

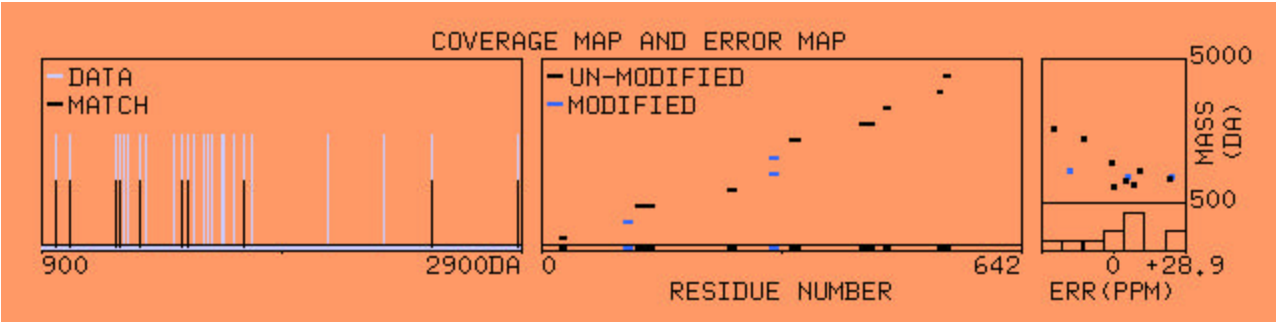
ProFound - Search Result Details


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Details for rank 1 candidate in search 20060330141902-1840-192168001107

1. FTTSGH1433 1292668 1290743 [-2 L=1926 r=-1.202] (FTT1269c 1292668 1290743 -)
====>sp|P48205|DNAK_FRATU Chaperone protein dnaK (Heat shock protein 70) (Heat shock
70 kDaprotein) (HSP70) Score = 1232 bits (3188), Expect = 0.0====>ref|YP_170225.1|
Chaperone protein dnaK (heat shock protein family 70 protein)[Francisella tularensis subsp.
tularensis Schu 4] Score = 1239 bits (3207), Expect = 0.0

Sample ID : Schu4 158 [Pass:0]
Measured peptides : 25
Matched peptides : 11
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
957.503	M	957.503	0	531	538	0	FHDLVTAR
1023.518	M	1023.509	9	26	34	0	VIENAEGHR
1210.640	M	1210.634	5	459	469	0	FDLADIPPAPR
1226.628	M	1226.600	23	539	549	0	NTADNLIHSSR
1310.685	M	1310.653	24	307	317	0	FESLVSDLVMR
							(1)+O@M;
1312.688	M	1312.680	6	112	123	0	MAPPQVSAEVL
							(1)+O@M;
1486.814	M	1486.798	11	334	347	0	SDITEVLLVGGQTR
1509.759	M	1509.786	-18	305	317	1	AKFESLVSDLVMR
							(1)+O@M;
1748.916	M	1748.916	0	249	263	1	EQGIDLHNDKLALQR
2525.220	M	2525.250	-12	425	447	0	SQVFSTAEDNQPAVTIHVLQGER
2884.307	M	2884.375	-24	128	153	0	TAEDYLGEPVTEAVITVPAYFNDSQR

Unmatched Monoisotopic Masses:

1249.661	1259.916	1335.686	1456.833	1539.849	1576.772	1593.772	1609.817	1654.849
1666.903	1702.512	1782.997	2094.963	2330.107				

Search again using unmatched masses:

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 in

All taxa