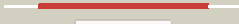



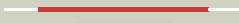

















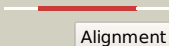

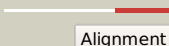





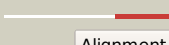

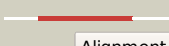







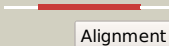
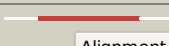
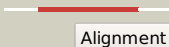


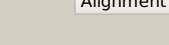
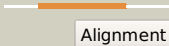
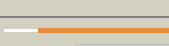


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2005c (-) _2251004_2251891
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	635e13cc17c2e8c5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2jaxA_</a>	 Alignment		100.0	57	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tb31.7; <b>PDBTitle:</b> universal stress protein rv2623 from mycobacterium2 tuberculosis
2	<a href="#">c3olqA_</a>	 Alignment		100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
3	<a href="#">c4r2jA_</a>	 Alignment		100.0	10	<b>PDB header:</b> metal binding protein, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
4	<a href="#">c3loqA_</a>	 Alignment		100.0	22	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
5	<a href="#">c3mt0A_</a>	 Alignment		100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1789; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
6	<a href="#">c3ab8B_</a>	 Alignment		100.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ttha0350; <b>PDBTitle:</b> crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
7	<a href="#">c3s3tD_</a>	 Alignment		99.9	33	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> nucleotide-binding protein, universal stress protein uspa <b>PDBTitle:</b> universal stress protein uspa from lactobacillus plantarum
8	<a href="#">d2z3va1</a>	 Alignment		99.9	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
9	<a href="#">d1tq8a_</a>	 Alignment		99.8	35	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
10	<a href="#">c3fh0A_</a>	 Alignment		99.8	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative universal stress protein kpn_01444; <b>PDBTitle:</b> crystal structure of putative universal stress protein kpn_01444 -2 atpase
11	<a href="#">c4wnyA_</a>	 Alignment		99.8	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei

12	<a href="#">c3hgmD_</a>	 Alignment		99.8	22	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> universal stress protein tead; <b>PDBTitle:</b> universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
13	<a href="#">c3dloC_</a>	 Alignment		99.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> structure of universal stress protein from archaeoglobus fulgidus
14	<a href="#">d1mjha_</a>	 Alignment		99.8	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
15	<a href="#">c5ahwC_</a>	 Alignment		99.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein msmeg_3811 in2 complex with camp
16	<a href="#">c4r2B_</a>	 Alignment		99.7	24	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> universal stress protein f; <b>PDBTitle:</b> crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
17	<a href="#">d1q77a_</a>	 Alignment		99.7	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
18	<a href="#">c3fg9B_</a>	 Alignment		99.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of universal stress protein uspa family; <b>PDBTitle:</b> the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
19	<a href="#">d2gm3a1</a>	 Alignment		99.6	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
20	<a href="#">c2dumD_</a>	 Alignment		99.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ph0823; <b>PDBTitle:</b> crystal structure of hypothetical protein, ph0823
21	<a href="#">d1jmva_</a>	 Alignment	not modelled	99.6	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
22	<a href="#">c2pfsA_</a>	 Alignment	not modelled	99.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein from nitrosomonas2 europaea
23	<a href="#">c3idfA_</a>	 Alignment	not modelled	99.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> usp-like protein; <b>PDBTitle:</b> the crystal structure of a usp-like protein from wolinnella2 succinogenes to 2.0a
24	<a href="#">c5gafi_</a>	 Alignment	not modelled	88.1	9	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein I10; <b>PDBTitle:</b> rnc in complex with srp
25	<a href="#">c5ol2E_</a>	 Alignment	not modelled	88.1	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
26	<a href="#">c5ow0B_</a>	 Alignment	not modelled	87.3	17	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein, beta subunit; <b>PDBTitle:</b> crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
27	<a href="#">c3g40A_</a>	 Alignment	not modelled	84.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> na-k-cl cotransporter; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
28	<a href="#">c2j37W_</a>	 Alignment	not modelled	82.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54);

