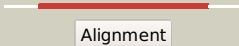



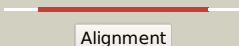

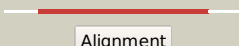
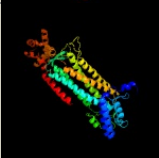
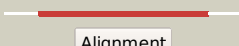

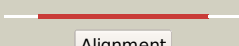
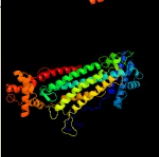
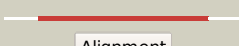


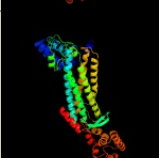





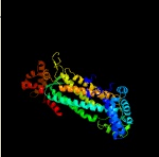


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1659\_(argH)\_1872646\_1874058  
 Date Fri Aug 2 13:30:25 BST 2019  
 Unique Job ID 014b28b1c3ca1caf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6igaB_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> argininosuccinate lyase; <b>PDBTitle:</b> crystal structure of argininosuccinate lyase from mycobacterium2 tuberculosis
2	<a href="#">d1tj7a_</a>	 Alignment		100.0	41	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
3	<a href="#">dli0aa_</a>	 Alignment		100.0	40	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
4	<a href="#">d1tjva_</a>	 Alignment		100.0	40	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
5	<a href="#">d1k62a_</a>	 Alignment		100.0	42	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
6	<a href="#">c6g3eA_</a>	 Alignment		100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate lyase; <b>PDBTitle:</b> crystal structure of edds lyase in complex with formate
7	<a href="#">d1hy0a_</a>	 Alignment		100.0	40	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
8	<a href="#">c2e9fC_</a>	 Alignment		100.0	43	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate lyase; <b>PDBTitle:</b> crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
9	<a href="#">c2pfmA_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
10	<a href="#">d1c3ca_</a>	 Alignment		100.0	16	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
11	<a href="#">d1q5na_</a>	 Alignment		100.0	18	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase

12	<a href="#">dlre5a_</a>	Alignment		100.0	20	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
13	<a href="#">c5vkwB_</a>	Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase ade13 from candida2 albicans
14	<a href="#">dlfuoa_</a>	Alignment		100.0	23	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
15	<a href="#">c3c8tA_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate lyase; <b>PDBTitle:</b> crystal structure of fumarate lyase from mesorhizobium sp. bnc1
16	<a href="#">c5xnzA_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cred; <b>PDBTitle:</b> crystal structure of cred complex with fumarate
17	<a href="#">c1yfmA_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarase; <b>PDBTitle:</b> recombinant yeast fumarase
18	<a href="#">dlyfma_</a>	Alignment		100.0	19	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
19	<a href="#">dlj3ua_</a>	Alignment		100.0	20	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
20	<a href="#">c2vd6B_</a>	Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
21	<a href="#">c4nleB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of apo adenylosuccinate lyase from mycobacterium2 smegmatis
22	<a href="#">c3gtdA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
23	<a href="#">c4hgvD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of a fumarate hydratase
24	<a href="#">d1vdka_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
25	<a href="#">c6n1mA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of fumarate hydratase class ii from legionella2 pneumophila philadelphia 1
26	<a href="#">c3no9C_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
27	<a href="#">c4eeiA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase from francisella2 tularensis complexed with amp and succinate
28	<a href="#">dljswa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
						<b>PDB header:</b> lyase

29	<a href="#">c3ocfB</a>	Alignment	not modelled	100.0	23	<b>Chain:</b> B: <b>PDB Molecule:</b> fumarate lyase:delta crystallin; <b>PDBTitle:</b> crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
30	<a href="#">c2qgaC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> plasmodium vivax adenylosuccinate lyase pv003765 with amp bound
31	<a href="#">c3e04A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate hydratase; <b>PDBTitle:</b> crystal structure of human fumarate hydratase
32	<a href="#">d1jswc</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
33	<a href="#">c3bhgA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase from legionella2 pneumophila
34	<a href="#">d1dofa</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
35	<a href="#">c4hgvC</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of a fumarate hydratase
36	<a href="#">c2ptsA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of wild type escherichia coli adenylosuccinate lyase
37	<a href="#">c3gtdB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
38	<a href="#">c3e04C</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarate hydratase; <b>PDBTitle:</b> crystal structure of human fumarate hydratase
39	<a href="#">c5eyvB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase from schistosoma mansoni2 in apo form.
40	<a href="#">c4efcA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase from trypanosoma brucei,2 tb427tmp.160.5560
41	<a href="#">c1yisA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> structural genomics of caenorhabditis elegans: adenylosuccinate lyase
42	<a href="#">c4mx2C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylosuccinate lyase; <b>PDBTitle:</b> crystal structure of adenylosuccinate lyase from leishmania donovani
43	<a href="#">c2fenA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-carboxy-cis,cis-muconate lactonizing enzyme; <b>PDBTitle:</b> 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
44	<a href="#">c3r6yG</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> aspartase; <b>PDBTitle:</b> crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1
45	<a href="#">d1f1oa</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
46	<a href="#">d1yqga1</a>	Alignment	not modelled	64.8	24	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> ProC C-terminal domain-like
47	<a href="#">c1x5bA</a>	Alignment	not modelled	49.2	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducing adaptor molecule 2; <b>PDBTitle:</b> the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
48	<a href="#">c2rcyB</a>	Alignment	not modelled	45.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrroline carboxylate reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
49	<a href="#">d1u5ta1</a>	Alignment	not modelled	26.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
50	<a href="#">c2ctoA</a>	Alignment	not modelled	26.0	58	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> novel protein; <b>PDBTitle:</b> solution structure of the hmg box like domain from human2 hypothetical protein flj14904
51	<a href="#">d2di4a1</a>	Alignment	not modelled	19.9	24	<b>Fold:</b> FtsH protease domain-like <b>Superfamily:</b> FtsH protease domain-like <b>Family:</b> FtsH protease domain-like
52	<a href="#">c2dd4H</a>	Alignment	not modelled	18.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> thiocyanate hydrolase beta subunit; <b>PDBTitle:</b> thiocyanate hydrolase (scnase) from thiobacillus thioparus recombinant2 apo-enzyme
53	<a href="#">c5eulY</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> protein transport <b>Chain:</b> Y: <b>PDB Molecule:</b> protein translocase subunit secy; <b>PDBTitle:</b> structure of the seca-secy complex with a translocating polypeptide2 substrate
54	<a href="#">c2ag8A</a>	Alignment	not modelled	18.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
						<b>PDB header:</b> oxidoreductase

55	<a href="#">c1p74B_</a>	Alignment	not modelled	17.5	12	<b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase (aroe) from haemophilus2 influenzae
56	<a href="#">c6e8dA_</a>	Alignment	not modelled	17.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta sliding clamp,dna mismatch repair protein mutl; <b>PDBTitle:</b> crystal structure of the bacillus subtilis sliding clamp-mutl complex.
57	<a href="#">c3exmA_</a>	Alignment	not modelled	17.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatase sc4828; <b>PDBTitle:</b> crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
58	<a href="#">c6iczX_</a>	Alignment	not modelled	16.6	46	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> prkr-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
59	<a href="#">c4omuA_</a>	Alignment	not modelled	15.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase (aroe) from pseudomonas2 putida
60	<a href="#">c5z4yB_</a>	Alignment	not modelled	15.7	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cys regulon transcriptional activator; <b>PDBTitle:</b> crystal structure of pacysb ntd domain with space group p4
61	<a href="#">c3o8qB_</a>	Alignment	not modelled	15.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase i alpha; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
62	<a href="#">c2xznC_</a>	Alignment	not modelled	14.9	21	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> kh domain containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
63	<a href="#">c3pgjB_</a>	Alignment	not modelled	14.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
64	<a href="#">d1nvtA2</a>	Alignment	not modelled	13.6	14	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Shikimate dehydrogenase-like
65	<a href="#">d2ahra1</a>	Alignment	not modelled	12.9	23	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> ProC C-terminal domain-like
66	<a href="#">c2zmeA_</a>	Alignment	not modelled	12.9	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar-sorting protein snf8; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
67	<a href="#">c2nloA_</a>	Alignment	not modelled	12.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
68	<a href="#">c3fbtB_</a>	Alignment	not modelled	12.6	14	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate mutase and shikimate 5-dehydrogenase fusion <b>PDBTitle:</b> crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum
69	<a href="#">c3bbnC_</a>	Alignment	not modelled	12.5	63	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal protein s3; <b>PDBTitle:</b> homology model of the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
70	<a href="#">d1vi2a2</a>	Alignment	not modelled	12.0	15	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Shikimate dehydrogenase-like
71	<a href="#">c2xgvA_</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> psiv capsid n-terminal domain; <b>PDBTitle:</b> structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
72	<a href="#">c5zdnA_</a>	Alignment	not modelled	11.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fomd; <b>PDBTitle:</b> the complex structure of fomd with cdp
73	<a href="#">c3ke2A_</a>	Alignment	not modelled	11.7	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yp_928783.1; <b>PDBTitle:</b> crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
74	<a href="#">c2digA_</a>	Alignment	not modelled	11.7	67	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lamin-b receptor; <b>PDBTitle:</b> solusion structure of the todor domain of human lamin-b2 receptor
75	<a href="#">c3egqB_</a>	Alignment	not modelled	11.7	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tet-family transcriptional regulator (af_1817)2 from archaeoglobus fulgidus at 2.55 a resolution
76	<a href="#">c5l3xB_</a>	Alignment	not modelled	11.5	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> negative elongation factor c/d; <b>PDBTitle:</b> crystal structure of negative elongation factor subcomplex nefl-ac
77	<a href="#">d1g3pa2</a>	Alignment	not modelled	11.0	20	<b>Fold:</b> N-terminal domains of the minor coat protein g3p <b>Superfamily:</b> N-terminal domains of the minor coat protein g3p <b>Family:</b> N-terminal domains of the minor coat protein g3p
78	<a href="#">c3zeyX_</a>	Alignment	not modelled	10.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s3, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
79	<a href="#">d1npya2</a>	Alignment	not modelled	10.7	21	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Shikimate dehydrogenase-like
						<b>PDB header:</b> oxidoreductase

80	<a href="#">c2ev9B_</a>	Alignment	not modelled	10.6	15	<b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
81	<a href="#">c3gt0A_</a>	Alignment	not modelled	10.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
82	<a href="#">c3w0kA_</a>	Alignment	not modelled	10.4	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional endomannanase/endoglucanase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase
83	<a href="#">c2izzE_</a>	Alignment	not modelled	10.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase 1; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate reductase
84	<a href="#">d1dlja1</a>	Alignment	not modelled	10.3	17	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
85	<a href="#">c1u5tA_</a>	Alignment	not modelled	10.3	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> appears to be functionally related to snf7; <b>PDBTitle:</b> structure of the escrt-ii endosomal trafficking complex
86	<a href="#">c3cuqA_</a>	Alignment	not modelled	10.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar-sorting protein snf8; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
87	<a href="#">c5dzsA_</a>	Alignment	not modelled	10.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase (nadp(+)); <b>PDBTitle:</b> 1.5 angstrom crystal structure of shikimate dehydrogenase 1 from2 peptoclostridium difficile.
88	<a href="#">c3izbB_</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein rps3 (s3p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
89	<a href="#">c1nvtA_</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate 5'-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
90	<a href="#">c3m1eA_</a>	Alignment	not modelled	9.6	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of benm_dbd
91	<a href="#">d1k6ya1</a>	Alignment	not modelled	9.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> N-terminal Zn binding domain of HIV integrase <b>Family:</b> N-terminal Zn binding domain of HIV integrase
92	<a href="#">c1nytC_</a>	Alignment	not modelled	9.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> shikimate dehydrogenase aroe complexed with nadp+
93	<a href="#">d1e8ga1</a>	Alignment	not modelled	9.2	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
94	<a href="#">d1e0ea_</a>	Alignment	not modelled	9.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> N-terminal Zn binding domain of HIV integrase <b>Family:</b> N-terminal Zn binding domain of HIV integrase
95	<a href="#">c2hk8B_</a>	Alignment	not modelled	8.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
96	<a href="#">c2wukD_</a>	Alignment	not modelled	8.9	20	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> septum site-determining protein diviva; <b>PDBTitle:</b> diviva n-terminal domain, f17a mutant
97	<a href="#">d1wjfa_</a>	Alignment	not modelled	8.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> N-terminal Zn binding domain of HIV integrase <b>Family:</b> N-terminal Zn binding domain of HIV integrase
98	<a href="#">c3toza_</a>	Alignment	not modelled	8.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
99	<a href="#">c5ybxA_</a>	Alignment	not modelled	8.6	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bouquet formation protein 4; <b>PDBTitle:</b> crystal structure of the n-terminal domain of bqt4 in s.pombe