

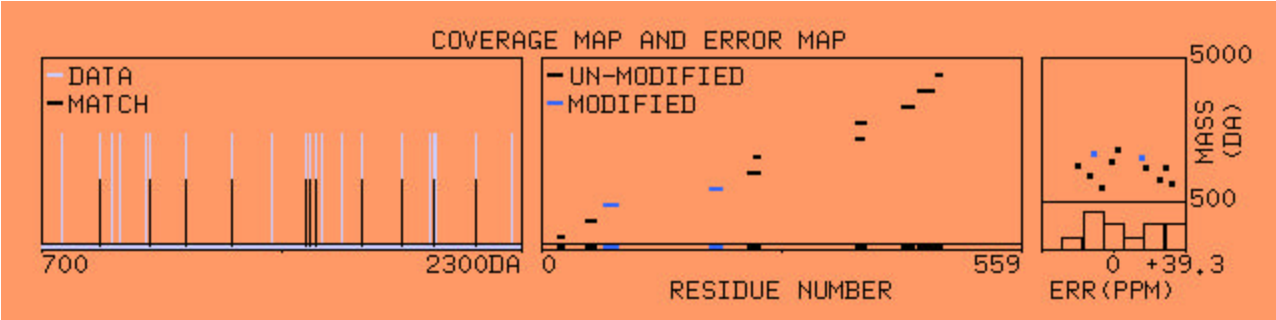
ProFound - Search Result Details


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Details for rank 1 candidate in search 20060404145732-1AE4-192168001107

1. FTTSGH1925 1764261 1765937 [+3 L=1677 r=-1.212] (FTT1696 1764306 1765937 +)
====>ref|YP_047391.1| chaperone Hsp60, peptide-dependent ATPase, heat shock
protein[Acinetobacter sp. ADP1] Score = 797 bits (2059), Expect = 0.0====>gb|AAT77113.1|
GroEL [Francisella tularensis subsp. tularensis]ref|YP_170601.1| Chaperone protein, groEL
[Francisella tularensis subsp. tularensis Score = 1037 bits (2682), Expect =
0.0====>emb|CAA67358.1| groEL [Francisella tularensis]sp|P94798|CH60_FRATU 60 kDa
chaperonin (Protein Cpn60) (groEL protein) Score = 1030 bits (2664), Expect = 0.0

Sample ID : Schu4 240 [Pass:0]
Measured peptides : 21
Matched peptides : 11
Min. sequence coverage: 24%



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
896.538	M	896.544	-6	460	467	1	KAIEAPLR
1063.564	M	1063.529	33	20	28	0	QVLFSDEAR
1182.715	M	1182.685	25	247	257	0	DLLPILEGVSK
1337.567	M	1337.584	-13	366	377	0	ANIAEANSYDR
1580.916	M	1580.888	18	420	436	0	AAVEEGIVAGGGVALIR
1594.767	M	1594.722	29	366	379	1	ANIAEANSYDREK
1618.862	M	1618.892	-19	52	66	1	NVVLDSFGTPTITK
1766.028	M	1766.029	-1	242	257	1	ISNIRDLLPILEGVSK
1900.843	M	1900.814	15	197	212	0	GFEDELVDVEGMQFDR
							(1)+O@M;
2007.961	M	2007.981	-10	74	90	1	EIELEDKFENMGAQIVK
							(1)+O@M;
2147.053	M	2147.048	2	440	459	0	ALDGLTGENDDQNYGIALLR

Unmatched Monoisotopic Masses:

769.555 935.534 962.434 1047.548 1470.900 1638.927 1703.258 1993.989 2013.110
2270.245

Search again using unmatched masses:

Search again

 in

All taxa