

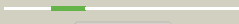
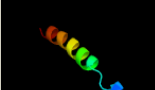

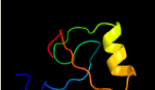







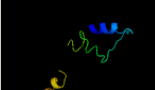

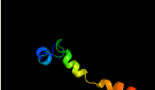

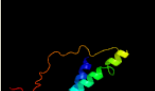







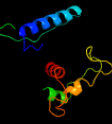

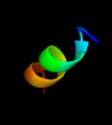

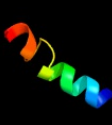
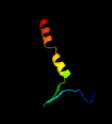


# Phyre2

Email	rachel.harding@utoronto.ca
Description	1201-2400
Date	Wed Mar 2 01:08:01 GMT 2016
Unique Job ID	Ocb1eb4777305840

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3n7nE_</a>	 Alignment		53.3	44	<b>PDB header:</b> replication <b>Chain:</b> E; <b>PDB Molecule:</b> monopolin complex subunit Irs4; <b>PDBTitle:</b> structure of csm1/Irs4 complex
2	<a href="#">c3n7nF_</a>	 Alignment		50.2	44	<b>PDB header:</b> replication <b>Chain:</b> F; <b>PDB Molecule:</b> monopolin complex subunit Irs4; <b>PDBTitle:</b> structure of csm1/Irs4 complex
3	<a href="#">c3na7A_</a>	 Alignment		43.6	14	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> hp0958; <b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
4	<a href="#">c3v6aA_</a>	 Alignment		39.5	19	<b>PDB header:</b> apoptosis inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> apoptosis inhibitor 5; <b>PDBTitle:</b> helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules
5	<a href="#">c3mkrB_</a>	 Alignment		38.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> coatamer subunit alpha; <b>PDBTitle:</b> crystal structure of yeast alpha/epsilon-cop subcomplex of the cop12 vesicular coat
6	<a href="#">c1z56B_</a>	 Alignment		36.8	22	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> ligase interacting factor 1; <b>PDBTitle:</b> co-crystal structure of lif1p-lig4p
7	<a href="#">d1zkda1</a>	 Alignment		27.5	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> RPA4359-like
8	<a href="#">c2l81A_</a>	 Alignment		25.0	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> enhancer of filamentation 1; <b>PDBTitle:</b> solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
9	<a href="#">c2kiwA_</a>	 Alignment		23.0	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> int protein; <b>PDBTitle:</b> solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
10	<a href="#">c2lzfA_</a>	 Alignment		18.5	31	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ykzf; <b>PDBTitle:</b> structure of the biofilm matrix promoter abba from b. subtilis
11	<a href="#">d2fzpa1</a>	 Alignment		18.5	27	<b>Fold:</b> NRDP1 C-terminal domain-like <b>Superfamily:</b> NRDP1 C-terminal domain-like <b>Family:</b> USP8 interacting domain

