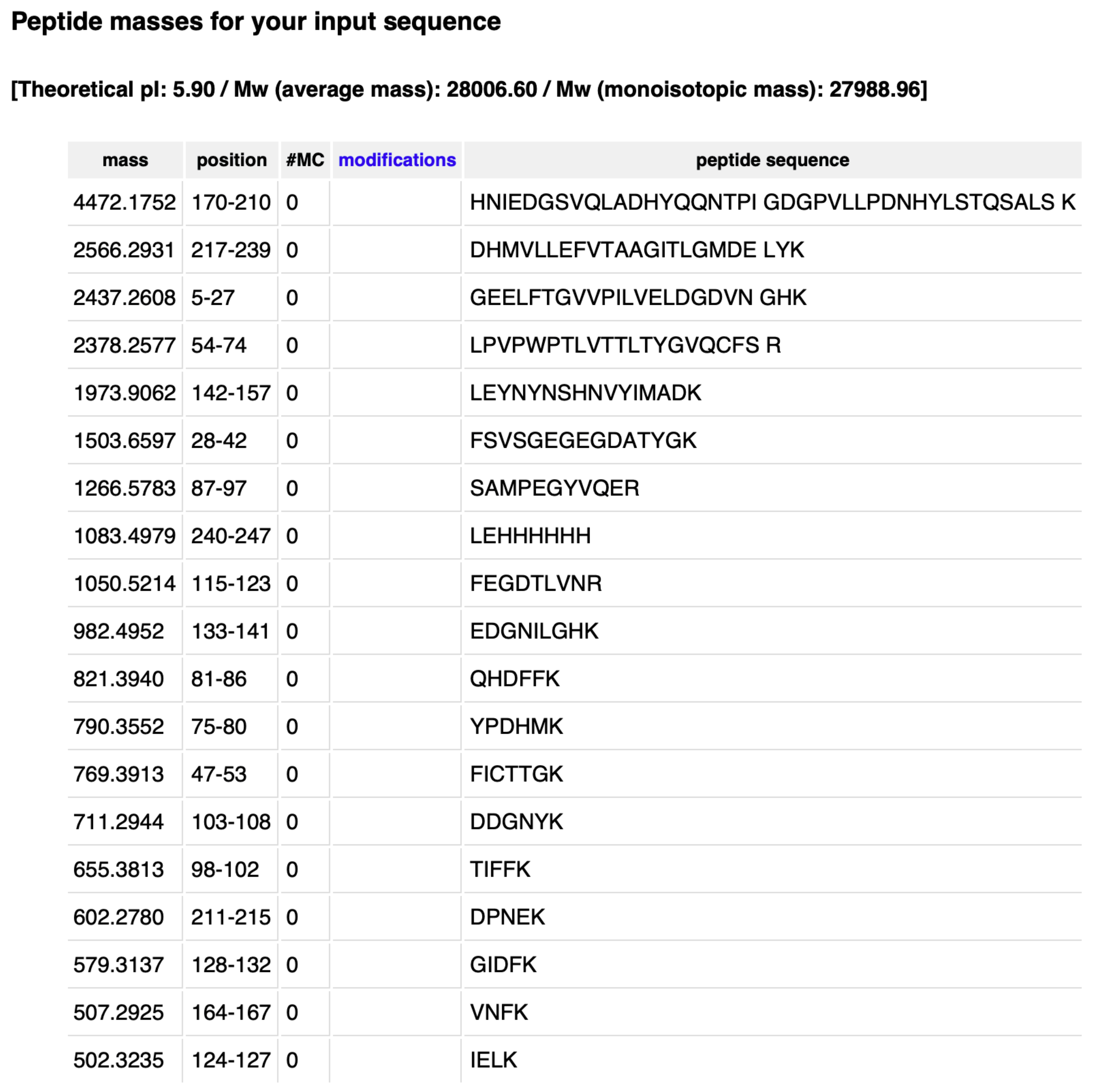

Peptide masses for your input sequence

[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