

BLAST Results

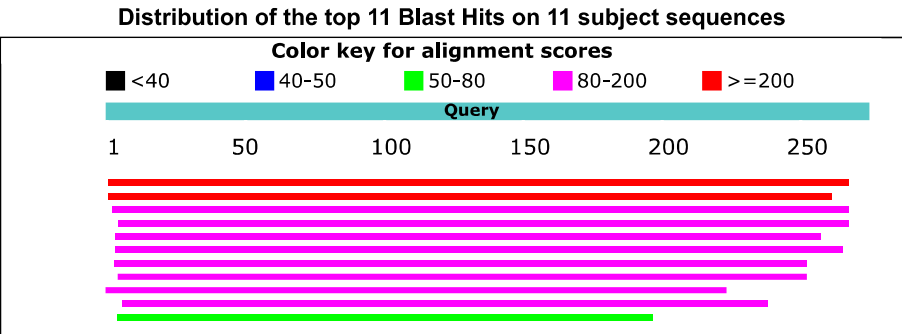
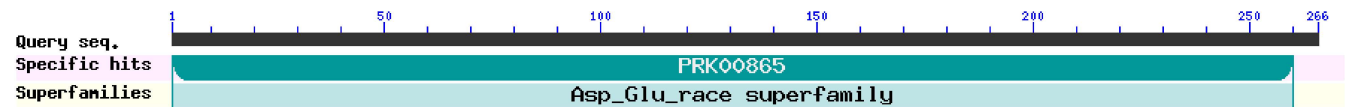
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Job title: BAB42246:glutamate racemase [Staphylococcus...

RID	2F60JXB1014 (Expires on 12-30 22:51 pm)	Database Name	SMARTBLAST/landmark
Query ID	BAB42246.1	Description	Landmark database for SmartBLAST
Description	glutamate racemase [Staphylococcus aureus subsp. aureus N315]	Program	BLASTP 2.8.1+
Molecule type	amino acid		
Query Length	266		

Graphic Summary.

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



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
glutamate racemase [Streptococcus pneumoniae R6]	233	233	98%	2e-75	45%	NP_359288.1
glutamate racemase [Clostridioides difficile 630]	207	207	96%	4e-65	40%	YP_001090085.1
glutamate racemase [Neisseria meningitidis MC58]	177	177	98%	2e-53	37%	NP_273505.1
glutamate racemase [Synechocystis sp. PCC 6803]	175	175	97%	1e-52	39%	WP_010872415.1
glutamate racemase [Mycobacterium tuberculosis H37Rv]	174	174	94%	2e-52	40%	NP_215854.1
glutamate racemase [Microcystis aeruginosa]	173	173	97%	1e-51	37%	WP_012267850.1
glutamate racemase [Deinococcus radiodurans R1]	139	139	92%	1e-37	33%	NP_295309.1
glutamate racemase [Pseudomonas aeruginosa PAO1]	130	130	92%	2e-35	33%	NP_253351.1
glutamate racemase Murl [Shewanella oneidensis MR-1]	114	114	82%	5e-29	32%	NP_715848.3
glutamate racemase [Escherichia coli str. K-12 substr. MG1655]	94.0	94.0	86%	3e-21	32%	NP_418402.2
glutamate racemase [Streptomyces coelicolor A3(2)]	62.0	62.0	71%	6e-10	29%	NP_625314.1

Alignments

glutamate racemase [Streptococcus pneumoniae R6]
Sequence ID: **NP_359288.1** Length: 264 Number of Matches: 1
Range 1: 3 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
233 bits(594)	2e-75()	Compositional matrix adjust.	119/264(45%)	169/264(64%)	3/264(1%)	
Features:						
Query	2	NKPIGVDSG+GGLTVAKEIMRQLPNETIYYLGDIGRCPYGRPRGEQVKQYTVETIARKLM	61			
Sbjct	3	NRPIGFSDSGVGGTLTVRELNRQLPHEEIVYIGDSARAPYGRPAEQIREYTWQLVNFLL	62			
Query	62	EFDIKMLVIACNTATAVALEYLQKTLSPVIGVIEPGARTAIMTTRNQNVVLGTGEGTIK	121			
Sbjct	63	TKDKVMIVACNTATAVWEEIKAQLDIPVLGVILPGASAAIKSSQGGKIGVIGTPMTVQ	122			
Query	122	SEAYRTHIKRINPHVEVHGACPGFVPLVEQMRYSDPTITSIVIHQTLKRWNRNSESQTVI	181			
Sbjct	123	SDIYRQKIHDLDPDLQVESLACPKFAPLVESGALST-SVTKKVYYETL-RPLVGKVDLSL	180			
Query	182	LGCTHYPLLYKPIYDFGGKKTVISSGLETAREVSALLTFSNEHASYTEHP-DHRFFATG	240			
Sbjct	181	LGCTHYPLLRPIIQNVMPKVLQIDSGAECVRDISVLLNYFEINRGRDAGPLHHRFYTTA	240			
Query	241	DPTHITNIIKEWLNLSVNVERISV	264			
Sbjct	241	SSQSFAQIGEEWLEKEIHVEHVEL	264			

glutamate racemase [Clostridioides difficile 630]
Sequence ID: **YP_001090085.1** Length: 268 Number of Matches: 1
Range 1: 3 to 258

Score	Expect	Method	Identities	Positives	Gaps	Frame
207 bits(526)	4e-65()	Compositional matrix adjust.	104/257(40%)	160/257(62%)	1/257(0%)	
Features:						
Query	2	NKPIGVDSG+GGLTVAKEIMRQLPNETIYYLGDIGRCPYGRPRGEQVKQYTVETIARKLM	61			
Sbjct	3	NKPIGVDSG+GGLTVKEIM+LPNEIYGD RPYGR E++YT+L	62			
Query	62	EFDIKMLVIACNTATAVALEYLQKTLSPVIGVIEPGARTAIMTTRNQNVVLGTGEGTIK	121			
Sbjct	63	TKGVKATVIACNTATARSLEAKQEKYDIPIIGVIEAGARTAVSSTKNKIVGIIGTEGTIS	122			
Query	122	SEAYRTHIKRINPHVEVHGACPGFVPLVEQMRYSDPTITSIVIHQTLKRWNRNSESQTVI	181			
Sbjct	123	SKAYNLEISKIDESIEIVNKACPLFVPIVEE-GWANTEVAKLTAKIYLQELKEKNIDSLV	181			
Query	182	LGCTHYPLLYKPIYDFGGKKTVISSGLETAREVSALLTFSNEHASYTEHPDHRFFATGD	241			
Sbjct	182	LGCTHYPLKRTIGEEVGEHIKLVNPAKETAKDLKKILEVQNIINNTEIHGTYQYVSDI	241			
Query	242	PTHITNIIKEWLNLSVN	258			
Sbjct	242	PEKFSDIAREFLKKKID	258			

glutamate racemase [Neisseria meningitidis MC58]
Sequence ID: **NP_273505.1** Length: 270 Number of Matches: 1
Range 1: 8 to 269

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(450)	2e-53()	Compositional matrix adjust.	98/264(37%)	152/264(57%)	4/264(1%)	
Features:						
Query	3	KPIGVDSGVGGLTVAKEIMROLPNETIYYLGDIGRCPYGPRPGEQVKQYTVETIARKLME				62
Sbjct	8	+PIGV DSG+GGLT + +M +LP E I Y GD R PYG + + + + + + I L+E				67
Query	63	FDIKMLVIACNTATAVALEYL-QKTLSPVIGVIEPGARTAIMTTRNQNVVLGTETGIK				121
Sbjct	68	D+K +VIACNT AVA + + OKT ++PV+ VI GA+ A+ TTRN + ++ T T+				127
Query	122	SEAYRTHIKRINPHVEVHGACPGFVPLVEQMRYSDPTITSIVIHQTLKRWNSSESDTVI				181
Sbjct	128	S AY I R NP V A P VPLVE+ + + +T + + + LK DT++				186
Query	182	LGCTHYPLLYKPIYDFGGKKTVISSGLETAREVSALLTFSNEHASYTEHPDHRFFATGD				241
Sbjct	187	LGCTHFLL-KPLIGREAGNALVDSAITTAEEARVLAQEGLLNTDNNNPDYRFYVSDI				245
Query	242	PTHITNIIKEWLNLSV-NVERISV 264				
Sbjct	246	P I + +L ++ +E +S+ PLKFRTIGERFLGRTEQIEMVSL 269				

glutamate racemase [Synechocystis sp. PCC 6803]
Sequence ID: **WP_010872415.1** Length: 279 Number of Matches: 1
Range 1: 9 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
175 bits(444)	1e-52()	Compositional matrix adjust.	102/264(39%)	147/264(55%)	12/264(4%)	
Features:						
Query	5	IGVIDSGVGGLTVAKEIMROLPNETIYYLGDIGRCPYGPRPGEQVKQYTVETIARKLMEFD				64
Sbjct	9	IGV DSGVGGLTV +E+ RQLP E+I Y GD R PYG R + + OY EI + + +				68
Query	65	IKMLVIACNTATAVALEYLQKTLSPVIGVIEPGARTAIMTTRNQNVVLGTETGIKSEA				124
Sbjct	69	+KM+++ACNT++A+ALE +O+ ++P++GVI PGAR A+ R + V+ T T S A				126
Query	125	YRTHIKRINPHVEVHGACPGFVPLVEQMRYSDPTITSIVIHQTLKRWNSSESDTVILGC				184
Sbjct	127	YRHAIEIITPDALVWQMACPEFVPLIEQNRLHDP-YTLEVAKGYLQPLLDADIDTLVFGC				185
Query	185	THYPLLYKPIYDFGGKKTVI---SSGLETAREVSALLTFSNEHASYTEHPDHRFFATG				240
Sbjct	186	THY L P++ + S ++ AR+ ++ N S RF +G				240
Query	241	DPTHITNIIKEWLNLSVNVVERISV 264				
Sbjct	241	P + +WL + VE+IS+ CPQQAELSHQWLGFTPMVEKISL 264				

glutamate racemase [Mycobacterium tuberculosis H37Rv]
Sequence ID: **NP_215854.1** Length: 271 Number of Matches: 1
Range 1: 7 to 256

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(442)	2e-52()	Compositional matrix adjust.	101/252(40%)	141/252(55%)	3/252(1%)	
Features:						
Query	4	PIGVDSGVGGLTVAKEIMROLPNETIYYLGDIGRCPYGPRPGEQVKQYTVETIARKLMEF				63
Sbjct	7	P+GV DSGVGGLTVA+ I+ QLP+E I Y+GD G PYGP +++ + + I L+				66
Query	64	DIKMLVIACNTATAVALEYLQKTLSPVIGVIEPGARTAIMTTRNQNVVLGTETGIKSE				123
Sbjct	67	+K LVIACN+A++ L ++ +PV+ VI P R A+ TRN + V+GT TI S				126
Query	124	AYRTHIKRINPHVEVHGACPGFVPLVEQMRYSDPTITSIVIHQTLKRWNSSESDTVILG				183
Sbjct	127	AY+ E+ VACP FV VE+ S + + L+ + +E DT++LG				184
Query	184	CTHYPLLYKPIYDFGGKKTVISSGLETAREVSALLTFSNEHASYTEHPDHRFF-ATGDP				242
Sbjct	185	CTHYPLL I G T++SS ETA+EV +LT + + P R F ATGDP				244
Query	243	THITNIIKEWLN 254				
Sbjct	245	T + +L EAFTKLAARFLG 256				

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