







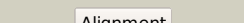

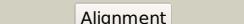

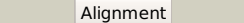
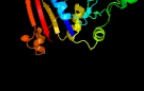
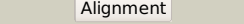

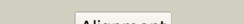

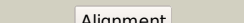
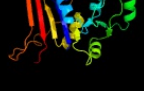
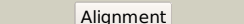







# Phyre2

Email	dlpeters@ualberta.ca
Description	vB_AbaM_DLP2_ dihydrofolate_reductase_Protein_translation
Date	Fri Jan 6 04:30:02 GMT 2023
Unique Job ID	51e1d1a5d42d34f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1juva_</a>	 Alignment		100.0	45	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
2	<a href="#">d2fzia1</a>	 Alignment		100.0	26	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
3	<a href="#">d1df7a_</a>	 Alignment		100.0	35	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
4	<a href="#">c3vc0A_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> schistosoma mansonii dihydrofolate reductase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
5	<a href="#">d8dfra_</a>	 Alignment		100.0	26	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
6	<a href="#">c7k6cD_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of dihydrofolate reductase (dhfr) from mycobacterium2 abscessus atcc 19977 / dsm 44196 with nadp and inhibitor p218 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
7	<a href="#">d1ra9a_</a>	 Alignment		100.0	27	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
8	<a href="#">d1j3ka_</a>	 Alignment		100.0	27	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
9	<a href="#">c6cxmA_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of a dihydrofolate reductase from mycobacterium2 smegmatis in complex with nadp and p218 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
10	<a href="#">c3tq8A_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> structure of the dihydrofolate reductase (folA) from coxiella burnetii2 in complex with trimethoprim <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
11	<a href="#">c1zdrB_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> dhfr from bacillus stearothermophilus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> oxidoreductase, transferase

12	<a href="#">c3dg8B_</a>	Alignment		100.0	26	<b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> quadruple mutant (n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase (pfdhfr-ts) complexed3 with rjf670, nadph, and dump <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
13	<a href="#">c3cseA_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> candida glabrata dihydrofolate reductase complexed with nadph and 2,4-2 diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
14	<a href="#">c4m7vA_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> dihydrofolate reductase from enterococcus faecalis complexed with2 nadp(h)and rab-propyl <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
15	<a href="#">c6drsA_</a>	Alignment		100.0	27	<b>PDB header:</b> antifungal protein/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase, putative; <b>PDBTitle:</b> dihydrofolate reductase (dhfr) of aspergillus flavus in complex with a2 small molecule inhibitor <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
16	<a href="#">c3ia5A_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> moritella profunda dihydrofolate reductase (dhfr) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
17	<a href="#">d1aoea_</a>	Alignment		100.0	23	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
18	<a href="#">c7rzoA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of a dihydrofolate reductase (fofa) from2 stenotrophomonas maltophilia <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
19	<a href="#">c3ix9B_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae dihydrofolate reductase2 - sp9 mutant <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
20	<a href="#">c3f0uX_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> trimethoprim-sensitive dihydrofolate reductase; <b>PDBTitle:</b> staphylococcus aureus f98y mutant dihydrofolate reductase complexed2 with nadph and 2,4-diamino-5-[3-(3-methoxy-5-phenylphenyl)but-1-3 ynyl]-6-methylpyrimidine <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
21	<a href="#">c4eckB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> crystal structure of the toxoplasma gondii ts-dhfr <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
22	<a href="#">d1vdra_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
23	<a href="#">c3e0bA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> bacillus anthracis dihydrofolate reductase complexed with nadph and 2,2 4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
24	<a href="#">c3clbA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhfr-ts; <b>PDBTitle:</b> structure of bifunctional tcdhfr-ts in complex with tmq <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
25	<a href="#">c2oipE_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> chain a, crystal structure of dhfr; <b>PDBTitle:</b> crystal structure of the s290g active site mutant of ts-dhfr from2 cryptosporidium hominis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
26	<a href="#">d1seja1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
27	<a href="#">c8f09A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of a trimethoprim-resistant dihydrofolate reductase2 (dhfr) enzyme from an uncultured soil bacterium <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a> <b>Fold:</b> Dihydrofolate reductase-like

28	<a href="#">d1kmva_</a>	Alignment	not modelled	100.0	22	<b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
29	<a href="#">c3jsuA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> quadruple mutant(n51i+c59r+s108n+i164l) plasmidum falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
30	<a href="#">c2blcA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> sp21 double mutant p. vivax dihydrofolate reductase in complex with2 des-chloropyrimethamine <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
31	<a href="#">c5eccA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrofolate reductase type i; <b>PDBTitle:</b> klebsiella pneumoniae dfra1 complexed with nadph and 6-ethyl-5-(3-(2-2 methoxy-5-(pyridin-4-yl)phenyl)prop-1-yn-1-yl)pyrimidine-2,4-diamine <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
32	<a href="#">c3rg9A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
33	<a href="#">c6rumA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> gfp-lama-g97 a gfp enhancer nanobody with cpdhfr insertion; <b>PDBTitle:</b> crystal structure of gfp-lama-g97 - a gfp enhancer nanobody with2 cpdhfr insertion and tmp and nadph <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
34	<a href="#">d3dfra_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
35	<a href="#">c3k2hA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase/thymidylate synthase; <b>PDBTitle:</b> co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
36	<a href="#">c7lrhD_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> c-terminal domain of ribd from brucella abortus (5-amino-6-2 ribosylamino-2,4(1h,3h)-pyrimidinedione 5'-phosphate reductase) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
37	<a href="#">d1d1ga_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
38	<a href="#">c2gd9A_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yyap; <b>PDBTitle:</b> crystal structure of a putative dihydrofolate reductase (bsu40760,2 yyap) from bacillus subtilis at 2.30 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
39	<a href="#">c7lrhC_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> c-terminal domain of ribd from brucella abortus (5-amino-6-2 ribosylamino-2,4(1h,3h)-pyrimidinedione 5'-phosphate reductase) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
40	<a href="#">c2hxvA_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- <b>PDBTitle:</b> crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
41	<a href="#">c2p4gA_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
42	<a href="#">d2hxva1</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> RibD C-terminal domain-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
43	<a href="#">c3kgvA_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional deaminase-reductase domain protein; <b>PDBTitle:</b> crystal structure of putative dihydrofolate reductase (yp_001636057.1)2 from chloroflexus aurantiacus j-10-fl at 1.50 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
44	<a href="#">c2xw7A_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> structure of mycobacterium smegmatis putative reductase ms0308 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
45	<a href="#">c5xuxC_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> conserved protein; <b>PDBTitle:</b> crystal structure of rib7 from methanosarcina mazei <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
46	<a href="#">c3znpA_</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribd;

46	<a href="#">c2p9A_</a>	Alignment	not modelled	98.2	13	<b>PDBTitle:</b> acinetobacter baumannii ribd, form 2 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
47	<a href="#">c3jtwB_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of putative dihydrofolate reductase (yp_805003.1)2 from pediococcus pentosaceus atcc 25745 at 1.90 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
48	<a href="#">c2o7pA_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
49	<a href="#">d2b3za1</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> RibD C-terminal domain-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
50	<a href="#">c2d5nB_</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
51	<a href="#">d2azna1</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> RibD C-terminal domain-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
52	<a href="#">c6p8cB_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,5-diamino-6-ribosylamino-4(3h)-pyrimidinone 5'-phosphate <b>PDBTitle:</b> 2,5-diamino-6-(ribosylamino)-4(3h)-pyrimidinone 5'-phosphate reductase2 (mthred) from methanothermobacter thermoautotrophicus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
53	<a href="#">c3ky8B_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative riboflavin biosynthesis protein; <b>PDBTitle:</b> crystal structure of putative riboflavin biosynthesis protein2 (yp_001092907.1) from shewanella sp. pv-4 at 2.12 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
54	<a href="#">c4xt6A_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rv2671; <b>PDBTitle:</b> crystal structure of rv2671 from mycobacterium tuberculosis in complex2 with the tetrahydropteridine ring of tetrahydrofolate (thf) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
55	<a href="#">c4ha7B_</a>	Alignment	not modelled	87.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,5-diamino-6-ribosylamino-4(3h)-pyrimidinone 5'-phosphate <b>PDBTitle:</b> structural insights into the reduction mechanism of saccharomyces2 cerevisia riboflavin biosynthesis reductase rib7 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
56	<a href="#">c4cvkA_</a>	Alignment	not modelled	82.9	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine ligase; <b>PDBTitle:</b> pamurf in complex with udp-murnac-tripeptide (mdap) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
57	<a href="#">c7waeB_</a>	Alignment	not modelled	81.5	28	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cyanophycin synthase; <b>PDBTitle:</b> trichodesmium erythraeum cyanophycin synthetase 1 (tecpha1) with2 atpgammas, 4x(beta-asp-arg), and aspartate <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
58	<a href="#">c7lgjC_</a>	Alignment	not modelled	69.2	28	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> cyanophycin synthase; <b>PDBTitle:</b> cyanophycin synthetase 1 from synechocystis sp. utex2470 with adpcp2 and 8x(asp-arg)-nh2 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
59	<a href="#">c7sy9B_</a>	Alignment	not modelled	65.6	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramoylalanine--d-glutamate ligase2 (murd) from pseudomonas aeruginosa pao1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
60	<a href="#">c6vr7A_</a>	Alignment	not modelled	65.1	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> mur ligase middle domain protein; <b>PDBTitle:</b> structure of a pseudomurein peptide ligase type c from methanothermus2 fervidus <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
61	<a href="#">c2xjaD_</a>	Alignment	not modelled	62.2	23	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure from m.tuberculosis with dipeptide and adp <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
62	<a href="#">c1j6uA_</a>	Alignment	not modelled	61.8	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
63	<a href="#">c7lgnB_</a>	Alignment	not modelled	55.8	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cyanophycin synthase; <b>PDBTitle:</b> cyanophycin synthetase 1 from t. morbirosei <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
64	<a href="#">c3zdrA_</a>	Alignment	not modelled	55.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase domain of the bifunctional <b>PDBTitle:</b> structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-1-phosphate dehydrogenase

65	<a href="#">c4rfIB_</a>	Alignment	not modelled	50.6	19	[nad(p)+]; <b>PDBTitle:</b> crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
66	<a href="#">c4c13A_</a>	Alignment	not modelled	50.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; <b>PDBTitle:</b> x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
67	<a href="#">c1e8cB_</a>	Alignment	not modelled	47.8	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamate--2,6-diaminopimelate <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
68	<a href="#">c7bvaB_</a>	Alignment	not modelled	47.4	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramic acid l-alanine ligase (murc)2 from mycobacterium bovis <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
69	<a href="#">d1gg4a1</a>	Alignment	not modelled	45.8	15	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
70	<a href="#">c7d27A_</a>	Alignment	not modelled	42.7	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2, 6-2 diaminopimelate ligase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
71	<a href="#">c1gqqa_</a>	Alignment	not modelled	41.7	5	<b>PDB header:</b> cell wall biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> murc - crystal structure of the apo-enzyme from haemophilus influenzae <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
72	<a href="#">c2f00A_</a>	Alignment	not modelled	38.6	8	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
73	<a href="#">c3uhjE_</a>	Alignment	not modelled	34.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> probable glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
74	<a href="#">c6csjD_</a>	Alignment	not modelled	33.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
75	<a href="#">c5fb3C_</a>	Alignment	not modelled	31.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerol-1-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> structure of glycerophosphate dehydrogenase in complex with nadph <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
76	<a href="#">c1o5zA_</a>	Alignment	not modelled	31.4	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase/dihydrofolate synthase; <b>PDBTitle:</b> crystal structure of folypolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
77	<a href="#">d2gc6a1</a>	Alignment	not modelled	28.4	21	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
78	<a href="#">c5zwoY_</a>	Alignment	not modelled	28.3	27	<b>PDB header:</b> splicing <b>Chain:</b> Y: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc26; <b>PDBTitle:</b> cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
79	<a href="#">d1o6da_</a>	Alignment	not modelled	27.4	24	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
80	<a href="#">d1j6ua2</a>	Alignment	not modelled	27.0	14	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
81	<a href="#">c3ox4D_</a>	Alignment	not modelled	26.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 2; <b>PDBTitle:</b> structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
82	<a href="#">c1xahA_</a>	Alignment	not modelled	25.1	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate synthase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+ <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
83	<a href="#">c3hl0B_</a>	Alignment	not modelled	24.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> maleylacetate reductase; <b>PDBTitle:</b> crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
84	<a href="#">c3uagA_</a>	Alignment	not modelled	23.4	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d-glutamate <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
85	<a href="#">c2dzaA_</a>	Alignment	not modelled	23.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate



						<b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a> <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus2 selenitireducens mls10, nysgrc target 029814. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
86	<a href="#">c4m1qB_</a>	Alignment	not modelled	22.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate- <b>PDBTitle:</b> crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
87	<a href="#">c1gg4A_</a>	Alignment	not modelled	22.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysin; <b>PDBTitle:</b> crystal structure of a wild type endolysin lysime-ef1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
88	<a href="#">c6istA_</a>	Alignment	not modelled	21.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
89	<a href="#">c1ta9A_</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
90	<a href="#">c5tpR_</a>	Alignment	not modelled	20.1	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> J: <b>PDB Molecule:</b> m-phase phosphoprotein 6 homolog; <b>PDBTitle:</b> crystal structure of the mpp6 exosome complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
91	<a href="#">c5okzJ_</a>	Alignment	not modelled	19.7	50	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine(9)-adenine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis. <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
92	<a href="#">c6emvA_</a>	Alignment	not modelled	19.1	20	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
93	<a href="#">d1jq5a_</a>	Alignment	not modelled	19.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus cereus atcc2 14579 complexed with calcium, nysgrc target 029452 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
94	<a href="#">c4ln1B_</a>	Alignment	not modelled	18.6	18	<b>PDB header:</b> cell cycle <b>Chain:</b> F: <b>PDB Molecule:</b> tubulin tyrosine ligase, ttl; <b>PDBTitle:</b> crystal structure of tubulin-stathmin-ttl-apo complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
95	<a href="#">c4ijjF_</a>	Alignment	not modelled	18.5	31	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
96	<a href="#">d1vlja_</a>	Alignment	not modelled	16.5	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramoylalanine-d-glutamate ligase2 from acinetobacter baumannii ab5075-uw <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
97	<a href="#">c7sirA_</a>	Alignment	not modelled	16.4	15	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
98	<a href="#">c1ldbA_</a>	Alignment	not modelled	16.4	19	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
99	<a href="#">d1ns5a_</a>	Alignment	not modelled	16.1	43	