12	<a href="#">c4cr2Z_</a>	Alignment		18.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn1; <b>PDBTitle:</b> deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
13	<a href="#">c2kj9A_</a>	Alignment		15.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
14	<a href="#">c3zqpB_</a>	Alignment		15.1	15	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> terminase small subunit; <b>PDBTitle:</b> crystal structure of the small terminase oligomerization2 domain from a spp1-like bacteriophage
15	<a href="#">c3n4qA_</a>	Alignment		14.2	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit ul89 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain, mn soaked
16	<a href="#">c3wofB_</a>	Alignment		13.8	56	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of p23-45 gp39 (6-132) bound to thermus thermophilus2 rna polymerase beta-flap domain
17	<a href="#">c3wodG_</a>	Alignment		13.8	45	<b>PDB header:</b> transferase/transcription <b>Chain:</b> G: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rna polymerase-gp39 complex
18	<a href="#">d2vrda1</a>	Alignment		12.6	67	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> HkH motif-containing C2H2 finger
19	<a href="#">c5af0B_</a>	Alignment		12.3	26	<b>PDB header:</b> unknown protein <b>Chain:</b> B: <b>PDB Molecule:</b> maelstrom; <b>PDBTitle:</b> mael domain from bombyx mori maelstrom
20	<a href="#">c1z23A_</a>	Alignment		12.1	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> crk-associated substrate; <b>PDBTitle:</b> the serine-rich domain from crk-associated substrate2 (p130cas)
21	<a href="#">c3zqoK_</a>	Alignment	not modelled	12.1	27	<b>PDB header:</b> dna-binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> terminase small subunit; <b>PDBTitle:</b> crystal structure of the small terminase oligomerization2 core domain from a spp1-like bacteriophage (crystal form 3)
22	<a href="#">d1wgnA_</a>	Alignment	not modelled	11.9	33	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
23	<a href="#">c3cw19_</a>	Alignment	not modelled	11.4	67	<b>PDB header:</b> splicing <b>Chain:</b> 9: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein c; <b>PDBTitle:</b> crystal structure of human spliceosomal u1 snrnp
24	<a href="#">c3lysC_</a>	Alignment	not modelled	11.3	7	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> prophage pi2 protein 01, integrase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
25	<a href="#">d1wjna_</a>	Alignment	not modelled	11.2	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
26	<a href="#">c4ybgA_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein maelstrom; <b>PDBTitle:</b> crystal structure of the mael domain of drosophila melanogaster2 maelstrom
27	<a href="#">c1vf6C_</a>	Alignment	not modelled	10.6	35	<b>PDB header:</b> protein binding/protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> maguk p55 subfamily member 5; <b>PDBTitle:</b> 2.1 angstrom crystal structure of the pals-1-l27n and patj2 l27 heterodimer complex
28	<a href="#">d1vf6c_</a>	Alignment	not modelled	10.6	35	<b>Fold:</b> L27 domain <b>Superfamily:</b> L27 domain <b>Family:</b> L27 domain

29	<a href="#">d2hw4a1</a>	Alignment	not modelled	10.6	33	<b>Fold:</b> PHP14-like <b>Superfamily:</b> PHP14-like <b>Family:</b> Janus/Ocnus
30	<a href="#">c2oxoA</a>	Alignment	not modelled	10.4	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
31	<a href="#">c2keyA</a>	Alignment	not modelled	10.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative phage integrase; <b>PDBTitle:</b> solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
32	<a href="#">dliapa</a>	Alignment	not modelled	10.3	36	<b>Fold:</b> Regulator of G-protein signaling, RGS <b>Superfamily:</b> Regulator of G-protein signaling, RGS <b>Family:</b> Regulator of G-protein signaling, RGS
33	<a href="#">c2km6A</a>	Alignment	not modelled	10.3	26	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> nacht, Irr and pyd domains-containing protein 7; <b>PDBTitle:</b> nmr structure of the nlrp7 pyrin domain
34	<a href="#">d1fo1a2</a>	Alignment	not modelled	10.2	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Non-canonical RBD domain
35	<a href="#">c2hw4A</a>	Alignment	not modelled	10.1	33	<b>PDB header:</b> structural genomics, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 14 kda phosphohistidine phosphatase; <b>PDBTitle:</b> crystal structure of human phosphohistidine phosphatase
36	<a href="#">d1g8fa3</a>	Alignment	not modelled	10.1	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ATP sulfurylase C-terminal domain
37	<a href="#">d1u6ra1</a>	Alignment	not modelled	10.1	13	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
38	<a href="#">c1htfF</a>	Alignment	not modelled	10.1	27	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> kiaa0380; <b>PDBTitle:</b> structure of the rgs-like domain from pdz-rhogeF
39	<a href="#">d1htfj</a>	Alignment	not modelled	10.1	27	<b>Fold:</b> Regulator of G-protein signaling, RGS <b>Superfamily:</b> Regulator of G-protein signaling, RGS <b>Family:</b> Regulator of G-protein signaling, RGS
40	<a href="#">d1rqga1</a>	Alignment	not modelled	10.0	6	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
41	<a href="#">d1vrpa1</a>	Alignment	not modelled	10.0	14	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
42	<a href="#">d1mwpa</a>	Alignment	not modelled	10.0	40	<b>Fold:</b> SRCR-like <b>Superfamily:</b> A heparin-binding domain <b>Family:</b> A heparin-binding domain
43	<a href="#">d1upka</a>	Alignment	not modelled	9.7	22	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> Mo25 protein
44	<a href="#">c1u9fA</a>	Alignment	not modelled	9.7	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15)(16)
45	<a href="#">d1i0ea1</a>	Alignment	not modelled	9.5	11	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
46	<a href="#">c3tekA</a>	Alignment	not modelled	9.5	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> thermodbp-single stranded dna binding protein; <b>PDBTitle:</b> thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
47	<a href="#">c4nfuA</a>	Alignment	not modelled	9.4	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> eds1; <b>PDBTitle:</b> structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
48	<a href="#">d1crka1</a>	Alignment	not modelled	9.4	18	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
49	<a href="#">c2e2zA</a>	Alignment	not modelled	9.4	17	<b>PDB header:</b> protein transport, chaperone regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tim15; <b>PDBTitle:</b> solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
50	<a href="#">c2rp4C</a>	Alignment	not modelled	9.4	26	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcription factor p53; <b>PDBTitle:</b> solution structure of the oligomerization domain in dmp53
51	<a href="#">d1qk1a1</a>	Alignment	not modelled	9.2	13	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
52	<a href="#">c1u9fB</a>	Alignment	not modelled	9.1	50	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15)(16)
53	<a href="#">c1u9fC</a>	Alignment	not modelled	9.1	50	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15)(16)
54	<a href="#">c1u9fD</a>	Alignment	not modelled	9.0	50	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15)(16)

55	<a href="#">c5bvlA_</a>	Alignment	not modelled	9.0	47	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed tim barrel stim11; <b>PDBTitle:</b> crystal structure of a de novo designed tim-barrel
56	<a href="#">c2kj8A_</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative prophage cps-53 integrase; <b>PDBTitle:</b> nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
57	<a href="#">c3cueJ_</a>	Alignment	not modelled	9.0	16	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> transport protein particle 22 kda subunit; <b>PDBTitle:</b> crystal structure of a trapp subassembly activating the rab ypt1p
58	<a href="#">c3zqnD_</a>	Alignment	not modelled	8.9	27	<b>PDB header:</b> dna-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> terminase small subunit; <b>PDBTitle:</b> crystal structure of the small terminase oligomerization2 core domain from a spp1-like bacteriophage (crystal form 2)
59	<a href="#">d1sxd1</a>	Alignment	not modelled	8.9	25	<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
60	<a href="#">c4dnnB_</a>	Alignment	not modelled	8.7	33	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> protein quaking; <b>PDBTitle:</b> crystal structure of the quaking qua1 homodimerization domain
61	<a href="#">c4v1an_</a>	Alignment	not modelled	8.6	29	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian2 mitochondrial ribosome, part 2 of 2
62	<a href="#">c3o0rC_</a>	Alignment	not modelled	8.6	38	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide reductase subunit c; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
63	<a href="#">c1shzF_</a>	Alignment	not modelled	8.6	36	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> rho guanine nucleotide exchange factor 1; <b>PDBTitle:</b> crystal structure of the p115rhogef rrgs domain in a2 complex with galpha(13):galpha(i1) chimera
64	<a href="#">c2kb2A_</a>	Alignment	not modelled	8.3	15	<b>PDB header:</b> signaling protein, hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> blrp1; <b>PDBTitle:</b> blrp1 bluf
65	<a href="#">c3ktmB_</a>	Alignment	not modelled	8.2	40	<b>PDB header:</b> cell adhesion, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> structure of the heparin-induced e1-dimer of the amyloid precursor2 protein (app)
66	<a href="#">c3ztaA_</a>	Alignment	not modelled	8.1	35	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-factor antagonist (stas) domain protein; <b>PDBTitle:</b> the bacterial stressosome: a modular system that has been adapted to2 control secondary messenger signaling
67	<a href="#">c2a2fX_</a>	Alignment	not modelled	8.1	18	<b>PDB header:</b> protein transport <b>Chain:</b> X: <b>PDB Molecule:</b> exocyst complex component sec15; <b>PDBTitle:</b> crystal structure of sec15 c-terminal domain
68	<a href="#">c5a1vV_</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> transport protein <b>Chain:</b> V: <b>PDB Molecule:</b> coatomer subunit gamma-1; <b>PDBTitle:</b> the structure of the copi coat linkage i
69	<a href="#">c4hv0B_</a>	Alignment	not modelled	8.0	28	<b>PDB header:</b> transcription, viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> avtr; <b>PDBTitle:</b> structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
70	<a href="#">c1x4qA_</a>	Alignment	not modelled	7.9	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
71	<a href="#">d1g0wa1</a>	Alignment	not modelled	7.8	14	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
72	<a href="#">c4p55A_</a>	Alignment	not modelled	7.8	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> viral irf2-like protein; <b>PDBTitle:</b> crystal structure of dna binding domain of k11 from kshv
73	<a href="#">c2r17C_</a>	Alignment	not modelled	7.8	14	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 35; <b>PDBTitle:</b> functional architecture of the retromer cargo-recognition complex
74	<a href="#">c4dwlA_</a>	Alignment	not modelled	7.8	28	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bbp7; <b>PDBTitle:</b> avd molecule from bordetella bacteriophage dgr
75	<a href="#">c1xc0A_</a>	Alignment	not modelled	7.7	83	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> pardaxin p-4; <b>PDBTitle:</b> twenty lowest energy structures of pa4 by solution nmr
76	<a href="#">c4xvvB_</a>	Alignment	not modelled	7.7	32	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> acid stress chaperone hdeb; <b>PDBTitle:</b> crystal structure of an acid stress chaperone hdeb (kpn_03484) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a3 resolution
77	<a href="#">c3odrA_</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> symplekin; <b>PDBTitle:</b> crystal structure of the n-terminal domain of human symplekin
78	<a href="#">d1ug7a_</a>	Alignment	not modelled	7.5	20	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain from hypothetical 2610208m17rik protein <b>Family:</b> Domain from hypothetical 2610208m17rik protein
79	<a href="#">d1eg3a2</a>	Alignment	not modelled	7.5	13	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
						<b>PDB header:</b> de novo protein

80	<a href="#">c2ag3A</a>	Alignment	not modelled	7.4	55	<b>Chain:</b> A: <b>PDB Molecule:</b> gcn4-pli; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: substitution of the k(15)-(16) amide with a triazole
81	<a href="#">c2b5dX</a>	Alignment	not modelled	7.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
82	<a href="#">c3rqsB</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxyacyl-coenzyme a dehydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership
83	<a href="#">c3n4pA</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit ul89 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain
84	<a href="#">c1avoD</a>	Alignment	not modelled	7.2	24	<b>PDB header:</b> proteasome activator <b>Chain:</b> D: <b>PDB Molecule:</b> 11s regulator; <b>PDBTitle:</b> proteasome activator reg(alpha)
85	<a href="#">d1lpba1</a>	Alignment	not modelled	7.1	36	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Colipase-like <b>Family:</b> Colipase-like
86	<a href="#">d1j36a</a>	Alignment	not modelled	7.1	14	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Neurolysin-like
87	<a href="#">c2agaA</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> machado-joseph disease protein 1; <b>PDBTitle:</b> de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
88	<a href="#">d1ik0a</a>	Alignment	not modelled	7.0	21	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
89	<a href="#">d1rw2a</a>	Alignment	not modelled	7.0	16	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> C-terminal domain of Ku80 <b>Family:</b> C-terminal domain of Ku80
90	<a href="#">c3a1bA</a>	Alignment	not modelled	6.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 3a, histone h3.1; <b>PDBTitle:</b> crystal structure of the dnmt3a add domain in complex with histone h3
91	<a href="#">c4lkuE</a>	Alignment	not modelled	6.9	27	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
92	<a href="#">c4lkuC</a>	Alignment	not modelled	6.9	27	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
93	<a href="#">c4lkuD</a>	Alignment	not modelled	6.9	27	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
94	<a href="#">c4dx8H</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> krev interaction trapped protein 1; <b>PDBTitle:</b> icap1 in complex with krit1 n-terminus
95	<a href="#">c2fv2A</a>	Alignment	not modelled	6.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rcd1 required for cell differentiation1 homolog; <b>PDBTitle:</b> crystal structure analysis of human rcd-1 conserved region
96	<a href="#">c2m5vA</a>	Alignment	not modelled	6.9	16	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> nacht, lrr and pyd domains-containing protein 10; <b>PDBTitle:</b> three-dimensional structure of human nlrp10/pynod pyrin domain
97	<a href="#">c1wsoA</a>	Alignment	not modelled	6.8	22	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> orexin-a; <b>PDBTitle:</b> the solution structures of human orexin-a
98	<a href="#">c1o1nA</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> A: <b>PDB Molecule:</b> hemoglobin alpha chain; <b>PDBTitle:</b> deoxy hemoglobin (a-glyglygly-c:v1m,l29w; b,d:v1m)
99	<a href="#">d1jmsa1</a>	Alignment	not modelled	6.8	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like