

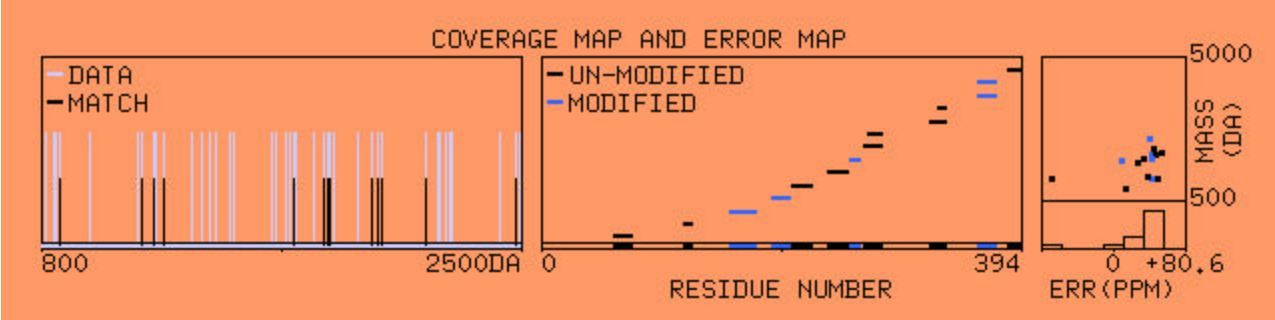
ProFound - Search Result Details


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Details for rank 1 candidate in search 20060330144555-19E4-192168001107

1. FTTSGH0150 150045 151226 [+3 L=1182 r=-1.259] (FTT0137 150045 151226 +)
====>gb|AAM35853.1| elongation factor Tu [Xanthomonas axonopodis pv. citri str.
306]gb|AAM35841.1| elongation factor Tu [Xanthomonas axonopodis pv. citri str. 306] Score =
673 bits (1737), Expect = 0.0====>ref|YP_169203.1| elongation factor Tu (EF-Tu) [Francisella
tularensis subsp.tularensis Schu 4] Score = 788 bits (2034), Expect = 0.0

Sample ID : Schu4 164 [Pass:0]
Measured peptides : 44
Matched peptides : 13
Min. sequence coverage: 40%



Note: click on the  symbol to change column format.

Measured	Avg/	Computed	Error	 Residues	Missed		
Mass(M)	Mono	Mass	 (ppm)	Start	To	Cut	Peptide sequence
866.509	M	866.497	14	118	124	0	EHILLSR
1155.608	M	1155.686	-67	383	394	1	TVGAGVVAKIIE
1155.608	M	1155.559	43	254	263	0	TTVTGVEMFR
							(1)+O@M;
1198.691	M	1198.630	51	269	280	0	GEAGDNVGILVR
1232.657	M	1232.609	39	326	334	0	GYRPQFYFR
1695.975	M	1695.926	29	265	280	1	LLDRGEAGDNVGILVR
1802.946	M	1802.926	11	359	374	0	MTITLINPIAMDEGLR
							(1)+O@M;
1815.937	M	1815.874	34	60	75	0	GITINTSHVEYESPNR
1819.001	M	1818.921	44	359	374	0	MTITLINPIAMDEGLR
							(2)+O@M;
1974.060	M	1973.976	43	189	205	0	IVELVQAMDDYIPAPER
							(1)+O@M;
1990.096	M	1990.000	49	320	334	1	HTPFFKGYRPQFYFR
2008.205	M	2008.094	55	235	253	0	GVVNIGDEVEVVGIRPTQK
2162.223	M	2162.125	46	206	224	0	DTEKPFILPIEDVFSISGR
2481.274	M	2481.172	41	156	177	0	ELLDQYEFPGDDTPVIMGSALR
							(1)+O@M;

Unmatched Monoisotopic Masses:

814.925 848.154 854.588 974.406 1140.026 1208.595 1337.763 1373.887 1395.788
1417.851 1419.354 1470.019 1486.858 1618.983 1634.829 1666.673 1681.482 1702.257
1765.797 1825.108 1834.218 1835.951 1840.131 1920.796 2206.300 2216.653 2236.102
2247.106 2256.846 2427.778 2498.309

Search again using unmatched masses:

Search again in All taxa