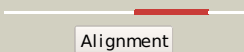

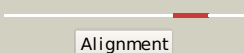
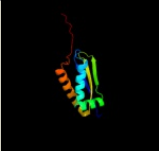
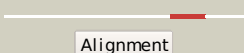
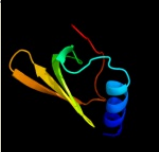
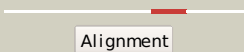
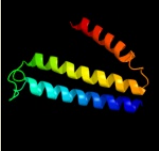
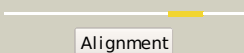

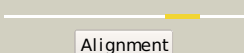
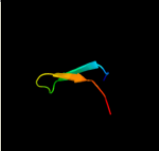


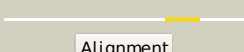

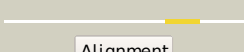

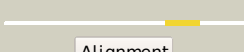

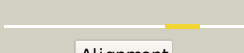
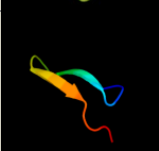





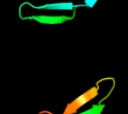
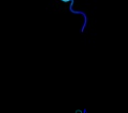

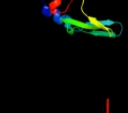


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vv5D_</a>	 Alignment		100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> the open structure of mscs
2	<a href="#">d2vv5a2</a>	 Alignment		99.4	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain <b>Family:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain
3	<a href="#">d2vv5a1</a>	 Alignment		99.0	28	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Mechanosensitive channel protein MscS (YggB), middle domain
4	<a href="#">d2vv5a3</a>	 Alignment		98.2	19	<b>Fold:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Family:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region
5	<a href="#">c2e6zA_</a>	 Alignment		78.1	16	<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
6	<a href="#">d1nz9a_</a>	 Alignment		77.8	33	<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
7	<a href="#">c2vfva_</a>	 Alignment		77.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> akap18 delta; <b>PDBTitle:</b> akap18 delta central domain
8	<a href="#">c2kvqG_</a>	 Alignment		76.9	22	<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
9	<a href="#">c2jvva_</a>	 Alignment		76.9	22	<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
10	<a href="#">d1nppa2</a>	 Alignment		76.4	43	<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
11	<a href="#">d2hqha1</a>	 Alignment		75.6	29	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain

12	<a href="#">d2dfaa1</a>	Alignment		75.2	23	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
13	<a href="#">c2zkrt</a>	Alignment		71.8	16	<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 an 2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
14	<a href="#">c3p8bB</a>	Alignment		69.9	20	<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="#">d2cqaa1</a>	Alignment		69.0	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TIP49 domain
16	<a href="#">d1v6ta</a>	Alignment		68.2	18	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
17	<a href="#">d2cp6a1</a>	Alignment		66.4	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
18	<a href="#">cloy8A</a>	Alignment		65.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
19	<a href="#">c2d5wA</a>	Alignment		65.5	15	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter, peptide-binding protein; <b>PDBTitle:</b> the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
20	<a href="#">d1t9ha1</a>	Alignment		64.3	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
21	<a href="#">d1u0la1</a>	Alignment	not modelled	63.0	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
22	<a href="#">c2x5cB</a>	Alignment	not modelled	62.8	21	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein orf131; <b>PDBTitle:</b> crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
23	<a href="#">c3ftjA</a>	Alignment	not modelled	60.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein <b>PDBTitle:</b> crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
24	<a href="#">d1whka</a>	Alignment	not modelled	59.7	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
25	<a href="#">c3ry3B</a>	Alignment	not modelled	58.1	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative solute-binding protein; <b>PDBTitle:</b> putative solute-binding protein from yersinia pestis.
26	<a href="#">d1vqot1</a>	Alignment	not modelled	55.9	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
27	<a href="#">d1h6za2</a>	Alignment	not modelled	55.0	26	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
28	<a href="#">c3pamB</a>	Alignment	not modelled	54.5	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein; <b>PDBTitle:</b> crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1

29	<a href="#">c2rcnA</a>	Alignment	not modelled	54.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
30	<a href="#">c4a1cS</a>	Alignment	not modelled	53.1	25	<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.
31	<a href="#">d1vqqq1</a>	Alignment	not modelled	52.7	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
32	<a href="#">d2coya1</a>	Alignment	not modelled	51.6	23	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
33	<a href="#">d1whma</a>	Alignment	not modelled	51.5	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
34	<a href="#">d2p13a1</a>	Alignment	not modelled	51.0	13	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
35	<a href="#">d1whja</a>	Alignment	not modelled	50.5	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
36	<a href="#">c1t9hA</a>	Alignment	not modelled	50.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> the crystal structure of yloq, a circularly permuted gtpase.
37	<a href="#">d2do3a1</a>	Alignment	not modelled	50.2	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
38	<a href="#">d2e3ia1</a>	Alignment	not modelled	50.2	15	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
39	<a href="#">d2cp5a1</a>	Alignment	not modelled	50.1	14	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
40	<a href="#">d2cp2a1</a>	Alignment	not modelled	48.8	25	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
41	<a href="#">c2e4hA</a>	Alignment	not modelled	48.8	27	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> restin; <b>PDBTitle:</b> solution structure of cytoskeletal protein in complex with2 tubulin tail
42	<a href="#">d2pls1</a>	Alignment	not modelled	48.6	20	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
43	<a href="#">c1m1gB</a>	Alignment	not modelled	48.3	43	<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)
44	<a href="#">c2z0wA</a>	Alignment	not modelled	48.1	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cap-gly domain-containing linker protein 4; <b>PDBTitle:</b> crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
45	<a href="#">d1khia1</a>	Alignment	not modelled	47.1	23	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
46	<a href="#">d2o1ra1</a>	Alignment	not modelled	47.0	14	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
47	<a href="#">d2coza1</a>	Alignment	not modelled	47.0	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
48	<a href="#">d1bkba1</a>	Alignment	not modelled	46.9	21	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
49	<a href="#">d2e3ha1</a>	Alignment	not modelled	46.9	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
50	<a href="#">d1ppje2</a>	Alignment	not modelled	46.7	4	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> ISP transmembrane anchor <b>Family:</b> ISP transmembrane anchor
51	<a href="#">c3nkuA</a>	Alignment	not modelled	45.9	28	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> drroa; <b>PDBTitle:</b> crystal structure of the n-terminal domain of drroa/sidm from2 legionella pneumophila
52	<a href="#">c2omdB</a>	Alignment	not modelled	45.7	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
53	<a href="#">c2jxfA</a>	Alignment	not modelled	45.1	18	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> the solution structure of hcv ns4b(40-69)
54	<a href="#">c3iz5Y</a>	Alignment	not modelled	45.1	19	<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

55	<a href="#">c3ftoA_</a>	Alignment	not modelled	45.1	16	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide-binding protein oppa; <b>PDBTitle:</b> crystal structure of oppa in a open conformation
56	<a href="#">d1dpea_</a>	Alignment	not modelled	44.9	25	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
57	<a href="#">c2qieA_</a>	Alignment	not modelled	44.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex2 with precursor z
58	<a href="#">c2grvC_</a>	Alignment	not modelled	44.6	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> lpqw; <b>PDBTitle:</b> crystal structure of lpqw
59	<a href="#">d1kbla2_</a>	Alignment	not modelled	44.5	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
60	<a href="#">d1iuha_</a>	Alignment	not modelled	44.3	12	<b>Fold:</b> LigT-like <b>Superfamily:</b> LigT-like <b>Family:</b> 2'-5' RNA ligase LigT
61	<a href="#">c3tpaA_</a>	Alignment	not modelled	44.2	14	<b>PDB header:</b> heme binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme-binding protein a; <b>PDBTitle:</b> structure of hbpa2 from haemophilus parasuis
62	<a href="#">d1iz6a1_</a>	Alignment	not modelled	43.4	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> elF5a N-terminal domain-like
63	<a href="#">d1u7ka_</a>	Alignment	not modelled	43.2	20	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
64	<a href="#">d1s04a_</a>	Alignment	not modelled	43.2	18	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> ProFAR isomerase associated domain
65	<a href="#">d2cowa1_</a>	Alignment	not modelled	43.1	32	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
66	<a href="#">c1u0lB_</a>	Alignment	not modelled	42.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> crystal structure of yjeq from thermotoga maritima
67	<a href="#">d1iwga1_</a>	Alignment	not modelled	42.4	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
68	<a href="#">d1xoca1_</a>	Alignment	not modelled	42.3	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
69	<a href="#">d2cp0a1_</a>	Alignment	not modelled	42.0	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
70	<a href="#">c2wctC_</a>	Alignment	not modelled	41.9	32	<b>PDB header:</b> rna-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> non-structural protein 3; <b>PDBTitle:</b> human sars coronavirus unique domain (triclinc form)
71	<a href="#">d1vbga2_</a>	Alignment	not modelled	41.0	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
72	<a href="#">c3dedB_</a>	Alignment	not modelled	40.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable hemolysin; <b>PDBTitle:</b> c-terminal domain of probable hemolysin from chromobacterium violaceum
73	<a href="#">d1vr5a1_</a>	Alignment	not modelled	40.9	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
74	<a href="#">c3lvuB_</a>	Alignment	not modelled	40.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
75	<a href="#">c3iz5U_</a>	Alignment	not modelled	40.3	34	<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
76	<a href="#">c2o7jA_</a>	Alignment	not modelled	40.0	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptide abc transporter, periplasmic <b>PDBTitle:</b> the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
77	<a href="#">c4a1aP_</a>	Alignment	not modelled	39.6	41	<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.
78	<a href="#">d2cp3a1_</a>	Alignment	not modelled	39.6	35	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
79	<a href="#">d2eyqa1_</a>	Alignment	not modelled	39.6	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> CarD-like <b>Family:</b> CarD-like
80	<a href="#">d3deda1_</a>	Alignment	not modelled	39.6	13	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like

81	<a href="#">d1whha_</a>	Alignment	not modelled	39.3	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
82	<a href="#">d1xnea_</a>	Alignment	not modelled	39.2	15	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> ProFAR isomerase associated domain
83	<a href="#">c2e70A_</a>	Alignment	not modelled	39.2	20	<b>PDB header:</b> transcription <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
84	<a href="#">c1ztyA_</a>	Alignment	not modelled	39.0	14	<b>PDB header:</b> sugar binding protein, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin oligosaccharide binding protein; <b>PDBTitle:</b> crystal structure of the chitin oligasaccharide binding2 protein
85	<a href="#">d2nqwa1</a>	Alignment	not modelled	39.0	19	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
86	<a href="#">d1m9dc_</a>	Alignment	not modelled	38.9	21	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
87	<a href="#">d2eifa1</a>	Alignment	not modelled	38.7	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
88	<a href="#">d1v6ga2</a>	Alignment	not modelled	37.9	27	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
89	<a href="#">d1yvca1</a>	Alignment	not modelled	37.7	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TRAM domain
90	<a href="#">d1e32a3</a>	Alignment	not modelled	37.7	18	<b>Fold:</b> Cdc48 domain 2-like <b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
91	<a href="#">c3llbA_</a>	Alignment	not modelled	37.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
92	<a href="#">d1m9fd_</a>	Alignment	not modelled	37.0	15	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
93	<a href="#">c2yv5A_</a>	Alignment	not modelled	36.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yjeq protein; <b>PDBTitle:</b> crystal structure of yjeq from aquifex aeolicus
94	<a href="#">d1bbua1</a>	Alignment	not modelled	36.4	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
95	<a href="#">d1zyna2</a>	Alignment	not modelled	35.8	13	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
96	<a href="#">d2pxrc1</a>	Alignment	not modelled	35.5	17	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
97	<a href="#">d1bcce2</a>	Alignment	not modelled	34.4	9	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> ISP transmembrane anchor <b>Family:</b> ISP transmembrane anchor
98	<a href="#">c2ivwA_</a>	Alignment	not modelled	34.4	20	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> pilp pilot protein; <b>PDBTitle:</b> the solution structure of a domain from the neisseria2 meningitidis pilp pilot protein.
99	<a href="#">c2fb0A_</a>	Alignment	not modelled	34.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
100	<a href="#">d1zlqa1</a>	Alignment	not modelled	34.2	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
101	<a href="#">c2zkrq_</a>	Alignment	not modelled	33.8	31	<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
102	<a href="#">c3t66A_</a>	Alignment	not modelled	33.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nickel abc transporter (nickel-binding protein); <b>PDBTitle:</b> crystal structure of nickel abc transporter from bacillus halodurans
103	<a href="#">d1x6oa1</a>	Alignment	not modelled	33.4	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
104	<a href="#">d1vgya2</a>	Alignment	not modelled	33.3	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
105	<a href="#">d1q40b_</a>	Alignment	not modelled	33.2	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> NTF2-like
106	<a href="#">d1g7sa1</a>	Alignment	not modelled	33.1	5	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
						<b>Fold:</b> Transmembrane helix hairpin

107	<a href="#">d1c99a_</a>	Alignment	not modelled	32.8	39	<b>Superfamily:</b> F1F0 ATP synthase subunit C <b>Family:</b> F1F0 ATP synthase subunit C
108	<a href="#">c3c5oD_</a>	Alignment	not modelled	32.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> upf0311 protein rpa1785; <b>PDBTitle:</b> crystal structure of the conserved protein of unknown function rpa17852 from rhodopseudomonas palustris
109	<a href="#">c1l6nA_</a>	Alignment	not modelled	32.4	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
110	<a href="#">d2plia1</a>	Alignment	not modelled	32.4	39	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
111	<a href="#">c2l66B_</a>	Alignment	not modelled	31.8	32	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
112	<a href="#">d1yeza1</a>	Alignment	not modelled	31.8	10	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TRAM domain
113	<a href="#">c2lc4A_</a>	Alignment	not modelled	31.8	28	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> pilp protein; <b>PDBTitle:</b> solution structure of pilp from pseudomonas aeruginosa
114	<a href="#">cls1iQ_</a>	Alignment	not modelled	31.4	31	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l21-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.
115	<a href="#">d2hi6a1</a>	Alignment	not modelled	31.2	41	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> AF0055-like
116	<a href="#">dlixda_</a>	Alignment	not modelled	31.2	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
117	<a href="#">d2if6a1</a>	Alignment	not modelled	31.0	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Yiix-like
118	<a href="#">d3d3ra1</a>	Alignment	not modelled	30.8	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
119	<a href="#">d2a7ya1</a>	Alignment	not modelled	30.0	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component <b>Family:</b> Rv2302-like
120	<a href="#">c2a7yA_</a>	Alignment	not modelled	30.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv2302/mt2359; <b>PDBTitle:</b> solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis