





























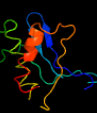


# Phyre2

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 Description RVBD0720\_(rplR)\_813943\_814311  
 Date Fri Jul 26 01:50:29 BST 2019  
 Unique Job ID 0041fac41a5531f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o60P_</a>	 Alignment		100.0	82	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	<a href="#">c3bboQ_</a>	 Alignment		100.0	47	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> ribosomal protein l18; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
3	<a href="#">c3j3vO_</a>	 Alignment		100.0	53	<b>PDB header:</b> ribosome <b>Chain:</b> O; <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
4	<a href="#">d2gycm1</a>	 Alignment		100.0	44	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
5	<a href="#">d1ovya_</a>	 Alignment		100.0	48	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
6	<a href="#">c4v19S_</a>	 Alignment		100.0	28	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> mitoribosomal protein ul18m, mrpl18; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
7	<a href="#">d2zjr1</a>	 Alignment		100.0	46	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
8	<a href="#">c2j18S_</a>	 Alignment		100.0	44	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
9	<a href="#">d2j01s1</a>	 Alignment		100.0	47	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
10	<a href="#">c4ce4S_</a>	 Alignment		100.0	29	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> mrpl18; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
11	<a href="#">d1vqon1</a>	 Alignment		100.0	31	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11

12	<a href="#">c3j21O_</a>	Alignment		99.9	29	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 50s ribosomal protein l18p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
13	<a href="#">c2zkrn_</a>	Alignment		99.6	25	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> N: <b>PDB Molecule:</b> rna expansion segment es27; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
14	<a href="#">c3j39D_</a>	Alignment		99.6	27	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
15	<a href="#">c3zf7u_</a>	Alignment		99.6	30	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l21e, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
16	<a href="#">c3j3bD_</a>	Alignment		99.6	23	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
17	<a href="#">c4a1aM_</a>	Alignment		99.6	27	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 3.
18	<a href="#">c3izcO_</a>	Alignment		99.5	30	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein rpl5 (l18p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
19	<a href="#">c3iz5O_</a>	Alignment		99.4	24	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l5 (l18p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
20	<a href="#">c1s1iE_</a>	Alignment		99.3	29	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
21	<a href="#">c5o5jK_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 30s ribosomal protein s11; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
22	<a href="#">d2uubk1</a>	Alignment	not modelled	97.4	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
23	<a href="#">c3j20M_</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 30s ribosomal protein s11p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
24	<a href="#">d2qalk1</a>	Alignment	not modelled	97.1	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
25	<a href="#">c3j6vK_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 28s ribosomal protein s11, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
26	<a href="#">c3bbnK_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> ribosomal protein s11; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
27	<a href="#">c2zkak_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> K: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
28	<a href="#">c3jyvK_</a>	Alignment	not modelled	94.5	21	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 40s ribosomal protein s14(a); <b>PDBTitle:</b> structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces

						lanuginosus ribosome at3 8.9a resolution
29	<a href="#">c2yfnA_</a>	Alignment	not modelled	69.3	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase-sucrose kinase agask; <b>PDBTitle:</b> galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
30	<a href="#">c2xn1B_</a>	Alignment	not modelled	64.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
31	<a href="#">c3mi6A_</a>	Alignment	not modelled	60.5	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
32	<a href="#">c5awqA_</a>	Alignment	not modelled	58.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isomaltodextranase; <b>PDBTitle:</b> arthrobacter globiformis t6 isomalto-dextranase complexed with panose
33	<a href="#">c2pohA_</a>	Alignment	not modelled	48.7	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> head completion protein; <b>PDBTitle:</b> structure of phage p22 tail needle gp26
34	<a href="#">c4fnrB_</a>	Alignment	not modelled	42.6	43	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosidase agaa; <b>PDBTitle:</b> crystal structure of gh36 alpha-galactosidase agaa from geobacillus2 stearothermophilus
35	<a href="#">c3ff4A_</a>	Alignment	not modelled	41.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
36	<a href="#">c4s1aB_</a>	Alignment	not modelled	37.2	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
37	<a href="#">c3mo4B_</a>	Alignment	not modelled	35.9	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,3/4-fucosidase; <b>PDBTitle:</b> the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
38	<a href="#">c6gn6A_</a>	Alignment	not modelled	35.2	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-fucosidase; <b>PDBTitle:</b> alpha-l-fucosidase isoenzyme 1 from paenibacillus thiaminolyticus
39	<a href="#">c4zrxA_</a>	Alignment	not modelled	34.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rf5/8 type c domain protein; <b>PDBTitle:</b> crystal structure of a putative alpha-l-fucosidase (bacova_04357) from2 bacteroides ovatus atcc 8483 at 1.59 a resolution
40	<a href="#">d1hl9a2</a>	Alignment	not modelled	33.4	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Putative alpha-L-fucosidase, catalytic domain
41	<a href="#">c1hl8B_</a>	Alignment	not modelled	33.3	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-l-fucosidase; <b>PDBTitle:</b> crystal structure of thermotoga maritima alpha-fucosidase
42	<a href="#">c3gzaB_</a>	Alignment	not modelled	32.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-l-fucosidase; <b>PDBTitle:</b> crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
43	<a href="#">c4fe4C_</a>	Alignment	not modelled	31.2	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> xylose operon regulatory protein; <b>PDBTitle:</b> crystal structure of apo e. coli xylr
44	<a href="#">d2q4oa1</a>	Alignment	not modelled	31.2	17	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
45	<a href="#">c2q4oA_</a>	Alignment	not modelled	31.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein at2g37210/t2n18.3; <b>PDBTitle:</b> ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
46	<a href="#">c2wvsD_</a>	Alignment	not modelled	27.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-l-fucosidase; <b>PDBTitle:</b> crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
47	<a href="#">c4ni3B_</a>	Alignment	not modelled	27.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-fucosidase gh29; <b>PDBTitle:</b> crystal structure of gh29 family alpha-l-fucosidase from fusarium2 graminearum in the closed form
48	<a href="#">c5oq3A_</a>	Alignment	not modelled	27.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cwp19; <b>PDBTitle:</b> high resolution structure of the functional region of cwp19 from2 clostridium difficile
49	<a href="#">c5k9hA_</a>	Alignment	not modelled	27.3	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 0940_gh29; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase 29 family member from an2 unknown rumen bacterium
50	<a href="#">c3eypB_</a>	Alignment	not modelled	27.0	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-l-fucosidase; <b>PDBTitle:</b> crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
51	<a href="#">d1np7a2</a>	Alignment	not modelled	26.5	19	<b>Fold:</b> Cryptochrome/photolyase, N-terminal domain <b>Superfamily:</b> Cryptochrome/photolyase, N-terminal domain <b>Family:</b> Cryptochrome/photolyase, N-terminal domain
52	<a href="#">c2juia_</a>	Alignment	not modelled	25.9	42	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> plne; <b>PDBTitle:</b> three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaricin ef
						<b>PDB header:</b> hydrolase

53	<a href="#">c6orfA_</a>	Alignment	not modelled	25.6	20	<b>Chain:</b> A: <b>PDB Molecule:</b> spgh29; <b>PDBTitle:</b> crystal structure of spgh29
54	<a href="#">c4c84B_</a>	Alignment	not modelled	25.5	47	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase znrf3; <b>PDBTitle:</b> zebrafish znrf3 ectodomain crystal form i
55	<a href="#">c3noyA_</a>	Alignment	not modelled	24.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
56	<a href="#">d1owla2</a>	Alignment	not modelled	23.9	23	<b>Fold:</b> Cryptochrome/photolyase, N-terminal domain <b>Superfamily:</b> Cryptochrome/photolyase, N-terminal domain <b>Family:</b> Cryptochrome/photolyase, N-terminal domain
57	<a href="#">c4c9vA_</a>	Alignment	not modelled	23.3	40	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rnf43; <b>PDBTitle:</b> xenopus rnf43 ectodomain in complex with xenopus rspo2 fu1-fu2
58	<a href="#">c3m0zD_</a>	Alignment	not modelled	23.1	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative aldolase; <b>PDBTitle:</b> crystal structure of putative aldolase from klebsiella pneumoniae.
59	<a href="#">d3cuma2</a>	Alignment	not modelled	22.9	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
60	<a href="#">c4nzjA_</a>	Alignment	not modelled	22.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha-galactosidase; <b>PDBTitle:</b> crystal structure of a putative alpha-galactosidase (bf1418) from bacteroides fragilis nctc 9343 at 1.57 a resolution
61	<a href="#">c4ad2C_</a>	Alignment	not modelled	22.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glycosyl hydrolase family 71; <b>PDBTitle:</b> structure of the gh99 endo-alpha-mannosidase from bacteroides2 xylanisolvens in complex with glucose-1,3-isofagomine
62	<a href="#">d1zpa2</a>	Alignment	not modelled	20.8	22	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
63	<a href="#">d1y81a1</a>	Alignment	not modelled	19.6	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
64	<a href="#">c2duwA_</a>	Alignment	not modelled	19.4	35	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
65	<a href="#">c3qk7C_</a>	Alignment	not modelled	19.3	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
66	<a href="#">c3qhaB_</a>	Alignment	not modelled	18.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
67	<a href="#">c4aczB_</a>	Alignment	not modelled	18.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-alpha-mannosidase; <b>PDBTitle:</b> structure of the gh99 endo-alpha-mannosidase from2 bacteroides thetaiotaomicron
68	<a href="#">c5u5gC_</a>	Alignment	not modelled	17.4	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> psf3 in complex with nadp+ and 2-opp
69	<a href="#">d1gtka2</a>	Alignment	not modelled	17.4	12	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
70	<a href="#">c3sbcC_</a>	Alignment	not modelled	17.2	27	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
71	<a href="#">d1u3da2</a>	Alignment	not modelled	17.1	14	<b>Fold:</b> Cryptochrome/photolyase, N-terminal domain <b>Superfamily:</b> Cryptochrome/photolyase, N-terminal domain <b>Family:</b> Cryptochrome/photolyase, N-terminal domain
72	<a href="#">d1pdaa2</a>	Alignment	not modelled	16.8	12	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
73	<a href="#">d2hc5a1</a>	Alignment	not modelled	16.2	14	<b>Fold:</b> FlaG-like <b>Superfamily:</b> FlaG-like <b>Family:</b> FlaG-like
74	<a href="#">c2w4iC_</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> human dcmp deaminase
75	<a href="#">c5k6iA_</a>	Alignment	not modelled	15.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> b-glucosidase; <b>PDBTitle:</b> structure of a gh3 b-glucosidase from cow rumen metagenome
76	<a href="#">c5ufhA_</a>	Alignment	not modelled	14.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> laci-type transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a laci-type transcription regulator from2 bifidobacterium animalis subsp. lactis dsm 10140
77	<a href="#">d1aopa1</a>	Alignment	not modelled	14.5	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
78	<a href="#">c3gybB_</a>	Alignment	not modelled	14.4	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulators (laci-family) <b>PDBTitle:</b> crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum <b>PDB header:</b> structural genomics, unknown function

79	<a href="#">c4jjaA_</a>	Alignment	not modelled	14.3	30	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0379) from <i>Bacteroides fragilis</i> nctc 9343 at 1.30 Å resolution
80	<a href="#">c3eywA_</a>	Alignment	not modelled	14.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of <i>E. coli</i> kefc in complex2 with keff
81	<a href="#">c4xtbA_</a>	Alignment	not modelled	14.0	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter
82	<a href="#">d2djia2</a>	Alignment	not modelled	14.0	33	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
83	<a href="#">d2i9ua1</a>	Alignment	not modelled	13.9	14	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
84	<a href="#">c6ndiB_</a>	Alignment	not modelled	13.8	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.60 Å resolution crystal structure of periplasmic binding and2 sugar binding domain of lacI family protein from <i>Klebsiella pneumoniae</i> .
85	<a href="#">d1vpda2</a>	Alignment	not modelled	13.7	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
86	<a href="#">c2cukC_</a>	Alignment	not modelled	13.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from <i>Thermophilus hb8</i>
87	<a href="#">c4k05B_</a>	Alignment	not modelled	13.1	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical exported protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0371) from <i>Bacteroides fragilis</i> nctc 9343 at 1.65 Å resolution
88	<a href="#">c4yyfC_</a>	Alignment	not modelled	13.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> the crystal structure of a glycosyl hydrolase of gh3 family member2 from <i>Mycobacterium smegmatis</i> str. mc2 155
89	<a href="#">d1kjqa2</a>	Alignment	not modelled	13.0	21	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
90	<a href="#">c2iz1C_</a>	Alignment	not modelled	12.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
91	<a href="#">c2uyyD_</a>	Alignment	not modelled	12.9	19	<b>PDB header:</b> cytokine <b>Chain:</b> D: <b>PDB Molecule:</b> n-pac protein; <b>PDBTitle:</b> structure of the cytokine-like nuclear factor n-pac
92	<a href="#">c1zy9A_</a>	Alignment	not modelled	12.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of alpha-galactosidase (ec 3.2.1.22) (melibiase)2 (tm1192) from <i>Thermotoga maritima</i> at 2.34 Å resolution
93	<a href="#">c1vpdA_</a>	Alignment	not modelled	12.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tartronate semialdehyde reductase; <b>PDBTitle:</b> x-ray crystal structure of tartronate semialdehyde reductase2 [ <i>Salmonella typhimurium</i> lt2]
94	<a href="#">c3toxG_</a>	Alignment	not modelled	12.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase in complex with2 nad(p) from <i>Sinorhizobium meliloti</i> 1021
95	<a href="#">d1hjqa_</a>	Alignment	not modelled	12.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
96	<a href="#">c5by4A_</a>	Alignment	not modelled	12.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein tolR; <b>PDBTitle:</b> structure and function of the <i>Escherichia coli</i> tol-pal stator protein2 tolR
97	<a href="#">c4ulif_</a>	Alignment	not modelled	11.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l15-a; <b>PDBTitle:</b> crystal structure of pactamycin bound to the yeast 80s ribosome
98	<a href="#">c4ujye_</a>	Alignment	not modelled	11.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein l15-a; <b>PDBTitle:</b> crystal structure of t-2 toxin bound to the yeast 80s ribosome
99	<a href="#">c4ukje_</a>	Alignment	not modelled	11.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein l15-a; <b>PDBTitle:</b> crystal structure of blasticidin s bound to the yeast 80s ribosome