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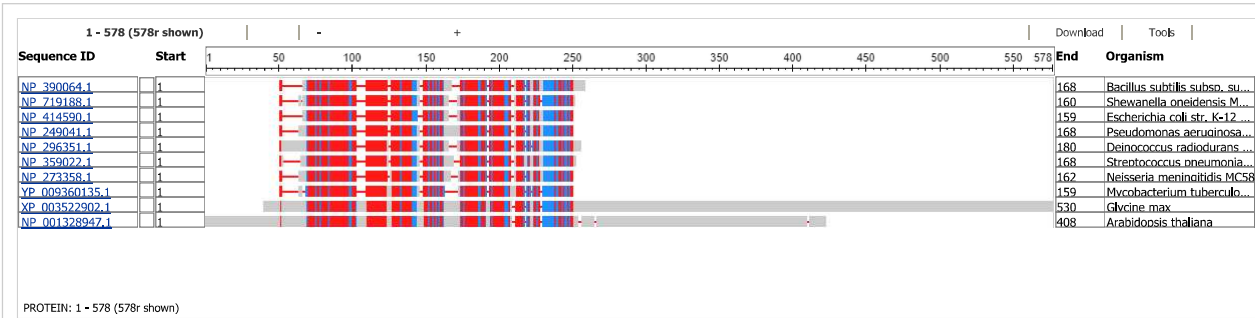
[COBALT](#) Constraint-based Multiple Alignment Tool

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Multiple Alignment Results - BAB42519: dihydrofolate reductase [Staphylococcus... - Cobalt RID 43HRMFSK211 (10 seqs)

Graphical Overview



Descriptions ☒ Select All [Re-align](#) [Alignment parameters](#)

Accession	Description	Links
<input checked="" type="checkbox"/> NP_390064.1	dihydrofolate reductase [Bacillus subtilis subsp. subtilis str. 168]	Related Information
<input checked="" type="checkbox"/> NP_719188.1	dihydrofolate reductase FdIA [Shewanella oneidensis MR-1]	Related Information
<input checked="" type="checkbox"/> NP_414590.1	dihydrofolate reductase [Escherichia coli str. K-12 substr. MG1655]	Related Information
<input checked="" type="checkbox"/> NP_249041.1	dihydrofolate reductase [Pseudomonas aeruginosa PAO1]	Related Information
<input checked="" type="checkbox"/> NP_296351.1	dihydrofolate reductase [Deinococcus radiodurans R1]	Related Information
<input checked="" type="checkbox"/> NP_359022.1	dihydrofolate reductase [Streptococcus pneumoniae R6]	Related Information
<input checked="" type="checkbox"/> NP_273358.1	dihydrofolate reductase [Neisseria meningitidis MC58]	Related Information
<input checked="" type="checkbox"/> YP_009360135.1	dihydrofolate reductase dhfr (dhfr) (tetrahydrofolate dehydrogenase) [Mycobacterium tuberculosis variant bovis AF2122/97]	Related Information
<input checked="" type="checkbox"/> XP_003522902.1	bifunctional dihydrofolate reductase-thymidylate synthase [Glycine max]	Related Information
<input checked="" type="checkbox"/> NP_001328947.1	thymidylate synthase 2 [Arabidopsis thaliana]	Related Information

Alignments ☒ Select All [Re-align](#) Mouse over the sequence identifier for sequence title

View Format: Compact ▾

Conservation Setting: 2 Bits ▾

NP_390064	1	M	---ISFIFAMDANRLIGKNDLPMHLPNDLAYFKITSG	HSIIMGRKTFESIG---RPLNPKRNIVVT	63
NP_719188	1	M	R--IAMIAAMANNRVIGKDNKMPWHLPEDLRHFKAMTLG	KPVVMGRKTFESIG---RPLPGRHNIVIS	64
NP_414590	1	M	---ISLSIAALAVDRVIGMENAMPWNLPAADLAWFKRNTLN	KPVMGRHTWESIG---RPLPGRKNILS	63
NP_249041	1	M	ARPLAMIAALGENRAIGIDNRLPWRLPADLKHFKAMTLG	KPVMGRKTWDSLG---RPLPGRNLNVS	66
NP_296351	1	M	[12]RQDVAIAAQTENRVIRGDDGMPWHLPAADFHFRLASVG	KPNIMGRKVFDTLRR--KPLPERVNI VLT	79
NP_359022	1	M	[1]-KKIVAIWAQDEELIGKENRLPMHLPALQHKETTLLN	HAILMGRVTFDGMGR--RLLPKRETLLT	67
NP_273358	1	M	LK-ITLIAACAENLCIGAGNMPWHPEDFAFFKAYITLG	KPVMGRKTWESLP--VKPLPGRRNIVIS	66
YP_009360135	1	M	VG---LIWAQATSGVIRGGDIPWRLPEDQAHFREITMG	HTIVMGRRTWDSLPAKVRPLPGRRNIVLS	66
XP_003522902	1	[11]Y[11]	RRTYQVLVAATQDWGIGKDGKLPWRLPTDLKFFKIDITVK	[7]NAIVMGRKTWESIPLeYRPLSGRLNVLT	98
NP_001328947	1	[51]L[10]	QSTYQVVVAATKEMGIGKDGKLPWNLPTDLKFFKDLTLS	[7]NAVVMGRKTWESIPKkYRPLSGRLNVLS	137
NP_390064	64	S	APDSEF---QSGTVVSLKDVLDICSGP	--EECFVIGGAQLYTDLPFY--ADRLYMTKIHHEFE---GDRHFPE-F	129
NP_719188	65	R	QADLQI---EGVTCVTSFEAAKRVAG--	DCEELVIGGGQLYKQLPQ--ADRLYLTQINLDVD---GDTFFPA-W	130
NP_414590	64	S	QPGTD---DRVTWVKSVDIEAACG--	DVPEIMVIGGGRVYEQFLPK--AQKLYLTHIDAEVE---GDTHFPD-Y	128
NP_249041	67	R	RQAGLAL---EGAEVFASLDAALARAFAE[4]DADELMLTGGAQLYAEALPR--AARLYLTVRGLAPE---GDAFFPE-I	138	
NP_296351	80	R	NENLKF---DGCCLIAHSPPEALQLAG--	DAPEIAIIGGEEIYRLYWR--LTRLEMLTHIAELD---GDTFFPE-I	145
NP_359022	68	R	NPEEKI---DGVATFDQVQSLDWYQDQ[1]-	KNLYITGGKQIFQAFEPY--LDEIVTHIHARVE---GDTYFPEEL	135
NP_273358	67	R	RQADYCA---AGAETAASLEAALACAG--	AEEAVIMGGAQIYQAMPL--ATDLRITEVDSLVE---GDAFFPA-I	132
YP_009360135	67	R	QADFMA---SGAEVVGSLLEALT-----	SPETWVIGGGQVYALALPY--ATRCVTEVDIGLPreaGDALAPV-L	131
XP_003522902	99	R	SGSFDIataENNVVTCGSMSSALELLAAS[4]SIEKFVFIGGGQIFREALNagpCEAIHLTEIQSSIEFc--DTFMPP-V	175	
NP_001328947	138	R	SGSFDIantENNVTCSSIDSALDLAAP[4]SIEKFVFIGGGQILREALNkpsCEAIHTEIDTSDIOc--DTFIPT-V	214	
NP_390064	130	D	ESNMKLVsEQGTCKDEKNPYDYFLMYEKKNs	[6]	168
NP_719188	131	E	DNEWQKT--ETQPISADGLEYNFNLVKKC-		160
NP_414590	129	E	PDDWESVFSFHDADAQNSHSYCFEILERR--		159
NP_249041	139	D	GAAWRLA--SSTHAADAPAYAFVWERR--		168
NP_296351	146	G	P-EFELaQETFRPADEKNRYDLTFQTRRRRGs	[3]	180
NP_359022	136	D	LSLLETVsSKFYAKDEKNPYDFTIQYRKKEV		168
NP_273358	133	D	RTHWKEA-ERTERRVSSKGRYAFVHYLRY--		162
YP_009360135	132	D	E-TWRGE--TGEWFRFSGLRRLYSYHRS--		159
XP_003522902	176	D	TFMFRPW--YSSFPKVENIRYCFTTYVRVRS	[324]	530
NP_001328947	215	D	TSAYQPW--CSSFPTICENGLRFSTTHVRVKS	[163]	408

