

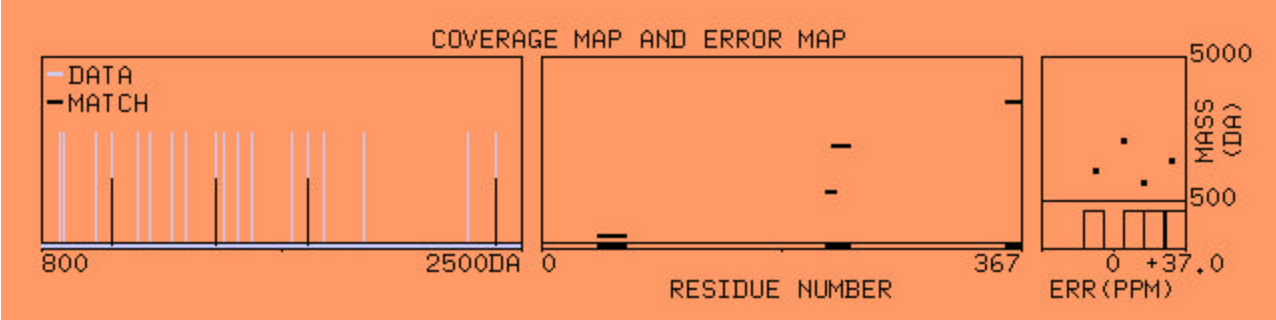
ProFound - Search Result Details


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Details for rank 1 candidate in search 20060404153133-1CAC-192168001107

1. FTTSGH0001 1558 2658 [+1 L=1101 r=-1.194] (FTT0002 1558 2658 +)
====>ref|ZP_00318458.1| COG0592: DNA polymerase sliding clamp subunit (PCNA homolog)[Microbulbifer degradans 2-40] Score = 286 bits (733), Expect = 6e-76====>ref|YP_169085.1| DNA polymerase III, beta chain [Francisella tularensis subsp.tularensis Schu 4] Score = 720 bits (1858), Expect = 0.0

Sample ID : Schu4 245 [Pass:0]
Measured peptides : 19
Matched peptides : 4
Min. sequence coverage: 15%



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
1050.606	M	1050.589	16	218	226	1	ICLGKNYLK
1420.732	M	1420.745	-9	356	367	1	DNSLFIIMPMKI
1747.983	M	1747.929	31	223	237	1	NYLKAIFGNYAFISK
2411.169	M	2411.155	6	44	66	0	ITASDLDTTEISCNIAVSCNTTIK

Unmatched Monoisotopic Masses:

864.467 868.484 882.512 996.563 1141.604 1183.696 1261.709 1314.696 1450.783
1495.779 1547.806 1685.880 1802.840 1940.966 2313.157

Search again using unmatched masses:

Search again in All taxa