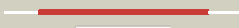
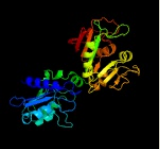





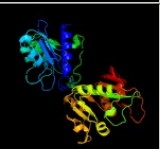











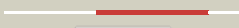












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1409_ribG_1585200_1586219
Date	Wed Jul 31 22:05:51 BST 2019
Unique Job ID	3b93442f5646f2c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2d5nB_</a>	 Alignment		100.0	41	<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
2	<a href="#">c3zpgA_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribd; <b>PDBTitle:</b> acinetobacter baumannii ribd, form 2
3	<a href="#">c2hvxA_</a>	 Alignment		100.0	33	<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
4	<a href="#">c2o7pA_</a>	 Alignment		100.0	42	<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
5	<a href="#">d2b3za2</a>	 Alignment		100.0	45	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
6	<a href="#">d2azna1</a>	 Alignment		100.0	32	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> RibD C-terminal domain-like
7	<a href="#">d2b3za1</a>	 Alignment		100.0	37	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> RibD C-terminal domain-like
8	<a href="#">c5xuxC_</a>	 Alignment		100.0	32	<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
9	<a href="#">c4xt6A_</a>	 Alignment		100.0	20	<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)
10	<a href="#">c2p4gA_</a>	 Alignment		100.0	19	<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
11	<a href="#">d2hxva1</a>	 Alignment		100.0	30	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> RibD C-terminal domain-like

12	<a href="#">d2hxva2</a>	Alignment		100.0	38	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
13	<a href="#">c4ha7B_</a>	Alignment		100.0	23	<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
14	<a href="#">c3jtwB_</a>	Alignment		100.0	17	<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
15	<a href="#">c2nx8A_</a>	Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific adenosine deaminase; <b>PDBTitle:</b> the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
16	<a href="#">c2xw7A_</a>	Alignment		100.0	21	<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
17	<a href="#">d2g84a1</a>	Alignment		100.0	31	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
18	<a href="#">c3kgyA_</a>	Alignment		100.0	18	<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
19	<a href="#">d1z3aa1</a>	Alignment		100.0	33	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
20	<a href="#">c2gd9A_</a>	Alignment		100.0	15	<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
21	<a href="#">d2b3ja1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
22	<a href="#">d1d1ga_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
23	<a href="#">c3ocqA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytosine/adenosine deaminase; <b>PDBTitle:</b> crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
24	<a href="#">d1p6oa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
25	<a href="#">c3ky8B_</a>	Alignment	not modelled	100.0	19	<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
26	<a href="#">c3dh1D_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-specific adenosine deaminase 2; <b>PDBTitle:</b> crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
27	<a href="#">c2w4IC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> human dcmp deaminase
28	<a href="#">d1wwra1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like

29	<a href="#">d1vq2a_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
30	<a href="#">c2hvwC_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> crystal structure of dcmp deaminase from streptococcus mutans
31	<a href="#">c4p9eA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
32	<a href="#">d2a8na1</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
33	<a href="#">d1wkqa_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
34	<a href="#">c5xkrA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cmp/dcmp deaminase, zinc-binding protein; <b>PDBTitle:</b> crystal structure of msmeg3575 in complex with benzoguanamine
35	<a href="#">c5jfyC_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidine deaminase; <b>PDBTitle:</b> crystal structure of a plant cytidine deaminase
36	<a href="#">d1seja1</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
37	<a href="#">c3ix9B_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant
38	<a href="#">c5eccA_</a>	Alignment	not modelled	99.6	13	<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
39	<a href="#">d1vdra_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
40	<a href="#">d3dfra_</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
41	<a href="#">c3e0bA_</a>	Alignment	not modelled	99.5	18	<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)
42	<a href="#">d1kmva_</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
43	<a href="#">d1df7a_</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
44	<a href="#">c3tq8A_</a>	Alignment	not modelled	99.4	16	<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 (foIa) from coxiella burnetii2 in complex with trimethoprim
45	<a href="#">d1ra9a_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
46	<a href="#">d8dfra_</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
47	<a href="#">c3k2hA_</a>	Alignment	not modelled	99.4	16	<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
48	<a href="#">c3ia5A_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> moritella profunda dihydrofolate reductase (dhfr)
49	<a href="#">c1zdrB_</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> dhfr from bacillus stearothermophilus
50	<a href="#">d2fzia1</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
51	<a href="#">c3vcoA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> schistosoma mansoni dihydrofolate reductase
52	<a href="#">c4m7vA_</a>	Alignment	not modelled	99.3	14	<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
53	<a href="#">c3f0uX_</a>	Alignment	not modelled	99.3	13	<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>Fold:</b> Dihydrofolate reductase-like

54	<a href="#">d1aoea_</a>	Alignment	not modelled	99.2	14	<b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
55	<a href="#">c6cxmA_</a>	Alignment	not modelled	99.1	18	<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
56	<a href="#">c2oipE_</a>	Alignment	not modelled	99.0	17	<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
57	<a href="#">c3clbA_</a>	Alignment	not modelled	98.8	15	<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
58	<a href="#">c4eckB_</a>	Alignment	not modelled	98.7	15	<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
59	<a href="#">c3cseA_</a>	Alignment	not modelled	98.7	15	<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)
60	<a href="#">c2blcA_</a>	Alignment	not modelled	98.6	13	<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
61	<a href="#">d1j3ka_</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
62	<a href="#">c3dg8B_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> oxidoreductase, transferase <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
63	<a href="#">c3jsuA_</a>	Alignment	not modelled	98.4	13	<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) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump
64	<a href="#">c3rg9A_</a>	Alignment	not modelled	98.4	19	<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
65	<a href="#">c6drsA_</a>	Alignment	not modelled	98.4	17	<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
66	<a href="#">d1juva_</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
67	<a href="#">d1mq0a_</a>	Alignment	not modelled	97.7	24	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
68	<a href="#">d1r5ta_</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
69	<a href="#">d2fr5a1</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
70	<a href="#">d1uwza_</a>	Alignment	not modelled	97.5	24	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
71	<a href="#">d1alna1</a>	Alignment	not modelled	97.5	26	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
72	<a href="#">d2d30a1</a>	Alignment	not modelled	97.4	25	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
73	<a href="#">c3jifX_</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
74	<a href="#">d2z3ga1</a>	Alignment	not modelled	97.2	29	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
75	<a href="#">c4eg2G_</a>	Alignment	not modelled	97.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of cytidine deaminase from vibrio2 cholerae in complex with zinc and uridine
76	<a href="#">c3oj6C_</a>	Alignment	not modelled	97.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> blasticidin-s deaminase; <b>PDBTitle:</b> crystal structure of blasticidin s deaminase from coccidioides immitis
77	<a href="#">c3r2nC_</a>	Alignment	not modelled	97.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase from mycobacterium leprae
78	<a href="#">c1alnA_</a>	Alignment	not modelled	97.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase complexed with 3-deazacytidine

79	<a href="#">c3dmoD</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei
80	<a href="#">c3b8fB</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative blastidicin s deaminase; <b>PDBTitle:</b> crystal structure of the cytidine deaminase from bacillus anthracis
81	<a href="#">c3g8qA</a>	Alignment	not modelled	96.7	40	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rna-binding protein, contains thump <b>PDBTitle:</b> a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
82	<a href="#">c5k83C</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> apolipoprotein b mrna editing enzyme, catalytic peptide- <b>PDBTitle:</b> crystal structure of a primate apobec3g n-domain, in complex with2 ssdna
83	<a href="#">d1alna2</a>	Alignment	not modelled	96.3	18	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
84	<a href="#">c5tkmA</a>	Alignment	not modelled	96.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna dc->du-editing enzyme apobec-3b; <b>PDBTitle:</b> crystal structure of human apobec3b n-terminal domain
85	<a href="#">c3vowB</a>	Alignment	not modelled	96.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable dna dc->du-editing enzyme apobec-3c; <b>PDBTitle:</b> crystal structure of the human apobec3c having hiv-1 vif-binding2 interface
86	<a href="#">c2nytB</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable c->u-editing enzyme apobec-2; <b>PDBTitle:</b> the apobec2 crystal structure and functional implications2 for aid
87	<a href="#">c2m65A</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna dc->du-editing enzyme apobec-3a; <b>PDBTitle:</b> nmr structure of human restriction factor apobec3a
88	<a href="#">c2mzZA</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> hydrolase, antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein b mrna-editing enzyme, catalytic <b>PDBTitle:</b> nmr structure of apobec3g ntd variant, sntd
89	<a href="#">c6b0bE</a>	Alignment	not modelled	94.8	21	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> apobec3h; <b>PDBTitle:</b> crystal structure of human apobec3h
90	<a href="#">c2kboA</a>	Alignment	not modelled	93.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna dc->du-editing enzyme apobec-3g; <b>PDBTitle:</b> structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
91	<a href="#">c6bwyA</a>	Alignment	not modelled	92.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protection of telomeres protein 1, dna dc->du-editing <b>PDBTitle:</b> dna substrate selection by apobec3g
92	<a href="#">c2h6rG</a>	Alignment	not modelled	68.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
93	<a href="#">d1xk7a1</a>	Alignment	not modelled	59.4	17	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
94	<a href="#">c4fq5B</a>	Alignment	not modelled	57.1	7	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> maleate cis-trans isomerase; <b>PDBTitle:</b> crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
95	<a href="#">c2xecD</a>	Alignment	not modelled	54.2	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative maleate isomerase; <b>PDBTitle:</b> nocardia farcinica maleate cis-trans isomerase bound to2 tris
96	<a href="#">c4a1oB</a>	Alignment	not modelled	53.2	22	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
97	<a href="#">d1j5ta</a>	Alignment	not modelled	51.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
98	<a href="#">d1zcza2</a>	Alignment	not modelled	50.7	29	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
99	<a href="#">c4ix1B</a>	Alignment	not modelled	48.8	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; opag_01669 from rhodococcus2 opacus pd630, target 016205 <b>PDBTitle:</b> crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
100	<a href="#">c2yx6C</a>	Alignment	not modelled	42.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein ph0822; <b>PDBTitle:</b> crystal structure of ph0822
101	<a href="#">c3qjaA</a>	Alignment	not modelled	38.5	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
102	<a href="#">d1pia2</a>	Alignment	not modelled	37.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
103	<a href="#">c2dgdD</a>	Alignment	not modelled	36.9	7	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 223aa long hypothetical arylmalonate decarboxylase; <b>PDBTitle:</b> crystal structure of st0656, a function unknown protein

						from2 sulfobolus tokodaii
104	<a href="#">c3b0vD_</a>	Alignment	not modelled	36.1	13	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
105	<a href="#">d1i4na_</a>	Alignment	not modelled	35.5	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
106	<a href="#">c5yx6D_</a>	Alignment	not modelled	35.2	29	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein rv3272; <b>PDBTitle:</b> crystal structure of rv3272 from m. tuberculosis orthorhombic form
107	<a href="#">c1piiA_</a>	Alignment	not modelled	33.5	19	<b>PDB header:</b> bifunctional(isomerase and synthase) <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
108	<a href="#">d1o13a_</a>	Alignment	not modelled	33.5	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
109	<a href="#">c1zczA_</a>	Alignment	not modelled	32.9	30	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
110	<a href="#">d1t3va_</a>	Alignment	not modelled	32.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
111	<a href="#">d1a53a_</a>	Alignment	not modelled	32.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
112	<a href="#">d1znn1</a>	Alignment	not modelled	31.3	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> PdxS-like
113	<a href="#">d1zczal</a>	Alignment	not modelled	31.1	17	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
114	<a href="#">c4hl6D_</a>	Alignment	not modelled	30.1	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein yfde; <b>PDBTitle:</b> yfde from escherichia coli
115	<a href="#">d1w0ma_</a>	Alignment	not modelled	29.3	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
116	<a href="#">c1znnF_</a>	Alignment	not modelled	28.8	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> plp synthase; <b>PDBTitle:</b> structure of the synthase subunit of plp synthase
117	<a href="#">c2g04B_</a>	Alignment	not modelled	27.8	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable fatty-acid-coa racemase far; <b>PDBTitle:</b> crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
118	<a href="#">c2r8rB_</a>	Alignment	not modelled	27.3	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
119	<a href="#">d2vjma1</a>	Alignment	not modelled	26.8	15	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
120	<a href="#">c6bmaA_</a>	Alignment	not modelled	26.4	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168