

BLAST Results

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PSI blast Iteration 1

Job title: T0866 MlaD, E. coli, 183 residues

RID [A6PF99ZU014](#) (Expires on 04-03 20:47 pm)

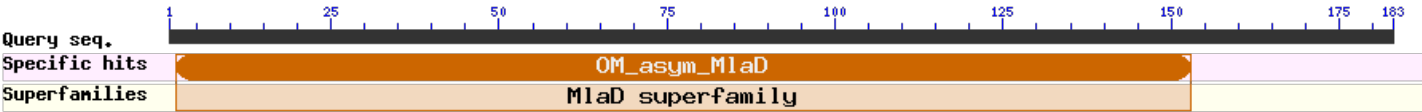
Query ID lcllQuery_130937
Description T0866 MlaD, E. coli, 183 residues
Molecule type amino acid
Query Length 183

Database Name pdb
Description PDB protein database
Program BLASTP 2.9.0+

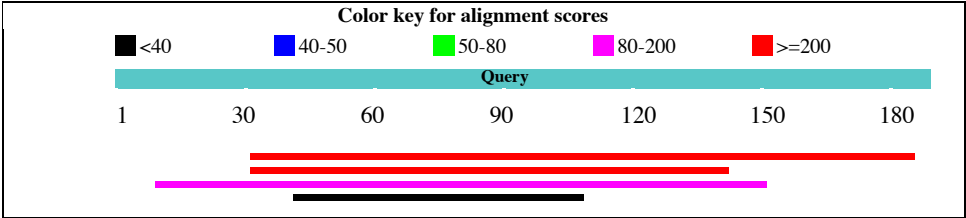
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Graphic Summary

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



Distribution of the top 4 Blast Hits on 4 subject sequences



Descriptions

Description	Max score	Total score	Query cover	E value	Per. Ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, Structure Of E. Coli Mce Protein Mlad, Periplasmic Domain	309	309	83%	5e-109	100.00%	5UW2_A (scored below threshold on previous iteration)		
Chain A, Structure Of E. Coli Mce Protein Mlad, Core Mce Domain	222	222	59%	3e-75	100.00%	5UW8_A (scored below threshold on previous iteration)		
Chain A, Toluene tolerance efflux transporter (ABC superfamily, PerI-bind)	81.6	81.6	76%	2e-19	31.55%	6IC4_A (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	Per. Ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, Crystal structure of Archaeometzincin (amzA) from Methanopyrus kandleri at 1.5 A resolution	27.7	27.7	36%	8.5	33.33%	2X7M_A (scored below threshold on previous iteration)		

Alignments

Chain A, Structure Of E. Coli Mce Protein Mlad, Periplasmic Domain
Sequence ID: **5UW2_A** Length: 165 Number of Matches: 1

See 2 more title(s)
Range 1: 14 to 165

Score	Expect	Method	Identities	Positives	Gaps	Frame
309 bits(791) 5e-109() Compositional matrix adjust. 152/152(100%) 152/152(100%) 0/152(0%)						
Features:						
Query	32	TSIRTEPTYTLYATFDNIGGLKARSPVSI	IGGVVGRVADITLDPKTYLPRVTLEIEQRYN	91		
Sbjct	14	TSIRTEPTYTLYATFDNIGGLKARSPVSI	IGGVVGRVADITLDPKTYLPRVTLEIEQRYN	73		
Query	92	HIPDTSSLSIRTSGLLGEQYLALNVGFEDPELGTAILKDGD	TIQDTKSAMVLEDLIGQFL	151		
Sbjct	74	HIPDTSSLSIRTSGLLGEQYLALNVGFEDPELGTAILKDGD	TIQDTKSAMVLEDLIGQFL	133		
Query	152	YGSKGDDNKNSGDAPAAAPGNNETTEPVGTTK	183			
Sbjct	134	YGSKGDDNKNSGDAPAAAPGNNETTEPVGTTK	165			

Chain A, Structure Of E. Coli Mce Protein Mlad, Core Mce Domain
Sequence ID: **5UW8_A** Length: 122 Number of Matches: 1

See 6 more title(s)
Range 1: 14 to 122

Score	Expect	Method	Identities	Positives	Gaps	Frame
222 bits(565)	3e-75()	Compositional matrix adjust.	109/109(100%)	109/109(100%)	0/109(0%)	
Features:						
Query	32	TSIRTEPTYTLYATFDNIGGLKARSPVSI	IGGVVVG	RVADITLDPKTYLPRVTLEIEQRYN		91
Sbjct	14	TSIRTEPTYTLYATFDNIGGLKARSPVSI	IGGVVVG	RVADITLDPKTYLPRVTLEIEQRYN		73
Query	92	HIPDTSSLSIRTSGLLGEQYLALNVGFEDPELGTAILKDGD	TIQDTKSA		140	
Sbjct	74	HIPDTSSLSIRTSGLLGEQYLALNVGFEDPELGTAILKDGD	TIQDTKSA		122	

Chain A, Toluene tolerance efflux transporter (ABC superfamily, PerI-bind)
Sequence ID: **6IC4_A** Length: 183 Number of Matches: 1

See 5 more title(s)
Range 1: 2 to 183

Score	Expect	Method	Identities	Positives	Gaps	Frame
81.6 bits(200)	2e-19()	Compositional matrix adjust.	59/187(32%)	85/187(45%)	52/187(27%)	
Features:						
Query	10	VGIFLLAALLAALFVCLKAANVTSIRTEPTYTLYATFDNIGGLKARSPVSI	IGGVVVG	RVAV		69
Sbjct	2	VGIFVVIIFGIALFFLAMKVSGLVGTNLSDGYTMKAQFDNVNGLKPRAKVTMSGVTIGRVD				61
Query	70	DITLDPKTYLPRVTLEI-----E	QRYN-----			91
Sbjct	62	SITLDPVTRLATVTFDLDGKLT	SFNAEQ	LKEVQKNALDELRYS	SDYTQATPAQQKTMEQQ	121
Query	92	-----HIPDTSSLSIRTSGLLGEQYLALNVGFEDPELGTAILKDGD	TIQDTKSAMV			142
Sbjct	122	LISNMNSITSIDEDAYIMVATNGLLGEKYLKIV-----PGGGLN	YLKRGDTISNTQGTMD			176
Query	143	LEDLIGQ				149
Sbjct	177	LEDLISK				183

Chain A, Crystal structure of Archaeometzincin (amzA) from Methanopyrus kandleri at 1.5 A resolution
Sequence ID: **2X7M_A** Length: 195 Number of Matches: 1
Range 1: 101 to 170

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.7 bits(60)	8.5()	Compositional matrix adjust.	24/72(33%)	31/72(43%)	8/72(11%)	
Features:						
Query	42	LYATFDNIGGLKARSPVSI	IGGVVVG	RVADITLDPKTYLPRVTLEIEQR-----YNH	IPD	95
Sbjct	101	LYAPGLNFVFGQARCPGREAVVSVARLLDP--DP	ELYLERVVKELTHELGHTFGLGHCPD			158
Query	96	TSSLSIRTSGLL				107
Sbjct	159	RNCVMSFSSSL				170

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