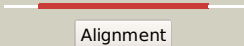

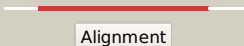

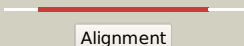







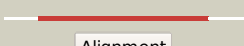






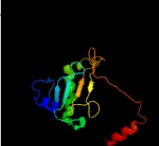




# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0619\_(galTb)\_712252\_712722  
 Date Fri Jul 26 01:50:18 BST 2019  
 Unique Job ID 42dfc799d5dde4f5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1guqa2</a>	 Alignment		100.0	27	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> Hexose-1-phosphate uridylyltransferase
2	<a href="#">c5in3A_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> galactose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of glucose-1-phosphate bound nucleotidylated human2 galactose-1-phosphate uridylyltransferase
3	<a href="#">c1gupC_</a>	 Alignment		100.0	27	<b>PDB header:</b> nucleotidyltransferase <b>Chain:</b> C: <b>PDB Molecule:</b> galactose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> structure of nucleotidyltransferase complexed with udp-2 galactose
4	<a href="#">d1z84a2</a>	 Alignment		100.0	22	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> Hexose-1-phosphate uridylyltransferase
5	<a href="#">c1zwwA_</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative galactose-1-phosphate uridylyl transferase; <b>PDBTitle:</b> x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
6	<a href="#">c3lb5B_</a>	 Alignment		100.0	16	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> hit-like protein involved in cell-cycle regulation; <b>PDBTitle:</b> crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
7	<a href="#">c3imiB_</a>	 Alignment		100.0	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hit family protein; <b>PDBTitle:</b> 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
8	<a href="#">c3o0mB_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hit family protein; <b>PDBTitle:</b> crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
9	<a href="#">d1y23a_</a>	 Alignment		100.0	12	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
10	<a href="#">c6iq1A_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine 5'-monophosphoramidase; <b>PDBTitle:</b> crystal structure of histidine triad nucleotide-binding protein from2 candida albicans
11	<a href="#">c3l7xA_</a>	 Alignment		100.0	16	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative hit-like protein involved in cell-cycle <b>PDBTitle:</b> the crystal structure of smu.412c from streptococcus mutans ua159

12	<a href="#">c3ksvA_</a>	Alignment		100.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> hypothetical protein from leishmania major
13	<a href="#">c3p0tB_</a>	Alignment		100.0	10	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
14	<a href="#">c3anoA_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ap-4-a phosphorylase; <b>PDBTitle:</b> crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
15	<a href="#">c2eo4A_</a>	Alignment		99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical histidine triad nucleotide-binding <b>PDBTitle:</b> crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfobolus tokodaii strain7
16	<a href="#">c4eguA_</a>	Alignment		99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad (hit) protein; <b>PDBTitle:</b> 0.95a resolution structure of a histidine triad protein from2 clostridium difficile
17	<a href="#">c3n1tE_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> hit-like protein hint; <b>PDBTitle:</b> crystal structure of the h101a mutant echint gmp complex
18	<a href="#">c6d6jB_</a>	Alignment		99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hit family hydrolase; <b>PDBTitle:</b> crystal structure of hit family hydrolase from legionella pneumophila2 philadelphia 1
19	<a href="#">c1xquA_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hit family hydrolase; <b>PDBTitle:</b> hit family hydrolase from clostridium thermocellum cth-393
20	<a href="#">d1xqua_</a>	Alignment		99.9	19	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
21	<a href="#">d1rzya_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
22	<a href="#">d1kpfa_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
23	<a href="#">d2oika1</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
24	<a href="#">c3r6fA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hit family protein; <b>PDBTitle:</b> crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
25	<a href="#">d1emsa1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
26	<a href="#">d1fita_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
27	<a href="#">c5cs2A_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad protein; <b>PDBTitle:</b> crystal structure of plasmodium falciparum diadenosine triphosphate2 hydrolase in complex with cyclamarin a
28	<a href="#">c4q61j_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> cell cycle <b>Chain:</b> J: <b>PDB Molecule:</b> uncharacterized hit-like protein hp_0404; <b>PDBTitle:</b> hit like protein from helicobacter pylori 26695
						<b>PDB header:</b> metal binding protein

29	<a href="#">c3oj7A_</a>	Alignment	not modelled	99.9	16	<b>Chain:</b> A: <b>PDB Molecule:</b> putative histidine triad family protein; <b>PDBTitle:</b> crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
30	<a href="#">c1emsB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> antitumor protein <b>Chain:</b> B: <b>PDB Molecule:</b> nit-fragile histidine triad fusion protein; <b>PDBTitle:</b> crystal structure of the c. elegans nitfhit protein
31	<a href="#">c4incA_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad nucleotide-binding protein 2, <b>PDBTitle:</b> human histidine triad nucleotide binding protein 2
32	<a href="#">c3nrdB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> histidine triad (hit) protein; <b>PDBTitle:</b> crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
33	<a href="#">c3i24B_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hit family hydrolase; <b>PDBTitle:</b> crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
34	<a href="#">c3i4sB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine triad protein; <b>PDBTitle:</b> crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
35	<a href="#">c4qvua_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4931 family protein (bce0241) from bacillus2 cereus atcc 10987 at 2.65 a resolution
36	<a href="#">c3oheA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad (hit) protein; <b>PDBTitle:</b> crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
37	<a href="#">c4ndgB_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> dna binding protein/rna/dna <b>Chain:</b> B: <b>PDB Molecule:</b> aprataxin; <b>PDBTitle:</b> human aprataxin (aptx) bound to rna-dna and zn -adenosine vanadate2 transition state mimic complex
38	<a href="#">c3jb9c_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> u5 snrna; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
39	<a href="#">c3splC_</a>	Alignment	not modelled	99.3	8	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> aprataxin-like protein; <b>PDBTitle:</b> crystal structure of aprataxin ortholog hnt3 in complex with dna and2 amp
40	<a href="#">c6id1U_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> splicing <b>Chain:</b> U: <b>PDB Molecule:</b> cwf19-like protein 2; <b>PDBTitle:</b> cryo-em structure of a human intron lariat spliceosome after prp432 loaded (ils2 complex) at 2.9 angstrom resolution
41	<a href="#">d1z84a1</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> Hexose-1-phosphate uridylyltransferase
42	<a href="#">c4i5wA_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5',5'''-p-1,p-4-tetraphosphate phosphorylase 2; <b>PDBTitle:</b> crystal structure of yeast ap4a phosphorylase apa2 in complex with amp
43	<a href="#">d3bl9a1</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> mRNA decapping enzyme Dcp5 C-terminal domain
44	<a href="#">c3bl9B_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> scavenger mrna-decapping enzyme dcps; <b>PDBTitle:</b> synthetic gene encoded dcps bound to inhibitor dg157493
45	<a href="#">c1xmlA_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock-like protein 1; <b>PDBTitle:</b> structure of human dcps
46	<a href="#">d1vlra1</a>	Alignment	not modelled	98.6	18	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> mRNA decapping enzyme Dcp5 C-terminal domain
47	<a href="#">c6gbsB_</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative mrna decapping protein; <b>PDBTitle:</b> crystal structure of the c. thermophilum scavenger decapping enzyme2 dcps apo form
48	<a href="#">c5bv3C_</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> m7gpppx diphosphatase; <b>PDBTitle:</b> yeast scavenger decapping enzyme in complex with m7gdp
49	<a href="#">d1guqa1</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> Hexose-1-phosphate uridylyltransferase
50	<a href="#">d2pofa1</a>	Alignment	not modelled	85.2	13	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> CDH-like
51	<a href="#">c4lvjA_</a>	Alignment	not modelled	82.3	12	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> plasmid recombination enzyme; <b>PDBTitle:</b> mobm relaxase domain (mobv; mob_pre) bound to plasmid pmv158 orit dna2 (22nt). mn-bound crystal structure at ph 5.5
52	<a href="#">c4ht4A_</a>	Alignment	not modelled	26.6	13	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> nicking enzyme; <b>PDBTitle:</b> molecular basis of vancomycin resistance transfer in staphylococcus2 aureus
53	<a href="#">c3bddD_</a>	Alignment	not modelled	21.5	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein marr; <b>PDBTitle:</b> crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator. marr family;

