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BLAST Results

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PSI blast Iteration 1

Job title: T0953s2 Adhesin tip, Salmonella phage vB_SenMS16,...

RID	9JG90J3T014 (Expires on 03-27 04:59 am)	Database Name	pdb
Query ID	lcIIQuery_229643	Description	PDB protein database
Description	T0953s2 Adhesin tip, Salmonella phage vB_SenMS16, subunit 2, 249 residues!	Program	BLASTP 2.9.0+
Molecule type	amino acid		
Query Length	249		

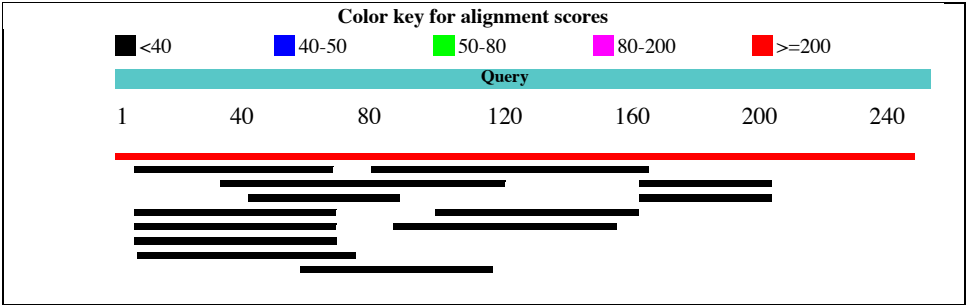
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Graphic Summary

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



Distribution of the top 14 Blast Hits on 14 subject sequences



Descriptions

Description	Max score	Total score	Query cover	E value	Perc. ident	Accession	Select for PSI blast	Used to build PSSM
Chain D, Receptor recognition protein	487	487	100%	4e-177	100.00%	6F45_D (scored below threshold on previous iteration)		

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	Perc. ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, The Crystal Structure Of The Domain Of The Putative Light And Redox Sensing Histidine Kinase From Haloarcula Marismortui	31.2	31.2	34%	0.45	25.00%	3EEH_A (scored below threshold on previous iteration)		
Chain A, 2.75 Angstrom Resolution Crystal Structure of UDP-N-acetylglucosamine 1-carboxyvinyltransferase from Pseudomonas putida in Complex with Uridine-diphosphate-2(n-acetylglucosaminy)l butyric acid, (2R)-2-(phosphonoxy)propanoic acid and Magnesium	30.8	30.8	35%	1.6	28.41%	6CN1_A (scored below threshold on previous iteration)		
Chain A, The crystal structure of Munc13-1 C1C2BMUN domain	30.4	30.4	24%	2.2	31.15%	5UE8_A (scored below threshold on previous iteration)		
Chain A, Crystal Structure Of Piwi/argonaute/zwillig(paz) Domain From Thermococcus Thioreducens	28.5	28.5	18%	4.9	38.30%	3DA5_A (scored below threshold on previous iteration)		
Chain A, Crystal Structure Of Munc13-1 Mun Domain	29.3	29.3	24%	5.1	30.65%	4Y21_A (scored below threshold on previous iteration)		
Chain A, CRYSTAL STRUCTURE OF MUNC13-1 MUN DOMAIN	29.3	29.3	24%	5.3	30.65%	5UF7_A (scored below threshold on previous iteration)		
Chain A, Homoserine dehydrogenase from Thermoplasma volcanium complexed with NAD	29.3	29.3	16%	5.3	40.00%	3JSA_A (scored below threshold on previous iteration)		
Chain A, Protein unc-13 homolog A	29.3	29.3	24%	5.4	30.65%	6A30_A (scored below threshold on previous iteration)		
Chain A, Crystal Structure Of Homoserine Dehydrogenase From Thermoplasma Volcanium	29.3	29.3	16%	5.4	40.00%	3C8M_A (scored below threshold on previous iteration)		

Chain A, Scabin (W155A) toxin from Streptomyces scabies	28.5	28.5	25%	7.2	26.98%	5UVQ_A (scored below threshold on previous iteration)	
Chain S, Solution Structure Of Nfgf-1	27.7	27.7	26%	8.0	27.54%	1FMM_S (scored below threshold on previous iteration)	
Chain A, X-Ray Analyses Of 3-Hydroxybutyrate Dehydrogenase From Alcaligenes Faecalis	28.1	28.1	23%	9.3	30.51%	2YZ7_A (scored below threshold on previous iteration)	
Chain A, The Reduced Form Of Mj0499	28.5	28.5	27%	9.9	25.71%	4NQY_A (scored below threshold on previous iteration)	

Alignments

Chain D, Receptor recognition protein
Sequence ID: **6F45_D** Length: 249 Number of Matches: 1
Range 1: 1 to 249

Score	Expect	Method	Identities	Positives	Gaps	Frame
487 bits(1254)	4e-177()	Compositional matrix adjust.	249/249(100%)	249/249(100%)	0/249(0%)	
Features:						
Query 1		MAVQGPWVGSSYVAETGQNWASLAANELRVTERPFWISSFIGRSKEEIWWTGENHSFNK				60
Sbjct 1		MAVQGPWVGSSYVAETGQNWASLAANELRVTERPFWISSFIGRSKEEIWWTGENHSFNK				60
Query 61		DWLIGELNRNGGTPVVINIRAHQVSYTPGAPLFEFPGDLPNAYITLNIYADIYGRGGTGG				120
Sbjct 61		DWLIGELNRNGGTPVVINIRAHQVSYTPGAPLFEFPGDLPNAYITLNIYADIYGRGGTGG				120
Query 121		VAYLGGNPGGDCIHNWIGNRLRINNQGWCIGGGGGGGGFRVGHTAAGGGGGRPLGAGGVS				180
Sbjct 121		VAYLGGNPGGDCIHNWIGNRLRINNQGWCIGGGGGGGGFRVGHTAAGGGGGRPLGAGGVS				180
Query 181		SLNLNGDNATLGAPGRGYQLGNDYAGNGGDVGNPGSASSAEMGGGAAGRAVVGTSPOWIN				240
Sbjct 181		SLNLNGDNATLGAPGRGYQLGNDYAGNGGDVGNPGSASSAEMGGGAAGRAVVGTSPOWIN				240
Query 241		VGNIAGSWL 249				
Sbjct 241		VGNIAGSWL 249				

Chain A, The Crystal Structure Of The Domain Of The Putative Light And Redox Sensing Histidine Kinase From Haloarcula Marismortui
Sequence ID: **3EEH_A** Length: 125 Number of Matches: 1
Range 1: 12 to 94

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.2 bits(69)	0.45()	Compositional matrix adjust.	23/92(25%)	35/92(38%)	15/92(16%)	
Features:						
Query 80		RAHQVSYTPGAPLFEFPGDLPNAYITLNIYADIYGRGGTGGVAYLGGNPGGDCIHNWI--				137
Sbjct 12		R+++L+EF DL++YDI+GRVA L NP H+++RVRELTEATNDILWEFTADLSEVLVINSAYEDIWGR----SVAKLRENP-----HDFLNG				62
Query 138		----GNRLRINNQGWCIGGGGGGGGFRVGHT 165				
Sbjct 63		L++G RV TEIHPEDRELMKDTMQSLMDGESADVECRVNATE 94				

Chain A, 2.75 Angstrom Resolution Crystal Structure of UDP-N-acetylglucosamine 1-carboxyvinyltransferase from Pseudomonas putida in Complex with Uridine-diphosphate-2(n-acetylglucosaminyI) butyric acid, (2R)-2-(phosphonoxy)propanoic acid and Magnesium
Sequence ID: **6CN1_A** Length: 424 Number of Matches: 1

See 7 more title(s)
Range 1: 262 to 329

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.8 bits(68)	1.6()	Compositional matrix adjust.	25/88(28%)	39/88(44%)	20/88(22%)	
Features:						
Query	34	PFWISSFIGRSKEEIEWWTGENHSFNKDWLIGELNRGGTPVVINIRAHQVSYPGAPLF				93
		P + + + + KE G + + +DW+ EL G P +N+R AP				
Sbjct	262	PTILEAVLEKLKE-----AGADINTGEDWI--ELDMHGKRPKAVNLRT-----APYP				306
Query	94	EFPGLPNAYITLNIYADIYGRGGTGGV				121
		FP D+ +I+LN A+ GTG V				
Sbjct	307	AFPTDMQAQFISLNAIAE-----GTGAV				329

Chain A, The crystal structure of Munc13-1 C1C2BMUN domain
Sequence ID: **5UE8_A** Length: 961 Number of Matches: 1

See 1 more title(s)
Range 1: 607 to 653

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.4 bits(67)	2.2()	Composition-based stats.	19/61(31%)	27/61(44%)	14/61(22%)	
Features:						
Query	7	WVGSSYVAETGQNWASLAANELRVTERPFWISSFIGRSKEEIEWWTGENHSFNKDWLIGE				66
		W+ + YVAE L + RV E P W F+ +W EN ++D+L G				
Sbjct	607	WLYNEYVAE-----LPTFKDRVPEYPAWFEPFV-----IQWLDENEEVSRDFLHGA				652
Query	67	L	67			
		L				
Sbjct	653	L	653			

Chain A, Crystal Structure Of Piwi/argonaute/zwille(paz) Domain From Thermococcus Thioreducens
Sequence ID: **3DA5_A** Length: 128 Number of Matches: 1

See 1 more title(s)
Range 1: 6 to 48

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.5 bits(62)	4.9()	Compositional matrix adjust.	18/47(38%)	26/47(55%)	5/47(10%)	
Features:						
Query	43	RSKEEIEWWTGENHSFNKDWLIGELNRGGTPVVINIRA-HQVSYP				88
		RSK+ +WE G NKD L L+ GT ++ +I + H+V Y P				
Sbjct	6	RSKKTLELVGR----NKDALRDFLKEHRGTILLRDIASEHKVVYKP				48

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