

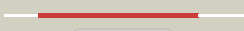



























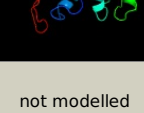







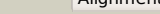






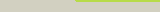

















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1juva_	 Alignment		100.0	46	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
2	d1df7a_	 Alignment		100.0	35	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
3	c2oipE_	 Alignment		100.0	26	PDB header: transferase, oxidoreductase Chain: E: PDB Molecule: chain a, crystal structure of dhfr; PDBTitle: crystal structure of the s290g active site mutant of ts-dhfr from <i>Mycobacterium tuberculosis</i> PDB Entry: PDBe RCSB PDBj
4	d2fzia1	 Alignment		100.0	25	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
5	c3tq8A_	 Alignment		100.0	27	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of the dihydrofolate reductase (folA) from <i>Escherichia coli</i> in complex with trimethoprim PDB Entry: PDBe RCSB PDBj
6	d1aoea_	 Alignment		100.0	26	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
7	c3vcoA_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: schistosoma mansoni dihydrofolate reductase PDB Entry: PDBe RCSB PDBj
8	c4m7vA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: dihydrofolate reductase from <i>Enterococcus faecalis</i> complexed with 2 NADP(H) and rab-propyl PDB Entry: PDBe RCSB PDBj
9	d8dfra_	 Alignment		100.0	26	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
10	c7k6cD_	 Alignment		100.0	29	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: D: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of dihydrofolate reductase (dhfr) from <i>Mycobacterium tuberculosis</i> abscessus atcc 19977 / dsm 44196 with nadp and inhibitor p218 PDB Entry: PDBe RCSB PDBj
11	c4eckB_	 Alignment		100.0	26	PDB header: transferase, oxidoreductase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: crystal structure of the toxoplasma gondii ts-dhfr PDB Entry: PDBe RCSB PDBj

12	c1zdrB_	Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: dhfr from bacillus stearothermophilus PDB Entry: PDBe RCSB PDBj
13	d1ra9a_	Alignment		100.0	27	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
14	c6cxmA_	Alignment		100.0	29	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of a dihydrofolate reductase from mycobacterium2 smegmatis in complex with nadp and p218 PDB Entry: PDBe RCSB PDBj
15	c6drsA_	Alignment		100.0	23	PDB header: antifungal protein/inhibitor Chain: A: PDB Molecule: dihydrofolate reductase, putative; PDBTitle: dihydrofolate reductase (dhfr) of aspergillus flavus in complex with a2 small molecule inhibitor PDB Entry: PDBe RCSB PDBj
16	c3clbA_	Alignment		100.0	28	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: dhfr-ts; PDBTitle: structure of bifunctional tcdhfr-ts in complex with tmq PDB Entry: PDBe RCSB PDBj
17	c3cseA_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with nadph and 2,4-2 diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b) PDB Entry: PDBe RCSB PDBj
18	c7rzoA_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of a dihydrofolate reductase (folA) from2 stenotrophomonas maltophilila PDB Entry: PDBe RCSB PDBj
19	c3f0uX_	Alignment		100.0	26	PDB header: oxidoreductase Chain: X: PDB Molecule: trimethoprim-sensitive dihydrofolate reductase; PDBTitle: 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 PDB Entry: PDBe RCSB PDBj
20	c8f09A_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of a trimethoprim-resistant dihydrofolate reductase2 (dhfr) enzyme from an uncultured soil bacterium PDB Entry: PDBe RCSB PDBj
21	c3ia5A_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: moritella profunda dihydrofolate reductase (dhfr) PDB Entry: PDBe RCSB PDBj
22	c3e0bA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: bacillus anthracis dihydrofolate reductase complexed with nadph and 2,2 4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b) PDB Entry: PDBe RCSB PDBj
23	c3ix9B_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of streptococcus pneumoniae dihydrofolate reductase2 - sp9 mutant PDB Entry: PDBe RCSB PDBj
24	d1kmya_	Alignment	not modelled	100.0	23	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
25	d1j3ka_	Alignment	not modelled	100.0	24	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
26	c3dg8B_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase, transferase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: quadruple mutant (n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase (pfdhfr-ts) complexed3 with rjf670, nadph, and dump PDB Entry: PDBe RCSB PDBj
27	d1ydra	Alignment	not modelled	100.0	28	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like

27	d1vvdA_	Alignment	not modelled	100.0	20	Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
28	c3rg9A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210 PDB Entry: PDBe RCSB PDBj
29	d1seja1	Alignment	not modelled	100.0	27	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
30	c2blcA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in complex with2 des-chloropyrimethamine PDB Entry: PDBe RCSB PDBj
31	c5eccA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: dehydrofolate reductase type i; PDBTitle: 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 PDB Entry: PDBe RCSB PDBj
32	d3dfra_	Alignment	not modelled	100.0	21	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
33	c3k2hA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: dihydrofolate reductase/thymidylate synthase; PDBTitle: co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp PDB Entry: PDBe RCSB PDBj
34	c3jsuA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump PDB Entry: PDBe RCSB PDBj
35	d1d1ga_	Alignment	not modelled	99.9	21	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases PDB entry: PDBe RCSB PDBj
36	c6rumA_	Alignment	not modelled	100.0	21	PDB header: protein binding Chain: A: PDB Molecule: gfp-lama-g97 a gfp enhancer nanobody with cpdhfr insertion; PDBTitle: crystal structure of gfp-lama-g97 - a gfp enhancer nanobody with2 cpdhfr insertion and tmp and nadph PDB Entry: PDBe RCSB PDBj
37	c2gd9A_	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein yyap; PDBTitle: crystal structure of a putative dihydrofolate reductase (bsu40760,2 yyap) from bacillus subtilis at 2.30 a resolution PDB Entry: PDBe RCSB PDBj
38	c7lrhD_	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: D: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: c-terminal domain of ribd from brucella abortus (5-amino-6-2 ribosylamino-2,4(1h,3h)-pyrimidinedione 5'-phosphate reductase) PDB Entry: PDBe RCSB PDBj
39	c2p4gA_	Alignment	not modelled	96.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution PDB Entry: PDBe RCSB PDBj
40	c2xw7A_	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of mycobacterium smegmatis putative reductase ms0308 PDB Entry: PDBe RCSB PDBj
41	c5xuxC_	Alignment	not modelled	97.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: conserved protein; PDBTitle: crystal structure of rib7 from methanosarcina mazei PDB Entry: PDBe RCSB PDBj
42	c3kgvA_	Alignment	not modelled	98.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional deaminase-reductase domain protein; PDBTitle: crystal structure of putative dihydrofolate reductase (yp_001636057.1)2 from chloroflexus aurantiacus j-10-fl at 1.50 a resolution PDB Entry: PDBe RCSB PDBj
43	c2hvxvA_	Alignment	not modelled	98.1	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- PDBTitle: crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution PDB Entry: PDBe RCSB PDBj
44	d2hxva1	Alignment	not modelled	98.3	17	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like PDB entry: PDBe RCSB PDBj
45	c2o7pA_	Alignment	not modelled	98.3	14	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain

						PDB Entry: PDBe RCSB PDBj PDB header: hydrolase, oxidoreductase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis PDB Entry: PDBe RCSB PDBj
46	c2d5nB_	 Alignment	not modelled	98.2	14	PDB header: hydrolase, oxidoreductase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis PDB Entry: PDBe RCSB PDBj
47	c3jtwB_	 Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of putative dihydrofolate reductase (yp_805003.1)2 from pediococcus pentosaceus atcc 25745 at 1.90 a resolution PDB Entry: PDBe RCSB PDBj
48	d2b3za1	 Alignment	not modelled	98.5	15	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like PDB entry: PDBe RCSB PDBj
49	c7lrhC_	 Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: C: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: c-terminal domain of ribd from brucella abortus (5-amino-6-2 ribosylamino-2,4(1h,3h)-pyrimidinedione 5'-phosphate reductase) PDB Entry: PDBe RCSB PDBj
50	c3ky8B_	 Alignment	not modelled	98.3	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative riboflavin biosynthesis protein; PDBTitle: crystal structure of putative riboflavin biosynthesis protein2 (yp_001092907.1) from shewanella sp. pv-4 at 2.12 a resolution PDB Entry: PDBe RCSB PDBj
51	c6p8cB_	 Alignment	not modelled	98.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 2,5-diamino-6-ribosylamino-4(3h)-pyrimidinone 5'-phosphate PDBTitle: 2,5-diamino-6-(ribosylamino)-4(3h)-pyrimidinone 5'-phosphate reductase2 (mthred) from methanothermobacter thermautotrophicus PDB Entry: PDBe RCSB PDBj
52	c3zpgA_	 Alignment	not modelled	98.0	13	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2 PDB Entry: PDBe RCSB PDBj
53	d2azna1	 Alignment	not modelled	98.3	14	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like PDB entry: PDBe RCSB PDBj
54	c4xt6A_	 Alignment	not modelled	97.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: rv2671; PDBTitle: crystal structure of rv2671 from mycobacterium tuberculosis in complex2 with the tetrahydropteridine ring of tetrahydrofolate (thf) PDB Entry: PDBe RCSB PDBj
55	c4cvkA_	 Alignment	not modelled	80.6	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine ligase; PDBTitle: pamurf in complex with udp-murnac-tripeptide (mdap) PDB Entry: PDBe RCSB PDBj
56	c7waeB_	 Alignment	not modelled	77.9	28	PDB header: ligase Chain: B: PDB Molecule: cyanophycin synthase; PDBTitle: trichodesmium erythraeum cyanophycin synthetase 1 (tecpha1) with2 atpgammas, 4x(beta-aspartate) PDB Entry: PDBe RCSB PDBj
57	c7sy9B_	 Alignment	not modelled	64.3	14	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: crystal structure of udp-n-acetylmuramoylalanine--d-glutamate ligase2 (murd) from pseudomonas aeruginosa pao1 PDB Entry: PDBe RCSB PDBj
58	c4ha7B_	 Alignment	not modelled	63.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2,5-diamino-6-ribosylamino-4(3h)-pyrimidinone 5'-phosphate PDBTitle: structural insights into the reduction mechanism of saccharomyces2 cerevisia riboflavin biosynthesis reductase rib7 PDB Entry: PDBe RCSB PDBj
59	c7lgjC_	 Alignment	not modelled	62.8	29	PDB header: ligase Chain: C: PDB Molecule: cyanophycin synthase; PDBTitle: cyanophycin synthetase 1 from synechocystis sp. utex2470 with adpcp2 and 8x(aspartate)-nh2 PDB Entry: PDBe RCSB PDBj
60	c2xjaD_	 Alignment	not modelled	60.1	21	PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp PDB Entry: PDBe RCSB PDBj
61	c1j6uA_	 Alignment	not modelled	59.2	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution PDB Entry: PDBe RCSB PDBj
62	c3uhjE_	 Alignment	not modelled	58.1	15	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021 PDB Entry: PDBe RCSB PDBj
63	c6vr7A_	 Alignment	not modelled	56.9	17	PDB header: ligase Chain: A: PDB Molecule: mur ligase middle domain protein; PDBTitle: structure of a pseudomurein peptide ligase type c from methanothermus2 fervidus PDB Entry: PDBe RCSB PDBj
64	c3zdrA_	 Alignment	not modelled	56.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3

						thermoglucoaldolase ncbi 11955 PDB Entry: PDBe RCSB PDBj
65	c4rf1B_	 Alignment	not modelled	54.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii PDB Entry: PDBe RCSB PDBj
66	c4c13A_	 Alignment	not modelled	47.0	14	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; PDBTitle: x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys PDB Entry: PDBe RCSB PDBj
67	c7lgnB_	 Alignment	not modelled	46.5	19	PDB header: ligase Chain: B: PDB Molecule: cyanophycin synthase; PDBTitle: cyanophycin synthetase 1 from t. moribirosei PDB Entry: PDBe RCSB PDBj
68	c7bvaB_	 Alignment	not modelled	42.1	11	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: crystal structure of udp-n-acetylmuramic acid l-alanine ligase (murc)2 from mycobacterium bovis PDB Entry: PDBe RCSB PDBj
69	c1e8cB_	 Alignment	not modelled	41.9	23	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamate--2,6-diaminopimelate PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli PDB Entry: PDBe RCSB PDBj
70	d1gg4a1	 Alignment	not modelled	39.9	15	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain PDB entry: PDBe RCSB PDBj
71	c6csjD_	 Alignment	not modelled	38.9	24	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity PDB Entry: PDBe RCSB PDBj
72	c6emvA_	 Alignment	not modelled	36.1	20	PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(9)-/adenine(9)-n1)-methyltransferase; PDBTitle: crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis. PDB Entry: PDBe RCSB PDBj
73	c7d27A_	 Alignment	not modelled	35.9	31	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- PDBTitle: structure of udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2, 6-2 diaminopimelate ligase PDB Entry: PDBe RCSB PDBj
74	c1gqqA_	 Alignment	not modelled	34.9	4	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae PDB Entry: PDBe RCSB PDBj
75	c3ox4D_	 Alignment	not modelled	34.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor PDB Entry: PDBe RCSB PDBj
76	c1o5zA_	 Alignment	not modelled	33.5	23	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution PDB Entry: PDBe RCSB PDBj
77	c2dzaA_	 Alignment	not modelled	32.5	18	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate PDB Entry: PDBe RCSB PDBj
78	c5fb3C_	 Alignment	not modelled	30.9	12	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph PDB Entry: PDBe RCSB PDBj
79	c6istA_	 Alignment	not modelled	29.8	31	PDB header: hydrolase Chain: A: PDB Molecule: lysin; PDBTitle: crystal structure of a wild type endolysin lysime-ef1 PDB Entry: PDBe RCSB PDBj
80	c2f00A_	 Alignment	not modelled	29.7	8	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc PDB Entry: PDBe RCSB PDBj
81	c5zwoY_	 Alignment	not modelled	29.1	27	PDB header: splicing Chain: Y: PDB Molecule: pre-mrna-splicing factor cwc26; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom PDB Entry: PDBe RCSB PDBj
82	c3hl0B_	 Alignment	not modelled	28.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens PDB Entry: PDBe RCSB PDBj
83	d1o6da_	 Alignment	not modelled	28.3	24	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like PDB entry: PDBe RCSB PDBj
84	c1xahA_	 Alignment	not modelled	27.4	15	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: crystal structure of staphylococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+

					PDB Entry: PDBe RCSB PDBj
85	d2gc6a1	Alignment	not modelled	24.2	22 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain PDB entry: PDBe RCSB PDBj
86	d1oj7a_	Alignment	not modelled	21.1	15 Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase PDB entry: PDBe RCSB PDBj
87	c1ta9A_	Alignment	not modelled	20.0	15 PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of a long form rnase z from yeast PDB Entry: PDBe RCSB PDBj
88	c5mtzA_	Alignment	not modelled	19.2	17 PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease z; PDBTitle: crystal structure of a long form rnase z from yeast PDB Entry: PDBe RCSB PDBj
89	d1vh0a_	Alignment	not modelled	18.4	24 Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like PDB entry: PDBe RCSB PDBj
90	d1j6ua2	Alignment	not modelled	18.3	14 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain PDB entry: PDBe RCSB PDBj
91	c5uurA_	Alignment	not modelled	18.2	18 PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic acid PDB Entry: PDBe RCSB PDBj
92	c5okzj_	Alignment	not modelled	18.0	50 PDB header: rna binding protein Chain: J: PDB Molecule: m-phase phosphoprotein 6 homolog; PDBTitle: crystal structure of the mpp6 exosome complex PDB Entry: PDBe RCSB PDBj
93	d1jq5a_	Alignment	not modelled	17.4	19 Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase PDB entry: PDBe RCSB PDBj
94	c3uagA_	Alignment	not modelled	17.3	18 PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d-glutamate PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase PDB Entry: PDBe RCSB PDBj
95	c3en2A_	Alignment	not modelled	16.7	6 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable primosomal replication protein n; PDBTitle: three-dimensional structure of the protein prib from ralstonia2 solanacearum at the resolution 2.3a. northeast structural genomics3 consortium target rsr213c. PDB Entry: PDBe RCSB PDBj
96	c5tprB_	Alignment	not modelled	15.7	12 PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound PDB Entry: PDBe RCSB PDBj
97	c7w9yB_	Alignment	not modelled	14.9	11 PDB header: oxidoreductase Chain: B: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of bacillus subtilis yugj in complex with nadp and2 nickel PDB Entry: PDBe RCSB PDBj
98	c2gruB_	Alignment	not modelled	14.9	16 PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scylo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbagluco-6-phosphate, nad+ and co2+ PDB Entry: PDBe RCSB PDBj
99	c1gg4A_	Alignment	not modelled	14.8	16 PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate- PDBTitle: crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution PDB Entry: PDBe RCSB PDBj