						<b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
29	<a href="#">c3zquA</a>	Alignment	not modelled	82.0	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> structure of a probable aromatic acid decarboxylase
30	<a href="#">c3a2kB</a>	Alignment	not modelled	81.1	23	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
31	<a href="#">c6qlgD</a>	Alignment	not modelled	80.3	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> flavin prenyltransferase pada1, mitochondrial; <b>PDBTitle:</b> crystal structure of anubix (pada1) in complex with fm and2 dimethylallyl pyrophosphate
32	<a href="#">c4kpuB</a>	Alignment	not modelled	76.8	11	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
33	<a href="#">c1ni5A</a>	Alignment	not modelled	76.3	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
34	<a href="#">d1o94c</a>	Alignment	not modelled	75.6	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
35	<a href="#">d3clsc1</a>	Alignment	not modelled	74.8	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
36	<a href="#">c2e21A</a>	Alignment	not modelled	70.5	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
37	<a href="#">c2ppvA</a>	Alignment	not modelled	69.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
38	<a href="#">c3dm5A</a>	Alignment	not modelled	68.8	11	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
39	<a href="#">c2p0yA</a>	Alignment	not modelled	67.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein lp_0780; <b>PDBTitle:</b> crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
40	<a href="#">c6eoaA</a>	Alignment	not modelled	66.0	29	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantothenoilcysteine decarboxylase; <b>PDBTitle:</b> crystal structure of hal3 from cryptococcus neoformans
41	<a href="#">c2j289</a>	Alignment	not modelled	65.9	9	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
42	<a href="#">c5h75B</a>	Alignment	not modelled	62.1	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mersacidin decarboxylase,immunoglobulin g-binding protein <b>PDBTitle:</b> crystal structure of the mrsd-protein a fusion protein
43	<a href="#">c2iy3A</a>	Alignment	not modelled	58.1	15	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
44	<a href="#">d2hzba1</a>	Alignment	not modelled	54.9	17	<b>Fold:</b> CofD-like <b>Superfamily:</b> CofD-like <b>Family:</b> CofD-like
45	<a href="#">c4hqnb</a>	Alignment	not modelled	54.6	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> sporozoite surface protein 2; <b>PDBTitle:</b> crystal structure of manganese-loaded plasmodium vivax trap protein
46	<a href="#">c6jlsA</a>	Alignment	not modelled	50.9	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavoprotein decarboxylase; <b>PDBTitle:</b> crystal structure of fm-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
47	<a href="#">d1ni5a1</a>	Alignment	not modelled	47.4	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
48	<a href="#">d1qzua</a>	Alignment	not modelled	47.4	29	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
49	<a href="#">d1g5qa</a>	Alignment	not modelled	45.7	3	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
50	<a href="#">c4rheB</a>	Alignment	not modelled	44.9	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-octaprenyl-4-hydroxybenzoate carboxylase; <b>PDBTitle:</b> crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
51	<a href="#">d1sbza</a>	Alignment	not modelled	44.1	15	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
52	<a href="#">d1efpb</a>	Alignment	not modelled	43.8	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits

53	<a href="#">c5ghaC</a>	Alignment	not modelled	43.2	24	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
54	<a href="#">c4nzpA</a>	Alignment	not modelled	42.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
55	<a href="#">c1vl2C</a>	Alignment	not modelled	42.8	15	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
56	<a href="#">c6fahB</a>	Alignment	not modelled	42.0	7	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit card; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
57	<a href="#">c2ejbA</a>	Alignment	not modelled	41.4	6	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
58	<a href="#">d1p5dx1</a>	Alignment	not modelled	38.9	21	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
59	<a href="#">d2g0ta1</a>	Alignment	not modelled	38.9	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
60	<a href="#">c3vrhA</a>	Alignment	not modelled	38.1	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
61	<a href="#">c1mvlA</a>	Alignment	not modelled	36.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ppc decarboxylase athal3a; <b>PDBTitle:</b> ppc decarboxylase mutant c175s
62	<a href="#">d1mvla</a>	Alignment	not modelled	36.0	12	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
63	<a href="#">c2yxbA</a>	Alignment	not modelled	35.8	8	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
64	<a href="#">d2ffea1</a>	Alignment	not modelled	33.6	15	<b>Fold:</b> CofD-like <b>Superfamily:</b> CofD-like <b>Family:</b> CofD-like
65	<a href="#">c4okuA</a>	Alignment	not modelled	33.4	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> micronemal protein mic2; <b>PDBTitle:</b> structure of toxoplasma gondii promic2
66	<a href="#">c1qzuB</a>	Alignment	not modelled	32.1	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein mds018; <b>PDBTitle:</b> crystal structure of human phosphopantothenoylcysteine decarboxylase
67	<a href="#">c1kh2D</a>	Alignment	not modelled	31.5	13	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
68	<a href="#">c5bmpA</a>	Alignment	not modelled	30.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglucomutase; <b>PDBTitle:</b> crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
69	<a href="#">d1np7a2</a>	Alignment	not modelled	29.8	12	<b>Fold:</b> Cryptochrome/photolyase, N-terminal domain <b>Superfamily:</b> Cryptochrome/photolyase, N-terminal domain <b>Family:</b> Cryptochrome/photolyase, N-terminal domain
70	<a href="#">c4l2iA</a>	Alignment	not modelled	29.0	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
71	<a href="#">c3qjgD</a>	Alignment	not modelled	27.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> epidermin biosynthesis protein epid; <b>PDBTitle:</b> epidermin biosynthesis protein epid from staphylococcus aureus
72	<a href="#">c3c04A</a>	Alignment	not modelled	27.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase/phosphoglucomutase; <b>PDBTitle:</b> structure of the p368g mutant of pmm/pgm from p. aeruginosa
73	<a href="#">d1p3y1</a>	Alignment	not modelled	27.6	18	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
74	<a href="#">c3mcf</a>	Alignment	not modelled	26.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
75	<a href="#">d1m7ja3</a>	Alignment	not modelled	26.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> D-aminoacylase, catalytic domain
76	<a href="#">c4hjhA</a>	Alignment	not modelled	25.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate
77	<a href="#">c2m9A</a>	Alignment	not modelled	24.1	9	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy;

77	<a href="#">c4y3A</a>	Alignment	not modelled	24.1	9	<b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy <b>PDB header:</b> oxidoreductase
78	<a href="#">c4n7bA</a>	Alignment	not modelled	24.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> lytb; <b>PDBTitle:</b> structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
79	<a href="#">d1to6a</a>	Alignment	not modelled	22.8	32	<b>Fold:</b> Glycerate kinase I <b>Superfamily:</b> Glycerate kinase I <b>Family:</b> Glycerate kinase I
80	<a href="#">d3clsd1</a>	Alignment	not modelled	22.7	8	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
81	<a href="#">c3ih5A</a>	Alignment	not modelled	21.7	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
82	<a href="#">c2nz2A</a>	Alignment	not modelled	21.4	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
83	<a href="#">c3dnfB</a>	Alignment	not modelled	20.9	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
84	<a href="#">c3urkA</a>	Alignment	not modelled	20.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> isph in complex with propynyl diphosphate (1061)
85	<a href="#">c3ke8A</a>	Alignment	not modelled	20.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> crystal structure of isph:hmbpp-complex
86	<a href="#">d1j20a1</a>	Alignment	not modelled	20.4	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
87	<a href="#">c3s40C</a>	Alignment	not modelled	20.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> diacylglycerol kinase; <b>PDBTitle:</b> the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
88	<a href="#">d1vbkA1</a>	Alignment	not modelled	19.7	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
89	<a href="#">d1xrsa</a>	Alignment	not modelled	19.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> D-lysine 5,6-aminomutase alpha subunit, KamD
90	<a href="#">c4hqfA</a>	Alignment	not modelled	19.6	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thrombospondin-related anonymous protein, trap; <b>PDBTitle:</b> crystal structure of plasmodium falciparum trap, i4 form
91	<a href="#">c3lqkA</a>	Alignment	not modelled	19.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit b; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
92	<a href="#">d3pmgA1</a>	Alignment	not modelled	18.5	26	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
93	<a href="#">c2f7IA</a>	Alignment	not modelled	18.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 455aa long hypothetical phospho-sugar mutase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
94	<a href="#">d1wy5a1</a>	Alignment	not modelled	17.6	9	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
95	<a href="#">c1o94D</a>	Alignment	not modelled	17.4	9	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
96	<a href="#">d1zuna1</a>	Alignment	not modelled	17.2	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
97	<a href="#">d2c5sa1</a>	Alignment	not modelled	16.8	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
98	<a href="#">c2obnA</a>	Alignment	not modelled	16.4	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1611 family protein (ava_3511) from anaena2 variabilis atcc 29413 at 2.30 a resolution
99	<a href="#">d1jeoa</a>	Alignment	not modelled	16.3	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain