
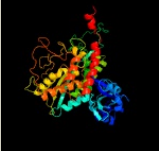
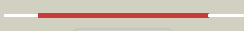












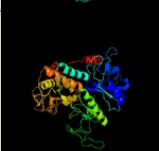










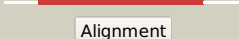



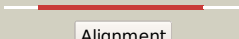

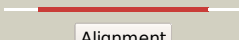

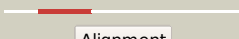





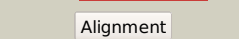



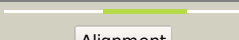





# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2860c\_glnA4\_3171637\_3173010  
 Date Wed Aug 7 12:50:53 BST 2019  
 Unique Job ID 9ce6fff32e86b244

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1fpyE_</a>	 Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> E; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
2	<a href="#">c3ng0A_</a>	 Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
3	<a href="#">c1htoB_</a>	 Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
4	<a href="#">c4hpaA_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> probable glutamine synthetase; <b>PDBTitle:</b> crystal structure of novel glutamine synthase homolog
5	<a href="#">c5zlpH_</a>	 Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> H; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from helicobacter pylori
6	<a href="#">c3qajL_</a>	 Alignment		100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> L; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
7	<a href="#">c4s17E_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> E; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703
8	<a href="#">c2j9iL_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> L; <b>PDB Molecule:</b> glutamate-ammonia ligase domain-containing protein 1; <b>PDBTitle:</b> lengsin is a survivor of an ancient family of class i glutamine2 synthetases in eukaryotes that has undergone evolutionary re-3 engineering for a tissue-specific role in the vertebrate eye lens.
9	<a href="#">c5dm3A_</a>	 Alignment		100.0	47	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> l-glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from chromohalobacter2 salexigens dsm 3043(csa1_0679, target efi-550015) with bound adp
10	<a href="#">d1f52a2</a>	 Alignment		100.0	27	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamine synthetase catalytic domain
11	<a href="#">d2bvca2</a>	 Alignment		100.0	28	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamine synthetase catalytic domain

12	<a href="#">c2qc8J_</a>	 Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> J: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
13	<a href="#">c4baxH_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from streptomyces2 coelicolor
14	<a href="#">c2d3aj_</a>	 Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> J: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
15	<a href="#">c3fkyD_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the glutamine synthetase gln1deltaN182 from the yeast saccharomyces cerevisiae
16	<a href="#">c4is4G_</a>	 Alignment		100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
17	<a href="#">c3o6xC_</a>	 Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
18	<a href="#">d2bvca1</a>	 Alignment		99.9	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Glutamine synthetase, N-terminal domain <b>Family:</b> Glutamine synthetase, N-terminal domain
19	<a href="#">d1f52a1</a>	 Alignment		99.9	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Glutamine synthetase, N-terminal domain <b>Family:</b> Glutamine synthetase, N-terminal domain
20	<a href="#">c1tt4B_</a>	 Alignment		98.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
21	<a href="#">d1tt4a_</a>	 Alignment	not modelled	98.8	15	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamate-cysteine ligase family 2 (GCS2)
22	<a href="#">d1r8ga_</a>	 Alignment	not modelled	98.7	16	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamate-cysteine ligase family 2 (GCS2)
23	<a href="#">c2gwcE_</a>	 Alignment	not modelled	98.1	18	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> glutamate cysteine ligase; <b>PDBTitle:</b> crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
24	<a href="#">d1ppva_</a>	 Alignment	not modelled	74.8	7	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
25	<a href="#">c5op0B_</a>	 Alignment	not modelled	65.9	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase ligd, polymerase domain; <b>PDBTitle:</b> structure of prim-polc from mycobacterium smegmatis
26	<a href="#">d1u8sa2</a>	 Alignment	not modelled	50.8	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Glycine cleavage system transcriptional repressor
27	<a href="#">d1neka3</a>	 Alignment	not modelled	43.8	15	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
28	<a href="#">d2bs2a3</a>	 Alignment	not modelled	43.2	21	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain

						<b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
29	<a href="#">c5knwA_</a>	Alignment	not modelled	33.2	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> la-related protein 7; <b>PDBTitle:</b> solution nmr structure of human larp7 xrrm2
30	<a href="#">c6bevB_</a>	Alignment	not modelled	32.0	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiosulfate sulfurtransferase/rhodanese-like domain- <b>PDBTitle:</b> human single domain sulfurtransferase tstd1
31	<a href="#">c3g12A_</a>	Alignment	not modelled	27.3	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a putative lactoylglutathione lyase from <i>Bdellovibrio bacteriovorus</i>
32	<a href="#">d1u8sa1</a>	Alignment	not modelled	25.6	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Glycine cleavage system transcriptional repressor
33	<a href="#">d1zpvA1</a>	Alignment	not modelled	24.7	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> SPO238-like
34	<a href="#">d2z1ea1</a>	Alignment	not modelled	24.5	5	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
35	<a href="#">c2btwA_</a>	Alignment	not modelled	24.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alr0975 protein; <b>PDBTitle:</b> crystal structure of alr0975
36	<a href="#">d1chua3</a>	Alignment	not modelled	21.3	19	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
37	<a href="#">d2bu3a1</a>	Alignment	not modelled	20.1	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Phytochelatin synthase
38	<a href="#">d1owxa_</a>	Alignment	not modelled	19.8	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
39	<a href="#">c1a8pA_</a>	Alignment	not modelled	17.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh\ferredoxin oxidoreductase; <b>PDBTitle:</b> ferredoxin reductase from <i>Azotobacter vinelandii</i>
40	<a href="#">c2jy5A_</a>	Alignment	not modelled	16.6	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-1; <b>PDBTitle:</b> nmr structure of ubiquitin 1 uba domain
41	<a href="#">c1u8sB_</a>	Alignment	not modelled	14.6	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional <b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor
42	<a href="#">c3p2oA_</a>	Alignment	not modelled	14.3	18	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from <i>Campylobacter jejuni</i>
43	<a href="#">c4tufC_</a>	Alignment	not modelled	14.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> major extracellular endoglucanase; <b>PDBTitle:</b> catalytic domain of the major endoglucanase from <i>Xanthomonas campestris</i> pv. <i>campestris</i>
44	<a href="#">d1z2la2</a>	Alignment	not modelled	14.2	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
45	<a href="#">c2nyiB_</a>	Alignment	not modelled	13.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> unknown protein; <b>PDBTitle:</b> crystal structure of an unknown protein from <i>Galdieria sulphuraria</i>
46	<a href="#">c5laaB_</a>	Alignment	not modelled	13.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tetrahydromethanopterin s-methyltransferase subunit a; <b>PDBTitle:</b> x-ray structure of the methyltransferase subunit a from <i>Methanothermus fervidus</i> in complex with cobalamin
47	<a href="#">c5l8xA_</a>	Alignment	not modelled	13.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydromethanopterin s-methyltransferase subunit a; <b>PDBTitle:</b> x-ray structure of apo methanocaldococcus jannaschii methyltransferase2 subunit a at 1.85 angstrom
48	<a href="#">c3ixzB_</a>	Alignment	not modelled	13.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
49	<a href="#">c2dr1A_</a>	Alignment	not modelled	13.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 386aa long hypothetical serine aminotransferase; <b>PDBTitle:</b> crystal structure of the ph1308 protein from <i>Pyrococcus horikoshii</i> ot3
50	<a href="#">c3mpoD_</a>	Alignment	not modelled	13.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted hydrolase of the had superfamily; <b>PDBTitle:</b> the crystal structure of a hydrolase from <i>Lactobacillus brevis</i>
51	<a href="#">c2jepB_</a>	Alignment	not modelled	13.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucanase; <b>PDBTitle:</b> native family 5 xyloglucanase from <i>Paenibacillus pabuli</i>
52	<a href="#">d2cxaa1</a>	Alignment	not modelled	12.7	6	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> LFTR-like
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl/phenylalanyl-trna-protein

53	<a href="#">c2cxaA_</a>	Alignment	not modelled	12.7	6	transferase; <b>PDBTitle:</b> crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
54	<a href="#">c4biyD_</a>	Alignment	not modelled	12.5	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (monoclinic form 2)
55	<a href="#">c3p2oB_</a>	Alignment	not modelled	12.5	18	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
56	<a href="#">c4o9uB_</a>	Alignment	not modelled	12.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
57	<a href="#">d1ysja2</a>	Alignment	not modelled	12.3	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
58	<a href="#">c3htnA_</a>	Alignment	not modelled	11.7	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
59	<a href="#">c4zonB_</a>	Alignment	not modelled	11.0	24	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> verruculogen synthase; <b>PDBTitle:</b> structure of ftmx1 with fumitremorgen b complex
60	<a href="#">d1a4ia2</a>	Alignment	not modelled	11.0	19	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Tetrahydrofolate dehydrogenase/cyclohydrolase
61	<a href="#">c2f59B_</a>	Alignment	not modelled	10.9	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 6,7-dimethyl-8-ribityllumazine synthase 1; <b>PDBTitle:</b> lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
62	<a href="#">c3d3aA_</a>	Alignment	not modelled	10.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
63	<a href="#">c2v5iA_</a>	Alignment	not modelled	10.8	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> salmonella typhimurium db7155 bacteriophage det7 tailspike; <b>PDBTitle:</b> structure of the receptor-binding protein of bacteriophage det7: a2 podoviral tailspike in a myovirus
64	<a href="#">c4ochA_</a>	Alignment	not modelled	10.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease muts2; <b>PDBTitle:</b> apo structure of smr domain of muts2 from deinococcus radiodurans
65	<a href="#">c6ithA_</a>	Alignment	not modelled	10.5	54	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
66	<a href="#">d1nxia_</a>	Alignment	not modelled	10.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Hypothetical protein VC0424 <b>Family:</b> Hypothetical protein VC0424
67	<a href="#">c3ln7A_</a>	Alignment	not modelled	10.1	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
68	<a href="#">c5z70B_</a>	Alignment	not modelled	10.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> oleate hydratase; <b>PDBTitle:</b> crystal structure of oleate hydratase from stentrophomonas sp. kctc2 12332
69	<a href="#">c5fn2B_</a>	Alignment	not modelled	9.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> cryo-em structure of gamma secretase in complex with a drug dapt
70	<a href="#">c3it5B_</a>	Alignment	not modelled	9.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease lasa; <b>PDBTitle:</b> crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
71	<a href="#">d1prtcl</a>	Alignment	not modelled	9.5	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
72	<a href="#">c4uirB_</a>	Alignment	not modelled	9.1	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oleate hydratase; <b>PDBTitle:</b> structure of oleate hydratase from elizabethkingia2 meningoseptica
73	<a href="#">d1ijcb2</a>	Alignment	not modelled	9.0	17	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
74	<a href="#">c6gcsF_</a>	Alignment	not modelled	8.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nufm subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
75	<a href="#">c4x0vH_</a>	Alignment	not modelled	8.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> beta-1,3-1,4-glucanase; <b>PDBTitle:</b> structure of a gh5 family lichenase from caldicellulosiruptor sp. f32
76	<a href="#">c5vymB_</a>	Alignment	not modelled	8.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase bgab; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bifidobacterium2 adolescentis
77	<a href="#">d1prtb1</a>	Alignment	not modelled	8.3	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
78	<a href="#">c2yvaA_</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cg10686-pa;

78	<a href="#">c4vxaA</a>	Alignment	not modelled	8.2	14	<b>PDBTitle:</b> solution structure of the lsm domain of drosophila2 melanogaster tral (trailer hitch) <b>PDB header:</b> hydrolase
79	<a href="#">c4htyA</a>	Alignment	not modelled	8.1	12	<b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of a metagenome-derived cellulase cel5a
80	<a href="#">c2igoG</a>	Alignment	not modelled	8.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> pyranose oxidase; <b>PDBTitle:</b> crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose
81	<a href="#">d2b0ja1</a>	Alignment	not modelled	8.0	26	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> HMD dimerization domain-like
82	<a href="#">c5iwyD</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtilis complexed with cmp and mg2+
83	<a href="#">d1wj5a</a>	Alignment	not modelled	7.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> An Obfc1 domain
84	<a href="#">c4v0bA</a>	Alignment	not modelled	7.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> escherichia coli ftsh hexameric n-domain
85	<a href="#">d1tg7a5</a>	Alignment	not modelled	7.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Glycosyl hydrolases family 35 catalytic domain
86	<a href="#">d2hzab1</a>	Alignment	not modelled	7.4	45	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
87	<a href="#">d1c41a</a>	Alignment	not modelled	7.3	16	<b>Fold:</b> Lumazine synthase <b>Superfamily:</b> Lumazine synthase <b>Family:</b> Lumazine synthase
88	<a href="#">c4rkkA</a>	Alignment	not modelled	7.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> laforin; <b>PDBTitle:</b> structure of a product bound phosphatase
89	<a href="#">d1gvha3</a>	Alignment	not modelled	6.8	16	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Flavo-hemoglobin, C-terminal domain
90	<a href="#">c2c2xB</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase- <b>PDBTitle:</b> three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
91	<a href="#">c6gmaA</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rb1-inducible coiled-coil protein 1; <b>PDBTitle:</b> crystal structure of the fip200 c-terminal region
92	<a href="#">c3b8eB</a>	Alignment	not modelled	6.6	14	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
93	<a href="#">c1q6xA</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> crystal structure of rat choline acetyltransferase
94	<a href="#">d1d4oa</a>	Alignment	not modelled	6.5	12	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
95	<a href="#">d1t3ta3</a>	Alignment	not modelled	6.3	29	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> FGAM synthase PurL, PurS-like domain
96	<a href="#">c5iwzA</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> synaptonemal complex protein 2; <b>PDBTitle:</b> synaptonemal complex protein
97	<a href="#">d2hh6a1</a>	Alignment	not modelled	6.1	37	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
98	<a href="#">d1t3ba2</a>	Alignment	not modelled	6.1	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> DsbC/DsbG N-terminal domain-like <b>Family:</b> DsbC/DsbG N-terminal domain-like
99	<a href="#">c1pt9B</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue