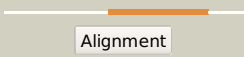
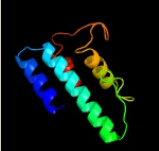
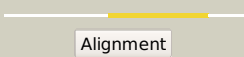

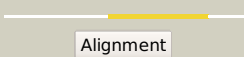

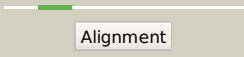
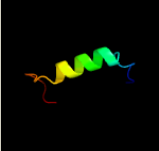
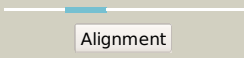
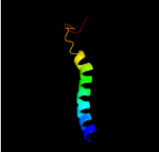
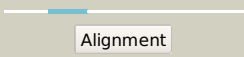
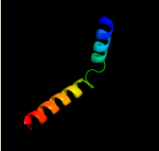
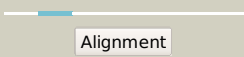
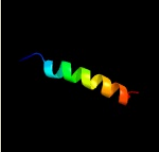
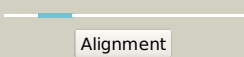
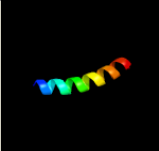
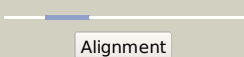
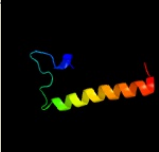
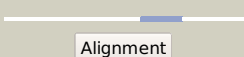
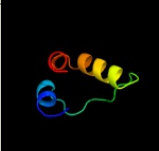

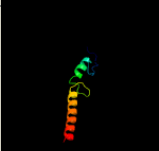

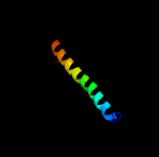

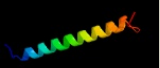


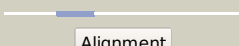

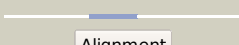

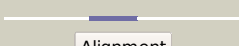

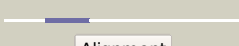




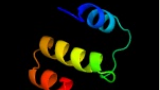




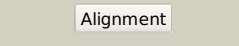

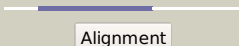



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3690_(-)_4131917_4132570
Date	Fri Aug 9 18:20:38 BST 2019
Unique Job ID	ce37844df49a1a60

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1wo1A_</a>	 Alignment		87.7	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 122aa long conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of st0689, an archaeal hepn homologue
2	<a href="#">c2hsbA_</a>	 Alignment		77.4	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0332 protein af0298; <b>PDBTitle:</b> crystal structure of a hepn domain containing protein (af_0298) from <i>Archaeoglobus fulgidus</i> at 1.95 Å resolution
3	<a href="#">d1ufba_</a>	 Alignment		71.8	19	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nucleotidyltransferase substrate binding subunit/domain <b>Family:</b> HEPN domain
4	<a href="#">d2b7oa1</a>	 Alignment		55.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class-II DAHP synthetase
5	<a href="#">c2kncA_</a>	 Alignment		35.7	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
6	<a href="#">c5v2sA_</a>	 Alignment		32.8	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type 1
7	<a href="#">c1r7gA_</a>	 Alignment		30.5	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> nmr structure of the membrane anchor domain (1-31) of the 2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
8	<a href="#">c1r7cA_</a>	 Alignment		30.5	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> nmr structure of the membrane anchor domain (1-31) of the 2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 50% tfe)
9	<a href="#">c5n9yB_</a>	 Alignment		29.0	9	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
10	<a href="#">c1v8cA_</a>	 Alignment		28.5	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> moad related protein; <b>PDBTitle:</b> crystal structure of moad related protein from <i>Thermophilus hb8</i>
11	<a href="#">c3j0cG_</a>	 Alignment		22.6	24	<b>PDB header:</b> virus <b>Chain:</b> G: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map

12	<a href="#">c2ks1A_</a>	 Alignment		21.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbB1 and erbB2 receptors enabling kinase activation
13	<a href="#">c2jwaA_</a>	 Alignment		21.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> erbB2 transmembrane segment dimer spatial structure
14	<a href="#">c5kwpA_</a>	 Alignment		21.0	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> designed peptide nc_eeh_d2; <b>PDBTitle:</b> nmr solution structure of designed peptide nc_eeh_d2
15	<a href="#">c2k1aA_</a>	 Alignment		20.4	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiB) transmembrane segment
16	<a href="#">c5a5tC_</a>	 Alignment		20.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit c; <b>PDBTitle:</b> structure of mammalian eIF3 in the context of the 43S preinitiation2 complex
17	<a href="#">c4u1cC_</a>	 Alignment		19.6	17	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit c; <b>PDBTitle:</b> crystal structure of the eIF3a/eIF3c PCI-domain heterodimer
18	<a href="#">c4ev6E_</a>	 Alignment		17.1	9	<b>PDB header:</b> metal transport <b>Chain:</b> E; <b>PDB Molecule:</b> magnesium transport protein Cora; <b>PDBTitle:</b> the complete structure of Cora magnesium transporter from <i>Methanocaldococcus jannaschii</i>
19	<a href="#">c3j7jC_</a>	 Alignment		17.0	15	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit c; <b>PDBTitle:</b> model of the human eIF3 PCI-MPN octamer docked into the 43S-hCV IRES2 EM map
20	<a href="#">c3j8bC_</a>	 Alignment		17.0	15	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit c; <b>PDBTitle:</b> model of the human eIF3 PCI-MPN octamer docked into the 43S-hCV IRES2 EM map
21	<a href="#">c3j8cC_</a>	 Alignment	not modelled	17.0	15	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit c; <b>PDBTitle:</b> model of the human eIF3 PCI-MPN octamer docked into the 43S EM map
22	<a href="#">c3j7kC_</a>	 Alignment	not modelled	17.0	15	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit c; <b>PDBTitle:</b> model of the human eIF3 PCI-MPN octamer docked into the 43S EM map
23	<a href="#">c2l8sA_</a>	 Alignment	not modelled	15.9	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution NMR structure of transmembrane and cytosolic regions of $\alpha$ 1 integrin in detergent micelles
24	<a href="#">c3dpiA_</a>	 Alignment	not modelled	13.3	13	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> Na <sup>+</sup> synthetase; <b>PDBTitle:</b> crystal structure of Na <sup>+</sup> synthetase from <i>Burkholderia pseudomallei</i>
25	<a href="#">c3o10D_</a>	 Alignment	not modelled	13.1	13	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> sacsin; <b>PDBTitle:</b> crystal structure of the HEPN domain from human sacsin
26	<a href="#">d1wpga4</a>	 Alignment	not modelled	12.2	13	<b>Fold:</b> Calcium ATPase, transmembrane domain M <b>Superfamily:</b> Calcium ATPase, transmembrane domain M <b>Family:</b> Calcium ATPase, transmembrane domain M
27	<a href="#">c2fvzC_</a>	 Alignment	not modelled	11.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> putative arsenical resistance protein; <b>PDBTitle:</b> crystal structure of an apo form of a flavin-binding protein from <i>Shigella flexneri</i>
28	<a href="#">c3mk7F_</a>	 Alignment	not modelled	11.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p;

						<b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase <b>PDB header:</b> membrane protein
29	<a href="#">c2n2aA_</a>	Alignment	not modelled	10.2	15	<b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> spatial structure of her2/erbB2 dimeric transmembrane domain in the presence of cytoplasmic juxtamembrane domains
30	<a href="#">c6mctH_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> H: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
31	<a href="#">c6mctO_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> O: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
32	<a href="#">c6mctC_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
33	<a href="#">c6mctJ_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
34	<a href="#">c6mctI_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
35	<a href="#">c6mctE_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
36	<a href="#">c6mctD_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
37	<a href="#">c6mctG_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
38	<a href="#">c6mctM_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> M: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
39	<a href="#">c6mctB_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
40	<a href="#">c6mctN_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> N: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
41	<a href="#">c6mctA_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
42	<a href="#">c6mctL_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> L: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
43	<a href="#">c6mctF_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
44	<a href="#">c6mq2D_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
45	<a href="#">c6mpwA_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
46	<a href="#">c6mctK_</a>	Alignment	not modelled	10.0	5	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
47	<a href="#">c2v1sD_</a>	Alignment	not modelled	9.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial import receptor subunit tom20 homolog; <b>PDBTitle:</b> crystal structure of rat tom20-aldh presequence complex
48	<a href="#">d1om2a_</a>	Alignment	not modelled	9.8	24	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Mitochondrial import receptor subunit Tom20 <b>Family:</b> Mitochondrial import receptor subunit Tom20
49	<a href="#">c6mq2E_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
50	<a href="#">c6mpwE_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
51	<a href="#">c6mq2A_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
52	<a href="#">c6mpwB_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
53	<a href="#">c6mq2C_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
54	<a href="#">c6mpwC_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein;

54	<a href="#">c6mpwC_</a>	Alignment	not modelled	9.0	5	<b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1 <b>PDB header:</b> de novo protein
55	<a href="#">c6mq2B_</a>	Alignment	not modelled	9.6	5	<b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
56	<a href="#">c6mpwD_</a>	Alignment	not modelled	9.6	5	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
57	<a href="#">d1o3ua_</a>	Alignment	not modelled	9.2	11	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nucleotidyltransferase substrate binding subunit/domain <b>Family:</b> HEPN domain
58	<a href="#">c5t42A_</a>	Alignment	not modelled	9.2	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
59	<a href="#">c2axtH_</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> electron transport <b>Chain:</b> H: <b>PDB Molecule:</b> photosystem ii reaction center h protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
60	<a href="#">d2axth1</a>	Alignment	not modelled	9.0	15	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II 10 kDa phosphoprotein PsbH <b>Family:</b> PsbH-like
61	<a href="#">c3urzB_</a>	Alignment	not modelled	8.4	10	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative protein binding protein (bacova_03105)2 from bacteroides ovatus atcc 8483 at 2.19 a resolution
62	<a href="#">c5fshA_</a>	Alignment	not modelled	8.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> csm6; <b>PDBTitle:</b> crystal structure of thermus thermophilus csm6
63	<a href="#">c4nqfB_</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of hepn domain protein
64	<a href="#">c6nk6B_</a>	Alignment	not modelled	7.9	20	<b>PDB header:</b> virus like particle/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> e1 glycoprotein; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya vlp in complex with mouse2 mxra8 receptor
65	<a href="#">c3q4gA_</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad synthetase from vibrio cholerae
66	<a href="#">c1zzaA_</a>	Alignment	not modelled	7.5	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin
67	<a href="#">c3u7rB_</a>	Alignment	not modelled	7.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-dependent fmn reductase; <b>PDBTitle:</b> ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
68	<a href="#">c4rvqA_</a>	Alignment	not modelled	7.2	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna splicing helicase-like protein; <b>PDBTitle:</b> pwi-like domain of chaetomium thermophilum brr2
69	<a href="#">d2f23a1</a>	Alignment	not modelled	7.0	15	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain <b>Family:</b> GreA transcript cleavage protein, N-terminal domain
70	<a href="#">c2xzeA_</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> hydrolase/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> stam-binding protein; <b>PDBTitle:</b> structural basis for amsh-escrt-iii chmp3 interaction
71	<a href="#">c3hy5A_</a>	Alignment	not modelled	6.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> retinaldehyde-binding protein 1; <b>PDBTitle:</b> crystal structure of cralbp
72	<a href="#">c4eu4A_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa:acetate coenzyme a transferase; <b>PDBTitle:</b> succinyl-coa: acetate coa-transferase (aarch6) in complex with coa2 (hexagonal lattice)
73	<a href="#">c4jhjD_</a>	Alignment	not modelled	6.5	71	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> dead/h (asp-glu-ala-asp/his) box polypeptide 19 (dbp5) <b>PDBTitle:</b> crystal structure of danio rerio slip1 in complex with dbp5
74	<a href="#">c4jhjC_</a>	Alignment	not modelled	6.5	71	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> dead/h (asp-glu-ala-asp/his) box polypeptide 19 (dbp5) <b>PDBTitle:</b> crystal structure of danio rerio slip1 in complex with dbp5
75	<a href="#">c2nvvF_</a>	Alignment	not modelled	6.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> acetyl-coa hydrolase/transferase family protein; <b>PDBTitle:</b> crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
76	<a href="#">c2vviA_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sgta protein; <b>PDBTitle:</b> crystal structure of the tpr domain of human sgt
77	<a href="#">c1p58F_</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
78	<a href="#">c1p58E_</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
79	<a href="#">d1rka2</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain

80	<a href="#">c3q49B_</a>	Alignment	not modelled	6.2	10	<b>PDB header:</b> ligase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> stip1 homology and u box-containing protein 1; <b>PDBTitle:</b> crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
81	<a href="#">c6mx4J_</a>	Alignment	not modelled	6.0	25	<b>PDB header:</b> virus <b>Chain:</b> J: <b>PDB Molecule:</b> e1; <b>PDBTitle:</b> cryoem structure of chimeric eastern equine encephalitis virus
82	<a href="#">c2I05A_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase b-raf; <b>PDBTitle:</b> solution nmr structure of the ras-binding domain of serine/threonine-2 protein kinase b-raf from homo sapiens, northeast structural genomics3 consortium target hr4694f
83	<a href="#">d1ecma_</a>	Alignment	not modelled	5.8	28	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> Dimeric chorismate mutase
84	<a href="#">c6agfB_</a>	Alignment	not modelled	5.8	2	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium channel subunit beta-1; <b>PDBTitle:</b> structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
85	<a href="#">c5hujB_</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nade from streptococcus pyogenes
86	<a href="#">c5yxiA_</a>	Alignment	not modelled	5.3	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> drafx6; <b>PDBTitle:</b> designed protein drafx6
87	<a href="#">c2q00B_</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> orf c02003 protein; <b>PDBTitle:</b> crystal structure of the p95883_sulso protein from sulfolobus2 solfataricus. nesg target ssr10.
88	<a href="#">d1xrsa_</a>	Alignment	not modelled	5.2	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