Phyre^2

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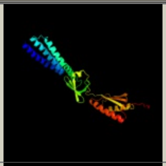
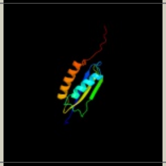
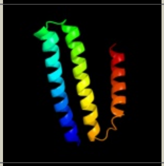
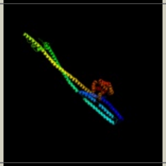
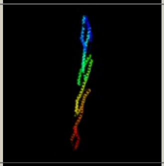
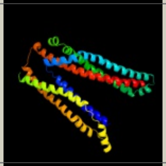
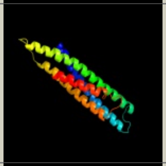
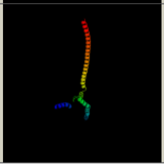
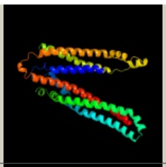
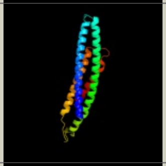
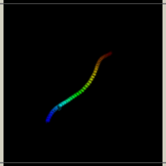
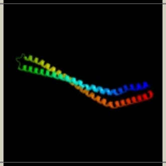
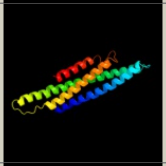
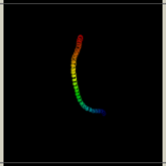
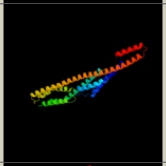
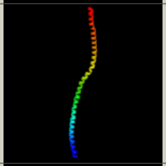
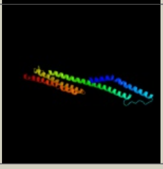
Description	P39285
Date	Thu Jan 5 11:58:57 GMT 2012
Unique Job ID	0106ad3fe443e7d2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vv5D_	Alignment		100.0	20	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
2	d2vv5a2	Alignment		99.6	20	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
3	d2vv5a1	Alignment		99.2	29	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
4	d2vv5a3	Alignment		98.7	12	**Fold:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Superfamily:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Family:**Mechanosensitive channel protein MscS (YggB), transmembrane region
5	c1ciiA_	Alignment		98.7	12	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
6	c1c1gA_	Alignment		98.5	12	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
7	c1yvlB_	Alignment		98.1	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
8	c1sjjB_	Alignment		97.9	10	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**actinin; **PDBTitle:** cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
9	c2oevA_	Alignment		97.7	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
10	c1bf5A_	Alignment		97.7	9	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
11	c3ojaB_	Alignment		97.5	12	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex

12	c2oexB_	Alignment		97.3	8	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** structure of alix/aip1 v domain
13	c1bg1A_	Alignment		97.2	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
14	c2efrB_	Alignment		97.0	7	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
15	c3na7A_	Alignment		96.9	10	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
16	c3cwgA_	Alignment		96.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
17	c3dtpA_	Alignment		96.5	12	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
18	c1f5nA_	Alignment		96.4	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1; **PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
19	c1ei3C_	Alignment		96.4	8	**PDB header:** **PDB COMPND:**
20	c1g8xB_	Alignment		96.4	9	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**myosin ii heavy chain fused to alpha-actinin 3; **PDBTitle:** structure of a genetically engineered molecular motor
21	c3ghgK_	Alignment	not modelled	96.1	9	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
22	c3hizB_	Alignment	not modelled	95.9	10	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
23	c2d3eD_	Alignment	not modelled	95.6	9	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
24	c2v71A_	Alignment	not modelled	95.6	9	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
25	c2ch7A_	Alignment	not modelled	95.4	10	**PDB header:**chemotaxis **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
26	c1jchC_	Alignment	not modelled	95.3	4	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
27	c1ei3E_	Alignment	not modelled	95.0	11	**PDB header:** **PDB COMPND:**
28	c3o0zD_	Alignment	not modelled	94.9	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human

