










Phyre2

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Description	RVBD2763c_(dfrA)_3073140_3073619
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1df7a_	Alignment		100.0	100	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
2	c6cxmA_	Alignment		100.0	65	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
3	c4m7vA_	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: dihydrofolate reductase from enterococcus faecalis complexed with2 nadp(h)and rab-propyl
4	c3tq8A_	Alignment		100.0	36	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
5	c3k2hA_	Alignment		100.0	29	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
6	c3f0uX_	Alignment		100.0	27	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
7	c1zdrB_	Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: dhfr from bacillus stearotherophilus
8	c2oipE_	Alignment		100.0	30	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 from2 cryptosporidium hominis
9	c4eckB_	Alignment		100.0	32	PDB header: transferase, oxidoreductase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: crystal structure of the toxoplasma gondii ts-dhfr
10	d1ra9a_	Alignment		100.0	36	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
11	c3cseA_	Alignment		100.0	33	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)

12	c3e0bA	Alignment		100.0	34	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)
13	c3ia5A	Alignment		100.0	35	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrofolate reductase; PDBTitle: moritella profunda dihydrofolate reductase (dhfr)
14	c3vcoA	Alignment		100.0	32	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrofolate reductase; PDBTitle: schistosoma mansoni dihydrofolate reductase
15	d2fzia1	Alignment		100.0	34	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
16	d3dfra	Alignment		100.0	33	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
17	d1kmya	Alignment		100.0	34	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
18	c3rg9A	Alignment		100.0	37	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A; PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210
19	d8dfra	Alignment		100.0	35	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
20	c3jsuA	Alignment		100.0	28	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
21	d1j3ka	Alignment	not modelled	100.0	27	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
22	c3dg8B	Alignment	not modelled	100.0	26	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
23	c3ix9B	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B; PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant
24	c6drsA	Alignment	not modelled	100.0	41	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
25	c2blcA	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in complex with2 des-chloropyrimethamine
26	d1aoea	Alignment	not modelled	100.0	29	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
27	d1vdra	Alignment	not modelled	100.0	32	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
28	c5eccA	Alignment	not modelled	100.0	29	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
29	d1seja1	Alignment	not modelled	100.0	30	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
30	c3clbA	Alignment	not modelled	100.0	44	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: dhfr-ts; PDBTitle: structure of bifunctional tcdhfr-ts in complex with tmq
31	d1juva	Alignment	not modelled	100.0	26	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
32	d1d1ga	Alignment	not modelled	100.0	29	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
33	c3jtwB	Alignment	not modelled	99.9	18	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
34	c2gd9A	Alignment	not modelled	99.9	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
35	c2xw7A	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of mycobacterium smegmatis putative reductase ms0308
36	c3ky8B	Alignment	not modelled	99.7	23	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
37	c3kgyA	Alignment	not modelled	99.7	20	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
38	d2hxva1	Alignment	not modelled	99.7	20	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
39	d2azna1	Alignment	not modelled	99.6	14	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
40	d2b3za1	Alignment	not modelled	99.5	17	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
41	c2hxA	Alignment	not modelled	99.5	19	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
42	c2d5nB	Alignment	not modelled	99.5	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
43	c5xuxC	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: C: PDB Molecule: conserved protein; PDBTitle: crystal structure of rib7 from methanosarcina mazei
44	c2o7pA	Alignment	not modelled	99.4	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
45	c4xt6A	Alignment	not modelled	99.3	16	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)
46	c3zpgA	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2
47	c2p4gA	Alignment	not modelled	99.0	24	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
48	c4ha7B	Alignment	not modelled	97.6	18	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
49	c4jwiA	Alignment	not modelled	36.3	23	PDB header: transferase Chain: A: PDB Molecule: trna (guanine(9)-n1)-methyltransferase; PDBTitle: crystal structure of sctrm10(84)-sah complex
50	c5nfiA	Alignment	not modelled	31.5	20	PDB header: transferase Chain: A: PDB Molecule: mitochondrial ribonuclease p protein 1; PDBTitle: crystal structure of the methyltransferase subunit of human2 mitochondrial ribonuclease p (mrpp1) bound to s-adenosyl-methionine3 (sam)
51	c4fmwA	Alignment	not modelled	29.8	23	PDB header: transferase Chain: A: PDB Molecule: rna (guanine-9-)-methyltransferase domain-containing PDBTitle: crystal structure of methyltransferase domain of human

						rna (guanine-9-2) methyltransferase domain containing protein 2
52	c4jwhB	Alignment	not modelled	27.9	23	PDB header: transferase Chain: B: PDB Molecule: trna (guanine(9)-n1)-methyltransferase; PDBTitle: crystal structure of sptm10(full length)-sah complex
53	c6emvA	Alignment	not modelled	19.7	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.
54	c5okzJ	Alignment	not modelled	14.9	29	PDB header: rna binding protein Chain: J: PDB Molecule: m-phase phosphoprotein 6 homolog; PDBTitle: crystal structure of the mpp6 exosome complex
55	c4rfIB	Alignment	not modelled	14.5	11	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii
56	d1udxa3	Alignment	not modelled	13.3	20	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
57	c3ihtB	Alignment	not modelled	12.2	24	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
58	c6emsA	Alignment	not modelled	11.8	17	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.
59	d1xbra	Alignment	not modelled	11.4	14	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box
60	c4cvkA	Alignment	not modelled	10.5	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine PDBTitle: pamurf in complex with udp-murnac-tripeptide (mdap)
61	d1h6fa	Alignment	not modelled	10.4	18	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box
62	c2x6vB	Alignment	not modelled	10.2	16	PDB header: transcription/dna Chain: B: PDB Molecule: t-box transcription factor tbx5; PDBTitle: crystal structure of human tbx5 in the dna-bound and dna-2 free form
63	c6q8iL	Alignment	not modelled	8.2	33	PDB header: splicing Chain: L: PDB Molecule: protein red; PDBTitle: nterminal domain of human smu1 in complex with human redmid
64	c5vzjL	Alignment	not modelled	8.2	38	PDB header: hydrolase/rna Chain: L: PDB Molecule: m-phase phosphoprotein 6 homolog; PDBTitle: structure of a twelve component mpp6-nuclear rna exosome complex bound2 to rna
65	c5t1jB	Alignment	not modelled	7.9	14	PDB header: transcription/dna Chain: B: PDB Molecule: t-box transcription factor tbx21; PDBTitle: crystal structure of the tbx dna binding domain of the transcription2 factor t-bet
66	c3iuwA	Alignment	not modelled	7.9	17	PDB header: rna binding protein Chain: A: PDB Molecule: activating signal cointegrator; PDBTitle: crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
67	d1q1ra2	Alignment	not modelled	7.6	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
68	d1vjda	Alignment	not modelled	7.1	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
69	c1kyqC	Alignment	not modelled	7.0	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.
70	c4ehjA	Alignment	not modelled	6.7	26	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: an x-ray structure of a putative phosphoglycerate kinase from2 francisella tularensis subsp. tularensis schu s4
71	c5a7yA	Alignment	not modelled	6.6	24	PDB header: transferase Chain: A: PDB Molecule: trna (adenine(9)-n1)-methyltransferase; PDBTitle: crystal structure of sulfobolus acidocaldarius trm10 in2 complex with s-adenosylhomocysteine
72	c5fb3C	Alignment	not modelled	6.4	23	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph
73	d1kyqa1	Alignment	not modelled	6.2	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
74	c6nm9A	Alignment	not modelled	6.0	50	PDB header: unknown function/rna Chain: A: PDB Molecule: acrva4; PDBTitle: cryoem structure of the lbcas12a-crrna-acrva4 dimer
75	c3uhjE	Alignment	not modelled	5.7	27	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
76	c3h10B	Alignment	not modelled	5.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase;

76	c3m6B_	Alignment	not modelled	5.7	23	PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
77	d1hdia_	Alignment	not modelled	5.6	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
78	c4a04B_	Alignment	not modelled	5.5	20	PDB header: transcription Chain: B: PDB Molecule: t-box transcription factor tbx1; PDBTitle: structure of the dna-bound t-box domain of human tbx1, a2 transcription factor associated with the digeorge syndrome
79	c4y68A_	Alignment	not modelled	5.5	12	PDB header: hydrolase Chain: A: PDB Molecule: putative nisin-resistance protein; PDBTitle: structure of a lipoprotein from streptococcus agalactiae
80	c4ia6B_	Alignment	not modelled	5.5	20	PDB header: immune system Chain: B: PDB Molecule: myosin-crossreactive antigen; PDBTitle: hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah)
81	c4c2dC_	Alignment	not modelled	5.4	20	PDB header: hydrolase/peptide Chain: C: PDB Molecule: carboxy-terminal processing protease ctpb; PDBTitle: crystal structure of the protease ctpb in an active state
82	c3dfzB_	Alignment	not modelled	5.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sirc, precorrin-2 dehydrogenase
83	c3zlbA_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae
84	c6oeeB_	Alignment	not modelled	5.3	19	PDB header: translocase Chain: B: PDB Molecule: type iv secretion system apparatus protein cagt; PDBTitle: structure of cagt from a cryo-em reconstruction of a t4ss
85	c1zmrA_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
86	d1qpga_	Alignment	not modelled	5.1	17	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase