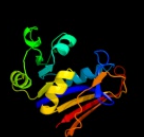
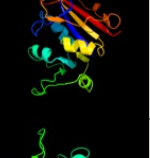
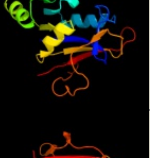
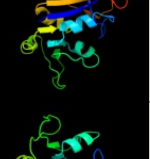
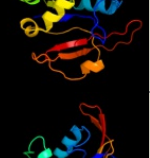
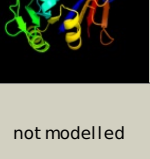


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ra9a_	 Alignment		100.0	99	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
2	c3tq8A_	 Alignment		100.0	43	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of the dihydrofolate reductase (folA) from coxiella burnetii2 in complex with trimethoprim
3	c3ia5A_	 Alignment		100.0	55	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: moritella profunda dihydrofolate reductase (dhfr)
4	c3e0bA_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: bacillus anthracis dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
5	c3f0uX_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: X: PDB Molecule: trimethoprim-sensitive dihydrofolate reductase; PDBTitle: staphylococcus aureus f98y mutant dihydrofolate reductase2 complexed with nadph and 2,4-diamino-5-[3-(3-methoxy-5-3 phenylphenyl)but-1-ynyl]-6-methylpyrimidine
6	c1zdrB_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: dhfr from bacillus stearothermophilus
7	c3k2hA_	 Alignment		100.0	34	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
8	c2oipE_	 Alignment		100.0	34	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-2 dhfr from cryptosporidium hominis
9	d3dfra_	 Alignment		100.0	28	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
10	c3cseA_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
11	c3ix9B_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant

12	d8dfra_	Alignment		100.0	32	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
13	d1aoea_	Alignment		100.0	35	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
14	c3jsuA_	Alignment		100.0	35	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
15	d1kmva_	Alignment		100.0	32	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
16	d1j3ka_	Alignment		100.0	35	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
17	d2fzia1	Alignment		100.0	35	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
18	c3dg8B_	Alignment		100.0	35	PDB header: oxidoreductase, transferase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate PDBTitle: quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
19	c3rg9A_	Alignment		100.0	32	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tdhfr) in complex with2 wr99210
20	d1df7a_	Alignment		100.0	36	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
21	c2blcA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine
22	d1vdra_	Alignment	not modelled	100.0	33	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
23	c3clbA_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: dhfr-ts; PDBTitle: structure of bifunctional tcdhfr-ts in complex with tmq
24	d1seja1	Alignment	not modelled	100.0	33	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
25	d1juva_	Alignment	not modelled	100.0	22	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
26	d1d1ga_	Alignment	not modelled	100.0	26	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
27	c3jtwB_	Alignment	not modelled	99.9	19	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
28	c2gd9A_	Alignment	not modelled	99.8	17	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

29	c2xw7A_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of mycobacterium smegmatis putative reductase ms0308
30	c3ky8B_	Alignment	not modelled	99.6	18	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
31	d2hxva1	Alignment	not modelled	99.5	20	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
32	c3kgyA_	Alignment	not modelled	99.4	19	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
33	d2azna1	Alignment	not modelled	99.4	16	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
34	d2b3za1	Alignment	not modelled	99.4	15	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
35	c2hvxA_	Alignment	not modelled	99.3	20	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
36	c2o7pA_	Alignment	not modelled	99.2	15	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
37	c2d5nB_	Alignment	not modelled	99.2	16	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
38	c2p4gA_	Alignment	not modelled	98.8	17	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
39	d1aoga2	Alignment	not modelled	66.2	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
40	d1q1ra2	Alignment	not modelled	47.6	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
41	d1gesa2	Alignment	not modelled	38.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
42	d1gera2	Alignment	not modelled	33.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
43	d3grsa2	Alignment	not modelled	32.9	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
44	d1onfa2	Alignment	not modelled	28.4	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
45	d1m6ia2	Alignment	not modelled	27.4	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
46	d1feca2	Alignment	not modelled	22.3	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
47	d1nhpa2	Alignment	not modelled	21.2	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
48	d1gv4a2	Alignment	not modelled	20.3	33	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
49	c3fq6A_	Alignment	not modelled	20.1	17	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
50	d1h6va2	Alignment	not modelled	18.3	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
51	c3ihtB_	Alignment	not modelled	16.7	11	PDB header: transferase Chain: B: PDB Molecule: s-adenosyl-l-methionine methyl transferase; PDBTitle: crystal structure of s-adenosyl-l-methionine methyl transferase2 (yp_165822.1) from silicibacter pomeroyi dss-3 at 1.80 a resolution
						Fold: FAD-binding/transporter-associated domain-like

52	d1rm6b2	Alignment	not modelled	16.2	11	Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
53	d1udxa3	Alignment	not modelled	15.8	18	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
54	c3q3vA	Alignment	not modelled	15.7	13	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
55	c1jb9A	Alignment	not modelled	15.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
56	c1zmrA	Alignment	not modelled	14.3	18	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
57	d1d7ya2	Alignment	not modelled	14.0	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
58	d1vjda	Alignment	not modelled	13.9	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
59	d1hdia	Alignment	not modelled	13.5	20	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
60	d1fw8a	Alignment	not modelled	13.3	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
61	d1vdca2	Alignment	not modelled	13.2	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
62	c3cqyA	Alignment	not modelled	12.5	30	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetyl/muramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
63	d1ojta2	Alignment	not modelled	11.8	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
64	c1rm6E	Alignment	not modelled	11.7	11	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
65	d1qpga	Alignment	not modelled	11.5	21	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
66	d1ebda2	Alignment	not modelled	11.3	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
67	d2b4ya1	Alignment	not modelled	11.1	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
68	d1lvla2	Alignment	not modelled	11.1	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
69	c3okfA	Alignment	not modelled	10.9	11	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
70	d1jeoa	Alignment	not modelled	10.7	27	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
71	d1gg4a1	Alignment	not modelled	10.5	21	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
72	d1ltkA	Alignment	not modelled	10.3	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
73	d1dxla2	Alignment	not modelled	9.0	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
74	d16pka	Alignment	not modelled	8.7	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
75	d1xhca2	Alignment	not modelled	8.5	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
76	d1phpa	Alignment	not modelled	8.5	26	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
77	c2jraB	Alignment	not modelled	8.5	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
78	d1vpea	Alignment	not modelled	8.4	21	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase

					Family: Phosphoglycerate kinase
79	d2gs5a1	Alignment	not modelled	8.1	12 Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
80	c2hjhB	Alignment	not modelled	8.1	23 PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
81	c1xahA	Alignment	not modelled	8.0	9 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+
82	d1v6sa	Alignment	not modelled	7.8	19 Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
83	d2i14a2	Alignment	not modelled	7.7	20 Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
84	c2cunA	Alignment	not modelled	7.5	24 PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii o3
85	c3h10B	Alignment	not modelled	7.3	20 PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
86	c3ce9A	Alignment	not modelled	6.7	16 PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
87	c3f3mA	Alignment	not modelled	6.6	25 PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenyltransferase; PDBTitle: six crystal structures of two phosphopantetheine2 adenyltransferases reveal an alternative ligand binding3 mode and an associated structural change
88	d1krha2	Alignment	not modelled	6.5	13 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
89	c1kyqC	Alignment	not modelled	6.5	38 PDB header: oxidoreductase, lyase Chain: C: PDB Molecule: siroheme biosynthesis protein met8; PDBTitle: met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
90	d1kyqa1	Alignment	not modelled	6.4	38 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
91	d2h3ka1	Alignment	not modelled	6.3	17 Fold: Immunoglobulin-like beta-sandwich Superfamily: NEAT domain-like Family: NEAT domain
92	d1fcda1	Alignment	not modelled	6.3	26 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
93	d1jb9a2	Alignment	not modelled	6.3	16 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
94	c3dfzB	Alignment	not modelled	6.3	18 PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sir, precorrin-2 dehydrogenase
95	d1fl2a2	Alignment	not modelled	6.1	29 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
96	c3hrdC	Alignment	not modelled	6.0	18 PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
97	d1ddga2	Alignment	not modelled	6.0	22 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
98	d1up7a1	Alignment	not modelled	5.8	43 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
99	d1v59a2	Alignment	not modelled	5.8	24 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains