

ProFound - Search Result Summary

Version 2002.03.01

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Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	1.18	FTTSGH1445 1301196 1300903 [-1 L= 294 r=-1.217] (FTT1281c 1301196 1300903 -) =====>emb CAA34495.1 ORF102 [Pseudomonas putida]pir T01754 hypothetical protein 102 - Pseudomonas putida Score = 107 bits (266), Expect = 1e-22=====>ref YP_170237.1 Sigma-54 modulation protein [Francisella tularensis subsp.tularensis Schu 4] Score = 198 bits (504), Expect = 4e-50 FTTSGH1496 1357102 1356791 [-2 L= 312 r=-1.294] (FTT1328 1356834 1354072 -) (FTT1328 1357102 1356836 -) =====>ref ZP_00514536.1 FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal[Crocospaera watsonii WH 8501] Score = 78.2 bits (191), Expect = 7e-14 FTTSGH0569 544186 544359 [+1 L= 174 r=-1.198] (FTT0521 543955 544362 +) =====>Hypothetical ORF FTTSGH569 FTTSGH1913 1757966 1757799 [-3 L= 168 r=-1.256] [ShadowedBy _1962] (None identical in .gff) =====>ref YP_069783.1 HAAAP family tyrosine:H+ symporter, tyrP [Yersiniapseudotuberculosis IP 32953] Score = 49.7 bits (117), Expect = 3e-05=====>ref YP_170593.1 aromatic amino acid transporter of the HAAAP family [Francisellatularensis subsp. tularensis Schu 4] Score = 107 bits (267), Expect = 1e-22 FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61 FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) =====>ref YP_169428.1 hypothetical	37	5.9	11.16	
2	1.2e-003	0.22	FTTSGH1496 1357102 1356791 [-2 L= 312 r=-1.294] (FTT1328 1356834 1354072 -) (FTT1328 1357102 1356836 -) =====>ref ZP_00514536.1 FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal[Crocospaera watsonii WH 8501] Score = 78.2 bits (191), Expect = 7e-14 FTTSGH0569 544186 544359 [+1 L= 174 r=-1.198] (FTT0521 543955 544362 +) =====>Hypothetical ORF FTTSGH569 FTTSGH1913 1757966 1757799 [-3 L= 168 r=-1.256] [ShadowedBy _1962] (None identical in .gff) =====>ref YP_069783.1 HAAAP family tyrosine:H+ symporter, tyrP [Yersiniapseudotuberculosis IP 32953] Score = 49.7 bits (117), Expect = 3e-05=====>ref YP_170593.1 aromatic amino acid transporter of the HAAAP family [Francisellatularensis subsp. tularensis Schu 4] Score = 107 bits (267), Expect = 1e-22 FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61 FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) =====>ref YP_169428.1 hypothetical	21	8.7	11.98	
3	9.3e-005	-	FTTSGH0569 544186 544359 [+1 L= 174 r=-1.198] (FTT0521 543955 544362 +) =====>Hypothetical ORF FTTSGH569 FTTSGH1913 1757966 1757799 [-3 L= 168 r=-1.256] [ShadowedBy _1962] (None identical in .gff) =====>ref YP_069783.1 HAAAP family tyrosine:H+ symporter, tyrP [Yersiniapseudotuberculosis IP 32953] Score = 49.7 bits (117), Expect = 3e-05=====>ref YP_170593.1 aromatic amino acid transporter of the HAAAP family [Francisellatularensis subsp. tularensis Schu 4] Score = 107 bits (267), Expect = 1e-22 FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61 FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) =====>ref YP_169428.1 hypothetical	14	9.8	6.83	
4	8.0e-006	-	FTTSGH1913 1757966 1757799 [-3 L= 168 r=-1.256] [ShadowedBy _1962] (None identical in .gff) =====>ref YP_069783.1 HAAAP family tyrosine:H+ symporter, tyrP [Yersiniapseudotuberculosis IP 32953] Score = 49.7 bits (117), Expect = 3e-05=====>ref YP_170593.1 aromatic amino acid transporter of the HAAAP family [Francisellatularensis subsp. tularensis Schu 4] Score = 107 bits (267), Expect = 1e-22 FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61 FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) =====>ref YP_169428.1 hypothetical	13	5.0	6.17	
5	1.1e-006	-	FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61 FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) =====>ref YP_169428.1 hypothetical	9	9.0	13.51	
6	6.6e-007	-	FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) =====>ref YP_169428.1 hypothetical	10	10.5	13.33	

protein FTT0383 [Francisella tularensis
subsp.tularensis Schu 4] Score = 231 bits
(590), Expect = 4e-60

NOTE:

1. To search again using [unmatched masses](#), click the symbol .

Input Summary

Search id 20060404165959-1DBC-192168001107
Sequences 2059
Date & Time Tue Apr 04 21:59:59 2006 UTC (Search Time: 0.05 sec.)
Sample ID Schu4 273
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 15 kDa
pI Range 0.0 -14.0
Digestion Trypsin
Missed Cuts 1
Modifications +O@M(Partial);
Charge State MH+
Masses (avg)
Tolerance (avg) 1.00 ppm
Masses (mon) 932.535 948.484 975.295 1387.741 1453.687 1703.606 1855.811
Tolerance (mon) 40.00 ppm
Number of 7
Peptides

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