  735
             +P   R  +A LIF  S+ W   + +  +  GLL G    L +AA    +    F+ +
Sbjct  656  EKPTDHR-LIADLIFANSSQWTQFQTSRRKNPGLLRGTIWFLGLAAYQTTRGLAYFLKDL  714

Query  736  ARRRRRHE  743
             R R  +E
Sbjct  715  GRSRAGNE  722


>TR:A0A7W7YUP6 A0A7W7YUP6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella fusca OX=544480 GN=HNQ66_002039 PE=4 SV=1
Length=722

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 316/715 (44%), Positives = 428/715 (60%), Gaps = 17/715 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V  +A++K    +   R + L+  + +V+R
Sbjct  8    ILWALVSALVILVITLPINLQTQLVASIAVVTFMAVIKVLRAEGTWRLIALAFGTAVVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   L++  E +S+ +  L+ F+ A P      R      L
Sbjct  68   YVYWRTTSTLPPVNQLENFIPGFLVYLAEMYSVMMLALSLFVVAMPMPPRKSRTAVDGRL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE   +L+ TLAAAK M YPA   TV L DDGGT+Q+  +     AQ A
Sbjct  128  PSVDVFVPSYNEDTALLANTLAAAKAMDYPADKLTVWLLDDGGTEQKRNAASVVEAQTAG  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R RELQ LC +LGV Y TR RNEHAKAGNM+  ++   GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHRELQALCHDLGVNYLTRARNEHAKAGNMNNGMQHSTGELIAVFDADHAPARDFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFADDPKLFLVQTPHFFLNPDPLERNLRTFETMPSENEMFYGIIQRGLDKWNAAFFCG  307
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Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRAALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL  +QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKRGLSPSQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+++ +L P
Sbjct  428  IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVISVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++  + +S I RP    F +     L ++ R+ + P    V  VVGGW
Sbjct  488  KPTFKVTAKDESIRVSRLSEISRPFFVIFAVLFVAFLMSIYRFYSEPYKADVTFVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E+ +R A+ RV ++         FG R   AT+ + S  G R+ V
Sbjct  548  LLNLLIAGCALGVVSERSERAASRRVTIKRRCSF---VFGGRDYPATLENVSAHGARMQV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
               G+    P + A   ++F    P   + E  +   IR+    G  V +G  F    P
Sbjct  605  F--GLETEAP-VGATAELRF---VPYGAEHEEALPVDIRNHENLGNVVAIGCRF---MPE  655

Query  680  AVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
              R    VA LIF  S  W   + +     GL+ G    LW    +L +T+R  +
Sbjct  656  IARHHALVADLIFANSNQWSDFQVSRRSNPGLVRG---TLWFLGIALYQTSRGLL  707


>TR:A0ABD5LD58 A0ABD5LD58_AGRRD Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium radiobacter OX=362 GN=bcsA PE=4 SV=1
Length=729

 Score = 563 bits (1451),  Expect = 0.0
 Identities = 322/711 (45%), Positives = 433/711 (61%), Gaps = 17/711 (2%)

Query  23   VALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAASMLVMRY  80
            V LLV   +LA   +  S Q  +  +A+  +L+A +K F  +   R + L   + +V+RY
Sbjct  9    VWLLVSLCVLAIVTMPVSLQTHLVATAISLILLATIKSFNGQGAWRLVALGFGTAIVLRY  68

Query  81   WFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELP  140
             +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P+  P
Sbjct  69   VYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPGSPDYRP  128

Query  141  TVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQE  200
            TVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +   AQ AQ
Sbjct  129  TVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVEAQAAQR  188

Query  201  RRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTV  260
            R  EL++LC EL V Y TRERN HAKAGN++  L    GELV VFDADH P+RDFL  TV
Sbjct  189  RHEELKKLCEELDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARDFLLETV  248

Query  261  GYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGS  320
            GYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAFFCGS
Sbjct  249  GYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAFFCGS  308

Query  321  AAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQR  380
            AAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI QR
Sbjct  309  AAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFASFIGQR  368

Query  381  GRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEI  440
             RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLFF ++I
Sbjct  369  SRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFFDLQI  428

Query  441  FVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRS  500
            FVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +  P
Sbjct  429  FVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVIFNPGK  488

Query  501  ARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAV  560
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              F VTAKDE+++E  +S I RP    F L +  +   + R  + P    V LVVGGW +
Sbjct  489  PTFKVTAKDESIAEARLSEISRPFFVIFALLVVAMAFAVWRIYSEPYKADVTLVVGGWNL  548

Query  561  LNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVR  620
            LN++  G AL  V+E+  + A+ R+ ++   E ++    +  + A++ + S  G  LL+
Sbjct  549  LNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SDAWVPASIDNVSVHG--LLIN  605

Query  621  LPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQP  678
            L    D    +E G   +++ +P     P  E M    +R+ + E G V +G  F   +
Sbjct  606  L---FDSATNIEKGATAIVKVKPHSEGVP--ETMPVNVVRTVKGE-GFVSIGCTFSPQRA  659

Query  679  IAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            +  R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  660  VDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706


>TR:A0A0J6TFL2 A0A0J6TFL2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
(Fragment) OS=Methylobacterium tarhaniae OX=1187852 GN=VQ03_01590
PE=4 SV=1
Length=745

 Score = 563 bits (1450),  Expect = 0.0
 Identities = 317/726 (44%), Positives = 427/726 (59%), Gaps = 30/726 (4%)

Query  32   LAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPP  91
            L + PV    Q  ++L+A+  +A L    D    RF+ L+  S++V+RY  WR+ +TLP
Sbjct  10   LLSQPVGTQNQLAMSLAAMAAMAGLWLLFDGPRARFVFLAMGSLVVLRYILWRVTDTLPS  69

Query  92   PALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNE  151
            P    SF F LLL   E + + I F++  ++A+P  R  P      +LP+VD+ VPSYNE
Sbjct  70   PGDPVSFGFGLLLLLCELYCVFILFVSLIINAEPLRRRPPAAAPAADLPSVDVFVPSYNE  129

Query  152  PADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRE  211
             A++L++TLAAA+ M YP    TV L DDGGTDQ+C  P+PE A  AQ RRRELQ LC E
Sbjct  130  DAEILAMTLAAARQMNYPPEKLTVWLLDDGGTDQKCADPNPEKAAAAQARRRELQALCAE  189

Query  212  LGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFL  271
            LG  Y TR RNEHAKAGN++  L    G+LV+V DADHVP R  L  TVGYF EDP LFL
Sbjct  190  LGARYLTRARNEHAKAGNLNNGLASATGDLVLVLDADHVPFRSLLNETVGYFAEDPKLFL  249

Query  272  VQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDE  331
            VQTPH F+NPDPI+RNL    R P ENEMFY     GLD+W G+FFCGSAA+LRR ALDE
Sbjct  250  VQTPHAFLNPDPIERNLRTFQRMPSENEMFYAVTQAGLDKWNGSFFCGSAALLRRAALDE  309

Query  332  AGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQML  391
            AGGFAG TITED ETA E+HSRGW S Y+DR +IAGLQP+T A FI QR RW  GM Q+L
Sbjct  310  AGGFAGITITEDCETAFELHSRGWTSAYVDRPLIAGLQPDTLADFIGQRSRWCQGMFQIL  369

Query  392  LLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAY  451
            LLKNP  +RGL   Q+L YL+SM+FWFFP+ R+ F+ APL+++FF ++IFVA+ +E +AY
Sbjct  370  LLKNPALQRGLKPIQKLAYLSSMTFWFFPIPRLAFMFAPLLHIFFDLKIFVASVDESIAY  429

Query  452  MPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDET  511
               Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL++AIV+ +  PR   F VT K  T
Sbjct  430  TATYIVINLMMQNYVYGKFRWPFVSELYEYVQGLYLSKAIVSVIWSPRKPTFNVTNKGAT  489

Query  512  LSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALR  571
            L  +++S +  P    + L L+G L    R++  PG  +++LVVG W + N+L  G AL
Sbjct  490  LDHDHLSALSLPFFAVYGLLLTGCLVAAWRYLFEPGVTNLMLVVGLWNLFNLLTAGAALG  549

Query  572  AVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPAL  631
              AE++Q    P   + +    Q+   G R++   +     S     VR+P       AL
Sbjct  550  VCAERRQLERTP--SLTINRRGQL-TLGGRAVDVAI--ERVSAEACTVRMPA------AL  598

Query  632  EAGGLIQFQPKFPDAPQLERMVRGRIRSARREGG-TVMVGVIFEAGQPIAVR--------  682
             A G  Q        P    +    +  AR  G   V++G +  +G     R
Sbjct  599  LAAGAGQ-------RPIPGTLTVVPVAGARPAGALPVILGPVTRSGADAVCRLAFGTLRT  651

Query  683  ---ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPARRR  739
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                 +A L++G++      +    R   L  G  + +W   A   +  R  +   ARR
Sbjct  652  QDYVALAGLMYGDAEAMLRFQLRRRRHKDLFTGTLQFVWWGLAEPVRALRYALAGEARRP  711

Query  740  RRHEEP  745
               E P
Sbjct  712  AAVEAP  717


>TR:A0ABZ2BLE2 A0ABZ2BLE2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Sinorhizobium chiapasense OX=501572 GN=bcsA PE=4 SV=1
Length=726

 Score = 563 bits (1450),  Expect = 0.0
 Identities = 313/705 (44%), Positives = 420/705 (60%), Gaps = 8/705 (1%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V    +W  L +    L   PV    Q + ++  V  +AL+K        R + L+  +
Sbjct  4    VAALAVWAFLSLCVVALITLPVNLQTQLIASVVVVTFMALIKLVNAGGRWRLIALAFGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R
Sbjct  64   IVLRYVYWRTTNTLPPVNQPENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPPRPSRAAT  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              + P VD+ VPSYNE A +L+ TLAAAK M YPA   TV L DDGGT Q+  S     A
Sbjct  124  AAKSPKVDVFVPSYNEEASLLANTLAAAKGMDYPADKLTVWLLDDGGTQQKRDSASLVEA  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q+A  R  +LQ+LC +LGV Y TRERNEHAKAGN++  +    GEL+ VFDADH P+RDF
Sbjct  184  QRAAARHLQLQELCADLGVRYLTRERNEHAKAGNLNNGMLHADGELIAVFDADHAPARDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  A
Sbjct  244  LLETVGYFEDDPRLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAA  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR ALD+AGGF+G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLRRAALDDAGGFSGSSITEDCETALALHGRGWNSVYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
            FI QR RWA GMMQ+L+   PL +RGL + QRLCY++S  FW FPL R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILMFHFPLLKRGLSLPQRLCYMSSALFWMFPLSRTIFLFAPLCYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  QA +L  A+ + L
Sbjct  424  FDLEIFTASGGEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQAVHLLPAVFSVL  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
              PR   F VTAKDE++ E+ +S I RP    F +    +L T  R  A P    + LVV
Sbjct  484  ASPRKPTFKVTAKDESIFESRLSEISRPFFVIFAVLFIALLITAYRVYAEPYKADITLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW   N++L G AL  V+E+ +R  + RV++    E        +   AT+ + S +G
Sbjct  544  GGWNFFNLVLAGCALGVVSERGERSGSRRVKVSRRCEF---GLNEKWYPATIENVSANGA  600

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            R  V++ G+GD +  ++    I+F+P +     L+ +    I++    G   +VG  +
Sbjct  601  R--VQVYGLGDGNLVIDTQAQIRFEP-YSGGGTLDTLPVA-IKNVESGGDITIVGCRY-L  655

Query  676  GQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
             +       VA LIF  S  W   +       GL+ G     W++
Sbjct  656  PEVARHHSLVADLIFANSQQWSEFQRLRRANPGLVRGTLWFWWLS  700


>TR:A0AA50H747 A0AA50H747_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella sumterensis OX=1967501 GN=bcsA PE=4 SV=1
Length=722

 Score = 563 bits (1450),  Expect = 0.0
```

```
 Identities = 313/710 (44%), Positives = 429/710 (60%), Gaps = 13/710 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V  +A++K    + + R + L+  + +V+R
Sbjct  8    ILWACVSALVILVITLPINLQTQLVASIAVVTFMAVIKVLRAEGIWRLIALAFGTAIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+   P           E L
Sbjct  68   YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVTLPLPSRKGSVTPLERL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE   +L+ TLAAAK M YPA   T+ L DDGGT+Q+  +     AQ A
Sbjct  128  PSVDVFVPSYNEDIGLLANTLAAAKAMDYPADKMTIWLLDDGGTEQKRNATAVVEAQIAT  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  ELQ LCR+LGV Y TR RNEHAKAGNM+  +   KGEL+ +FDADH P+RDFL  T
Sbjct  188  ARHAELQALCRDLGVNYLTRARNEHAKAGNMNNGMLHSKGELIAIFDADHAPARDFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +FFCG
Sbjct  248  VGYFADDPKLFLVQTPHFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNASFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRTALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL + QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKRGLSLPQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428  IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE+++   +S I RP    F +     L ++ R+ A P    V  VVG W
Sbjct  488  KPTFKVTAKDESIAVARLSEISRPFFVIFAVLFIAFLMSIYRFYAEPYKADVTFVVGAWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E+ ++ A+ RV   V       + G R   AT+ + S +G R  V
Sbjct  548  LLNLLIAGCALGVVSERSEKAASRRV--TVKRRCTFLSEG-REYPATLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+ D H A  A G ++F+P      + E  +   IR+    G  +++G  F   Q
Sbjct  603  QVFGLED-HIATGAEGALRFKPY---GGEHEEALPVEIRNTETTGSVMVIGCRF-TPQDA  657

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                 VA LIF  S  W   + +     G+ G    LW    +  +T+R
Sbjct  658  RHHSLVADLIFANSNQWSDFQVSRRYNPGIFRG---TLWFLGIAAYQTSR  704


>TR:A0A9X3QZK9 A0A9X3QZK9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium salinitolerans OX=1183413 GN=bcsA PE=4
SV=1
Length=729

 Score = 563 bits (1450),  Expect = 0.0
 Identities = 311/706 (44%), Positives = 429/706 (61%), Gaps = 12/706 (2%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
            +  ++W+ + V    +   PV+     +    +++L+A +K F  +   R + L   + +
Sbjct  5    ITIIVWLLVSVCVLAIVTMPVSLQTHLVATAISLILLATIKSFNGQGAWRLVALGFGTAI  64

Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
            V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP  P
Sbjct  65   VLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVIMLALSLVIVSMPLPSRKARPGSP  124

Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
            +  PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +   AQ
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Sbjct  125  DYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVEAQ  184

Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
             AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RDFL
Sbjct  185  AAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARDFL  244

Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
              TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W GAF
Sbjct  245  LETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNGAF  304

Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
            FCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASF
Sbjct  305  FCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFASF  364

Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
            I QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YLFF
Sbjct  365  IGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYLFF  424

Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
             ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +
Sbjct  425  DLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVIF  484

Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
             P    F VTAKDE+++E  +S I RP    F L +  +   + R  + P    V LVVG
Sbjct  485  NPGKPTFKVTAKDESIAEARLSEISRPFFVIFALLVVAMAFAVWRIYSEPYKADVTLVVG  544

Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVR  616
            GW +LN++  G AL  V+E+  + A+ R+ ++   E ++    +  + A++ + S  G
Sbjct  545  GWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SDAWVPASIDNVSVHG--  601

Query  617  LLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
            LL+ L    D    +E G   +++ +P     P  E M    +R+ + E G + +G  F
Sbjct  602  LLINL---FDSATTIEKGATAIVKVRPHSEGVP--ETMPVNVVRTVKGE-GFISIGCTFS  655

Query  675  AGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMA  720
              + +  R  +A LIF  S  W   +    +  GL+ G A  L +A
Sbjct  656  PQRAVDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFLAIA  700


>TR:A0ABN0HLS1 A0ABN0HLS1_RHILU Cellulose synthase catalytic subunit [UDP-forming]
OS=Bradyrhizobium lupini HPC(L) OX=1229491 GN=C241_11413
PE=4 SV=1
Length=729

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 320/717 (45%), Positives = 433/717 (60%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  +L+A +K F  + V R + L   +
Sbjct  5    ITIIVW--LLVSLCVLAIITMPVSLQTHLVATAISLILLATIKGFNGQGVWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLALSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P   P VD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPTYRPAVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNAANIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
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Sbjct  303  AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLF+RGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFKRGLTFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L +  ++  + R  + P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFGLLVVAMIFAVWRIYSEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++        + T + AS
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG------SDTWVPASIDN  596

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
            V +   L  + D    +E G   +++ +P     P  E M    +R+ R E G + +G
Sbjct  597  VSVHGLLINLFDNATTVEKGETAIVRVKPHSEGVP--ETMPLNIVRTVRGE-GFISIGCT  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + +  R  +A LIF  S  W   +    R  GL+ G A  L   A SL +T R
Sbjct  654  FSPQRAVDHR-LIADLIFANSEQWSEFQRVRRRNPGLIRGTATFL---AISLFQTQR  706


>TR:A0A549THQ6 A0A549THQ6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium straminoryzae OX=1387186 GN=bcsA PE=4 SV=1
Length=719

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 310/697 (44%), Positives = 427/697 (61%), Gaps = 18/697 (3%)

Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
            PV+   Q +++ + +VL+ +LK  A +   R + L+  + +V+RY FWR  ET+PP +
Sbjct  24   PVSMQTQLVLSFTIIVLITVLKITAPEGKWRLVTLALGTSIVIRYVFWRTTETIPPISQL  83

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
             +F+   L++  E +S+ +  L+ F+ A P        L  + LP VD+ VPSYNE  D+
Sbjct  84   ENFIPGFLVYLAEMYSVMMLGLSLFIVALPLPTRPEHTLDRKALPHVDVFVPSYNEDHDL  143

Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAAK + YP     + L DDGGT Q+  S D   A+ A  R R L QLC  L V
Sbjct  144  LANTLAAAKALDYPEDKLQIWLLDDGGTQQKQHSHDVREAETAIARSRALSQLCELLEVN  203

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TRERNEHAKAGN++  L    GEL+ VFDADH P+R+FL  TVG+F +DP LFLVQTP
Sbjct  204  YLTRERNEHAKAGNLNNGLAHSTGELIAVFDADHAPARNFLLETVGHFQDDPKLFLVQTP  263

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFFINPDP++RNL   +R P ENEMFYG I +GLDRW  AFFCGSAAVLRR AL E+ GF
Sbjct  264  HFFINPDPLERNLQTFERMPSENEMFYGIIQKGLDRWNAAFFCGSAAVLRRTALQESNGF  323

Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
             G +ITED ETA+ +HS GW S+Y+D+ +IAGLQP TFASFI QR RWA GMMQ+L  K
Sbjct  324  NGVSITEDCETAIVLHSAGWNSIYVDKPLIAGLQPATFASFIAQRSRWAQGMMQILRFKA  383

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PL RRGL + QRLCY++S  FW FP  R+ FL+APL YLFFG+EIF ++  E LAY   Y
Sbjct  384  PLLRRGLSLPQRLCYMSSTLFWLFPFTRITFLLAPLAYLFFGLEIFTSSGGEFLAYTSAY  443

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            + V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +L PR   F VTAKDET+S +
Sbjct  444  MLVNMMLQNYLYGSFRWPWISELYEYIQTVHLLPAVVSVMLNPRKPTFKVTAKDETVSSD  503

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
            ++S + RP    F + ++  L T+ R    P +  V+LVVGGW +LN+++ G AL  V+E
Sbjct  504  HVSELGRPFFIIFAVLVAAFLVTIYRIYTEPYNADVILVVGGWNLLNIIIAGCALGVVSE  563
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Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            ++ R ++ R ++    E     F  +   A++ D S  G+RL      +G      ++
Sbjct  564  RRDRASSRRFRVRRRCEL---GFEGQWYPASIEDVSVGGMRLQAYGKDLGT--LTHDSAV  618

Query  636  LIQFQPK-FPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRE--TVAYLIFGE  692
             I+F+P    D   L  +V    R+A+  G    +G  +    P   R+   +A LIF
Sbjct  619  EIRFKPHGGEDMAHLSLLV----RTAQSSGEMATLGCKY---MPANARDHRWIADLIFAN  671

Query  693  SAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            S+ W   +    +  GLL G    +W    +L +T+R
Sbjct  672  SSQWEQFQRGRRKNPGLLRGS---IWFLGLALYQTSR  705


>TR:A0ABP2BN87 A0ABP2BN87_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Agrobacterium genomosp. 13 str. CFBP 6927 OX=1183428
GN=bcsA PE=4 SV=1
Length=729

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 323/717 (45%), Positives = 434/717 (61%), Gaps = 19/717 (3%)

Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAV--VLVALLKPFADKMVPRFLLLSAAS  74
            +  ++W  LLV   +LA   +  S Q  +  +A+  VL+A +K F  +   R + L   +
Sbjct  5    ITIIVW--LLVSLCVLAIITMPISLQTHLVATAISLVLLATIKSFNGQGAWRLVALGFGT  62

Query  75   MLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPL  134
             +V+RY +WR   TLPP     +F+   LL+  E +S+ +  L+  + + P      RP
Sbjct  63   AIVLRYVYWRTTSTLPPVNQLENFIPGFLLYLAEMYSVVMLGLSLVIVSMPLPSRKTRPG  122

Query  135  QPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPEL  194
             P+  PTVD+ VPSYNE A++L+ TLAAAKNM YPA   TV L DDGG+ Q+  + +
Sbjct  123  SPDYRPTVDVFVPSYNEDAELLANTLAAAKNMDYPADRFTVWLLDDGGSVQKRNASNIVE  182

Query  195  AQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRD  254
            AQ AQ R  EL++LC +L V Y TRERN HAKAGN++  L    GELV VFDADH P+RD
Sbjct  183  AQAAQRRHEELKKLCEDLDVRYLTRERNVHAKAGNLNNGLAHSTGELVTVFDADHAPARD  242

Query  255  FLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGG  314
            FL  TVGYF EDP LFLVQTPHFF+NPDPI+RNL   +  P ENEMFYG I RGLD+W G
Sbjct  243  FLLETVGYFEEDPRLFLVQTPHFFVNPDPIERNLRTFETMPSENEMFYGIIQRGLDKWNG  302

Query  315  AFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFA  374
            AFFCGSAAVLRR AL +  GF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFA
Sbjct  303  AFFCGSAAVLRREALQDTEGFSGVSITEDCETALALHSRGWNSIYVDKPLIAGLQPATFA  362

Query  375  SFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYL  434
            SFI QR RWA GMMQ+L+ + PLFRRGL   QRLCY++S  FW FP  R +FL APL YL
Sbjct  363  SFIGQRSRWAQGMMQILIFRQPLFRRGLSFTQRLCYMSSTLFWLFPFPRTIFLFAPLFYL  422

Query  435  FFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTT  494
            FF ++IFVA+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+
Sbjct  423  FFDLQIFVASGGEFLAYTAAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSV  482

Query  495  LLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLV  554
            +  P    F VTAKDE+++E  +S I RP    F L +  +     R  + P    V LV
Sbjct  483  IFNPGKPTFKVTAKDESIAEARLSEISRPFFVIFALLVVAMAFAAWRIYSEPYKADVTLV  542

Query  555  VGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG  614
            VGGW +LN++  G AL  V+E+  + A+ R+ ++   E ++       + A++ + S  G
Sbjct  543  VGGWNLLNLIFAGCALGVVSERGDKSASRRITVKRRCEVKLEG-SEAWVPASIENVSVHG  601

Query  615  VRLLVRLPGVGDPHPALEAG--GLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVI  672
              LL+ L    D   A+E     +++ +P     P  E M    +R+ R E G V +G
Sbjct  602  --LLINL---FDNSTAIEKNTTAIVKVKPHSEGVP--ETMPINVVRTVRGE-GFVSIGCT  653

Query  673  FEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            F   + +  R  +A LIF  S  W   +    +  GL+ G A  L   A SL +T R
Sbjct  654  FSPQRAVDHR-LIADLIFANSEQWSEFQRVRRKNPGLIRGTAIFL---AISLFQTQR  706
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>TR:A0A6N8SBI2 A0A6N8SBI2_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella kummerowiae OX=417745 GN=bcsA PE=4 SV=1
Length=722

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 313/715 (44%), Positives = 432/715 (60%), Gaps = 17/715 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V  +A++K    + + R + L+  + +V+R
Sbjct  8    ILWALVSALVILVITLPINLQTQLIASIAVVTFMAVIKVLRAEGIWRLIALAFGTAVVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R      L
Sbjct  68   YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPPRKSRAAGGGPL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE   +L+ TLAAAK M YPA   T+ L DDGGT+Q+  +     AQ A
Sbjct  128  PSVDVFVPSYNEDTALLANTLAAAKAMDYPADKLTIWLLDDGGTEQKRNAAAVIEAQTAT  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R RELQ LCR+L V Y TR RNEHAKAGNM+  ++   GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHRELQALCRDLDVNYLTRARNEHAKAGNMNNGMQHSTGELIAVFDADHAPARDFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFADDPKLFLVQTPHFFLNPDPLERNLRTFETMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAA+L RRAL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAALLSRRALNEAGGFSGLSITEDCETALALHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL + QRLCY++SM FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKRGLSLPQRLCYMSSMLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428  IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++  + +S I RP    F +     L ++ R+ + P    V  VVGGW
Sbjct  488  KPTFKVTAKDESIKVSRLSEISRPFFVIFGILFIAFLMSIYRFYSEPYKADVTFVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+++ G AL  V+E+ +R ++ RV ++      I   G R   +T+ + S +G R  V
Sbjct  548  LLNLIIAGCALGVVSERSERASSRRVTVKRRCTFII---GEREYPSTLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+ +P  A+     ++F P      + E  +   +R+    G  V VG  F    P
Sbjct  603  QVFGL-EPDIAVGENCFLRFMPY---GSEQEETLPVDVRNVENLGSVVAVGCRF---MPQ  655

Query  680  AVR--ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
            A R    VA LIF  S  W   + +     GL  G    LW    ++ +T+R  +
Sbjct  656  AARHHSLVADLIFANSNQWSDFQVSRRYNPGLFRGS---LWFLGIAVYQTSRGLL  707


>TR:A0ABV3X165 A0ABV3X165_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Neoaquamicrobium sediminum OX=1849104 GN=bcsA PE=4
SV=1
Length=731

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 321/721 (45%), Positives = 434/721 (60%), Gaps = 26/721 (4%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQ---GLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +LL L+W  +      + A P+        G I L+ ++ + LL+P       R + L+
Sbjct  4    LLLGLVWAIVAACVIFIVALPINLQTHLIAGAIVLTMMMTLKLLRPDGTW---RLIALAL  60
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Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             + +V+RY +WR   T+PP +   +F+  LLL+  E +S+ +  L+ F+ A P
Sbjct  61   GTAIVLRYVYWRTTSTIPPVSQLENFIPGLLLYLAEMYSVFMLALSLFIVAKPLPSRAAS  120

Query  133  PLQPEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDP  192
            P+   +LP VD+ +PSYNE   +L+ T+AAAK M YP    TV L DDGGT Q+  + +
Sbjct  121  PIDDADLPFVDVFIPSYNEEPALLADTIAAAKAMDYPQERLTVWLLDDGGTVQKRNAVNI  180

Query  193  ELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPS  252
              AQ A ER  EL+QLC +LG  Y TRERNEHAKAGN++  L    G+LV VFDADH P+
Sbjct  181  IEAQAAGERHEELKQLCADLGANYLTRERNEHAKAGNLNNGLANSTGQLVAVFDADHAPA  240

Query  253  RDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRW  312
            R FL  TVGYF EDP LFLVQTPHFF+NPDP++RNL   D  P ENEMFYG I RGLD+W
Sbjct  241  RSFLRETVGYFAEDPRLFLVQTPHFFLNPDPLERNLKTFDTMPSENEMFYGIIQRGLDKW  300

Query  313  GGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPET  372
              +FFCGSAAVLRR AL+E  GF+G +ITED ETA+E+HSRGW S+Y+D+ +IAGLQP T
Sbjct  301  NASFFCGSAAVLRREALEETDGFSGISITEDCETAVELHSRGWNSVYVDKPLIAGLQPAT  360

Query  373  FASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLI  432
            FASFI QR RWA GMMQ+L  + P  +RGL + QRLCY++S  FW FP  R +FL APL
Sbjct  361  FASFIGQRSRWAQGMMQILRFRFPPLKRGLSLPQRLCYMSSTLFWLFPFPRTIFLFAPLF  420

Query  433  YLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIV  492
            YLFF ++IF A+  E LAY   Y+ V+ ++QN L+ R RWP +SE+YE  Q  +L  A+V
Sbjct  421  YLFFDLQIFTASGGEFLAYTLSYMVVNLMMQNYLYGRFRWPWISELYEYIQTVHLLPAVV  480

Query  493  TTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVL  552
            + +L PR   F VTAKDE+++ + +S + RP    F + L GV  +  R  A P    V
Sbjct  481  SVMLNPRKPTFKVTAKDESITISRLSELSRPFFVIFAVLLVGVAVSAWRIYAEPWKSDVT  540

Query  553  LVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRS--LTATVLDA  610
            LVVGGW +LN++L G AL  V+E++QR A  RV++    +     FG+    L A + D
Sbjct  541  LVVGGWNLLNLILAGCALGVVSERRQRTATRRVKVNRRCD-----FGHDGLWLPAMIEDV  595

Query  611  STSGVRLLVRLPGVGDPHPALEAGGL--IQFQPKFPDAPQLERMVRGRIRSARREGGTVM  668
            S +G R+ V     G     L A G   I+F       P     +   IR++ +EG  V
Sbjct  596  SVNGARIKVH----GGKASELIALGQANIRFATLSGGEP---ATLPVNIRNSEKEGDGVA  648

Query  669  VGVIFEAGQPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTA  728
            VG  +    P   R  VA LIF  +  W   +++  R +G++ G    LW    +L +T
Sbjct  649  VGCQYLRSAPEHHR-AVADLIFANAEQWTEFQQSRRRNLGVVIG---TLWFLRLALFQTW  704

Query  729  R  729
            R
Sbjct  705  R  705


>TR:A0ABS4EPM3 A0ABS4EPM3_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium herbae OX=508661 GN=J2Z75_003416 PE=4 SV=1
Length=728

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 313/714 (44%), Positives = 431/714 (60%), Gaps = 16/714 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            + L W    +     L   P+    Q + +++ V  +A+LK    +   R   L+  + +V
Sbjct  6    IILFWAIASLCVIALVTLPINLQTQLIASIAVVTFMAVLKILRAEGTWRLTALAFGTAIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            MRY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ + P      R   P
Sbjct  66   MRYVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVSMPLPSRPSRAASPG  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            + P+VD+ VP+YNE + +L+ TLAAAK M YPA   TV L DDGGT Q+  S +    Q
Sbjct  126  KYPSVDVFVPTYNEDSHLLANTLAAAKAMDYPADKLTVWLLDDGGTLQKRTSANLLEDQM  185
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Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A+ R +ELQ L  +LGV Y TR+RNEHAKAGN++  ++  +GEL+ VFDADH P+RDFL
Sbjct  186  AKARHQELQILSEDLGVRYLTRDRNEHAKAGNLNNGMKHSQGELIAVFDADHAPARDFLL  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TVGYF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +FF
Sbjct  246  ETVGYFEDDPRLFLVQTPHFFLNPDPVERNLRTFEKMPSENEMFYGIIQRGLDKWNASFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR+ALD+ GGF+G +ITED ETA+++H+ GW S+Y+DR +IAGLQP TFASFI
Sbjct  306  CGSAAVLRRQALDQTGGFSGVSITEDCETAIDLHASGWNSVYVDRPLIAGLQPATFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  K PL +RGL I QRLCY++S  FW FP  R +FL APL YLFF
Sbjct  366  GQRSRWAQGMMQILRFKFPLLKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAPLCYLFFD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            +EIF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ ++
Sbjct  426  LEIFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSAIVN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR   F VTAKDE++  + +S I RP    F + L  +L T  R    P    V LVVGG
Sbjct  486  PRKPSFKVTAKDESVLVSRLSEISRPFFIIFAVLLFALLVTAYRVYTEPYKADVTLVVGG  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN++L G AL  V+E+ ++ A  RV++    E       +    AT+ D S  G R+
Sbjct  546  WNLLNLILAGCALGVVSERGEKSATRRVKVTRRCEF---GLDDNWYPATIDDVSVHGARI  602

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
             V    +G    A++  GLI+F+P   D   +E ++   +R+ + +G  V +G  +
Sbjct  603  NVYAKSIG--LLAVDTRGLIRFKPHGSD---IEEILPVAVRNTQVDGDIVTIGCQY---L  654

Query  678  PIAVR--ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            P A R    VA LIF  S  W   + +     GL  G    LW    +  +T+R
Sbjct  655  PEAARHHSLVADLIFANSQQWTEFQLSRRGNPGLFRG---TLWFFGLAFYQTSR  705


>TR:A0ABS7HGD6 A0ABS7HGD6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium herbae OX=508661 GN=bcsA PE=4 SV=1
Length=728

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 318/728 (44%), Positives = 434/728 (60%), Gaps = 19/728 (3%)

Query  16   VLLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASM  75
            V + L W+   +    L   P+    Q + +++ V  +A++K    +   R   L+  +
Sbjct  4    VAIILSWIITSLGVIALVTLPINLQTQLIASIAVVTFMAVIKILRAEGTWRLTALAFGTA  63

Query  76   LVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQ  135
            +VMRY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ + P      R
Sbjct  64   IVMRYVYWRTTSTLPPFNQLENFIPGFLLYLAEMYSVMMLGLSLFVVSMPLPPRPSRAAS  123

Query  136  PEELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELA  195
              + P+VD+ VPSYNE A++L+ TLAAAK M YPA   TV L DDGGT Q+  SP+
Sbjct  124  EGKYPSVDVFVPSYNEDAELLANTLAAAKAMDYPAEKLTVWLLDDGGTLQKRTSPNLLED  183

Query  196  QKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDF  255
            Q A+ R +ELQ LC +L V Y TR+RNEHAKAGN++  +    GEL+ VFDADH P+RDF
Sbjct  184  QMAKARHQELQILCNDLDVRYLTRDRNEHAKAGNLNNGMRHSTGELIAVFDADHAPTRDF  243

Query  256  LARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGA  315
            L  TVGYF +DP LFLVQTPHFF+NPDP++RNL   +R P ENEMFYG I RGLD+W  +
Sbjct  244  LLETVGYFEDDPKLFLVQTPHFFLNPDPVERNLRTFERMPSENEMFYGIIQRGLDKWNAS  303

Query  316  FFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFAS  375
            FFCGSAAVLRR+ALD+ GGF+G +ITED ETA+ +H+ GW S+Y+DR +IAGLQP TFAS
Sbjct  304  FFCGSAAVLRRQALDQTGGFSGLSITEDCETAIALHASGWNSVYVDRPLIAGLQPATFAS  363

Query  376  FIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLF  435
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            FI QR RWA GMMQ+L  + PL +RGL I QRLCY++S  FW FP  R +FL APL YLF
Sbjct  364  FIGQRSRWAQGMMQILRFRFPLLKRGLSIPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLF  423

Query  436  FGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTL  495
            F +EIF+A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +
Sbjct  424  FDLEIFMASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTIHLLPAVVSAI  483

Query  496  LRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVV  555
            + PR   F VTAKDE++  + +S I RP    F + L  VL T  R    P    V LVV
Sbjct  484  VNPRKPSFKVTAKDESVLVSRLSEISRPFFVIFAVLLLAVLVTAYRVYTEPYKADVTLVV  543

Query  556  GGWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGV  615
            GGW +LN+LL G  L  V+E+ +  A  RV++    E        +   AT+ + S +G
Sbjct  544  GGWNLLNLLLAGCGLGVVSERGELTATRRVKVARRCEF---GLDEQWYPATIDNVSVNGA  600

Query  616  RLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEA  675
            R+ V    +G     L+  GLI+F P    +   E ++   +R+ +  G  V VG ++
Sbjct  601  RVNVYAKNLGT--LPLDKRGLIRFTPY---SSGHEEILPVAVRNTQVAGDIVTVGCLY--  653

Query  676  GQPIAVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARD---  730
              P A R+   +A LIF  S  W   + +     GLL G    +W    +L +T+R
Sbjct  654  -LPEAARDHSLIADLIFANSQQWTQFQMSRRGNPGLLRG---TIWFLGLALYQTSRGIIY  709

Query  731  FMDEPARR  738
            F   P  R
Sbjct  710  FFSSPGAR  717


>TR:A0A6M1S6N4 A0A6M1S6N4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium daejeonense OX=240521 GN=bcsA PE=4 SV=1
Length=719

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 316/712 (44%), Positives = 422/712 (59%), Gaps = 16/712 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  + V   ++   PV+  AQ + +LS V  +AL+K        R + L+  + +V+R
Sbjct  8    ILWAVISVLMIVVITLPVSLQAQLICSLSVVAFMALIKVLKAGGKWRLIALAFGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR  ETLPP     +F+  LLL+  E +S+ +  L+ F+ A P           +
Sbjct  68   YVYWRTTETLPPINQPENFIPGLLLYLAEMYSVMMLALSLFIVAMPLPSRSSHARDRKRF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            PTVD+ VPSYNE   +L+ TLAAAK M YP     + L DDGGT Q+  S +   A+ A
Sbjct  128  PTVDVFVPSYNEDPALLANTLAAAKAMDYPQDKVQIWLLDDGGTLQKQRSSNIRDAETAV  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R REL QLC ELGV Y TRERNEHAKAGN++  L+  +GELV VFDADH P+ DFL  T
Sbjct  188  TRNRELSQLCEELGVNYLTRERNEHAKAGNLNNGLKHSQGELVAVFDADHAPAHDFLMET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFFINPDP++RNL   +  P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFEDDPKLFLVQTPHFFINPDPLERNLQTFESMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL R+AL+   GF+G +ITED ETAL +HS+GW S+YID+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLNRKALETTDGFSGISITEDCETALALHSQGWNSIYIDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+RGL + QRLCY++S  FW FP  R +FL APL YL F +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKRGLSLPQRLCYMSSTLFWLFPFPRTIFLFAPLFYLLFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ +L PR
Sbjct  428  IFTASGGEFLGYTFAYMIVNLMMQNYLYGSFRWPWISELYEYIQTVHLLPAVISVMLNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++S + +S I RP    F      +L    R    P +  V LVVGGW
```

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Sbjct  488  KPTFKVTAKDESVSVSRLSEIGRPFFVIFAALFVALLVAAYRVYTEPYNADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            + N+++ G AL  V+E++ R ++ R ++    E  I    +    A+V D S  G RL V
Sbjct  548  LFNLIMAGCALGVVSERKDRASSRRFKINRRCEFGI---DDTWYPASVEDVSAGGARLQV  604

Query  620  RLPGVGDPHPALEAGGLIQ--FQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
                 G   P+L  G  +Q  F P   +   L  +    +R+ +  G    VG  +
Sbjct  605  ----FGRDIPSLREGNTVQIRFTPHNGEGTALLPLA---VRNFQISGDITAVGCEYAPAS  657

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
             +  R  +A LIF  S+ W   + A  R  GL  G    +W    S+ +T+R
Sbjct  658  ALDHR-WIADLIFANSSQWEEFQRARRRNPGLFRG---TIWFLGLSMYQTSR  705


>TR:A0ABS7GT74 A0ABS7GT74_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium mesosinicum OX=335017 GN=bcsA PE=4 SV=1
Length=732

 Score = 562 bits (1449),  Expect = 0.0
 Identities = 321/733 (44%), Positives = 439/733 (60%), Gaps = 16/733 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            L+W  + +    L   PV    Q + +++ V ++AL+K    +   R + L+  + +V+R
Sbjct  8    LIWAVVSLCVIALITLPVNLQTQLIASITVVTIMALIKVAKGEGTWRLVALAFGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP    A+F+  LLL+  E +S+ +  L+ F+ A P      R  + E
Sbjct  68   YVYWRTTNTLPPVNQLANFIPGLLLYLAEMYSVMMLALSLFIVATPLPPRPSRAGKLERF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P VD+ VPSYNE A +L+ TLAAAK M YPA    V L DDGGT Q+  S     AQ A
Sbjct  128  PHVDVFVPSYNEDAGLLANTLAAAKAMDYPADKLHVWLLDDGGTLQKRNSGKLIEAQAAA  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  EL+QLC +L V Y TR+RNEHAKAGN++  ++  +GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHAELKQLCVDLDVNYLTRDRNEHAKAGNLNNGMQHSRGELIAVFDADHAPARDFLLET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFFINPDP++RNL   D+ P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFDDDPKLFLVQTPHFFINPDPLERNLRTFDKMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVL RRAL    GF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRRALQSTNGFSGVSITEDCETALALHGAGWNSIYLDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PL +RGL + QRLCY++S  FW FP  R +FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRLPLLKRGLTLPQRLCYMSSSLFWLFPFPRTIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+V+ +L PR
Sbjct  428  IFTASGGEFLAYTLAYMIVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVVSVMLNPR  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE+++ + +S I RP    F + +  V  T+ +  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDESIALSRLSEISRPFFVIFAVQIIAVAITIYKIYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            ++N++L G AL  V+E+ +R ++ RV++    E  I   G++  TA++ D S  G RL +
Sbjct  548  IINLILAGCALGVVSERGERASSRRVRVNRRCEFCI---GDQWYTASIEDVSVHGARLHI  604

Query  620  RLPGVGDPHPALEAGGL--IQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
                      A++ G L  I+F+P       LE +    +R+    G    VG  ++
Sbjct  605  ----FSKHFDAVQVGALGEIRFRPY--SGADLETLPL-IVRNIEPSGDITNVGCQYQPKS  657

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFMDEPAR  737
             +  R  +A LIF  S  W   + +  R  GL+ G    +W    SL +T+R  +
Sbjct  658  ALDHR-LIADLIFANSDQWSQFQASRRRNPGLIKG---TVWFLGLSLYQTSRGLVYFFRS  713
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Query  738  RRRRHEEPKEKQA  750
             R   E  +++QA
Sbjct  714  MRPEREAHRQQQA  726


>TR:A0ABT8X7H5 A0ABT8X7H5_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Shinella curvata OX=1817964 GN=bcsA PE=4 SV=1
Length=723

 Score = 562 bits (1448),  Expect = 0.0
 Identities = 314/715 (44%), Positives = 431/715 (60%), Gaps = 17/715 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            +LW  +     L+   P+    Q + +++ V L+A++K    + + R + L+  + +V+R
Sbjct  8    ILWAFVSALVILVITLPINLQTQLIASIAVVTLMAVIKVLRAEGIWRLIALAFGTAVVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ A P      R  +   L
Sbjct  68   YVYWRTTSTLPPLNQLENFIPGFLLYLAEMYSVMMLALSLFVVAMPLPSRKSRMAEEGRL  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE   +L+ TLAAAK M YPA   TV L DDGGT+Q+  +     AQ A+
Sbjct  128  PSVDVFVPSYNEDIGLLANTLAAAKAMDYPADKLTVWLLDDGGTEQKRNAAAVIEAQTAE  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R RELQ LCR+LGV Y TR RNEHAKAGNM+  ++   GEL+ +FDADH P+RDFL  T
Sbjct  188  ARHRELQALCRDLGVNYLTRARNEHAKAGNMNNGMQYSTGELIAIFDADHAPARDFLRET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VG+F +DP LFLVQTPHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  +FFCG
Sbjct  248  VGFFADDPKLFLVQTPHFFLNPDPLERNLRTFENMPSENEMFYGIIQRGLDKWNASFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
            SAAVLRR AL+EAGGF+G +ITED ETAL +HSRGW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLRRTALNEAGGFSGLSITEDCETALSLHSRGWNSVYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PLF+ GL + QRLCY++SM FW FP  R +FLVAPL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLFKGGLSLPQRLCYMSSMLFWLFPFPRTIFLVAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E L Y   Y+ V+ ++QN L+   RWP +SE+YE  Q+ +L  A+V+ +L P
Sbjct  428  IFTASGGEFLGYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQSVHLLPAVVSVMLNPT  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++S + +S I RP    F +     L ++ R+ A P    V  VVGGW
Sbjct  488  KPTFKVTAKDESISVSRLSEISRPFFVIFGVLFVAFLVSVYRFYAEPFKADVTFVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            +LN+L+ G AL  V+E+ +R ++ RV ++      I     R   +T+ + S +G R  V
Sbjct  548  LLNLLIAGCALGVVSERSERASSRRVTVKRRCTFVI---DGRDYPSTLENVSANGAR--V  602

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
            ++ G+     A    G ++F    P     E  +   +R+    G  + VG  F    P
Sbjct  603  QVFGLEGQIEA-NTRGYLRFT---PSGATEEESLPVEVRNVESLGSVMAVGCRF---MPE  655

Query  680  AVR--ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
              R    VA LIF  S  W   + +     GL  G    LW    +  +T+R  +
Sbjct  656  VARHHSLVADLIFANSNQWSDFQVSRRYNPGLFRG---TLWFLGIAAYQTSRGLL  707


>TR:A0A8J6Q509 A0A8J6Q509_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Oryzicola mucosus OX=2767425 GN=bcsA PE=4 SV=1
Length=730

 Score = 562 bits (1448),  Expect = 0.0
 Identities = 314/737 (43%), Positives = 443/737 (60%), Gaps = 14/737 (2%)
```

```
Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            LFLLW  L     +L   P++   Q +  +  ++ + +LK    +   R + L+  + +V
Sbjct  6    LFLLWAFLGFCMLVLVTLPISLETQFITGMVVLIAMMILKLLGSEGNLRLIALAFGTAVV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY +WR   TLPP     +F+   LL+  E +S+ +  L+ F+ + P      R    +
Sbjct  66   LRYAYWRTTSTLPPFNQLENFIPGFLLYLAEMYSVMMLALSLFVVSRPLPPRPSRRNANK  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
              PTVD+ +P+YNE AD+L+ T+AAAK M YPA   TV L DDGGT Q+  S     A
Sbjct  126  RFPTVDVFIPTYNEDADLLANTMAAAKQMEYPADKLTVWLLDDGGTVQKRNSEKIIDANA  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A++R R+LQ+L  +L V Y TRERNEHAKAGNM+ AL++ +GEL+V+FDADH P+RDFL
Sbjct  186  AEQRFRDLQKLAADLDVRYLTRERNEHAKAGNMNNALDQSEGELIVIFDADHAPARDFLL  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
             TV YF +DP LFLVQTPHFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  +FF
Sbjct  246  ETVSYFDDDPKLFLVQTPHFFLNPDPVERNLRTFEKMPSENEMFYGIIQRGLDKWDASFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAAVLRR AL E  GF+G +ITED ETA+E+HSRGW SLYIDR +IAGLQP TFASFI
Sbjct  306  CGSAAVLRRTALAETNGFSGVSITEDCETAVELHSRGWSSLYIDRPLIAGLQPATFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P  +RGL + QRLCY++S  FW FP  R +FLVAPL YLFF
Sbjct  366  GQRSRWAQGMMQILRFRFPPLKRGLSLPQRLCYMSSTLFWLFPFPRAIFLVAPLCYLFFD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            ++IF A+  E +AY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ +L
Sbjct  426  LQIFTASGGEFMAYTLSYMLVNLMMQNYLYGAFRWPWISELYEYVQTVHLLPAVISVILN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
            PR   F VTAKDE+++ + +S I  P    F + +  V  T+ R    P    V LVVGG
Sbjct  486  PRKPTFKVTAKDESIARSRLSEIAAPFFVIFFVLIIAVFVTIYRVYTEPFKADVTLVVGG  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN+++ G AL  V+E+ ++ A  RV +    + ++   G+  L  T+ + S +G R
Sbjct  546  WNLLNLIMAGCALGVVSERGEKAATRRVAVSRRCDFKL---GDTWLQGTIENVSVNGAR-  601

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQ  677
             V L G       ++    ++F+     +   + ++   IR+  R G  V++G  +   +
Sbjct  602  -VNLIGAIPEGITIDDRAELRFK---THSDGNQGVLPVEIRNVERGGQNVVIGCRYHP-E  656

Query  678  PIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARD--FMDEP  735
              A  + VA LIF  SA W   + +     GLL G     W    +L +T R   ++
Sbjct  657  GAAHHKLVADLIFANSAQWTQFQLSRRGNPGLLRG---TFWFLRLALYQTYRGLVYLGRA  713

Query  736  ARRRRRHEEPKEKQAHL  752
            AR R   +     ++HL
Sbjct  714  ARDRGSDKSASMAESHL  730


>TR:A0ABV2QYT9 A0ABV2QYT9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Kaistia defluvii OX=410841 GN=ABIE08_001586 PE=4 SV=1
Length=734

 Score = 562 bits (1448),  Expect = 0.0
 Identities = 312/712 (44%), Positives = 434/712 (61%), Gaps = 15/712 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            LLW    +    L   P++  A  +   + +  + +LK F    V R + L+  + +V+R
Sbjct  8    LLWAVAAIVMAFLITLPISLQAHLIAGTAVLGAMVVLKTFTSGGVWRQIALALGTSIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADP-TDRPFPRPLQPEE  138
            Y +WR   TLPP     +F+   L++  E +SI + FL+ F+   P   R         +
Sbjct  68   YAYWRTTSTLPPINELQNFIPGFLVYICEMYSIFMLFLSLFVVMLPHPSRNLKISSSDPD  127

Query  139  LPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKA  198
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            LPTVD+ VP+YNE  ++L+ TLAAAK M YPA   TV L DDGGT Q+  + + + AQ+A
Sbjct  128  LPTVDVFVPTYNEEPELLATTLAAAKAMDYPADKLTVWLLDDGGTVQKRNAENMQAAQEA  187

Query  199  QERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLAR  258
            +ER   LQ+L  ++G  Y TRERN HAKAGNM+  L+   GELVVVFDADH P+RDFL
Sbjct  188  EERYITLQKLAEDMGCRYLTRERNVHAKAGNMNNGLQVATGELVVVFDADHAPARDFLLY  247

Query  259  TVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFC  318
            TVGYF EDP LFLVQ+PHFF+NPDP++RNL   +  P ENEMFYG I RGLD+W  +FFC
Sbjct  248  TVGYFKEDPKLFLVQSPHFFLNPDPVERNLRTFETMPSENEMFYGIIQRGLDKWDASFFC  307

Query  319  GSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQ  378
            GSAAVLRR ALD+ GGF+G +ITEDAETALE+H+ GW S+Y+DR +IAGLQP TFASFI
Sbjct  308  GSAAVLRRGALDQTGGFSGVSITEDAETALELHASGWHSVYVDRPLIAGLQPATFASFIG  367

Query  379  QRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGI  438
            QR RW  GM Q+L  + P  +RGL I QRLCY++S  FWFFP+ R +FL+APL YLFF +
Sbjct  368  QRSRWGQGMYQILRFRFPPGKRGLSIPQRLCYMSSTLFWFFPITRWIFLLAPLCYLFFNL  427

Query  439  EIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRP  498
            EIF A+  E +AY   Y+ V+ ++QN L+ R RWP +SE+YE  Q+ YL  A+V+ +L P
Sbjct  428  EIFTASAGEFVAYSATYMVVNLMMQNYLYGRFRWPWISELYEYVQSVYLLPALVSVILNP  487

Query  499  RSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGW  558
                F VT+K E+L    +S + RP    F + +  V  T  R +  P    V LVVGGW
Sbjct  488  SKPTFKVTSKSESLDTARVSELSRPFFIIFAVLVLAVFMTAWRVINEPWKADVALVVGGW  547

Query  559  AVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLL  618
             +LN+++ G AL  V+E+++ R + RV ++   E  +   G++   AT+ DAS  G R
Sbjct  548  NLLNLVIAGCALGVVSERRENRGSRRVDVKRRCEILV---GDKVFPATIEDASVGGAR--  602

Query  619  VRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQP  678
            + +  V  P  + +    ++F+   P    +    +    +RS  R    VM+GV +E
Sbjct  603  INMGNVKVPEISRDLYCDVRFKTNVPIPTEAMPI---SVRSMTRTPDGVMLGVRYE--PT  657

Query  679  IAVR-ETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            IA   + ++ L+F  S  W   + +    IG+L G    +W  + S+ +T R
Sbjct  658  IADHYKLISDLVFASSDLWTKFQWSRRTNIGILRG---TIWFLSLSIYQTGR  706


>TR:A0A1C3WWX6 A0A1C3WWX6_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Rhizobium miluonense OX=411945 GN=GA0061102_104417
PE=4 SV=1
Length=729

 Score = 562 bits (1448),  Expect = 0.0
 Identities = 309/710 (44%), Positives = 432/710 (61%), Gaps = 12/710 (2%)

Query  20   LLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMR  79
            L+W  + +   +L   PV    Q +    AV ++A++K    +   R + L+  + +V+R
Sbjct  8    LIWAVIALCGVVLITLPVNLQTQLIAGTVAVTIMAIIKILKRQGTWRLVALAFGTAIVLR  67

Query  80   YWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEEL  139
            Y +WR   TLPP     +F+  LLL+  E +++++  L+ F+ A P      R L+ ++
Sbjct  68   YVYWRTTSTLPPLNQPENFIPGLLLYLAEVYNVAMLMLSLFIVATPLPPRTARALKTQDF  127

Query  140  PTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQ  199
            P+VD+ VPSYNE  ++L+ TLA+AK M YPA    V L DDGGT Q+  S     +Q A
Sbjct  128  PSVDVFVPSYNEDTNLLANTLASAKAMDYPADKLKVWLLDDGGTAQKRNSTKVLESQVAI  187

Query  200  ERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLART  259
             R  EL+QLC +L V Y TRERNEHAKAGN++  LE   GEL+ VFDADH P+RDFL  T
Sbjct  188  ARHDELKQLCADLDVEYLTRERNEHAKAGNLNNGLEHSTGELIAVFDADHAPARDFLMET  247

Query  260  VGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCG  319
            VGYF +DP LFLVQTPHFFINPDP++RNL   D  P ENEMFYG I RGLD+W  AFFCG
Sbjct  248  VGYFEDDPRLFLVQTPHFFINPDPLERNLRTFDTMPSENEMFYGIIQRGLDKWNAAFFCG  307

Query  320  SAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQ  379
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            SAAVL RRAL+   GF+G +ITED ETAL +H  GW S+Y+D+ +IAGLQP TFASFI Q
Sbjct  308  SAAVLSRRALESQNGFSGISITEDCETALALHGAGWNSIYVDKPLIAGLQPATFASFIGQ  367

Query  380  RGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIE  439
            R RWA GMMQ+L  + PL +RGL + QR CY++S  FW FP  R++FL APL YLFF +E
Sbjct  368  RSRWAQGMMQILRFRFPLLKRGLTLPQRFCYMSSTLFWLFPFPRVIFLFAPLFYLFFDLE  427

Query  440  IFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPR  499
            IF A+  E LAY   Y+ V+ ++QN L+   RWP +SE+YE  Q  +L  A+++ +L P
Sbjct  428  IFTASGSEFLAYTLAYMLVNLMMQNYLYGSFRWPWISELYEYVQTVHLLPAVISVMLNPH  487

Query  500  SARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWA  559
               F VTAKDE++S + +S I RP    F + +  +  T+ R  A P    V LVVGGW
Sbjct  488  KPTFKVTAKDESISVSRLSEISRPFFVIFAVQIIALAVTIYRVYAEPYKADVTLVVGGWN  547

Query  560  VLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLV  619
            ++N+++ G AL  V+E+ +R ++ RV+++  +E      G++  +A++ D S  G +L V
Sbjct  548  LINLIMSGCALGVVSERGERASSRRVRVDRRSEF---GTGDKWNSASIEDVSVHGAKLNV  604

Query  620  RLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPI  679
                +G      E  G ++FQP +  A  +   V   IR+    G    +G  +   +
Sbjct  605  FNKDLGPIKVGSE--GTLRFQP-YSGAEMVTLSV--VIRNIEPMGDITAIGCQY-VPKGA  658

Query  680  AVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
            A    +A L+F  S  W   ++A  R  G++ G    +W    SL +T+R
Sbjct  659  ADHRLIADLVFANSDQWTKFQQARRRNPGIIRG---TIWFLGLSLYQTSR  705


>TR:A0ABU1MD03 A0ABU1MD03_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
OS=Brucella pseudogrignonensis OX=419475 GN=J2782_003397
PE=4 SV=1
Length=732

 Score = 562 bits (1448),  Expect = 0.0
 Identities = 307/713 (43%), Positives = 438/713 (61%), Gaps = 14/713 (2%)

Query  18   LFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLV  77
            + + W+   V        P+  + Q  + +S +VLVA+LK F      R +++   S +V
Sbjct  6    IVICWILSAVGVLFFCFIPINLATQLSLGISVLVLVAVLKHFRIGGPWRLVVVGLCSAIV  65

Query  78   MRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPE  137
            +RY +WR  +T+PP +   +F+  +LL+  E +S+ +  L+ F+ + P   P    L  +
Sbjct  66   LRYVYWRTTQTIPPVSQLQNFIPGILLYMAELYSVMMLALSVFVVSLPRKSPDSVDLVED  125

Query  138  ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQK  197
            ++P+VD+ +PSYNE A++L+ T+AAA NM YPA    + L DDGGTDQ+C S D   +++
Sbjct  126  DMPSVDVFIPSYNEDANLLANTIAAAVNMDYPADKLAIWLLDDGGTDQKCGSSDLLASRR  185

Query  198  AQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLA  257
            A ERR  L+ LC + G+ Y TR RNEHAKAGN++  L   KGEL+ VFDADH P+R+FL
Sbjct  186  ATERRATLKALCADFGINYLTRARNEHAKAGNLNNGLAHSKGELIAVFDADHAPARNFLT  245

Query  258  RTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFF  317
            +TVGYFV++  LFLVQTPHFFINPDP++RNL   ++ P ENEMFYG I RGLD+W  AFF
Sbjct  246  QTVGYFVQNRKLFLVQTPHFFINPDPVERNLRTFNQMPSENEMFYGMIQRGLDKWNAAFF  305

Query  318  CGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFI  377
            CGSAA+L R AL    GF+G +ITED ETA+ +H++GW+S+YIDR +IAGLQP TFASFI
Sbjct  306  CGSAALLSREALSTTDGFSGVSITEDCETAVNLHAQGWESVYIDRPLIAGLQPATFASFI  365

Query  378  QQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFG  437
             QR RWA GMMQ+L  + P F  GL + QRLCY++S  FW FP  RM FLVAPL YLFF
Sbjct  366  GQRSRWAQGMMQILRYRFPPFLPGLALPQRLCYMSSTLFWLFPFARMTFLVAPLFYLFFD  425

Query  438  IEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLR  497
            ++IFVA+  E LAY   YL ++ L+QN L+   RWP +SE+YE  Q+ +L  AI++ LL
Sbjct  426  LQIFVASGGEFLAYTLIYLFINLLLQNYLYGNYRWPWISELYEYVQSVHLFPAIISVLLN  485

Query  498  PRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGG  557
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            P+   F VTAKDE+++ + +S I RP    F++ +  +L    R    P    VL+VVGG
Sbjct  486  PKKPTFNVTAKDESITVSRLSEISRPFFIIFIVLVIALLYAAYRVYTEPYKADVLIVVGG  545

Query  558  WAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRL  617
            W +LN+++ G AL  V+E+ +  +  RV++   +   I    N   TAT+ D S +G+ L
Sbjct  546  WTLLNLIMAGCALGVVSERGEWSSTVRVKVTRRSSVLINGEWN---TATIDDVSVNGMHL  602

Query  618  LVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLER-MVRGRIRSARREGGTVMVGVIFEAG  676
             V          AL  G   +   +F     ++   +   +R+ + EG  + VG +F+
Sbjct  603  TVYATDAN----ALSVGQ--RTSARFQTLATMDSDELPIEVRNVKLEGDLLSVGCLFKPT  656

Query  677  QPIAVRETVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTAR  729
                 R  VA LIF  S  W+ +++      G+L      LW  + S+ +T R
Sbjct  657  TADHHR-LVADLIFANSERWKEIQQERRTNPGVLRA---TLWFLSLSIYQTGR  705


>TR:A0A9Q8YF04 A0A9Q8YF04_ENSAD Cellulose synthase catalytic subunit [UDP-forming]
OS=Ensifer adhaerens OX=106592 GN=bcsA PE=4 SV=1
Length=725

 Score = 562 bits (1448),  Expect = 0.0
 Identities = 311/685 (45%), Positives = 418/685 (61%), Gaps = 8/685 (1%)

Query  36   PVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASMLVMRYWFWRLFETLPPPALD  95
            PV    Q ++++  V  +A+LK        R + L+  + +V+RY +WR   TLPP
Sbjct  24   PVNLQTQLIVSVLIVTFMAVLKLANAGGRWRLIALAFGTAIVLRYVYWRTTSTLPPLNQL  83

Query  96   ASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQPEELPTVDILVPSYNEPADM  155
             +F+   LL+  E +S+ +  L+ F+ A P        + P + P VD+ VPSYNE A +
Sbjct  84   ENFIPGFLLYLAEMYSVMMLSLSLFVVAMPLPPRKASSISPGKFPKVDVFVPSYNEDAGL  143

Query  156  LSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQKAQERRRELQQLCRELGVV  215
            L+ TLAAAK M YPA   TV L DDGGT Q+  S +   AQ+A  R  ELQ LC +LGV
Sbjct  144  LANTLAAAKAMDYPADKLTVWLLDDGGTLQKRNSANLVEAQRASARNAELQALCDDLGVR  203

Query  216  YSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFLARTVGYFVEDPDLFLVQTP  275
            Y TRERNEHAKAGN++  +    GEL+ VFDADH P+RDFL  TVGYF +DP LFLVQTP
Sbjct  204  YLTRERNEHAKAGNLNNGMLHSDGELIAVFDADHAPARDFLLETVGYFEQDPKLFLVQTP  263

Query  276  HFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAFFCGSAAVLRRRALDEAGGF  335
            HFF+NPDP++RNL   ++ P ENEMFYG I RGLD+W  AFFCGSAAVLRR+AL++  GF
Sbjct  264  HFFLNPDPLERNLRTFEKMPSENEMFYGIIQRGLDKWNAAFFCGSAAVLRRKALEDTEGF  323

Query  336  AGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASFIQQRGRWATGMMQMLLLKN  395
            +G +ITED ETAL +H RGW S+Y+DR +IAGLQP TFASFI QR RWA GMMQ+L+ +
Sbjct  324  SGMSITEDCETALALHGRGWNSIYVDRPLIAGLQPATFASFIGQRSRWAQGMMQILIFRF  383

Query  396  PLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFFGIEIFVATFEEVLAYMPGY  455
            PLF+ GL I QRLCY++S  FW FP+ R +FL APL YLFF +EIF A+  E LAY   Y
Sbjct  384  PLFKGGLSIPQRLCYMSSTLFWLFPIPRTIFLFAPLFYLFFDLEIFTASGGEFLAYTLAY  443

Query  456  LAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLLRPRSARFAVTAKDETLSEN  515
            + V+ ++QN L+   RWP +SE+YE AQ  +L  A+++ LLRP    F VTAKDE++ E+
Sbjct  444  MVVNLMMQNYLYGSFRWPWISELYEFAQTVHLLPAVISVLLRPSRPTFKVTAKDESILES  503

Query  516  YISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVGGWAVLNVLLVGFALRAVAE  575
             +S I RP    F +    +L T+ R    P    V LVVGGW +LN+++ G  L  V+E
Sbjct  504  RLSEIARPFFVIFAVLFVALLMTVYRVYTEPYKADVTLVVGGWNLLNLIMAGCVLGVVSE  563

Query  576  KQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSGVRLLVRLPGVGDPHPALEAGG  635
            + +R A+ RV++    E  +    ++   AT+ D S  G R  V++ G+       +  G
Sbjct  564  RGERAASRRVKVSRRCEFGV---ADKWYPATIEDVSAHGAR--VQVYGIDASTLPTDTEG  618

Query  636  LIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFEAGQPIAVRETVAYLIFGESAH  695
             I+F+P       +   +   IR+    G   ++G  +   Q       VA LIF  S
Sbjct  619  GIRFEPY--SGSGVAETLPVAIRNKEVAGDITIMGCRY-LPQVARHHSLVADLIFANSRQ  675

Query  696  WRTMREATMRPIGLLHGMARILWMA  720
            W   + A     GL+ G    LW+A
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  Sbjct  676  WSEFQSARRGNPGLVRGTFWFLWLA  700


  >TR:A0AA37WTB9 A0AA37WTB9_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
  OS=Methylobacterium tardum OX=374432 GN=GCM10007890_40670
  PE=4 SV=1
  Length=794

   Score = 561 bits (1447),  Expect = 0.0
   Identities = 316/777 (41%), Positives = 449/777 (58%), Gaps = 17/777 (2%)

  Query  17   LLFLLWVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSAASML  76
              L +L WV   V    L + PV   AQ  ++L+A+ ++ +L    D    RF+ ++  S++
  Sbjct  5    LRWLAWVGATVASLALLSQPVGTQAQLAMSLAAMAVMIVLWAVFDGPRTRFVFMALGSLV  64

  Query  77   VMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPRPLQP  136
              V+RY  WRL  TLP P    SF F L+L   E + + I F++  ++ADP  R  P
  Sbjct  65   VLRYILWRLTNTLPSPGDPVSFGFGLILLVAELYCVFILFVSLIINADPLRRDPPPAAPA  124

  Query  137  EELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPDPELAQ  196
               +LP VD+ VPSYNE A +L++TLAAA+ + YP    TV L DDGGTDQ+C   D   A
  Sbjct  125  ADLPAVDVFVPSYNEDATILAMTLAAARQLNYPPDKLTVWLLDDGGTDQKCSDADAAKAA  184

  Query  197  KAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVPSRDFL  256
               A+ RR EL+ LC ELG  Y TR RNEHAKAGN++  L   +G+LV V DADHVP R FL
  Sbjct  185  AARARRSELKALCDELGARYLTRARNEHAKAGNLNNGLAHARGDLVAVLDADHVPFRSFL  244

  Query  257  ARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDRWGGAF  316
                TVGYF +DP LFLVQTPH F+NPDP++RNL   +R P ENEMFY    RGLD+W G+F
  Sbjct  245  TETVGYFAQDPRLFLVQTPHAFLNPDPVERNLRTFERMPSENEMFYAVTQRGLDKWNGSF  304

  Query  317  FCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPETFASF  376
              FCGSAA+LRR ALDEAGGF+G TITED ETA E+HSR W S Y+D+ +IAGLQP+T   F
  Sbjct  305  FCGSAALLRRTALDEAGGFSGITITEDCETAFELHSRNWTSAYVDKPLIAGLQPDTLTDF  364

  Query  377  IQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPLIYLFF  436
              I QR RW  GM Q+LLLKNP+F++GL   Q++ YL+SM+FWFFP+ R++F+ APL+++FF
  Sbjct  365  IGQRSRWCQGMFQILLLKNPVFQKGLKPIQKIAYLSSMAFWFFPVPRLIFMFAPLLHIFF  424

  Query  437  GIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAIVTTLL  496
               ++IFVA+ +E +AY   Y+ ++ ++QN ++ + RWP VSE+YE  Q  YL +AIV+ +
  Sbjct  425  DLKIFVASVDESIAYTLTYIIINLMIQNYVYGKFRWPFVSELYEYIQGVYLVKAIVSVIA  484

  Query  497  RPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSVLLVVG  556
               PR   F VT K  TL  ++IS +  P    +LL + G      R++  PG  +++LVVG
  Sbjct  485  SPRKPTFNVTNKGATLDHDHISSLALPFFLIYLLLMLGCAVAAWRYLYEPGVTNLMLVVG  544

  Query  557  GWAVLNVLLVGFALRAVAEKQQRRAAPRVQMEVPAEAQIPAFGNRSLTATVLDASTSG--  614
               W   N+L  G +L   AE++Q    P + ++       +     S+  ++   S  G
  Sbjct  545  LWNFFNLLTAGASLGVCAERRQLERTPSLAID---RRGVLTLSGHSVDVSIERVSAEGCT  601

  Query  615  VRLLVRLPGVGDPHPALEAGGLIQFQPKFPDAPQLERMVRGRIRSARREGGTVMVGVIFE  674
              +RLL      G   P L   G +  +P      +    +   +  A R+G  +++ + F
  Sbjct  602  LRLLSGALDQGLTRPQLR--GTLSVEP--TAGARRTAPLPVHLDQATRDGRELVMRMNFG  657

  Query  675  AGQPIAVRE--TVAYLIFGESAHWRTMREATMRPIGLLHGMARILWMAAASLPKTARDFM  732
                  +A+R+   +A L++G++   R  +    R   +  G  +  W       +  R  +
  Sbjct  658  T---LAIRDYTALAGLMYGDAEAMRRFQLRRRRHKDIPSGTLQFAWWGLVEPFRALRYLL  714

  Query  733  DEPARRRRRHEEPKEKQAHLLAFGTDFSTE-PDWAGELLDPTAQVSARPNTVAWGSN  788
                   R    EEP    A L  F    S   P  AG    P+  ++A+P+    G +
  Sbjct  715  ASRQPRPVEIEEPPVYDAPLGVFAPAPSVPGPATAGAA--PSLSMAAKPSDAESGDD  769


  >TR:A0A2U8W6R4 A0A2U8W6R4_9HYPH Cellulose synthase catalytic subunit [UDP-forming]
  OS=Methylobacterium durans OX=2202825 GN=bcsA PE=4 SV=1
  Length=815

   Score = 561 bits (1447),  Expect = 0.0
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 Identities = 282/577 (49%), Positives = 387/577 (67%), Gaps = 3/577 (1%)

Query  14   VPVLLFLL-WVALLVPFGLLAAAPVAPSAQGLIALSAVVLVALLKPFADKMVPRFLLLSA  72
            +P+ L  L W+       +L   PV  + Q  ++L AV ++  L  F       ++ L
Sbjct  1    MPIFLTRLSWLVTAAAVIVLLLQPVGTAVQLEMSLGAVAVMTALWLFTRGRASHYIFLGI  60

Query  73   ASMLVMRYWFWRLFETLPPPALDASFLFALLLFAVETFSISIFFLNGFLSADPTDRPFPR  132
             S++V++Y++WRL  TLP  A   S    L+L A E + + I FL+ F++ADP  R  P
Sbjct  61   GSLVVIKYFYWRLTRTLPWSADPLSLTAGLVLLAAELYYLYILFLSLFINADPLKRA-PV  119

Query  133  PLQPE-ELPTVDILVPSYNEPADMLSVTLAAAKNMIYPARLRTVVLCDDGGTDQRCMSPD  191
            PL  E +LP+VDI VPSYNE A +L+ TLAAA+++ YPA   TV L DDGGTDQ+C  PD
Sbjct  120  PLGSETDLPSVDIFVPSYNEDASILATTLAAARSLEYPADKLTVWLLDDGGTDQKCADPD  179

Query  192  PELAQKAQERRRELQQLCRELGVVYSTRERNEHAKAGNMSAALERLKGELVVVFDADHVP  251
            P+ + +A+ RR  LQ+LC ELGV Y TR RN HAKAGN++  L+   G++VVV DADHVP
Sbjct  180  PQKSSEARARRAGLQRLCEELGVRYLTRRRNLHAKAGNLNNGLKHATGDIVVVLDADHVP  239

Query  252  SRDFLARTVGYFVEDPDLFLVQTPHFFINPDPIQRNLALGDRCPPENEMFYGKIHRGLDR  311
             R FL  T+G+F +DP LFLVQTPH F+NPDPI+RNL   +R P ENEMFY     GLD+
Sbjct  240  FRSFLRETIGHFAQDPRLFLVQTPHAFLNPDPIERNLRTFERMPSENEMFYAIGQPGLDK  299

Query  312  WGGAFFCGSAAVLRRRALDEAGGFAGETITEDAETALEIHSRGWKSLYIDRAMIAGLQPE  371
            W G+FFCGSAA+LRR ALDEAGGF+G TITED ETA E+HSRGW S+Y+D+ +IAGLQP+
Sbjct  300  WNGSFFCGSAALLRRAALDEAGGFSGITITEDCETAFELHSRGWTSIYVDKPLIAGLQPD  359

Query  372  TFASFIQQRGRWATGMMQMLLLKNPLFRRGLGIAQRLCYLNSMSFWFFPLVRMMFLVAPL  431
            T   FI QR RW  GM+Q+LLLKNP+ +RGL   QRLCY+++M++WFFP+  M+F+ APL
Sbjct  360  TLRDFIGQRSRWCQGMLQILLLKNPVLKRGLKPIQRLCYMSNMTYWFFPVPCMIFMFAPL  419

Query  432  IYLFFGIEIFVATFEEVLAYMPGYLAVSFLVQNALFARQRWPLVSEVYEVAQAPYLARAI  491
            +Y+FF ++I VA  +E +AY   Y+ V+ ++QN L+ R RWP VSE+YE  Q  +L +A
Sbjct  420  LYIFFDMKIVVANVDEAIAYTATYIVVNLMMQNYLYGRVRWPFVSELYEYVQGLFLIKAT  479

Query  492  VTTLLRPRSARFAVTAKDETLSENYISPIYRPLLFTFLLCLSGVLATLVRWVAFPGDRSV  551
             + +L PR   F VTAK+ TL ++++SP+  P    + + L G L    R+   PG  ++
Sbjct  480  ASVILSPRKPTFNVTAKNVTLDQDHLSPLALPFFVVYAILLGGSLVAAYRYAFEPGITNL  539

Query  552  LLVVGGWAVLNVLLVGFALRAVAEKQQRRAAPRVQME  588
            +LVVG W  +NV+  G AL   AE++Q  + P + ++
Sbjct  540  MLVVGLWNFVNVIKAGAALGVAAERRQTESTPSLPVD  576



Lambda      K        H
   0.326    0.139    0.426 

Gapped
Lambda      K        H
   0.267   0.0410    0.140 

Effective search space used: 20033165833660


  Database: uniprotkb_refprotswissprot
    Posted date:  Jan 9, 2026  2:46 AM
  Number of letters in database: 55,731,415,880
  Number of sequences in database:  142,881,524



Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Neighboring words threshold: 11
Window for multiple hits: 40
```