Phyre^2

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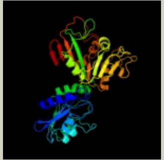
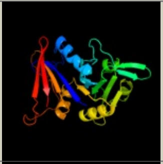
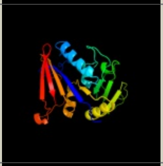
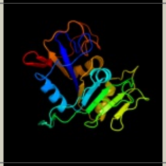
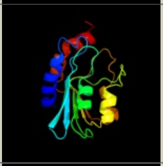
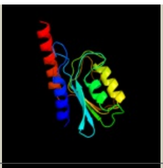
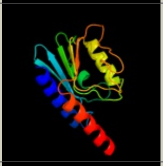
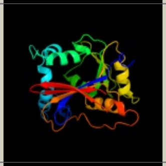
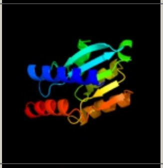
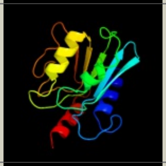
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d5nB_	Alignment		100.0	42	**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
2	c2o7pA_	Alignment		100.0	97	**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
3	c2hxvA_	Alignment		100.0	34	**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
4	d2b3za1	Alignment		100.0	32	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**RibD C-terminal domain-like
5	d2azna1	Alignment		100.0	32	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**RibD C-terminal domain-like
6	c2p4gA_	Alignment		100.0	16	**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
7	d2b3za2	Alignment		100.0	57	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
8	d2hxva1	Alignment		100.0	26	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**RibD C-terminal domain-like
9	d2hxva2	Alignment		100.0	44	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
10	d1z3aa1	Alignment		100.0	33	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
11	c3ocqA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/adenosine deaminase; **PDBTitle:** crystal structure of trna-specific adenosine deaminase from salmonella2 enterica

12	c2nx8A_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-specific adenosine deaminase; **PDBTitle:** the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
13	d2b3ja1	Alignment		100.0	30	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
14	d2g84a1	Alignment		100.0	25	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
15	c3kgyA_	Alignment		100.0	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
16	d1wwra1	Alignment		100.0	30	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
17	d1p6oa_	Alignment		100.0	28	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
18	c3jtwB_	Alignment		100.0	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
19	c3dh1D_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**trna-specific adenosine deaminase 2; **PDBTitle:** crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
20	c2gd9A_	Alignment		100.0	19	**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
21	c2xw7A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** structure of mycobacterium smegmatis putative reductase ms0308
22	d1d1ga_	Alignment	not modelled	100.0	21	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
23	d1wkqa_	Alignment	not modelled	100.0	27	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
24	d1vq2a_	Alignment	not modelled	100.0	36	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
25	d2a8na1	Alignment	not modelled	100.0	33	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
26	c2w4lC_	Alignment	not modelled	100.0	32	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** human dcmp deaminase
27	c2hvwC_	Alignment	not modelled	100.0	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** crystal structure of dcmp deaminase from streptococcus2 mutans
28	c3ky8B_	Alignment	not modelled	100.0	21	**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

29	d1seja1	Alignment	not modelled	99.7	14	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
30	d1vdra_	Alignment	not modelled	99.6	13	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
31	c3ix9B_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant
32	d3dfra_	Alignment	not modelled	99.4	15	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
33	d1kmva_	Alignment	not modelled	99.4	16	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
34	c3k2hA_	Alignment	not modelled	99.3	17	**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
35	d8dfra_	Alignment	not modelled	99.3	18	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
36	d2fzia1	Alignment	not modelled	99.2	20	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
37	c3e0bA_	Alignment	not modelled	99.2	15	**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)
38	c1zdrB_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** dhfr from bacillus stearothermophilus
39	d1df7a_	Alignment	not modelled	99.2	17	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
40	c3tq8A_	Alignment	not modelled	99.2	17	**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
41	c3ia5A_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** moritella profunda dihydrofolate reductase (dhfr)
42	d1ra9a_	Alignment	not modelled	99.1	14	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
43	c2oipE_	Alignment	not modelled	99.0	18	**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
44	c3f0uX_	Alignment	not modelled	99.0	16	**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
45	d1j3ka_	Alignment	not modelled	98.9	12	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
46	d1aoea_	Alignment	not modelled	98.8	12	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
47	c2blcA_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase; **PDBTitle:** sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine
48	c3dg8B_	Alignment	not modelled	98.7	13	**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
49	c3jsuA_	Alignment	not modelled	98.7	12	**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
50	c3clbA_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**dhfr-ts; **PDBTitle:** structure of bifunctional tcdhfr-ts in complex with tmq
51	c3cseA_	Alignment	not modelled	98.5	15	**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)
52	c3rg9A_	Alignment	not modelled	98.1	16	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate synthase; **PDBTitle:** trypanosoma brucei dihydrofolate reductase (tbdhfr) in

						complex with2 wr99210
53	d1uwza_	Alignment	not modelled	97.7	21	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
54	c3g8qA_	Alignment	not modelled	97.7	34	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump **PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
55	d2d30a1	Alignment	not modelled	97.6	21	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
56	d1juva_	Alignment	not modelled	97.5	22	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
57	d1alna1	Alignment	not modelled	97.4	26	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
58	c3ijfX_	Alignment	not modelled	97.3	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
59	d1r5ta_	Alignment	not modelled	97.2	20	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
60	c3dmoD_	Alignment	not modelled	97.1	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytidine deaminase; **PDBTitle:** 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei
61	c1alnA_	Alignment	not modelled	97.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase complexed with 3-deazacytidine
62	d1mq0a_	Alignment	not modelled	97.0	20	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
63	c3r2nC_	Alignment	not modelled	96.9	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae
64	c2nytB_	Alignment	not modelled	96.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
65	d2fr5a1	Alignment	not modelled	96.8	14	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
66	c3oj6C_	Alignment	not modelled	96.3	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**blasticidin-s deaminase; **PDBTitle:** crystal structure of blasticidin s deaminase from coccidioides immitis
67	d2z3ga1	Alignment	not modelled	96.2	21	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
68	c3b8fB_	Alignment	not modelled	96.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative blasticidin s deaminase; **PDBTitle:** crystal structure of the cytidine deaminase from bacillus anthracis
69	c2kboA_	Alignment	not modelled	95.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g; **PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
70	d1alna2	Alignment	not modelled	95.7	16	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
71	d1j5ta_	Alignment	not modelled	74.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
72	d1o60a_	Alignment	not modelled	71.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
73	c3qjaA_	Alignment	not modelled	66.4	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
74	d1zcza2	Alignment	not modelled	65.3	42	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
75	c4a1oB_	Alignment	not modelled	59.6	37	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
76	c2h6rG_	Alignment	not modelled	54.2	11	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
77	c2gm2A_	Alignment	not modelled	53.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
78	c2xecD_	Alignment	not modelled	49.8	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase;

78	c2xecD_	Alignment	not modelled	49.8	20	**PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
79	c1zczA_	Alignment	not modelled	49.0	42	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
80	d1o13a_	Alignment	not modelled	47.2	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
81	d1d9ea_	Alignment	not modelled	46.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
82	c2wfbA_	Alignment	not modelled	46.7	27	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
83	c1piiA_	Alignment	not modelled	46.4	25	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
84	d1i4na_	Alignment	not modelled	45.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
85	c2c3zA_	Alignment	not modelled	44.1	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
86	d1piia2	Alignment	not modelled	43.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
87	c2yx6C_	Alignment	not modelled	40.7	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
88	c2c4kD_	Alignment	not modelled	40.1	8	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
89	c3sz8D_	Alignment	not modelled	39.7	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
90	d1a53a_	Alignment	not modelled	38.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
91	d2fb5a1	Alignment	not modelled	37.7	35	**Fold:**YojJ-like **Superfamily:**YojJ-like **Family:**YojJ-like
92	c2k2eA_	Alignment	not modelled	37.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bp2786; **PDBTitle:** solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
93	c2gewA_	Alignment	not modelled	36.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
94	d2q4qa1	Alignment	not modelled	36.5	21	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
95	d1xk7a1	Alignment	not modelled	35.9	15	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
96	d1g5ha1	Alignment	not modelled	34.3	23	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
97	d1zbfa1	Alignment	not modelled	33.0	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
98	c3gxgA_	Alignment	not modelled	31.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphatase (duf442); **PDBTitle:** crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
99	d1u9ya2	Alignment	not modelled	31.1	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
100	d1vc4a_	Alignment	not modelled	30.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
101	c3efhB_	Alignment	not modelled	29.6	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
102	c3b0vD_	Alignment	not modelled	29.4	11	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase;

102	c3b0vD_	Alignment	not modelled	29.4	11	**PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
103	d2f5va1	Alignment	not modelled	29.3	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
104	d1ewna_	Alignment	not modelled	28.7	28	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**3-methyladenine DNA glycosylase (AAG, ANPG, MPG)
105	d1eo1a_	Alignment	not modelled	28.7	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
106	c1u9yD_	Alignment	not modelled	28.7	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
107	d2fi9a1	Alignment	not modelled	28.2	6	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
108	c3ggmB_	Alignment	not modelled	27.7	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bt9727_2919; **PDBTitle:** crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
109	c2jugB_	Alignment	not modelled	27.5	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
110	d1znna1	Alignment	not modelled	26.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
111	d1rdua_	Alignment	not modelled	26.5	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
112	d1dkua2	Alignment	not modelled	26.5	25	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
113	d1wu7a1	Alignment	not modelled	26.1	15	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
114	c1znnF_	Alignment	not modelled	25.7	16	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
115	d2g4ca1	Alignment	not modelled	25.4	20	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
116	d1t3va_	Alignment	not modelled	24.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
117	d1w0ma_	Alignment	not modelled	24.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
118	d2vjma1	Alignment	not modelled	23.5	9	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
119	d2fvta1	Alignment	not modelled	22.4	5	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
120	c2qtdA_	Alignment	not modelled	22.3	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein mj0327; **PDBTitle:** crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution