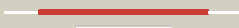


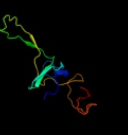

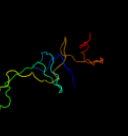
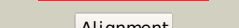
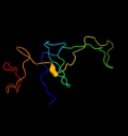
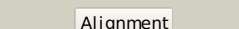







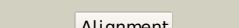

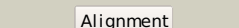

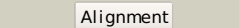



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2gycs1</a>	 Alignment		100.0	100	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
2	<a href="#">d2zjrr1</a>	 Alignment		100.0	43	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
3	<a href="#">c3bboW_</a>	 Alignment		100.0	34	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> ribosomal protein l24; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
4	<a href="#">d2j01y1</a>	 Alignment		100.0	43	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
5	<a href="#">c2ftcN_</a>	 Alignment		100.0	30	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> mitochondrial ribosomal protein l24; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
6	<a href="#">c3iz5Y_</a>	 Alignment		99.9	28	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l26 (l24p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
7	<a href="#">dlvqot1</a>	 Alignment		99.9	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
8	<a href="#">c4a1cS_</a>	 Alignment		99.9	32	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> rpl26; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
9	<a href="#">c1s1iU_</a>	 Alignment		99.8	29	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l26-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
10	<a href="#">c2zkrt_</a>	 Alignment		99.2	33	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> T: <b>PDB Molecule:</b> rna expansion segment es39 part iii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
11	<a href="#">c2kvqG_</a>	 Alignment		96.2	19	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of nuse:nusg-ctd complex

12	<a href="#">c2jvvA_</a>	Alignment		96.2	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of e. coli nusg carboxyterminal domain
13	<a href="#">d1npa2</a>	Alignment		96.0	25	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
14	<a href="#">c3p8bB_</a>	Alignment		95.7	28	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
15	<a href="#">d1nz9a_</a>	Alignment		95.5	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
16	<a href="#">d2joya1</a>	Alignment		95.3	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal protein L14e
17	<a href="#">d2do3a1</a>	Alignment		95.0	28	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
18	<a href="#">c2ckkA_</a>	Alignment		94.0	16	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> kin17; <b>PDBTitle:</b> high resolution crystal structure of the human kin172 c-terminal domain containing a kow motif3 kin17.
19	<a href="#">c2xhcA_</a>	Alignment		93.0	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
20	<a href="#">c1mlgB_</a>	Alignment		92.3	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
21	<a href="#">c4a19F_</a>	Alignment	not modelled	91.0	26	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> rpl14; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
22	<a href="#">c3izcN_</a>	Alignment	not modelled	90.7	23	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein rpl14 (l14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
23	<a href="#">c3iz5N_</a>	Alignment	not modelled	90.3	23	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein l14 (l14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
24	<a href="#">c3izcG_</a>	Alignment	not modelled	89.9	24	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein rpl6 (l16e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
25	<a href="#">c2e6zA_</a>	Alignment	not modelled	87.6	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the second kow motif of human2 transcription elongation factor spt5
26	<a href="#">c4a1dE_</a>	Alignment	not modelled	83.9	35	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> rpl6; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
27	<a href="#">c4a18N_</a>	Alignment	not modelled	82.2	30	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> rpl27; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
						<b>PDB header:</b> transcription

28	<a href="#">c2e70A_</a>	Alignment	not modelled	78.6	31	<b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the fifth kow motif of human2 transcription elongation factor spt5
29	<a href="#">c3iz5G_</a>	Alignment	not modelled	74.8	32	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l6 (l6e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
30	<a href="#">c2xzmW_</a>	Alignment	not modelled	56.5	16	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 40s ribosomal protein s4; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
31	<a href="#">c3kbgA_</a>	Alignment	not modelled	49.5	12	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s4e; <b>PDBTitle:</b> crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
32	<a href="#">c3iz6D_</a>	Alignment	not modelled	44.8	29	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein s4 (s4e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
33	<a href="#">d1vhka1</a>	Alignment	not modelled	43.3	18	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> YggJ N-terminal domain-like
34	<a href="#">c3izca_</a>	Alignment	not modelled	42.1	25	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 60s ribosomal protein rpl1 (l1p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
35	<a href="#">c4a1aP_</a>	Alignment	not modelled	35.8	32	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l21; <b>PDBTitle:</b> t thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
36	<a href="#">c3iz5a_</a>	Alignment	not modelled	35.4	28	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 60s ribosomal protein l1 (l1p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
37	<a href="#">d1nxza1</a>	Alignment	not modelled	30.1	15	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> YggJ N-terminal domain-like
38	<a href="#">c2dxcG_</a>	Alignment	not modelled	28.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> thiocyanate hydrolase subunit alpha; <b>PDBTitle:</b> recombinant thiocyanate hydrolase, fully-matured form
39	<a href="#">d1o12a1</a>	Alignment	not modelled	24.8	29	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA
40	<a href="#">c3k7aM_</a>	Alignment	not modelled	22.8	15	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor iib; <b>PDBTitle:</b> crystal structure of an rna polymerase ii-tfiib complex
41	<a href="#">d1ng2a2</a>	Alignment	not modelled	22.8	14	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
42	<a href="#">c2kmmA_</a>	Alignment	not modelled	20.7	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine-3',5'-bis(diphosphate) 3'- <b>PDBTitle:</b> solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
43	<a href="#">c3qz9D_</a>	Alignment	not modelled	20.3	33	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> co-type nitrile hydratase beta subunit; <b>PDBTitle:</b> crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
44	<a href="#">d1wlpb2</a>	Alignment	not modelled	20.1	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
45	<a href="#">c3izbD_</a>	Alignment	not modelled	19.3	23	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein rps4 (s4e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
46	<a href="#">c3gqhB_</a>	Alignment	not modelled	19.3	19	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> preneck appendage protein; <b>PDBTitle:</b> crystal structure of the bacteriophage phi29 gene product2 12 c-terminal fragment
47	<a href="#">d1pfta_</a>	Alignment	not modelled	18.9	14	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
48	<a href="#">d1tova_</a>	Alignment	not modelled	18.9	29	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
49	<a href="#">d1jb0e_</a>	Alignment	not modelled	18.7	23	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
50	<a href="#">d1dl6a_</a>	Alignment	not modelled	18.3	3	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
51	<a href="#">d1psea_</a>	Alignment	not modelled	18.0	36	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
52	<a href="#">c2k6dA_</a>	Alignment	not modelled	16.9	30	<b>PDB header:</b> sh3 domain/ubiquitin <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-containing kinase-binding protein 1; <b>PDBTitle:</b> cin85 sh3-c domain in complex with ubiquitin
						<b>Fold:</b> SH3-like barrel

53	<a href="#">dlugpb_</a>	Alignment	not modelled	16.7	30	<b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Nitrile hydratase beta chain
54	<a href="#">d1p7ba1</a>	Alignment	not modelled	15.1	26	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Cytoplasmic domain of inward rectifier potassium channel
55	<a href="#">d1qp3a_</a>	Alignment	not modelled	14.5	36	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
56	<a href="#">c3dclC_</a>	Alignment	not modelled	14.4	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> tm1086; <b>PDBTitle:</b> crystal structure of tm1086
57	<a href="#">d1k4us_</a>	Alignment	not modelled	14.4	35	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
58	<a href="#">c2ed0A_</a>	Alignment	not modelled	14.2	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> abl interactor 2; <b>PDBTitle:</b> solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2)
59	<a href="#">c2eyxA_</a>	Alignment	not modelled	13.6	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crk sarcoma virus ct10 oncogene homolog <b>PDBTitle:</b> c-terminal sh3 domain of ct10-regulated kinase
60	<a href="#">c2gb5B_</a>	Alignment	not modelled	13.5	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
61	<a href="#">d1v29b_</a>	Alignment	not modelled	13.3	11	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Nitrile hydratase beta chain
62	<a href="#">d2dk3a1</a>	Alignment	not modelled	12.8	38	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Mib/herc2 domain-like <b>Family:</b> Mib/herc2 domain
63	<a href="#">c2l0aA_</a>	Alignment	not modelled	12.4	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducing adapter molecule 1; <b>PDBTitle:</b> solution nmr structure of signal transducing adapter molecule 1 stam-12 from homo sapiens, northeast structural genomics consortium target3 hr4479e
64	<a href="#">d2cona1</a>	Alignment	not modelled	12.4	25	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> NOB1 zinc finger-like <b>Family:</b> NOB1 zinc finger-like
65	<a href="#">d2c78a1</a>	Alignment	not modelled	12.2	24	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
66	<a href="#">c2drnB_</a>	Alignment	not modelled	11.8	39	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> acanthamoeba myosin ib; <b>PDBTitle:</b> acanthamoeba myosin i sh3 domain bound to acan125
67	<a href="#">c2dnuA_</a>	Alignment	not modelled	11.8	22	<b>PDB header:</b> structural genomics, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 multiple domains 1; <b>PDBTitle:</b> solution structure of rsgi ruh-061, a sh3 domain from human
68	<a href="#">c2xzm1_</a>	Alignment	not modelled	11.8	31	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> ribosomal protein s28e containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
69	<a href="#">d1xl4a1</a>	Alignment	not modelled	11.7	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Cytoplasmic domain of inward rectifier potassium channel
70	<a href="#">d1ne3a_</a>	Alignment	not modelled	11.2	38	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
71	<a href="#">d1nlqa_</a>	Alignment	not modelled	11.1	9	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Nucleoplasmin-like core domain <b>Family:</b> Nucleoplasmin-like core domain
72	<a href="#">d1ppya_</a>	Alignment	not modelled	10.9	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Pyruvoyl dependent aspartate decarboxylase, ADC
73	<a href="#">d1ny4a_</a>	Alignment	not modelled	10.8	46	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
74	<a href="#">d1gria2</a>	Alignment	not modelled	10.8	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
75	<a href="#">d1ka5a_</a>	Alignment	not modelled	10.7	28	<b>Fold:</b> HPr-like <b>Superfamily:</b> HPr-like <b>Family:</b> HPr-like
76	<a href="#">c2csqA_</a>	Alignment	not modelled	10.7	14	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> rim binding protein 2; <b>PDBTitle:</b> solution structure of the second sh3 domain of human rim-2 binding protein 2
77	<a href="#">c1x2qA_</a>	Alignment	not modelled	10.6	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducing adapter molecule 2; <b>PDBTitle:</b> solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2
78	<a href="#">d2hpra_</a>	Alignment	not modelled	10.5	22	<b>Fold:</b> HPr-like <b>Superfamily:</b> HPr-like <b>Family:</b> HPr-like
79	<a href="#">c1wi7A_</a>	Alignment	not modelled	10.3	26	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sh3-domain kinase binding protein 1; <b>PDBTitle:</b> solution structure of the sh3 domain of sh3-domain

						kinase2 binding protein 1
80	<a href="#">c3t07D_</a>	Alignment	not modelled	10.3	19	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
81	<a href="#">c1u4fD_</a>	Alignment	not modelled	10.1	25	<b>PDB header:</b> allergen <b>Chain:</b> D: <b>PDB Molecule:</b> inward rectifier potassium channel 2; <b>PDBTitle:</b> crystal structure of cytoplasmic domains of irk1 (kir2.1)2 channel
82	<a href="#">d2b1ya1</a>	Alignment	not modelled	10.0	26	<b>Fold:</b> Atu1913-like <b>Superfamily:</b> Atu1913-like <b>Family:</b> Atu1913-like
83	<a href="#">c2bz8B_</a>	Alignment	not modelled	10.0	22	<b>PDB header:</b> sh3 domain <b>Chain:</b> B: <b>PDB Molecule:</b> sh3-domain kinase binding protein 1; <b>PDBTitle:</b> n-terminal sh3 domain of cin85 bound to cbl-b peptide
84	<a href="#">d1n9pa_</a>	Alignment	not modelled	9.8	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Cytoplasmic domain of inward rectifier potassium channel
85	<a href="#">d1mxaa2</a>	Alignment	not modelled	9.8	40	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
86	<a href="#">d1cm3a_</a>	Alignment	not modelled	9.7	17	<b>Fold:</b> HPr-like <b>Superfamily:</b> HPr-like <b>Family:</b> HPr-like
87	<a href="#">c3ihsB_</a>	Alignment	not modelled	9.6	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphocarrier protein hpr; <b>PDBTitle:</b> crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
88	<a href="#">d2nzul1</a>	Alignment	not modelled	9.5	22	<b>Fold:</b> HPr-like <b>Superfamily:</b> HPr-like <b>Family:</b> HPr-like
89	<a href="#">c3iz5U_</a>	Alignment	not modelled	9.5	31	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l21 (l21e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
90	<a href="#">c1wxba_</a>	Alignment	not modelled	9.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor pathway <b>PDBTitle:</b> solution structure of the sh3 domain from human epidermal2 growth factor receptor pathway substrate 8-like protein
91	<a href="#">c2zkrq_</a>	Alignment	not modelled	9.1	36	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Q: <b>PDB Molecule:</b> rna expansion segment es31 part ii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
92	<a href="#">d1uhfa_</a>	Alignment	not modelled	8.9	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
93	<a href="#">c2bzxA_</a>	Alignment	not modelled	8.8	22	<b>PDB header:</b> sh3 domain <b>Chain:</b> A: <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> atomic model of crkl-sh3c monomer
94	<a href="#">d1ug1a_</a>	Alignment	not modelled	8.8	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
95	<a href="#">c2djga_</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain containing ring finger 2; <b>PDBTitle:</b> the solution structure of the first sh3 domain of mouse sh32 domain containing ring finger 2
96	<a href="#">d1ptfa_</a>	Alignment	not modelled	8.7	22	<b>Fold:</b> HPr-like <b>Superfamily:</b> HPr-like <b>Family:</b> HPr-like
97	<a href="#">d1wlpb1</a>	Alignment	not modelled	8.6	13	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
98	<a href="#">c2wh7A_</a>	Alignment	not modelled	8.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronidase-phage associated; <b>PDBTitle:</b> the partial structure of a group a streptococcal phage-2 encoded tail fibre hyaluronate lyase hylp2
99	<a href="#">c2e4fa_</a>	Alignment	not modelled	8.2	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> g protein-activated inward rectifier potassium channel 2; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2