Phyre^2

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Description	A0JNW5
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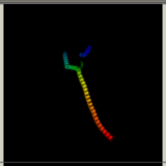
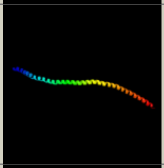
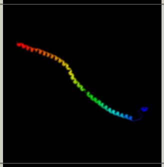
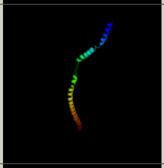
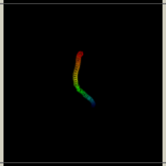
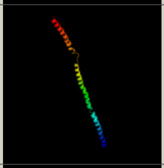
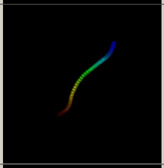
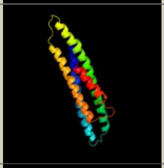
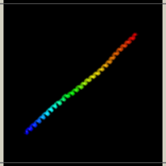
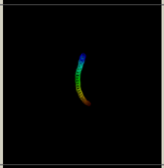
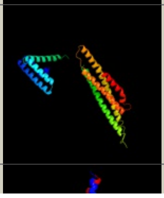
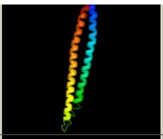
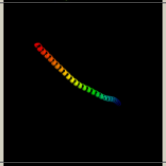
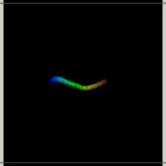
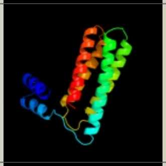
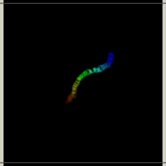
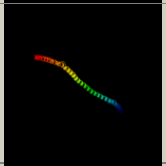
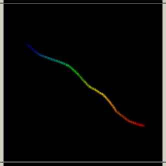
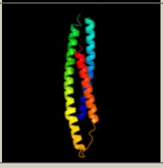
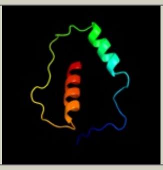
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ojaB_	Alignment		97.0	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
2	c3dtpA_	Alignment		94.3	8	**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
3	c1ei3C_	Alignment		92.4	7	**PDB header:** **PDB COMPND:**
4	c1deqF_	Alignment		92.3	8	**PDB header:** **PDB COMPND:**
5	c2d3eD_	Alignment		91.8	7	**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
6	c1deqO_	Alignment		91.5	9	**PDB header:** **PDB COMPND:**
7	c2efrB_	Alignment		91.4	6	**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
8	c1bf5A_	Alignment		91.0	8	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
9	c3u59C_	Alignment		90.9	13	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
10	c2fxmB_	Alignment		90.9	7	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
11	c1yvlB_	Alignment		90.6	6	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1

12	c3hizB_	Alignment		90.0	6	**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
13	c3q8tB_	Alignment		89.4	9	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**beclin-1; **PDBTitle:** crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
14	c2b9cA_	Alignment		87.5	11	**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
15	c1y4cA_	Alignment		87.4	8	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
16	c3ghgK_	Alignment		87.4	5	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
17	c1ei3E_	Alignment		87.1	8	**PDB header:** **PDB COMPND:**
18	d1ev0a_	Alignment		86.4	22	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
19	c1c1gA_	Alignment		82.7	6	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
20	c3cwgA_	Alignment		81.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
21	c1jchC_	Alignment	not modelled	80.1	9	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
22	c3hnwB_	Alignment	not modelled	77.1	13	**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
23	c3vkgB_	Alignment	not modelled	75.3	8	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** crystal structure of an motor protein
24	c3ol1A_	Alignment	not modelled	74.8	9	**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
25	c2i1jA_	Alignment	not modelled	73.3	11	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
26	c2y3aB_	Alignment	not modelled	70.5	9	**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
27	c3ojaA_	Alignment	not modelled	68.0	6	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
28	c1bg1A_	Alignment	not modelled	67.4	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex

29	c2jeeA_	Alignment	not modelled	64.1	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
30	c3o0zD_	Alignment	not modelled	63.5	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human rock i
31	c4a55B_	Alignment	not modelled	62.4	7	**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	c2kxoA_	Alignment	not modelled	60.8	31	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
33	c1g8xB_	Alignment	not modelled	60.3	6	**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
34	c1wt6B_	Alignment	not modelled	59.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**myotonin-protein kinase; **PDBTitle:** coiled-coil domain of dmpk
35	c2gl2B_	Alignment	not modelled	59.4	7	**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
36	c2zvnF_	Alignment	not modelled	57.8	12	**PDB header:**signaling protein/transcription **Chain:** F: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cozi domain incomplex with diubiquitin in p2121212 space group
37	c3n4xB_	Alignment	not modelled	55.5	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
38	c3ipkA_	Alignment	not modelled	55.2	7	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
39	c3r9jD_	Alignment	not modelled	54.8	22	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
40	c2v4hA_	Alignment	not modelled	54.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
41	d1etea_	Alignment		52.0	19	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
42	c3qh9A_	Alignment	not modelled	48.3	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
43	c3vkhD_	Alignment	not modelled	45.5	10	**PDB header:**motor protein **Chain:** D: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** crystal structure of an motor protein
44	d1gsma2	Alignment	not modelled	45.0	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
45	c3a7pB_	Alignment	not modelled	44.4	10	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
46	c2rd0B_	Alignment	not modelled	44.0	6	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a human p110alpha/p85alpha complex
47	c1ciiA_	Alignment	not modelled	42.5	13	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
48	c1l8dB_	Alignment	not modelled	41.9	10	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
49	c2w6aB_	Alignment	not modelled	41.2	24	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
50	c1debA_	Alignment	not modelled	40.8	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
51	c2oevA_	Alignment	not modelled	39.9	5	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
52	c2eqbC_	Alignment	not modelled	36.9	17	**PDB header:**endocytosis/exocytosis **Chain:** C: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
53	d1pugb_	Alignment	not modelled	35.4	28	**Fold:**YbaB-like **Superfamily:**YbaB-like

						Family: YbaB-like
54	d1hn6a_	Alignment	not modelled	34.9	11	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
55	c1deqD_	Alignment	not modelled	34.6	9	**PDB header:** **PDB COMPND:**
56	c1ybxA_	Alignment	not modelled	33.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
57	d1tlta2	Alignment	not modelled	32.2	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
58	d1xeaa2	Alignment	not modelled	32.0	6	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
59	c2v1yB_	Alignment	not modelled	31.8	6	**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
60	c2x7aB_	Alignment	not modelled	31.7	21	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
61	d1mvha_	Alignment	not modelled	31.6	27	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
62	c1mvhA_	Alignment	not modelled	31.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cryptic loci regulator 4; **PDBTitle:** structure of the set domain histone lysine2 methyltransferase clr4
63	d1kb0a1	Alignment	not modelled	30.8	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
64	c3c9jD_	Alignment	not modelled	30.7	35	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
65	d1pvga1	Alignment	not modelled	30.7	33	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
66	c3c9jC_	Alignment	not modelled	30.6	35	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
67	c2rlfA_	Alignment	not modelled	29.6	26	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**matrix protein 2; **PDBTitle:** proton channel m2 from influenza a in complex with2 inhibitor rimantadine
68	c2v71A_	Alignment	not modelled	29.1	7	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
69	c3vkhB_	Alignment	not modelled	29.0	5	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** crystal structure of an motor protein
70	c3o0rC_	Alignment	not modelled	27.8	19	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
71	c3ddyA_	Alignment	not modelled	27.8	27	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**lumazine protein; **PDBTitle:** structure of lumazine protein, an optical transponder of luminescent2 bacteria
72	c2wpqA_	Alignment	not modelled	27.2	4	**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)
73	c3m9hB_	Alignment	not modelled	27.2	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
74	d1ccra_	Alignment	not modelled	27.2	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
75	c2xzrA_	Alignment	not modelled	27.1	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
76	c3f42A_	Alignment	not modelled	27.0	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hp0035; **PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
77	d2rspa_	Alignment	not modelled	26.9	19	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
78	d1an2a_	Alignment	not modelled	26.8	6	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain

						Family:HLH, helix-loop-helix DNA-binding domain
79	d1puga_	Alignment	not modelled	26.7	26	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
80	d1j8ba_	Alignment	not modelled	26.5	15	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
81	c3c9jB_	Alignment	not modelled	26.5	35	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
82	d2cs3a1	Alignment	not modelled	26.2	33	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain
83	c4e61A_	Alignment	not modelled	26.0	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** crystal structure of the eb1-like motif of bim1p
84	d2au5a1	Alignment	not modelled	26.0	18	**Fold:**EF2947-like **Superfamily:**EF2947-like **Family:**EF2947-like
85	c3a35B_	Alignment	not modelled	26.0	33	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**lumazine protein; **PDBTitle:** crystal structure of lump complexed with riboflavin
86	d2b9ea1	Alignment	not modelled	25.9	33	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
87	c3na7A_	Alignment	not modelled	25.8	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
88	d1ynra1	Alignment	not modelled	25.8	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
89	c3mkxC_	Alignment	not modelled	25.8	11	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
90	c3pbpL_	Alignment	not modelled	25.7	45	**PDB header:**transport protein,structural protein **Chain:** L: **PDB Molecule:**nucleoporin nup159; **PDBTitle:** structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
91	c2r3aA_	Alignment	not modelled	25.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv39h2; **PDBTitle:** methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
92	c2zzsW_	Alignment	not modelled	25.6	25	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
93	c3idwA_	Alignment	not modelled	25.6	18	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
94	c2no2A_	Alignment	not modelled	25.4	9	**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
95	c2v66C_	Alignment	not modelled	25.4	10	**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
96	c3c9jA_	Alignment	not modelled	25.2	35	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
97	c2rd0A_	Alignment	not modelled	25.1	11	**PDB header:**transferase/oncoprotein **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** structure of a human p110alpha/p85alpha complex
98	c2wvrB_	Alignment	not modelled	25.1	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**geminin; **PDBTitle:** human cdt1:geminin complex
99	c3oa7A_	Alignment	not modelled	25.1	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**head morphogenesis protein, chaotic nuclear migration **PDBTitle:** structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
100	c1ci6A_	Alignment	not modelled	25.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
101	c3u1aC_	Alignment	not modelled	24.9	11	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
102	c2wxoA_	Alignment	not modelled	24.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
103	c1kzlA_	Alignment	not modelled	24.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** riboflavin synthase from s.pombe bound to2 carboxyethyllumazine

104	d1e6ya1	Alignment	not modelled	24.6	13	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
105	d1m70a2	Alignment	not modelled	24.6	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
106	c3kltB_	Alignment	not modelled	23.9	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of a vimentin fragment
107	c1i8dB_	Alignment	not modelled	23.9	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of riboflavin synthase
108	c3h6lA_	Alignment	not modelled	23.7	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd2; **PDBTitle:** methyltransferase domain of human set domain-containing protein 2
109	c3bnwA_	Alignment	not modelled	23.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase, putative; **PDBTitle:** crystal structure of riboflavin kinase from trypanosoma brucei
110	d1mjsa_	Alignment	not modelled	23.5	30	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
111	c1gd2G_	Alignment	not modelled	23.4	8	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
112	c3q0xA_	Alignment	not modelled	23.4	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centriole protein; **PDBTitle:** n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
113	c2gk4A_	Alignment	not modelled	23.4	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
114	d1cc5a_	Alignment	not modelled	23.2	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
115	c2y3aA_	Alignment	not modelled	23.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
116	c2kqtD_	Alignment	not modelled	23.0	33	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
117	c2kqtB_	Alignment	not modelled	23.0	33	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
118	c2kqtA_	Alignment	not modelled	23.0	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
119	c2kqtC_	Alignment	not modelled	23.0	33	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
120	c2wt7B_	Alignment	not modelled	22.9	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna