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BLAST Results

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PSI blast Iteration 1

Job title: T0949 B7JAQ5_ACIF2, Acidithiobacillus ferrooxidans,...

RID [766P5WC1014](#) (Expires on 02-26 05:29 am)

Query ID	lcIIQuery_84350	Database Name	pdb
Description	T0949 B7JAQ5_ACIF2, Acidithiobacillus ferrooxidans, 183 residuesl	Description	PDB protein database
Molecule type	amino acid	Program	BLASTP 2.8.1+
Query Length	183		

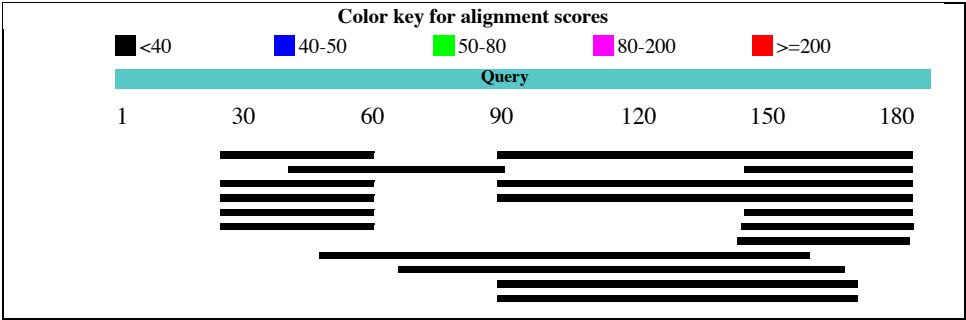
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Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 17 Blast Hits on 17 subject sequences



Descriptions

Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
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Select:AllNone Selected:0

[Alignments](#) [Download](#) [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) [Show/hide columns of the table presenting sequences with E-value WORSE than threshold](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, Structure Of Copper-containing Nitrite Reductase From Geobacillus Thermodenitrificans Without Chloride	33.1	33.1	51%	0.15	29.29%	3X1E_A (scored below threshold on previous iteration)		✓
Chain A, H294m Mutant Of Copper-containing Nitrite Reductase From Geobacillus Thermodenitrificans	33.1	33.1	20%	0.15	42.50%	3X1F_A (scored below threshold on previous iteration)		✓
Chain A, Copper-containing Nitrite Reductase From Geobacillus Thermodenitrificans In Complex With Formate	33.1	33.1	51%	0.16	29.29%	3WKQ_A (scored below threshold on previous iteration)		✓
Chain A, Crystal Structure Of The N-terminal 1-37 Residues Deleted Mutant Of Geobacillus Copper Nitrite Reductase	33.1	33.1	51%	0.16	29.29%	3WIA_A (scored below threshold on previous iteration)		✓
Chain A, Crystal Structure Of Copper Nitrite Reductase From Geobacillus Kaustophilus	33.1	33.1	20%	0.17	42.50%	3W19_A (scored below threshold on previous iteration)		✓
Chain A, Nitrite-bound Thermostable Copper Nitrite Reductase At 320 K	31.2	31.2	21%	0.71	36.00%	3X1N_A (scored below threshold on previous iteration)		✓
Chain A, C135a Mutant Of Geobacillus Thermodenitrificans Copper-containing Nitrite Reductase In Complex With Nitrite	30.8	30.8	21%	0.83	36.00%	3WKP_A (scored below threshold on previous iteration)		✓
Chain L, Crystal Structure Of Rv144-elicited Antibody Ch58 In Complex With V2 Peptide	29.6	29.6	61%	2.0	26.61%	4HPO_L (scored below threshold on previous iteration)		✓
Chain A, RED COPPER PROTEIN NITROCYANIN FROM NITROSOMONAS EUROPAEA	28.5	28.5	26%	2.5	30.61%	1IBY_A (scored below threshold on previous iteration)		✓
Chain A, Crystal Structure Of A Zinc Containing Peptidase From Vibrio Cholerae	28.9	28.9	55%	3.4	24.76%	2GU1_A (scored below threshold on previous iteration)		✓
Chain B, Crystal Structure Analysis Of Bovine Bc1 With Azoxystrobin	28.1	28.1	19%	6.5	43.24%	1SQB_B (scored below threshold on previous iteration)		✓
Chain O, Cytochrome Bc1 Bound To The 4(1h)-pyridone Gw844520	28.1	28.1	19%	6.5	43.24%	4D6T_O (scored below threshold on previous iteration)		✓
Chain B, Cytochrome b-c1 complex subunit 2,	28.1	28.1	19%	6.7	43.24%	6HAW_B (scored below threshold on previous iteration)		✓

mitochondrial						previous iteration)	
Chain B, Cytochrome Bc1 Complex From Bovine	28.1	28.1	19%	6.8	43.24%	1BGY_B (scored below threshold on previous iteration)	
Chain B, Crystal Structure Of Bovine Mitochondrial Cytochrome Bc1 Complex, Alpha Carbon Atoms Only	28.1	28.1	19%	7.1	43.24%	1QCR_B (scored below threshold on previous iteration)	
Chain A, Endo-beta-1,2-glucanase From Chitinophaga Pinensis - Ligand Free Form	28.1	28.1	44%	8.5	28.57%	5GZH_A (scored below threshold on previous iteration)	
Chain A, Endo-beta-1,2-glucanase From Chitinophaga Pinensis - Sophorotriose And Glucose Complex	27.7	27.7	44%	9.1	28.57%	5GZK_A (scored below threshold on previous iteration)	

Alignments

Chain A, Structure Of Copper-containing Nitrite Reductase From Geobacillus Thermodenitrificans Without Chloride
Sequence ID: **3X1E_A** Length: 352 Number of Matches: 1
Range 1: 110 to 188

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	0.15()	Compositional matrix adjust.	29/99(29%)	39/99(39%)	24/99(24%)	
Features:						
Query	88	SIGRTLVS RDNGFPKS---QAI AVGWKDNFFDGV PITSGGQTGPV PAFSVSLNGGQKYTF				144
		+I TL + D P S A+ +F D +P SG T P				
Sbjct	110	TIHFTLKNMDPVVPHSMD FHAVHASPSKDFIDVMPNKS GTFTYPA-----				154
Query	145	SFVVPNKPGKWEYGCFLQ-TGQHFMNGMHGILDILPAQG			182	
		NKPG + Y C + QH NGMHG++ + P G				
Sbjct	155	-----NKPGVFMYHCGTKPVLQHIANGMHGVIIVKPKNG			188	

Chain A, H294m Mutant Of Copper-containing Nitrite Reductase From Geobacillus Thermodenitrificans
Sequence ID: **3X1F_A** Length: 352 Number of Matches: 1

See 1 more title(s)
Range 1: 149 to 188

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	0.15()	Compositional matrix adjust.	17/40(43%)	23/40(57%)	2/40(5%)	
Features:						
Query	145	SFVVP-NKPGKWEYGCFLQ-TGQHFMNGMHGILDILPAQG +F P NKPG + Y C + QH NGMHG++ + P G		182		
Sbjct	149	TFTYPANKPGVFMYHCGTKPVLQHIANGMHGVIIKPKNG		188		

Chain A, Copper-containing Nitrite Reductase From Geobacillus Thermodenitrificans In Complex With Formate
Sequence ID: **3WKQ_A** Length: 323 Number of Matches: 1

See 13 more title(s)
Range 1: 81 to 159

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	0.16()	Compositional matrix adjust.	29/99(29%)	39/99(39%)	24/99(24%)	
Features:						
Query	88	SIGRTLVS RDNGFPKS---QAI AVGWKDNFFDGV PITSGGQTGPVPAFSVSLNGGQKYTF				144
		+I TL + D P S A+ +F D +P SG T P				
Sbjct	81	TIHFTLKNMDPVVPHSMD FHAVHASPSKDFIDVMPNKS GTFTYPA-----				125
Query	145	SFVVPNKP GKWEYGCFLQ-TGQHFMNGMHGILDILPAQG		182		
		NKPG + Y C + QH NGMHG++ + P P G				
Sbjct	126	-----NKPGVFMYHCGTKPVLQHIANGMHGVIIVKPKNG		159		

Chain A, Crystal Structure Of The N-terminal 1-37 Residues Deleted Mutant Of Geobacillus Copper Nitrite Reductase
Sequence ID: **3WIA_A** Length: 287 Number of Matches: 1

See 8 more title(s)
Range 1: 45 to 123

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	0.16()	Compositional matrix adjust.	29/99(29%)	39/99(39%)	24/99(24%)	
Features:						
Query	88	SIGRTLVSRDNGFPKS---QAIAVGWKDNFFDGVPIITSGGQTGPVPAFSVSLNGGQKYTF				144
		+I TL + D P S A+ +F D +P SG T P				
Sbjct	45	TIHFTLKNMDPVVPHSMDFHAVHASPSKDFIDVMPNKSGTFTYPA-----				89
Query	145	SFVVVPNKPGKWEYGCFLQ-TGQHFMNGMHGILDILPAQG				182
		NKPG + Y C + QH NGMHG++ + P G				
Sbjct	90	-----NKPGVFMYHCGTKPVLQHIANGMHGVIIIVKPKNG				123

Chain A, Crystal Structure Of Copper Nitrite Reductase From Geobacillus Kaustophilus
Sequence ID: **3WI9_A** Length: 324 Number of Matches: 1
Range 1: 121 to 160

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	0.17()	Compositional matrix adjust.	17/40(43%)	23/40(57%)	2/40(5%)	
Features:						
Query	145	SFVVVP-NKPGKWEYGCFLQ-TGQHFMNGMHGILDILPAQG				182
		+F P NKPG + Y C + QH NGMHG++ + P G				
Sbjct	121	TFTYPANKPGVFMYHCGTKPVLQHIANGMHGVIIIVKPKNG				160

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