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29	c2fxmB_	Alignment	not modelled	94.8	13	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
30	c3ojaA_	Alignment	not modelled	94.7	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
31	c4a55B_	Alignment	not modelled	94.7	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
32	c1y4cA_	Alignment	not modelled	94.7	12	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
33	c1deqF_	Alignment	not modelled	94.5	5	**PDB header:** **PDB COMPND:**
34	c2dfsA_	Alignment	not modelled	94.1	10	**PDB header:**contractile protein/transport protein **Chain:** A: **PDB Molecule:**myosin-5a; **PDBTitle:** 3-d structure of myosin-v inhibited state
35	c2v1yB_	Alignment	not modelled	94.0	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
36	c2y3aB_	Alignment	not modelled	93.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
37	c1deqO_	Alignment	not modelled	93.8	9	**PDB header:** **PDB COMPND:**
38	c2b9cA_	Alignment	not modelled	93.6	12	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**striated-muscle alpha tropomyosin; **PDBTitle:** structure of tropomyosin's mid-region: bending and binding2 sites for actin
39	c2j69D_	Alignment	not modelled	92.1	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
40	c3u59C_	Alignment	not modelled	91.2	15	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
41	c1hciB_	Alignment	not modelled	91.1	11	**PDB header:**triple-helix coiled coil **Chain:** B: **PDB Molecule:**alpha-actinin 2; **PDBTitle:** crystal structure of the rod domain of alpha-actinin
42	c3ipkA_	Alignment	not modelled	89.6	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
43	c1deqD_	Alignment	not modelled	87.8	10	**PDB header:** **PDB COMPND:**
44	d2ap3a1	Alignment	not modelled	87.4	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**MW0975(SA0943)-like **Family:**MW0975(SA0943)-like
45	c3hnwB_	Alignment	not modelled	84.8	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
46	c2zkrt_	Alignment	not modelled	84.8	24	**PDB header:**ribosomal protein/rna **Chain:** T: **PDB Molecule:**rna expansion segment es39 part iii; **PDBTitle:** 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
47	c3ol1A_	Alignment	not modelled	84.8	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
48	c2v66C_	Alignment	not modelled	84.5	11	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** crystal structure of the coiled-coil domain of ndel1 (a.a.2 58 to 169)c
49	c3r6nA_	Alignment	not modelled	84.1	5	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**desmoplakin; **PDBTitle:** crystal structure of a rigid four spectrin repeat fragment of the2 human desmoplakin plakin domain
50	c2gl2B_	Alignment	not modelled	83.5	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
51	c3g67A_	Alignment	not modelled	83.3	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
52	c3l9oA_	Alignment	not modelled	80.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
53	d2hqha1	Alignment	not modelled	80.5	33	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain

						Family: Cap-Gly domain
54	d2cqaa1	Alignment	not modelled	79.8	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
55	c2rd0B_	Alignment	not modelled	77.6	10	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a human p110alpha/p85alpha complex
56	c3edvB_	Alignment	not modelled	76.3	10	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**spectrin beta chain, brain 1; **PDBTitle:** crystal structure of repeats 14-16 of beta2-spectrin
57	c1l8dB_	Alignment	not modelled	74.4	7	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
58	c2zv4O_	Alignment	not modelled	74.3	13	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
59	d2cp6a1	Alignment	not modelled	74.2	30	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
60	d1nz9a_	Alignment	not modelled	74.0	35	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
61	c3kbtA_	Alignment	not modelled	73.9	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin beta chain, erythrocyte; **PDBTitle:** crystal structure of the ankyrin binding domain of human erythroid2 beta spectrin (repeats 13-15) in complex with the spectrin binding3 domain of human erythroid ankyrin (zu5-ank)
62	d1nppa2	Alignment	not modelled	72.0	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
63	c2wpqA_	Alignment	not modelled	71.6	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment; **PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
64	c2kvqG_	Alignment	not modelled	70.9	18	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
65	c2jvvA_	Alignment	not modelled	70.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
66	c4a1cS_	Alignment	not modelled	70.5	40	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** 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.
67	d1vqot1	Alignment	not modelled	68.6	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
68	c3iz5Y_	Alignment	not modelled	67.0	35	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
69	c3lssA_	Alignment	not modelled	66.5	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
70	c2e6zA_	Alignment	not modelled	66.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
71	d1whka_	Alignment	not modelled	65.9	13	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
72	d2plsa1	Alignment	not modelled	65.2	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
73	c2vfyA_	Alignment	not modelled	65.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
74	d1whma_	Alignment	not modelled	63.3	23	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
75	d2coya1	Alignment	not modelled	63.2	27	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
76	c2i1jA_	Alignment	not modelled	62.8	11	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
77	d2cp5a1	Alignment	not modelled	62.5	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
78	d1t9ha1	Alignment	not modelled	61.5	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						Fold:SH3-like barrel

79	d2coza1	Alignment	not modelled	60.8	27	**Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
80	c2e7sM_	Alignment	not modelled	60.8	7	**PDB header:**endocytosis/exocytosis **Chain:** M: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the yeast sec2p gef domain
81	c1i84V_	Alignment	not modelled	60.6	18	**PDB header:**contractile protein **Chain:** V: **PDB Molecule:**smooth muscle myosin heavy chain; **PDBTitle:** cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
82	c1l2fA_	Alignment	not modelled	60.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
83	d2cp2a1	Alignment	not modelled	60.5	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
84	c2qihA_	Alignment	not modelled	60.5	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein uspa1; **PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
85	c3cnrA_	Alignment	not modelled	59.6	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**type iv fimbriae assembly protein; **PDBTitle:** crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
86	d1yeza1	Alignment	not modelled	59.5	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
87	c2jeeA_	Alignment	not modelled	59.5	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
88	d1whja_	Alignment	not modelled	59.4	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
89	d2e3ha1	Alignment	not modelled	59.4	30	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
90	c2k52A_	Alignment	not modelled	58.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1198; **PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
91	d2do3a1	Alignment	not modelled	57.1	28	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
92	d2p13a1	Alignment	not modelled	57.0	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
93	c2no2A_	Alignment	not modelled	56.9	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of the dllrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
94	c2e4hA_	Alignment	not modelled	56.6	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
95	d2e3ia1	Alignment	not modelled	56.3	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
96	c2rcnA_	Alignment	not modelled	55.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
97	c1e0tD_	Alignment	not modelled	55.2	18	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
98	c2zdiA_	Alignment	not modelled	55.1	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**prefoldin subunit beta; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
99	d2cp3a1	Alignment	not modelled	54.5	35	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
100	d1h6za2	Alignment	not modelled	54.3	38	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
101	d1vqoq1	Alignment	not modelled	54.1	27	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
102	c2p03A_	Alignment	not modelled	54.1	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**alpha-2-macroglobulin receptor-associated **PDBTitle:** the structure of receptor-associated protein(rap)
103	c2z0wA_	Alignment	not modelled	53.7	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cap-gly domain-containing linker protein 4; **PDBTitle:** crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
104	d2cowa1	Alignment	not modelled	53.7	32	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain

105	c1q46A_	Alignment	not modelled	53.3	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
106	c2v4hA_	Alignment	not modelled	52.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
107	c3b7kA_	Alignment	not modelled	52.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
108	c2wctC_	Alignment	not modelled	52.7	37	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**non-structural protein 3; **PDBTitle:** human sars coronavirus unique domain (triclinic form)
109	d2essa1	Alignment	not modelled	52.1	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
110	c1hh2P_	Alignment	not modelled	52.0	20	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
111	d1yvca1	Alignment	not modelled	51.9	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
112	d1ppje2	Alignment	not modelled	51.5	22	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
113	c3iz5U_	Alignment	not modelled	51.4	24	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
114	d2o1ra1	Alignment	not modelled	51.3	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
115	d1whha_	Alignment	not modelled	51.3	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
116	c4a1aP_	Alignment	not modelled	51.2	28	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **PDBTitle:** 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.
117	c3a7pB_	Alignment	not modelled	50.9	8	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
118	d2f9ha1	Alignment	not modelled	50.8	26	**Fold:**PTSIIA/GutA-like **Superfamily:**PTSIIA/GutA-like **Family:**PTSIIA/GutA-like
119	c3dedB_	Alignment	not modelled	50.4	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable hemolysin; **PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum
120	d1y7ua1	Alignment	not modelled	50.4	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like