
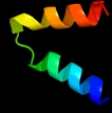
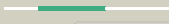
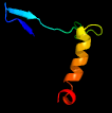




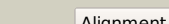


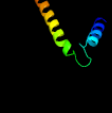

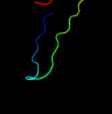


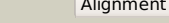

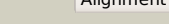
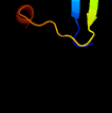
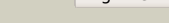
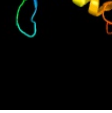
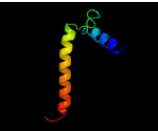

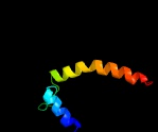

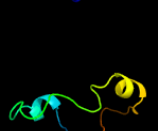
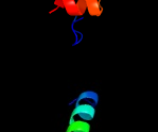





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1025_(-)_1146565_1147032
Date	Wed Jul 31 22:05:09 BST 2019
Unique Job ID	405850c9e17402cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2gnoa1</a>	 Alignment		52.8	17	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
2	<a href="#">c4is4G_</a>	 Alignment		42.0	22	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
3	<a href="#">c5z58w_</a>	 Alignment		37.1	31	<b>PDB header:</b> splicing <b>Chain:</b> W: <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
4	<a href="#">c6g90T_</a>	 Alignment		35.3	23	<b>PDB header:</b> splicing <b>Chain:</b> T: <b>PDB Molecule:</b> pre-mrna-splicing factor prp9; <b>PDBTitle:</b> prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
5	<a href="#">c2kz3A_</a>	 Alignment		33.3	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rad51l3; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
6	<a href="#">c3tgnA_</a>	 Alignment		25.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
7	<a href="#">d1biha2</a>	 Alignment		20.4	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
8	<a href="#">d2ouwa1</a>	 Alignment		18.2	20	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> TTHA0727-like
9	<a href="#">c2e5eA_</a>	 Alignment		17.3	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> advanced glycosylation end product-specific <b>PDBTitle:</b> solution structure of variable-type domain of human2 receptor for advanced glycation endproducts
10	<a href="#">c2r85B_</a>	 Alignment		15.5	26	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> purp protein pf1517; <b>PDBTitle:</b> crystal structure of purp from pyrococcus furiosus complexed with amp
11	<a href="#">c1vw4L_</a>	 Alignment		15.0	26	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 54s ribosomal protein l8, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit

12	<a href="#">c5hsmA</a>	Alignment		14.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv2887; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis marr family protein2 rv2887
13	<a href="#">c5b42A</a>	Alignment		13.7	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna mismatch repair protein mutl; <b>PDBTitle:</b> crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
14	<a href="#">c4fx0A</a>	Alignment		13.3	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> probable transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of m. tuberculosis transcriptional regulator mosr
15	<a href="#">c5yhxB</a>	Alignment		12.6	10	<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 zitri, wild type
16	<a href="#">c5iooA</a>	Alignment		12.3	32	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> avpa; <b>PDBTitle:</b> accommodation of massive sequence variation in nanoarchaeota by the c-2 type lectin fold
17	<a href="#">c2wx4C</a>	Alignment		11.9	22	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> decapping protein 1; <b>PDBTitle:</b> asymmetric trimer of the drosophila melanogaster dcp1 c-2 terminal domain
18	<a href="#">c2nplX</a>	Alignment		11.6	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> X; <b>PDB Molecule:</b> cox sackievirus and adenovirus receptor; <b>PDBTitle:</b> nmr structure of card d2 domain
19	<a href="#">c2odaB</a>	Alignment		11.6	24	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein pspto_2114; <b>PDBTitle:</b> crystal structure of pspto_2114
20	<a href="#">c5oa30</a>	Alignment		10.3	30	<b>PDB header:</b> translation <b>Chain:</b> 0; <b>PDB Molecule:</b> eukaryotic translation initiation factor 2d; <b>PDBTitle:</b> human 40s-eif2d-re-initiation complex
21	<a href="#">d1biha3</a>	Alignment	not modelled	10.0	13	<b>Fold:</b> immunoglobulin-like beta-sandwich <b>Superfamily:</b> immunoglobulin <b>Family:</b> ! set domains
22	<a href="#">c4l22A</a>	Alignment	not modelled	9.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphorylase; <b>PDBTitle:</b> crystal structure of putative glycogen phosphorylase from2 streptococcus mutans
23	<a href="#">c3qajL</a>	Alignment	not modelled	9.3	22	<b>PDB header:</b> ligase <b>Chain:</b> L; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
24	<a href="#">c5xr2D</a>	Alignment	not modelled	9.2	21	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> protein/nucleic acid deglycase hcha; <b>PDBTitle:</b> sav0551
25	<a href="#">c2d3aj</a>	Alignment	not modelled	9.1	26	<b>PDB header:</b> ligase <b>Chain:</b> J; <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
26	<a href="#">c3kp3B</a>	Alignment	not modelled	9.1	4	<b>PDB header:</b> transcription regulator/antibiotic <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator tcar; <b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin
27	<a href="#">c2l4aA</a>	Alignment	not modelled	9.0	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
28	<a href="#">c3kblA</a>	Alignment	not modelled	9.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> female germline-specific tumor suppressor gld-1; <b>PDBTitle:</b> crystal structure of the gld-1 homodimerization domain from2 caenorhabditis elegans n169a mutant at 2.28 a resolution
29	<a href="#">c1a7hA</a>	Alignment	not modelled	8.7	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein;

29	<a href="#">c1q7nA</a>	Alignment	not modelled	8.7	20	<b>PDBTitle:</b> structure of a conserved pua domain protein from thermoplasma2 acidophilum
30	<a href="#">c5u07B</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cse2; <b>PDBTitle:</b> crispr rna-guided surveillance complex
31	<a href="#">d2q79a1</a>	Alignment	not modelled	8.6	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
32	<a href="#">c3kkaD</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> co-crystal structure of the sam domains of epha1 and epha2
33	<a href="#">d1a7ge</a>	Alignment	not modelled	8.3	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
34	<a href="#">d2bopa</a>	Alignment	not modelled	8.2	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
35	<a href="#">d1civa2</a>	Alignment	not modelled	8.2	12	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
36	<a href="#">c2mpeA</a>	Alignment	not modelled	8.1	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bpsl1050; <b>PDBTitle:</b> solution nmr structure for b. pseudomallei bpsl1050
37	<a href="#">d1wwca</a>	Alignment	not modelled	8.0	27	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
38	<a href="#">c1zs7A</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ape0525; <b>PDBTitle:</b> the structure of gene product ape0525 from aeropyrum pernix
39	<a href="#">d1f9fa</a>	Alignment	not modelled	7.9	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
40	<a href="#">c3beyC</a>	Alignment	not modelled	7.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> conserved protein o27018; <b>PDBTitle:</b> crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
41	<a href="#">c3ddsB</a>	Alignment	not modelled	7.7	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen phosphorylase, liver form; <b>PDBTitle:</b> crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
42	<a href="#">c6m8sM</a>	Alignment	not modelled	7.6	29	<b>PDB header:</b> signaling protein <b>Chain:</b> M: <b>PDB Molecule:</b> btb/poz domain-containing protein kctd12; <b>PDBTitle:</b> crystal structure of the kctd12 h1 domain in complex with gbeta1gamma22 subunits
43	<a href="#">d1zxqa1</a>	Alignment	not modelled	7.5	27	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
44	<a href="#">c3boqB</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
45	<a href="#">d1dbda</a>	Alignment	not modelled	7.3	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
46	<a href="#">d1he7a</a>	Alignment	not modelled	7.2	35	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
47	<a href="#">d1r8ha</a>	Alignment	not modelled	7.2	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
48	<a href="#">c3j6vl</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 28s ribosomal protein s9, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
49	<a href="#">d1ku2a1</a>	Alignment	not modelled	7.0	40	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
50	<a href="#">c4yifE</a>	Alignment	not modelled	6.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> marr family protein rv0880; <b>PDBTitle:</b> crystal structure of rv0880
51	<a href="#">d2fbka1</a>	Alignment	not modelled	6.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
52	<a href="#">c4blgB</a>	Alignment	not modelled	6.6	39	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> latency-associated nuclear antigen; <b>PDBTitle:</b> crystal structure of mhv-68 latency-associated nuclear antigen (lana)2 c-terminal dna binding domain
53	<a href="#">c3g12A</a>	Alignment	not modelled	6.6	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
54	<a href="#">d2atia1</a>	Alignment	not modelled	6.6	9	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
55	<a href="#">c4zhaA</a>	Alignment	not modelled	6.6	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat-containing protein; <b>PDBTitle:</b> n-terminal structure of ankyrin repeat-containing protein lega11 from2 legionella pneumophila

