

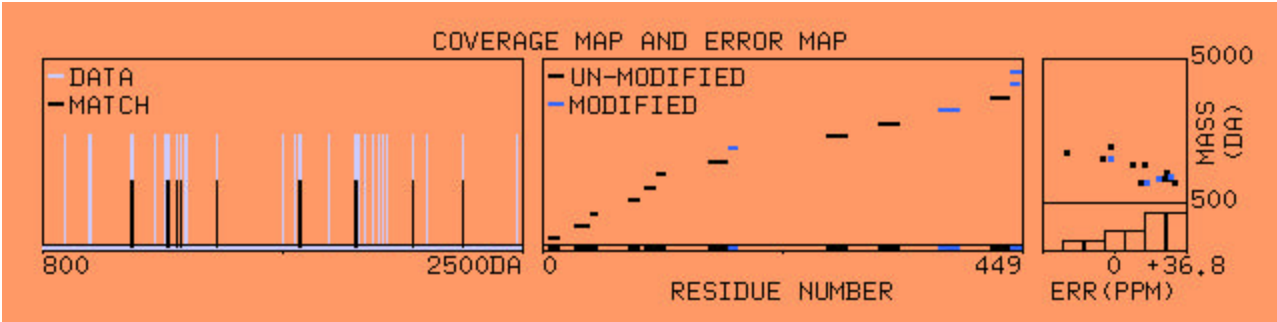
ProFound - Search Result Details


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Details for rank 1 candidate in search 20060404153533-1E94-192168001107

1. FTTSGH0411 383364 382018 [-1 L=1347 r=-1.217] (FTT0380c 383364 382018 -)
====>emb|CAA77805.1| Glutamate Dehydrogenase [Clostridium symbiosum]pir||S22403
glutamate dehydrogenase (EC 1.4.1.2) - Clostridium symbiosum Score = 578 bits (1489),
Expect = e-163====>ref|YP_169425.1| NAD(P)-specific glutamate dehydrogenase [Francisella
tularensissubsp. tularensis Schu 4] Score = 905 bits (2338), Expect = 0.0

Sample ID : Schu4 246 [Pass:0]
Measured peptides : 33
Matched peptides : 14
Min. sequence coverage: 41%



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
1113.600	M	1113.585	13	108	116	0	FLGFEEQVFK
1117.573	M	1117.554	17	439	448	0	VAEAMIQQGR
							(1)+O@M;
1119.626	M	1119.592	31	45	53	0	YIEENILAR
1240.658	M	1240.623	28	82	92	0	YQFNGAIGPFK
1246.702	M	1246.670	25	97	107	0	FHPSVYSGIIK
1280.647	M	1280.618	23	439	449	1	VAEAMIQQGRY
							(1)+O@M;
1294.602	M	1294.565	29	175	184	0	EIGYMYGQYR
							(1)+O@M;
1419.810	M	1419.772	27	6	17	1	YIDSVIAQVEKR
1708.941	M	1708.914	16	30	44	0	EVFSTLKPALHNPK
1715.899	M	1715.883	9	157	174	0	HIGPDIDVPAGDIGVGK
1904.897	M	1904.900	-2	372	391	0	AANAGGVAVSGLEMSQNSAR
							(1)+O@M;
1912.957	M	1912.968	-5	421	438	0	YNLGYNLVAGANLAGFEK
2110.986	M	2111.037	-24	316	335	0	ADIAIPAATQNEIDVEDAQK
2287.168	M	2287.172	-2	267	286	1	GFVHDPEGITTDEKIEFLK

Unmatched Monoisotopic Masses:

882.520 963.562 975.069 1199.706 1233.662 1243.624 1309.634 1311.640 1652.918
1696.957 1816.871 1920.532 1940.934 1975.000 1993.976 2009.131 2024.025 2163.170
2482.184

Search again using unmatched masses:

Search again in