

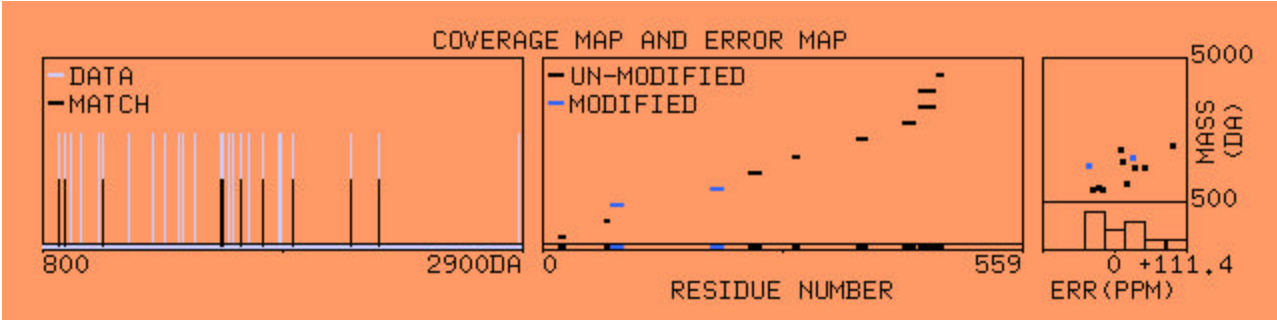
ProFound - Search Result Details

Copyright © 1997-2002 ProteoMetrics LLC

Details for rank 1 candidate in search 20060330142321-1B50-192168001107

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 159 [Pass:0]  
Measured peptides : 25  
Matched peptides : 10  
Min. sequence coverage: 22%



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
874.413	M	874.441	-31	293	300	1	APGFGDRR
874.413	M	874.428	-17	74	80	0	EIELEDK
896.523	M	896.544	-23	460	467	1	KAIEAPLR
1063.551	M	1063.529	20	20	28	0	QVLFSDEAR
1580.939	M	1580.888	33	420	436	0	AAVEEGIVAGGGVALIR
1594.799	M	1594.722	49	366	379	1	ANIAEANSYDREK
1665.773	M	1665.839	-39	81	95	1	FENMGAQIVKEVASK
							(1)+O@M;
1766.053	M	1766.029	14	242	257	1	ISNIRDLLPILEGVSK
1900.869	M	1900.814	29	197	212	0	GFEDEL DVVEGMQFDR
							(1)+O@M;
2147.071	M	2147.048	11	440	459	0	ALDGLTGENDDQNYGIALLR
2275.354	M	2275.143	93	440	460	1	ALDGLTGENDDQNYGIALLRK

Unmatched Monoisotopic Masses:

925.520 974.446 1047.547 1184.670 1288.087 1337.821 1395.833 1417.898 1470.078  
1618.992 1634.897 1702.345 1834.310 1847.746 2888.841

Search again using unmatched masses:

Search again

 in 

All taxa