54	<a href="#">c2qwwB_</a>	Alignment	not modelled	17.6	20	<b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
55	<a href="#">d2fbka1</a>	Alignment	not modelled	12.5	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
56	<a href="#">d2nvna1</a>	Alignment	not modelled	12.4	14	<b>Fold:</b> ssDNA-binding transcriptional regulator domain <b>Superfamily:</b> ssDNA-binding transcriptional regulator domain <b>Family:</b> PMN2A0962/syc2379c-like
57	<a href="#">c3txxD_</a>	Alignment	not modelled	12.2	10	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putrescine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of putrescine transcarbamylase from enterococcus2 faecalis
58	<a href="#">c2mwqA_</a>	Alignment	not modelled	11.6	17	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 3, chloroplastic; <b>PDBTitle:</b> solution structure of psbq from spinacia oleracea
59	<a href="#">c5n6yC_</a>	Alignment	not modelled	11.4	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein delta chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
60	<a href="#">c5ubaA_</a>	Alignment	not modelled	11.0	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna pseudouridylate synthase domain-containing protein 4; <b>PDBTitle:</b> human rna pseudouridylate synthase domain containing 4
61	<a href="#">d1duvg1</a>	Alignment	not modelled	10.8	10	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
62	<a href="#">c3oopA_</a>	Alignment	not modelled	10.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
63	<a href="#">c5nngA_</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctatc; <b>PDBTitle:</b> aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
64	<a href="#">c5vbbA_</a>	Alignment	not modelled	10.2	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna pseudouridylate synthase domain-containing protein 1; <b>PDBTitle:</b> human rna pseudouridylate synthase domain containing 1
65	<a href="#">c3tpfF_</a>	Alignment	not modelled	9.9	4	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
66	<a href="#">c5yhxH_</a>	Alignment	not modelled	9.8	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zittr, wild type
67	<a href="#">d1ml4a1</a>	Alignment	not modelled	9.2	7	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
68	<a href="#">d1vlva1</a>	Alignment	not modelled	9.2	14	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
69	<a href="#">d1v9ka_</a>	Alignment	not modelled	9.1	8	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase RsuA/RLuD
70	<a href="#">d1dxha1</a>	Alignment	not modelled	9.1	17	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
71	<a href="#">c3sdsA_</a>	Alignment	not modelled	9.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase, mitochondrial; <b>PDBTitle:</b> crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
72	<a href="#">c3siiA_</a>	Alignment	not modelled	8.9	29	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> poly(adp-ribose) glycohydrolase; <b>PDBTitle:</b> the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
73	<a href="#">d1vr7a1</a>	Alignment	not modelled	8.7	17	<b>Fold:</b> S-adenosylmethionine decarboxylase <b>Superfamily:</b> S-adenosylmethionine decarboxylase <b>Family:</b> Bacterial S-adenosylmethionine decarboxylase
74	<a href="#">d1ji8a_</a>	Alignment	not modelled	8.6	9	<b>Fold:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Superfamily:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Family:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase
75	<a href="#">d2a61a1</a>	Alignment	not modelled	8.6	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
76	<a href="#">d2at2a1</a>	Alignment	not modelled	8.4	12	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
77	<a href="#">d1ekxa1</a>	Alignment	not modelled	8.2	7	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
78	<a href="#">d2v4jc1</a>	Alignment	not modelled	8.1	12	<b>Fold:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Superfamily:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Family:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase
79	<a href="#">c2ef0A_</a>	Alignment	not modelled	7.9	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus

80	<a href="#">c2i82D</a>	 Alignment	not modelled	7.8	8	<b>PDB header:</b> lyase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
81	<a href="#">c1lqvD</a>	 Alignment	not modelled	7.7	0	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> vitamin-k dependent protein c; <b>PDBTitle:</b> crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.
82	<a href="#">c3jtcC</a>	 Alignment	not modelled	7.7	0	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> vitamin k-dependent protein c; <b>PDBTitle:</b> importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxyglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
83	<a href="#">c3jtcD</a>	 Alignment	not modelled	7.7	0	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> vitamin k-dependent protein c; <b>PDBTitle:</b> importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxyglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
84	<a href="#">c1lqvC</a>	 Alignment	not modelled	7.7	0	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> vitamin-k dependent protein c; <b>PDBTitle:</b> crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.
85	<a href="#">d1otha1</a>	 Alignment	not modelled	7.7	17	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
86	<a href="#">d1tuga1</a>	 Alignment	not modelled	7.4	7	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
87	<a href="#">c3cyyA</a>	 Alignment	not modelled	7.3	24	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> the crystal structure of zo-1 pdz2 in complex with the cx43 peptide
88	<a href="#">c5kciA</a>	 Alignment	not modelled	7.2	6	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ypl067c; <b>PDBTitle:</b> crystal structure of htc1
89	<a href="#">c1qyuA</a>	 Alignment	not modelled	7.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d; <b>PDBTitle:</b> structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
90	<a href="#">d1pvva1</a>	 Alignment	not modelled	7.1	10	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
91	<a href="#">d1uf0a</a>	 Alignment	not modelled	7.0	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Doublecortin (DC) <b>Family:</b> Doublecortin (DC)
92	<a href="#">d2it9a1</a>	 Alignment	not modelled	6.9	13	<b>Fold:</b> ssDNA-binding transcriptional regulator domain <b>Superfamily:</b> ssDNA-binding transcriptional regulator domain <b>Family:</b> PMN2A0962/syc2379c-like
93	<a href="#">c1vr7A</a>	 Alignment	not modelled	6.8	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine decarboxylase proenzyme; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine decarboxylase proenzyme2 (tm0655) from thermotoga maritima at 1.2 a resolution
94	<a href="#">c2ns6A</a>	 Alignment	not modelled	6.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mobilization protein a; <b>PDBTitle:</b> crystal structure of the minimal relaxase domain of moba from plasmid2 r1162
95	<a href="#">c2rodB</a>	 Alignment	not modelled	6.5	38	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> noxa; <b>PDBTitle:</b> solution structure of mcl-1 complexed with noxaa
96	<a href="#">c2osgB</a>	 Alignment	not modelled	6.3	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> tight junction protein zo-2; <b>PDBTitle:</b> solution structure and binding property of the domain-2 swapped dimer of zo2pdz2
97	<a href="#">d1hska2</a>	 Alignment	not modelled	6.3	6	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
98	<a href="#">d1wgva</a>	 Alignment	not modelled	6.3	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
99	<a href="#">d2gkpa1</a>	 Alignment	not modelled	6.2	19	<b>Fold:</b> NMB0488-like <b>Superfamily:</b> NMB0488-like <b>Family:</b> NMB0488-like