

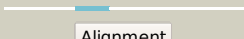
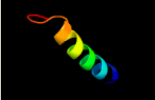
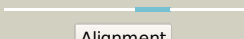


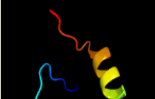
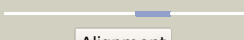
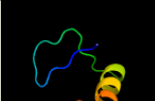



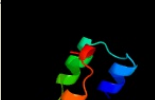



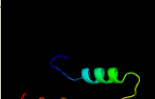



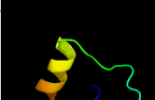


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2543_(lppA)_2866478_2867137
Date	Wed Aug 7 12:50:17 BST 2019
Unique Job ID	7695d1bf881299e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2v7sA_</a>	 Alignment		100.0	99	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved lipoprotein lppa; <b>PDBTitle:</b> crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
2	<a href="#">c6h3uA_</a>	 Alignment		33.1	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> schmalleberg virus glycoprotein gc head domain in complex with scfv2 4b6
3	<a href="#">c6bs7A_</a>	 Alignment		33.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
4	<a href="#">d1dj2a_</a>	 Alignment		32.0	18	<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
5	<a href="#">c3r7tA_</a>	 Alignment		29.4	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
6	<a href="#">c6h3xA_</a>	 Alignment		28.7	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> oropouche virus glycoprotein gc head domain
7	<a href="#">c4ps2A_</a>	 Alignment		27.8	16	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative type vi secretion protein; <b>PDBTitle:</b> structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule
8	<a href="#">c5civA_</a>	 Alignment		27.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sibling bacteriocin; <b>PDBTitle:</b> sibling lethal factor precursor - dfsb
9	<a href="#">d2oqea2</a>	 Alignment		26.7	24	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
10	<a href="#">c5j34B_</a>	 Alignment		26.6	26	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
11	<a href="#">d1qf5a_</a>	 Alignment		26.5	21	<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

12	<a href="#">c6h3wA_</a>	Alignment		25.6	9	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> la crosse virus glycoprotein gc head domain
13	<a href="#">cliweB_</a>	Alignment		25.6	15	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> imp complex of the recombinant mouse-muscle adenylosuccinate2 synthetase
14	<a href="#">c1wd6B_</a>	Alignment		25.5	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> protein ydhr; <b>PDBTitle:</b> crystal structure of jw1657 from escherichia coli
15	<a href="#">d1nvmB2</a>	Alignment		25.5	24	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
16	<a href="#">d1iwea_</a>	Alignment		25.4	15	<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
17	<a href="#">c5lnk2_</a>	Alignment		24.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 2; <b>PDB Molecule:</b> mitochondrial complex i, 24 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
18	<a href="#">d1dj3a_</a>	Alignment		24.6	18	<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
19	<a href="#">c3k6gA_</a>	Alignment		24.5	28	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> telomeric repeat-binding factor 2-interacting protein 1; <b>PDBTitle:</b> crystal structure of rap1 and trf2 complex
20	<a href="#">c3ls1A_</a>	Alignment		24.0	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> A; <b>PDB Molecule:</b> sll1638 protein; <b>PDBTitle:</b> crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
21	<a href="#">d2pv4a1</a>	Alignment	not modelled	23.0	39	<b>Fold:</b> Sama2622-like <b>Superfamily:</b> Sama2622-like <b>Family:</b> Sama2622-like
22	<a href="#">d1jl3a_</a>	Alignment	not modelled	23.0	17	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
23	<a href="#">c6h3sA_</a>	Alignment	not modelled	23.0	23	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> schmallenberg virus glycoprotein gc head/stalk domains
24	<a href="#">d1p9ba_</a>	Alignment	not modelled	22.7	24	<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
25	<a href="#">c4jn6B_</a>	Alignment	not modelled	20.7	29	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> acetaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
26	<a href="#">c4clvB_</a>	Alignment	not modelled	19.7	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
27	<a href="#">c2mt3A_</a>	Alignment	not modelled	18.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> structure of -24 dna binding domain of sigma 54 from e.coli
28	<a href="#">c4m0gB_</a>	Alignment	not modelled	18.3	26	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> the crystal structure of an adenylosuccinate synthetase from bacillus2 anthracis str. ames ancestor.

29	<a href="#">c1nvmB_</a>	Alignment	not modelled	17.5	25	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase (acylating); <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
30	<a href="#">d1xbpg2</a>	Alignment	not modelled	17.0	53	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
31	<a href="#">c2o8kA_</a>	Alignment	not modelled	17.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
32	<a href="#">c4dknB_</a>	Alignment	not modelled	16.7	39	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> amphioxus green fluorescent protein, gfpa1; <b>PDBTitle:</b> crystal structure of amphioxus green fluorescent protein, gfpa1
33	<a href="#">c4fgiH_</a>	Alignment	not modelled	16.6	32	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> tse1; <b>PDBTitle:</b> structure of the effector - immunity system tse1 / tsi1 from2 pseudomonas aeruginosa
34	<a href="#">c4f6oA_</a>	Alignment	not modelled	16.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metacaspase-1; <b>PDBTitle:</b> crystal structure of the yeast metacaspase yca1
35	<a href="#">d2gycg2</a>	Alignment	not modelled	15.3	41	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
36	<a href="#">d2csga1</a>	Alignment	not modelled	15.0	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> YbiU-like
37	<a href="#">c6h3vA_</a>	Alignment	not modelled	14.9	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> bunyamwera virus glycoprotein gc head domain
38	<a href="#">c2wyfF_</a>	Alignment	not modelled	14.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> l-ascorbate-6-phosphate lactonase ulag; <b>PDBTitle:</b> apo structure of a metallo-b-lactamase
39	<a href="#">c3vpjF_</a>	Alignment	not modelled	14.6	32	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> tse1-specific immunity protein; <b>PDBTitle:</b> crystal structure of type vi effector tse1 from pseudomonas aeruginosa2 in complex with immune protein tsi1
40	<a href="#">c4xhpA_</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sparm hybrid fusion protein; <b>PDBTitle:</b> bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
41	<a href="#">c5xf9E_</a>	Alignment	not modelled	13.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
42	<a href="#">d2zjrp1</a>	Alignment	not modelled	13.2	22	<b>Fold:</b> Ribosomal protein L22 <b>Superfamily:</b> Ribosomal protein L22 <b>Family:</b> Ribosomal protein L22
43	<a href="#">c2ahqA_</a>	Alignment	not modelled	12.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
44	<a href="#">c3uoaB_</a>	Alignment	not modelled	12.6	44	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> mucosa-associated lymphoid tissue lymphoma translocation <b>PDBTitle:</b> crystal structure of the malt1 paracaspase (p21 form)
45	<a href="#">d1d6za2</a>	Alignment	not modelled	12.2	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
46	<a href="#">d1w2za2</a>	Alignment	not modelled	11.9	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
47	<a href="#">c5y00A_</a>	Alignment	not modelled	11.9	27	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> acid-tolerant monomeric gfp, gamillus, fluorescence (on) state
48	<a href="#">c5todD_</a>	Alignment	not modelled	11.7	17	<b>PDB header:</b> lipid transport <b>Chain:</b> D: <b>PDB Molecule:</b> transmembrane protein 24; <b>PDBTitle:</b> transmembrane protein 24 smp domain
49	<a href="#">c4dkmH_</a>	Alignment	not modelled	11.0	39	<b>PDB header:</b> fluorescent protein <b>Chain:</b> H: <b>PDB Molecule:</b> amphioxus green fluorescent protein, gfpc1a; <b>PDBTitle:</b> crystal structure of amphioxus gfpc1a
50	<a href="#">d2fug21</a>	Alignment	not modelled	10.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
51	<a href="#">c5z43A_</a>	Alignment	not modelled	10.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ambp1; <b>PDBTitle:</b> crystal structure of prenyltransferase ambp1 apo structure
52	<a href="#">d1mmsa2</a>	Alignment	not modelled	10.8	53	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
53	<a href="#">d1w6ga2</a>	Alignment	not modelled	10.6	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
54	<a href="#">c4ce4W_</a>	Alignment	not modelled	10.6	15	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> mrpl22; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
55	<a href="#">c3uo9A_</a>	Alignment	not modelled	10.5	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase;

55	<a href="#">c3ue9A</a>	Alignment	not modelled	10.5	12	<b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis <b>PDB header:</b> fluorescent protein
56	<a href="#">c5ltrA</a>	Alignment	not modelled	10.2	24	<b>Chain:</b> A: <b>PDB Molecule:</b> mneongreen; <b>PDBTitle:</b> structure of the yellow-green fluorescent protein mneongreen from2 branchiostoma lanceolatum at the near physiological ph 8.0 <b>PDB header:</b> unknown function
57	<a href="#">c5cqvb</a>	Alignment	not modelled	9.9	12	<b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein q8dww2 from streptococcus2 agalactiae
58	<a href="#">c5mmi7</a>	Alignment	not modelled	9.6	50	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> 50s ribosomal protein 6, chloroplastic; <b>PDBTitle:</b> structure of the large subunit of the chloroplast ribosome
59	<a href="#">d1o57a1</a>	Alignment	not modelled	9.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of Bacillus PurR
60	<a href="#">c5mlc8</a>	Alignment	not modelled	9.4	50	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> psrp6, chloroplastic; <b>PDBTitle:</b> cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
61	<a href="#">c4v19W</a>	Alignment	not modelled	9.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> mitoribosomal protein ul22m, mrp122; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
62	<a href="#">c2n99A</a>	Alignment	not modelled	9.2	27	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> ly-6/neurotoxin-like protein 1; <b>PDBTitle:</b> solution structure of the slurp-2, a secreted isoform of lynx1
63	<a href="#">c5od4A</a>	Alignment	not modelled	9.1	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> secreted in xylem 3; <b>PDBTitle:</b> avr2 effector protein from the fungal plant pathogen fusarium2 oxysporum
64	<a href="#">c2yufA</a>	Alignment	not modelled	8.9	42	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ngfi-a-binding protein 1; <b>PDBTitle:</b> solution structure of the ncd2 domain in human2 transcriptional repressor nab1 protein
65	<a href="#">c2vdcF</a>	Alignment	not modelled	8.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadh] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
66	<a href="#">c1lm1A</a>	Alignment	not modelled	8.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
67	<a href="#">c6bwqB</a>	Alignment	not modelled	8.4	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel <b>PDBTitle:</b> larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
68	<a href="#">c3bjjC</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein gsu0716; <b>PDBTitle:</b> crystal structure of protein gsu0716 from geobacter sulfurreducens.2 northeast structural genomics target gsr13
69	<a href="#">c4ee7A</a>	Alignment	not modelled	8.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> prenyltransferase; <b>PDBTitle:</b> crystal structure of the novel phenazine prenyltransferase epzp in2 complex with s-thiolodiphosphate (methylated)
70	<a href="#">c5l7uB</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase; <b>PDBTitle:</b> crystal structure of bvgh123 with bound galnac
71	<a href="#">d3c9ua1</a>	Alignment	not modelled	8.2	8	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
72	<a href="#">c3vtiD</a>	Alignment	not modelled	8.2	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of hype-hypf complex
73	<a href="#">c1pbyA</a>	Alignment	not modelled	8.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinohemoprotein amine dehydrogenase 60 kda subunit; <b>PDBTitle:</b> structure of the phenylhydrazine adduct of the quinohemoprotein amine2 dehydrogenase from paracoccus denitrificans at 1.7 a resolution
74	<a href="#">c4mjgB</a>	Alignment	not modelled	7.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4853 family protein (actodo_00621) from2 actinomyces odontolyticus atcc 17982 at 2.65 a resolution
75	<a href="#">d2rm0w1</a>	Alignment	not modelled	7.8	10	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
76	<a href="#">c5mlcU</a>	Alignment	not modelled	7.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l22, chloroplastic; <b>PDBTitle:</b> cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
77	<a href="#">c1vw4O</a>	Alignment	not modelled	7.6	12	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 54s ribosomal protein l22, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
78	<a href="#">c3a9rA</a>	Alignment	not modelled	7.6	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-arabinose isomerase; <b>PDBTitle:</b> x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
						<b>Fold:</b> Ribosomal L11/L12e N-terminal domain

79	<a href="#">d3cjsb1</a>	Alignment	not modelled	7.6	53	<b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
80	<a href="#">c4jeoB</a>	Alignment	not modelled	7.4	44	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> red fluorescent protein blfp-r5; <b>PDBTitle:</b> crystal structure of red fluorescent protein lanrfdam exposed to2 prolonged x-ray irradiation
81	<a href="#">d1m1la</a>	Alignment	not modelled	7.3	40	<b>Fold:</b> Suppressor of Fused, N-terminal domain <b>Superfamily:</b> Suppressor of Fused, N-terminal domain <b>Family:</b> Suppressor of Fused, N-terminal domain
82	<a href="#">c4n4qD</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate lyase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
83	<a href="#">c4a8xB</a>	Alignment	not modelled	7.3	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hook-like, isoform a; <b>PDBTitle:</b> structure of the core asap complex
84	<a href="#">c5wuqD</a>	Alignment	not modelled	7.1	3	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> anti-sigma-w factor rsiw; <b>PDBTitle:</b> crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
85	<a href="#">d1fca2</a>	Alignment	not modelled	7.1	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1
86	<a href="#">d1hw8a2</a>	Alignment	not modelled	7.1	15	<b>Fold:</b> Substrate-binding domain of HMG-CoA reductase <b>Superfamily:</b> Substrate-binding domain of HMG-CoA reductase <b>Family:</b> Substrate-binding domain of HMG-CoA reductase
87	<a href="#">c6g90Q</a>	Alignment	not modelled	7.1	30	<b>PDB header:</b> splicing <b>Chain:</b> Q: <b>PDB Molecule:</b> cold sensitive u2 snrna suppressor 1; <b>PDBTitle:</b> prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
88	<a href="#">c6gioB</a>	Alignment	not modelled	7.1	9	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid amide racemase; <b>PDBTitle:</b> structure of amino acid amide racemase from ochrobactrum anthropi
89	<a href="#">c2zauB</a>	Alignment	not modelled	7.1	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
90	<a href="#">c5j9wA</a>	Alignment	not modelled	7.0	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetophenone carboxylase delta subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
91	<a href="#">d2a21a1</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
92	<a href="#">c2lkyA</a>	Alignment	not modelled	6.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysm.17112.b
93	<a href="#">d1pu1a</a>	Alignment	not modelled	6.9	11	<b>Fold:</b> Hypothetical protein MTH677 <b>Superfamily:</b> Hypothetical protein MTH677 <b>Family:</b> Hypothetical protein MTH677
94	<a href="#">d1fuia1</a>	Alignment	not modelled	6.9	39	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> FucI/AraA C-terminal domain-like <b>Family:</b> L-fucose isomerase, C-terminal domain
95	<a href="#">c4ffcD</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate aminotransferase (gabt); <b>PDBTitle:</b> crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
96	<a href="#">c1jmxA</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amine dehydrogenase; <b>PDBTitle:</b> crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
97	<a href="#">d2fh1a2</a>	Alignment	not modelled	6.6	32	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Gelsolin-like
98	<a href="#">c6gh5M</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> rna polymerase sigma-54 factor,rna polymerase sigma-54 <b>PDBTitle:</b> cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
99	<a href="#">d1d0na5</a>	Alignment	not modelled	6.4	32	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Gelsolin-like