PeptideMass - Results

Submission

Sequence:

```
        10         20         30         40         50         60
MVSKGEELFT GVVPILVELD GDVNGHKFSV SGEGEGDATY GKLTLKFICT TGKLPVPWPT

        70         80         90        100        110        120
LVTTLTYGVQ CFSRYPDHMK QHDFFKSAMP EGYVQERTIF FKDDGNYKTR AEVKFEGDTL

       130        140        150        160        170        180
VNRIELKGID FKEDGNILGH KLEYNYNSHN VYIMADKQKN GIKVNFKIRH NIEDGSVQLA

       190        200        210        220        230        240
DHYQQNTPIG DGPVLLPDNH YLSTQSALSK DPNEKRDHMV LLEFVTAAGI TLGMDELYKL


EHHHHHH
```

Selected enzyme:
Trypsin
Maximum number of missed cleavages (MC):
0
Cysteines modifications:
All cysteines in reduced form
Methionines modifications:
Methionines have not been oxidized.
Mass of displayed peptides:
> 500 Dalton
Mass calculation:
Using monoisotopic masses of the occurring amino acid residues and giving peptide masses as [M+H]$^+$.

Peptide masses for your input sequence

[Theoretical pI: 5.90 / Mw (average mass): 28006.60 / Mw (monoisotopic mass): 27988.96]

mass	position	#MC	modifications	peptide sequence
4472.1752	170-210	0		HNIEDGSVQLADHYQQNTPI GDGPVLLPDNHYLSTQSALS K
2566.2931	217-239	0		DHMVLLEFVTAAGITLGMDE LYK
2437.2608	5-27	0		GEELFTGVVPILVELDGDVN GHK
2378.2577	54-74	0		LPVPWPTLVTTLTYGVQCFS R
1973.9062	142-157	0		LEYNYNSHNVYIMADK
1503.6597	28-42	0		FSVSGEGEGDATYGK
1266.5783	87-97	0		SAMPEGYVQER
1083.4979	240-247	0		LEHHHHHH
1050.5214	115-123	0		FEGDTLVNR
982.4952	133-141	0		EDGNILGHK

821.3940	81-86	0		QHDFFK
790.3552	75-80	0		YPDHMK
769.3913	47-53	0		FICTTGK
711.2944	103-108	0		DDGNYK
655.3813	98-102	0		TIFFK
602.2780	211-215	0		DPNEK
579.3137	128-132	0		GIDFK
507.2925	164-167	0		VNFK
502.3235	124-127	0		IELK

90.7% of sequence covered (you may modify the input parameters to display also peptides < 500 Da):

```
        10         20         30         40         50         60
mvskGEELFT GVVPILVELD GDVNGHKFSV SGEGEGDATY GKltlkFICT TGKLPVPWPT

        70         80         90        100        110        120
LVTTLTYGVQ CFSRYPDHMK QHDFFKSAMP EGYVQERTIF FKDDGNYKtr aevkFEGDTL

       130        140        150        160        170        180
VNRIELKGID FKEDGNILGH KLEYNYNSHN VYIMADKqkn gikVNFKirH NIEDGSVQLA

       190        200        210        220        230        240
DHYQQNTPIG DGPVLLPDNH YLSTQSALSK DPNEKrDHMV LLEFVTAAGI TLGMDELYKL


EHHHHHH
```