

BLAST Results

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PSI blast Iteration 1

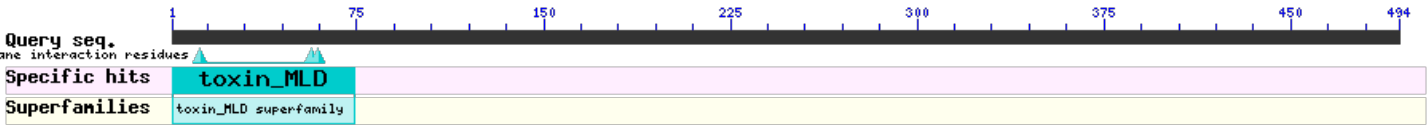
Job title: T0966 Ras/Rap1 site-specific endopeptidase...

RID	9JFW3GX3015 (Expires on 03-27 04:52 am)	Database Name	pdb
Query ID	lcIIQuery_29120	Description	PDB protein database
Description	T0966 Ras/Rap1 site-specific endopeptidase , Vibrio vulnificus CMCP6, 494 residues!	Program	BLASTP 2.9.0+
Molecule type	amino acid		
Query Length	494		

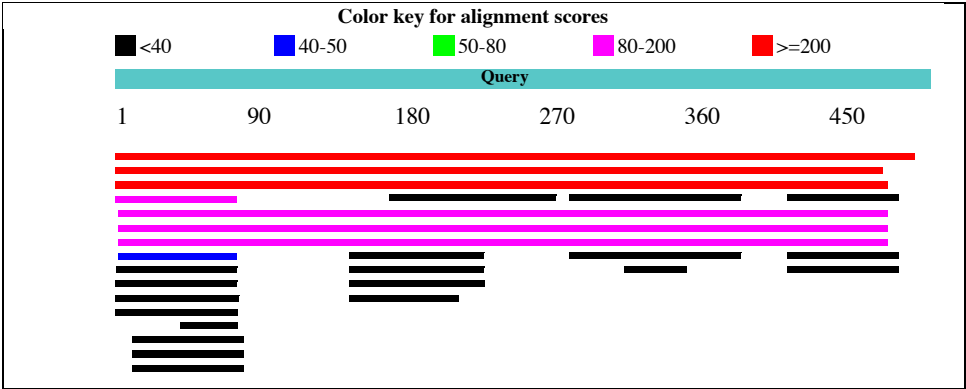
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Graphic Summary

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



Distribution of the top 27 Blast Hits on 27 subject sequences



## Descriptions

Description	Max score	Total score	Query cover	E value	Perc. ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, Crystal Structure of RRSP, a MARTX Toxin Effector Domain from <i>Vibrio vulnificus</i> CMCP6	981	981	100%	0.0	97.57%	<a href="#">5W6L_A</a> (scored below threshold on previous iteration)		
Chain A, RTX toxin	974	974	95%	0.0	100.00%	<a href="#">6A8J_A</a> (scored below threshold on previous iteration)		
Chain A, RTX toxin	972	972	96%	0.0	99.58%	<a href="#">6A7H_A</a> (scored below threshold on previous iteration)		
Chain A, 1.55 Angstrom Crystal Structure of the Four Helical Bundle Membrane Localization Domain (4HBM) of the <i>Vibrio vulnificus</i> MARTX Effector Domain DUF5	152	152	14%	2e-44	100.00%	<a href="#">4ERR_A</a> (scored below threshold on previous iteration)		
Chain X, Crystal Structures Reveal A Thiol-Protease Like Catalytic Triad In The C-Terminal Region Of <i>Pasteurella Multocida</i> Toxin	128	128	96%	4e-31	25.15%	<a href="#">2EBH_X</a> (scored below threshold on previous iteration)		
Chain A, Crystal Structures Reveal A Thiol-Protease Like Catalytic Triad In The C-Terminal Region Of <i>Pasteurella Multocida</i> Toxin	128	128	96%	4e-31	25.15%	<a href="#">2EC5_A</a> (scored below threshold on previous iteration)		
Chain X, Crystal Structures Reveal A Thiol-Protease Like Catalytic Triad In The C-Terminal Region Of <i>Pasteurella Multocida</i> Toxin	128	128	96%	4e-31	25.15%	<a href="#">2EBF_X</a> (scored below threshold on previous iteration)		
Chain A, Solution NMR Structure of the membrane localization domain from <i>Pasteurella multocida</i> toxin	44.7	44.7	14%	1e-05	38.36%	<a href="#">2N9V_A</a> (scored below threshold on previous iteration)		

Select:AllNone Selected:0

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Description	Max score	Total score	Query cover	E value	Perc. ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, Crystal Structure Of The Effector Domain Rid Of <i>Vibrio Vulnificus</i> Martx Toxin	39.3	39.3	14%	0.010	39.24%	<a href="#">5XN7_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure the N-terminal domain of <i>E. coli</i> HisB. Apo Mg model	35.0	35.0	21%	0.089	29.51%	<a href="#">2FPR_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal Structure of the N-terminal Domain of <i>E.coli</i> HisB-Phosphoaspartate intermediate	35.0	35.0	21%	0.090	29.51%	<a href="#">2FPW_A</a> (scored below threshold on previous iteration)		

Chain A, Lytr-Cps2a-Psr Family Protein With Bound Octaprenyl Pyrophosphate Lipid And Manganese Ion	33.9	33.9	13%	0.49	34.33%	<a href="#">3TEL_A</a> (scored below threshold on previous iteration)	
Chain A, Lytr-Cps2a-Psr Family Protein With Bound Octaprenyl Pyrophosphate Lipid And Magnesium Ion	33.9	33.9	13%	0.50	34.33%	<a href="#">3TEP_A</a> (scored below threshold on previous iteration)	
Chain A, Lytr-Cps2a-Psr Family Protein With Bound Octaprenyl Monophosphate Lipid	33.9	33.9	13%	0.50	34.33%	<a href="#">4DE8_A</a> (scored below threshold on previous iteration)	
Chain A, Retinoschisin R141H Mutant	32.0	32.0	20%	1.2	27.88%	<a href="#">5N6W_A</a> (scored below threshold on previous iteration)	
Chain A, STRUCTURE OF PROTEIN KINASE CK2 CATALYTIC SUBUNIT (ISOFORM CK2ALPHA') IN COMPLEX WITH THE INDENOINDOLE-TYPE INHIBITOR 4P	31.6	31.6	16%	2.3	30.00%	<a href="#">5OOI_A</a> (scored below threshold on previous iteration)	
Chain A, Structure Of A Human Ck2alpha Prime, The Paralog Isoform Of The Catalytic Subunit Of Protein Kinase Ck2 From Homo Sapiens	31.6	31.6	16%	2.4	30.00%	<a href="#">3OFM_A</a> (scored below threshold on previous iteration)	
Chain A, ORTHORHOMBIC COMPLEX STRUCTURE OF HUMAN PROTEIN KINASE CK2 CATALYTIC SUBUNIT (ISOFORM CK2ALPHA') WITH THE INHIBITOR 4'-CARBOXY-6,8-CHLORO- FLAVONOL (FLC21)	31.6	31.6	16%	2.5	30.00%	<a href="#">5M4U_A</a> (scored below threshold on previous iteration)	
Chain X, Crystal Structure Of Catalytic Subunit Of Human Protein Kinase Ck2alpha Prime With A Potent Indazole-Derivative Inhibitor	31.2	31.2	13%	3.4	31.08%	<a href="#">3E3B_X</a> (scored below threshold on previous iteration)	
Chain A, Clostridium difficile Toxin B (TcdB) glucosyltransferase domain in complex with U2F	30.8	30.8	14%	5.1	29.49%	<a href="#">5UQM_A</a> (scored below threshold on previous iteration)	
Chain A, Toxin B	30.4	30.4	15%	6.8	29.11%	<a href="#">6AR6_A</a> (scored below threshold on previous iteration)	
Chain A, Clostridium difficile TcdB-GTD bound to PA41 Fab	30.4	30.4	14%	6.8	29.49%	<a href="#">5VQM_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of The Catalytic Domain Of Alpha-Toxin From Clostridium Novyi	30.4	30.4	6%	7.0	36.36%	<a href="#">2VK9_A</a> (scored below threshold on previous iteration)	
Chain A, Trichoderma harzianum GH1 beta-glucosidase ThBg12	30.0	30.0	7%	8.4	47.37%	<a href="#">5JBO_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of The Gt Domain Of Clostridium Difficile Toxin A	30.0	30.0	13%	9.2	25.71%	<a href="#">4DMV_A</a> (scored below threshold on previous iteration)	
Chain A, Clostridium Difficile Toxin A (TcdA) Glucosyltransferase Domain Bound To Udp-Glucose	29.6	29.6	13%	9.4	25.71%	<a href="#">3SRZ_A</a> (scored below threshold on previous iteration)	
Chain A, Clostridium difficile toxin A (TcdA) glucosyltransferase domain in complex with U2F	29.6	29.6	13%	9.6	25.71%	<a href="#">5UQK_A</a> (scored below threshold on previous iteration)	

## Alignments

Chain A, Crystal Structure of RRSP, a MARTX Toxin Effector Domain from *Vibrio vulnificus* CMCP6  
Sequence ID: **5W6L\_A** Length: 518 Number of Matches: 1

See 1 more title(s)  
Hange 1: 25 to 518

Score	Expect	Method	Identities	Positives	Gaps	Frame
981 bits(2536)	0.0()	Compositional matrix adjust.	482/494(98%)	482/494(97%)	0/494(0%)	
Features:						
Query	1	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				60
Sbjct	25	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				84
Query	61	QALTQLKEQVTSALFIGKMQVAQAGIDAIQTRPELAARIFMVAIEEANGKHVGLTDMMV				120
Sbjct	85	QALTQLKEQVTSALFIGKQVAQAGIDAIQTRPELAARIFXVAIEEANGKHVGLTDXXV				144
Query	121	RWANEDPYLAPKHGKGETPSDLGFDKDYHVDLGEHYADFKQWLETSQSNGLLSKATLDE				180
Sbjct	145	RWANEDPYLAPKHGKGETPSDLGFDKDYHVDLGEHYADFKQWLETSQSNGLLSKATLDE				204
Query	181	STKTVHLGYSYQELQDLTGAESVQMAFYFLKEAAKKADPISGDSAEMILLKKFADQSYLS				240
Sbjct	205	STKTVHLGYSYQELQDLTGAESVQAFYFLKEAAKKADPISGDSAEXILLKKFADQSYLS				264
Query	241	QLDSDRMDQIEGIYRSSHETDIDAWDRRYSGTGYDELTKNLASATGVDEQLAVLLDDRKG				300
Sbjct	265	QLDSDRMDQIEGIYRSSHETDIDAWDRRYSGTGYDELTKNLASATGVDEQLAVLLDDRKG				324
Query	301	LLIGEVHGSVDVNGLRVNEQMDALKKQGVTVIGLEHLRSDLAQPLIDRYLATGVMSSSELS				360
Sbjct	325	LLIGEVHGSVDVNGLRVNEQMDALKKQGVTVIGLEHLRSDLAQPLIDRYLATGVXSSELS				384
Query	361	AMLKTKHLDVTLFENARANGMRIVALDANSSARPVQGTGHEGLMYRAGAANNIAVEVLQN				420
Sbjct	385	A LKTKHLDVTLFENARANG RIVALDANSSARPVQGTGHEGL YRAGAANNIAVEVLQN				444
Query	421	LPDGEKFVAIYGKAHLQSHKGIEGFVPGITHRLDLPALKVSDSNQFTVEQDDVSLRVVYD				480
Sbjct	445	LPDGEKFVAIYGKAHLQSHKGIEGFVPGITHRLDLPALKVSDSNQFTVEQDDVSLRVVYD				504
Query	481	DVANKPKITTFKGSL 494				
Sbjct	505	DVANKPKITTFKGSL 518				

Chain A, RTX toxin  
Sequence ID: **6A8J\_A** Length: 478 Number of Matches: 1

See 3 more title(s)  
Hange 1: 5 to 478

Score	Expect	Method	Identities	Positives	Gaps	Frame
974 bits(2518)	0.0()	Compositional matrix adjust.	474/474(100%)	474/474(100%)	0/474(0%)	
Features:						
Query	1	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				60
Sbjct	5	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				64
Query	61	QALTQLKEQVTSALFIGKMQVAQAGIDAIQTRPELAARIFMVAIEEANGKHVGLTDMMV				120
Sbjct	65	QALTQLKEQVTSALFIGKMQVAQAGIDAIQTRPELAARIFMVAIEEANGKHVGLTDMMV				124
Query	121	RWANEDPYLAPKHGKGETPSDLGFDKDYHVDLGEHYADFKQWLETSQSNGLLSKATLDE				180
Sbjct	125	RWANEDPYLAPKHGKGETPSDLGFDKDYHVDLGEHYADFKQWLETSQSNGLLSKATLDE				184
Query	181	STKTVHLGYSYQELQDLTGAESVQMAFYFLKEAAKKADPISGDSAEMILLKKFADQSYLS				240
Sbjct	185	STKTVHLGYSYQELQDLTGAESVQMAFYFLKEAAKKADPISGDSAEMILLKKFADQSYLS				244
Query	241	QLDSDRMDQIEGIYRSSHETDIDAWDRRYSGTGYDELTKNLASATGVDEQLAVLLDDRKG				300
Sbjct	245	QLDSDRMDQIEGIYRSSHETDIDAWDRRYSGTGYDELTKNLASATGVDEQLAVLLDDRKG				304
Query	301	LLIGEVHGSVDVNGLRVNEQMDALKKQGVTVIGLEHLRSDLAQPLIDRYLATGVMSSSELS				360
Sbjct	305	LLIGEVHGSVDVNGLRVNEQMDALKKQGVTVIGLEHLRSDLAQPLIDRYLATGVMSSSELS				364
Query	361	AMLKTKHLDVTLFENARANGMRIVALDANSSARPVQGTGHEGLMYRAGAANNIAVEVLQN				420
Sbjct	365	AMLKTKHLDVTLFENARANGMRIVALDANSSARPVQGTGHEGLMYRAGAANNIAVEVLQN				424
Query	421	LPDGEKFVAIYGKAHLQSHKGIEGFVPGITHRLDLPALKVSDSNQFTVEQDDVS				474
Sbjct	425	LPDGEKFVAIYGKAHLQSHKGIEGFVPGITHRLDLPALKVSDSNQFTVEQDDVS				478

Chain A, RTX toxin  
Sequence ID: **6A7H\_A** Length: 481 Number of Matches: 1

See 3 more title(s)  
Range 1: 5 to 481

Score	Expect	Method	Identities	Positives	Gaps	Frame
972 bits(2514)	0.0()	Compositional matrix adjust.	475/477(99%)	475/477(99%)	0/477(0%)	
Features:						
Query	1	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				60
Sbjct	5	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				64
Query	61	QALTQLKEQVTSALFIGKMQVAQAGIDAIQTRPELAARIFMVAIEEANGKHVGLTDMMV				120
Sbjct	65	QALTQLKEQVTSALFIGKMQVAQAGIDAIQTRPELAARIFMVAIEEANGKHVGLTDMMV				124
Query	121	RWANEDPYLAPKHGYKGETPSDLGFDKAYHVDLGEHYADFKQWLETSQSNGLLSKATLDE				180
Sbjct	125	RWANEDPYLAPKHGYKGETPSDLGFDKAYHVDLGEHYADFKQWLETSQSNGLLSKATLDE				184
Query	181	STKTVHLGYSYQELQDLTGAESVQMAFYFLKEAAKKADPISGDSAEMILLKKFADQSYLS				240
Sbjct	185	STKTVHLGYSYQELQDLTGAESVQMAFYFLKEAAKKADPISGDSAEMILLKKFADQSYLS				244
Query	241	QLDSDRMDQIEGIYRSSHETDIDAWDRRYSGTGYDELTKNLASATGVDEQLAVLLDDRKG				300
Sbjct	245	QLDSDRMDQIEGIYRSSHETDIDAWDRRYSGTGYDELTKNLASATGVDEQLAVLLDDRKG				304
Query	301	LLIGEVHGSVDVNGLRVNEQMDALKKQGVTVIGLEHLRSDLAQPLIDRYLATGVMSSSELS				360
Sbjct	305	LLIGEVHGSVDVNGLRVNEQMDALKKQGVTVIGLHLRSDLAQPLIDRYLATGVMSSSELS				364
Query	361	AMLKTKHLDVDTLFENARANGMRIVALDANSSARPNVQGTTEHGLMYRAGAANNIAVEVLQN				420
Sbjct	365	AMLKTKHLDVDTLFENARANGMRIVALDANSSARPNVQGTTEHGLMYRAGAANNIAVEVLQN				424
Query	421	LPDGEKFVAIYGKALQSHKGIEGFVPGITHRLDLPALKVSDSNQFTVEQDDVSLRV				477
Sbjct	425	LPDGEKFVAIYGKALQSHKGIEGFVPGITHRLDLPALKVSDSNQFTVEQDDVSLRV				481

Chain A, 1.55 Angstrom Crystal Structure of the Four Helical Bundle Membrane Localization Domain (4HBM) of the Vibrio vulnificus  
MARTX Effector Domain DUF5  
Sequence ID: **4ERR\_A** Length: 90 Number of Matches: 1

See 2 more title(s)  
Range 1: 8 to 81

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(383)	2e-44()	Compositional matrix adjust.	74/74(100%)	74/74(100%)	0/74(0%)	
Features:						
Query	1	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				60
Sbjct	8	QELKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASFELNKKINDYIAEHPTSGRN				67
Query	61	QALTQLKEQVTSAL				74
Sbjct	68	QALTQLKEQVTSAL				81

Chain X, Crystal Structures Reveal A Thiol-Protease Like Catalytic Triad In The C-Terminal Region Of Pasteurella Multocida Toxin  
Sequence ID: **2EBH\_X** Length: 746 Number of Matches: 1  
Range 1: 57 to 548

Score	Expect	Method	Identities	Positives	Gaps	Frame
128 bits(321)	4e-31()	Compositional matrix adjust.	129/513(25%)	218/513(42%)	59/513(11%)	
Features:						
Query	3	LKERAKVFAKPIGASYQGILDQLDLVHQAKGRDQIAASF-ELNKKINDYIAEHPTSGRNQ				61
Sbjct	57	LK RA V KPIG SY+ IL +L +H + D+ EL + I+ Y P+S R				116
Query	62	ALTQLKEQVTSALFIGKMQVAQAGIDAIQTRPELAARIFMVAIEEANGKHVGLTDMMV				121
Sbjct	117	A +L+ Q+ AL++ +M+ + I I A + A+ E GK T ++R				176

Query	122	WANEDPYL-APKHGYKGETPSDLGFDAKYHVD-----LGEHYAD---FKQW-----	163
		+A +D + AP GY G P + F KY ++ + +Y + ++ W	
Sbjct	177	FALQDQTVISAPFRGYAGAIPEAIDFPVKYVIEDISVFDKIQTNYWELPAYESWNEGSNSA	236
Query	164	-----LETSQSNGLLSKATLDESTKTVHLGYSYQEL-----QDLTGAESVQMAFYFLK	211
		L SQS G+LSK + E+ ++++G+SY+E+ + G F F	
Sbjct	237	LLPGLLRESQSKGMLSKCRIIEN--SLYIGHSEEMFYFYSISPYSNQVGGPYELYPFTFFS	294
Query	212	EAAKKADPISGDSAEMILLKKFADQSYLSQLDSRMDQIEGIYRSSHETDIDAWDRRYSG	271
		+ + GD + + FA +++ + L SDR+ +E + D WD Y	
Sbjct	295	MLQE---VQGD---LGFEQAFATRNFFNTLVSDRLSLMENTMLLTESFDYTPWDAIYGD	347
Query	272	TGYDELTNKLASATGVDEQLAVLLDDRKGLLIGEVHGSVDVNGLRVNEQMDALKKQGVTV	331
		YDE +A ++E++ ++ +G+ S + F + G+T	
Sbjct	348	INDEQF----AAMSINERIEKCMNTYRGVAFQNSSKS----IDFFLNNLTTFIDNGLTE	399
Query	332	IGLEHLRSDLAQPLIDRYLATGVMSSSELSAML-KTKHLDVT-----LFENARANGMRIVA	385
		I + L D+ Q I ++L L AML D+ L ++A+ N ++ A	
Sbjct	400	IAISDLPYDIVQQEISQFLQGSNEWKTLDAMLFNLDKGDINGAFRKLLQSAKDNNIKFRA	459
Query	386	LDANSSARPNVQGTEHGLMYRAGAANNIAVEVLQNLNLP-DGEKFVAIYGKAHLQSHKGIEG	444
		+ + ++ P L Y+ NI E ++ L +G+KFV + L S G	
Sbjct	460	IGHSDNSVPPFNNPYKSLYYKG---NIIAEAEIEKLDREGQKFVVFADSSLLNSTPGTGR	515
Query	445	FVPGITHRLDLPALKVSDSNQFTVEQDDVSLRV	477
		+PG+ L +PA V + D S RV	
Sbjct	516	PMPGLVQYLKIPATVVDSGAWQFLPDVASSRV	548

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