56	<a href="#">d1l5wa_</a>	Alignment	not modelled	6.5	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
57	<a href="#">d1vk3a1</a>	Alignment	not modelled	6.5	42	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
58	<a href="#">c4hedA</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> zebrafish chemokine cx11
59	<a href="#">c3o4oC_</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> interleukin-1 receptor type 2; <b>PDBTitle:</b> crystal structure of an interleukin-1 receptor complex
60	<a href="#">c4zyaA_</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase, cytoplasmic; <b>PDBTitle:</b> the n-terminal extension domain of human asparaginyl-trna synthetase
61	<a href="#">c4hblA_</a>	Alignment	not modelled	6.3	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of abfr of staphylococcus epidermidis
62	<a href="#">d2nxyb2</a>	Alignment	not modelled	6.3	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
63	<a href="#">c4b8xB_</a>	Alignment	not modelled	6.2	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible marr-transcriptional regulator; <b>PDBTitle:</b> near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
64	<a href="#">d1iray1</a>	Alignment	not modelled	6.2	24	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
65	<a href="#">c2lsmA_</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dna-packaging protein fi; <b>PDBTitle:</b> solution structure of gpfi c-terminal domain
66	<a href="#">d1t3ta1</a>	Alignment	not modelled	6.1	40	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> FGAM synthase PurL, linker domain <b>Family:</b> FGAM synthase PurL, linker domain
67	<a href="#">c4lqqB_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> transferase/transferase activator <b>Chain:</b> B: <b>PDB Molecule:</b> cbk1 kinase activator protein mob2; <b>PDBTitle:</b> crystal structure of the cbk1(t743e)-mob2 kinase-coactivator complex2 in crystal form b
68	<a href="#">d2ctxa_</a>	Alignment	not modelled	6.1	35	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Snake venom toxins
69	<a href="#">d1tnna_</a>	Alignment	not modelled	6.0	35	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
70	<a href="#">c2konA_</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
71	<a href="#">d2frha1</a>	Alignment	not modelled	5.9	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
72	<a href="#">c5zc2B_</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
73	<a href="#">d1zymA1</a>	Alignment	not modelled	5.7	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain <b>Family:</b> Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
74	<a href="#">c1ag7A_</a>	Alignment	not modelled	5.5	35	<b>PDB header:</b> neurotoxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin gs; <b>PDBTitle:</b> conotoxin gs, nmr, 20 structures
75	<a href="#">d1ag7a_</a>	Alignment	not modelled	5.5	35	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Conotoxin
76	<a href="#">c2nziA_</a>	Alignment	not modelled	5.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> titin; <b>PDBTitle:</b> crystal structure of domains a168-a170 from titin
77	<a href="#">c3hiuB_</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of protein (xcc3681) from xanthomonas2 campestris pv. campestris str. atcc 33913
78	<a href="#">d3deua1</a>	Alignment	not modelled	5.3	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
79	<a href="#">c5aiqD_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of ligand-free nadr
80	<a href="#">c3of6D_</a>	Alignment	not modelled	5.1	86	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> pre t-cell antigen receptor alpha; <b>PDBTitle:</b> human pre-t cell receptor crystal structure
81	<a href="#">d2fxaa1</a>	Alignment	not modelled	5.1	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
82	<a href="#">c3q3uA_</a>	Alignment	not modelled	5.1	71	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lignin peroxidase;

					<b>PDBTitle:</b> trametes cervina lignin peroxidase
83	<a href="#">c2akfC_</a>	Alignment	not modelled	5.1	31 <b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
84	<a href="#">c2akfA_</a>	Alignment	not modelled	5.1	31 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
85	<a href="#">d2cfxa1</a>	Alignment	not modelled	5.1	30 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
86	<a href="#">c3mtrA_</a>	Alignment	not modelled	5.0	17 <b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> neural cell adhesion molecule 1; <b>PDBTitle:</b> crystal structure of the ig5-fn1 tandem of human ncam
87	<a href="#">c5z08D_</a>	Alignment	not modelled	5.0	27 <b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cenp-h; <b>PDBTitle:</b> the crystal structure of kinetochore subunits cenp-h/i/k triple2 complex