

BLAST Results

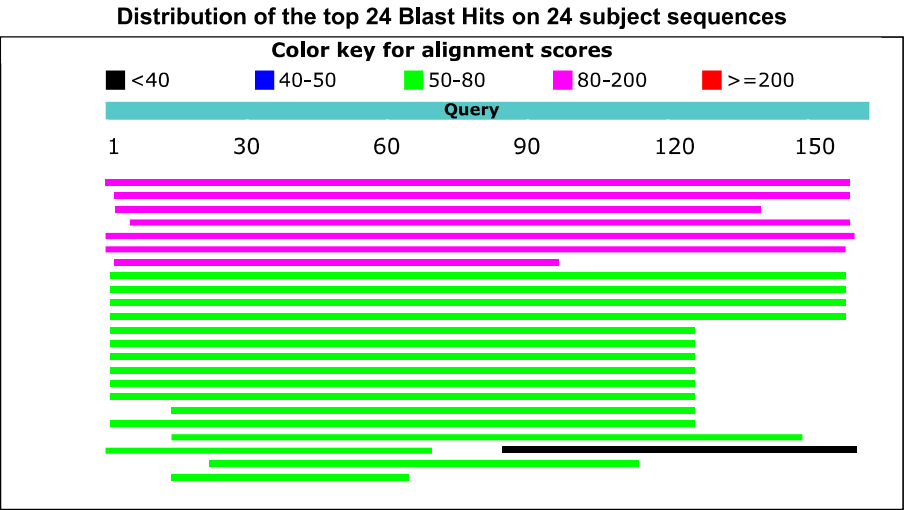
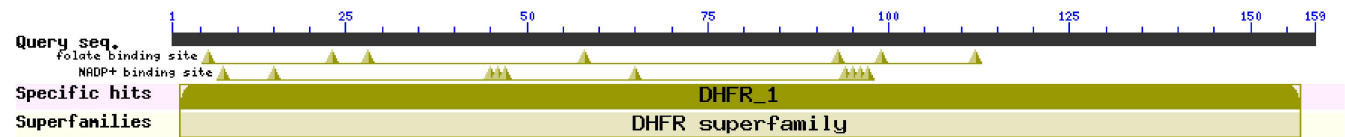
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Job title: BAB42519: dihydrofolate reductase [Staphylococcus...

RID	2F65VDV501R (Expires on 12-30 22:54 pm)	Database Name	SMARTBLAST/landmark
Query ID	BAB42519.1	Description	Landmark database for SmartBLAST
Description	dihydrofolate reductase [Staphylococcus aureus subsp. aureus N315]	Program	BLASTP 2.8.1+
Molecule type	amino acid		
Query Length	159		

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
dihydrofolate reductase FcIA [Shewanella oneidensis MR-1]	125	125	99%	4e-36	36%	gij24375145 NP_719188.1
dihydrofolate reductase [Escherichia coli str. K-12 substr. MG1655]	108	108	98%	2e-29	35%	gij16128042 NP_414590.1
dihydrofolate reductase [Pseudomonas aeruginosa PAO1]	108	108	86%	2e-29	34%	gij15595547 NP_249041.1
dihydrofolate reductase [Deinococcus radiodurans R1]	107	107	96%	1e-28	38%	gij15807612 NP_296351.1
dihydrofolate reductase [Streptococcus pneumoniae R6]	94.0	94.0	100%	1e-23	35%	gij15903472 NP_359022.1
dihydrofolate reductase [Neisseria meningitidis MC58]	89.0	89.0	98%	8e-22	30%	gij15676226 NP_273358.1
dihydrofolate reductase [Mycobacterium tuberculosis H37Rv]	81.6	81.6	59%	7e-19	39%	gij15609900 NP_217279.1
PREDICTED: bifunctional dihydrofolate reductase-thymidylate synthase-like [Glycine max]	76.3	76.3	98%	2e-15	32%	gij356508312 XP_003522902.1
PREDICTED: bifunctional dihydrofolate reductase-thymidylate synthase isoform X1 [Glycine max]	75.5	75.5	98%	3e-15	32%	gij571458152 XP_006581064.1
bifunctional dihydrofolate reductase-thymidylate synthase [Glycine max]	75.5	75.5	98%	3e-15	32%	gij351725903 NP_001238644.1
PREDICTED: bifunctional dihydrofolate reductase-thymidylate synthase isoform X2 [Glycine max]	75.1	75.1	98%	3e-15	32%	gij571458156 XP_006581066.1
thymidylate synthase 2 [Arabidopsis thaliana]	73.2	73.2	77%	2e-14	36%	gij1063726786 NP_001328947.1
thymidylate synthase 2 [Arabidopsis thaliana]	72.4	72.4	77%	4e-14	36%	gij1063726788 NP_001328949.1
thymidylate synthase 2 [Arabidopsis thaliana]	72.0	72.0	77%	4e-14	36%	gij1063726790 NP_001328950.1
thymidylate synthase 1 [Arabidopsis thaliana]	70.9	70.9	77%	1e-13	34%	gij1063703862 NP_001324592.1
thymidylate synthase 2 [Arabidopsis thaliana]	70.9	70.9	77%	1e-13	36%	gij30690081 NP_195183.2
thymidylate synthase 1 [Arabidopsis thaliana]	70.9	70.9	77%	1e-13	34%	gij15227185 NP_179230.1
PREDICTED: bifunctional dihydrofolate reductase-thymidylate synthase-like [Glycine max]	68.6	68.6	69%	7e-13	35%	gij356538745 XP_003537861.1
PREDICTED: bifunctional dihydrofolate reductase-thymidylate synthase-like [Glycine max]	68.6	68.6	77%	7e-13	33%	gij356545155 XP_003541010.1
dihydrofolate reductase, isoform A [Drosophila melanogaster]	59.3	59.3	84%	3e-10	29%	gij24647458 NP_732147.1
dihydrofolate reductase [Dictyostelium discoideum AX4]	58.9	58.9	43%	5e-10	40%	gij66807877 XP_637661.1
dihydrofolate reductase [Thermotoga maritima MSB8]	56.6	56.6	57%	3e-09	38%	gij15644389 NP_229441.1
dihydrofolate reductase [Saccharomyces cerevisiae S288C]	53.9	53.9	31%	4e-08	42%	gij6324810 NP_014879.1
adducin 3 (gamma) b [Danio rerio]	32.3	32.3	47%	2.3	30%	gij321400069 NP_001189456.1

Alignments

dihydrofolate reductase FcIA [Shewanella oneidensis MR-1]
Sequence ID: [gij24375145|NP_719188.1](#) Length: 160 Number of Matches: 1
Range 1: 1 to 159

Score	Expect	Method	Identities	Positives	Gaps	Frame
125 bits(315)	4e-36()	Compositional matrix adjust.	59/164(36%)	98/164(59%)	11/164(6%)	
Features:						
Query	1	MTLSILVAHDLQRVIGFENQLPWHLPNDLKHVKKLSGTHTLVMGKRTFESIGKPLPNRRN	60			
		M +++++ A RVIG +N++PWHLP DL+H K ++ G +VMGRKTFESIG+PLP R N				
Sbjct	1	MRIAMIAAMANNRVIGKDNKMPWHLPEDLRHFKAMTLGKPVVMGRKTFESIGRPLPGRHN	60			

Query 61 VVLTSDTSFNVEGVVDIHSIEDIYQLPG---HVFIFGGQTLFEEMIDKVDDMYITVIEGK 117
+V++ +EGV + S E ++ G + + GG L+++++ + D +Y+T I
Sbjct 61 IVISRQADLQIEGVTCVTSFEAAKRVAGDCEELVVIGGGQLYKQLLPQADRLYLTQINLD 120

Query 118 FRGDTFFPPYTFEDW---EVASSVEGKLDEKNTIPHTFLHLIRK 158
GDTFFP + +W E S+ + + + F++L++K
Sbjct 121 VDGDTFFPAWEDNEWQKTETQPSISA-----DGLEYNFINLVKK 159

dihydrofolate reductase [Escherichia coli str. K-12 substr. MG1655]

Sequence ID: **gi|16128042|NP_414590.1** Length: 159 Number of Matches: 1
Range 1: 2 to 159

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(271)	2e-29()	Compositional matrix adjust.	56/159(35%)	92/159(57%)	4/159(2%)	
Features:						
Query 3	LSILVAHDLQRVIGFENQLPWHLPNDLKHVKKLSTGHTLMGRKTFESIGKPLPNRRNVV	62				
Sbjct 2	ISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLNKPVIMGRHTWESIGRPLPGRKNII	61				
Query 63	LTSDTSFNVEGVVDIHSIEDIYQLPGHV---FIFGGQTLFEEMIDKVDDMYITVIEGKFR	119				
Sbjct 62	LSSQPGTD-DRVTWVKSVDEAIAACGDVPEIMVIGGRVYEQFLPKAQKLYLTHIDAEVE	120				
Query 120	GDTFFPPYTFEDWEVASSVEGKLDEKNTIPHTFLHLIRK	158				
Sbjct 121	GDTFFPDYEPDDWESVFSEFHDADAQNSHSCYCFEILERR	159				

dihydrofolate reductase [Pseudomonas aeruginosa PAO1]

Sequence ID: **gi|15595547|NP_249041.1** Length: 168 Number of Matches: 1
Range 1: 5 to 150

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(271)	2e-29()	Compositional matrix adjust.	50/146(34%)	80/146(54%)	9/146(6%)	
Features:						
Query 3	LSILVAHDLQRVIGFENQLPWHLPNDLKHVKKLSTGHTLMGRKTFESIGKPLPNRRNVV	62				
Sbjct 5	LAMIAALGENRAIGIDNRLPWRLPADLKHFKAMTLGKPVIMGRKTWDSLGRPLPGRLNLV	64				
Query 63	LTSDTSFNVEGVVDIHSIEDIYQL-----PGHVFIFGGQTLFEEMIDKVDDMYITV	113				
Sbjct 65	VSRQAGLALGAEVFASLDAALARAEEAWAQAEDAELMLIGGAQLYAEALPRAARLYLTR	124				
Query 114	IEGKFRGDTFFPPYTFEDWEVASSVE	139				
Sbjct 125	VGLAPEGDAFFPEIDGAAWRLASSIE	150				

dihydrofolate reductase [Deinococcus radiodurans R1]

Sequence ID: **gi|15807612|NP_296351.1** Length: 180 Number of Matches: 1
Range 1: 20 to 175

Score	Expect	Method	Identities	Positives	Gaps	Frame
107 bits(266)	1e-28()	Compositional matrix adjust.	59/157(38%)	85/157(54%)	5/157(3%)	
Features:						
Query 6	LVAHDLQRVIGFENQLPWHLPNDLKHVKKLSTGHTLMGRKTFESI-GKPLPNRRNVVLT	64				
Sbjct 20	IAAQTENRVIGRDGGMPWHLPADFAHFRALSVGKPNIMGRKVFDTLRRKPLPERVNIVLT	79				
Query 65	SDTSFNVEGVVDIHSIEDIYQLPG---HVFIFGGQTLFEEMIDKVDDMYITVIEGKFRGD	121				
Sbjct 80	RNENLKFDGCLIAHSPEEALQLAGDAPEIAIIGGEEIYRLYWRDLTRLEMTLIHAELDGD	139				
Query 122	TFFPPYTFEDWEVASSVEGKLDEKNTIPHTFLHLIRK	158				
Sbjct 140	TFFPEIGPE-WELAQETFRPADEKNRYDLTFQTWRRR	175				

dihydrofolate reductase [Streptococcus pneumoniae R6]

Sequence ID: **gi|15903472|NP_359022.1** Length: 168 Number of Matches: 1
Range 1: 1 to 165

Score	Expect	Method	Identities	Positives	Gaps	Frame
94.0 bits(232)	1e-23()	Compositional matrix adjust.	59/167(35%)	94/167(56%)	10/167(5%)	
Features:						
Query 1	MTLSILV--AHDLQRVIGFENQLPWHLPNDLKHVKKLSTGHTLMGRKTFESIGKP-LPN	57				
Sbjct 1	MTKKIVAIWAQDEELIGKENRLPWHLPALQHFKETTLNHAILMGRVTFDGMGRRLLPK	60				
Query 58	RRNVVLTSDTSFNVEGVVDV---IHSIEDIYQ-LPGHVIFGGQTLFEEMIDKVDDMYITV	113				
Sbjct 61	RETILILTRNPEEKIDGVATFQDVQSVLDWYQDQEKNLVIIGGKQIFQAFEPYLDDEVIVTH	120				
Query 114	IEGKFRGDTFFP-PYTFEDWEVASSVEGKLDEKNTIPHTFLHLIRK	159				
Sbjct 121	IHARVEGDTYFPEELDSLFLFETVSSKFYAKDEKN--PYDFTIQYRK	165				

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