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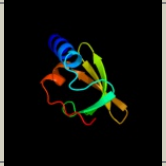
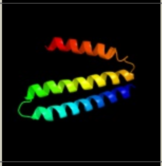
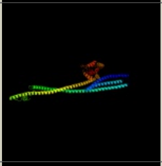
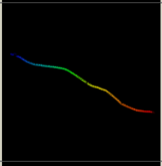
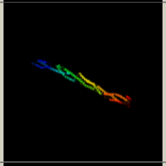
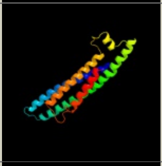
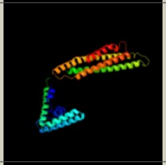
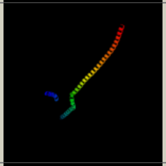
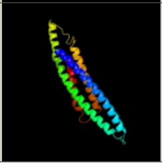
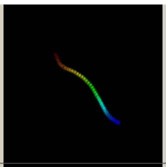
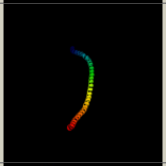
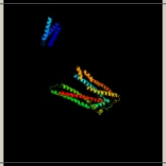
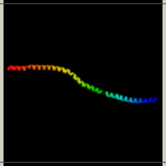
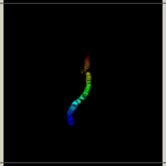
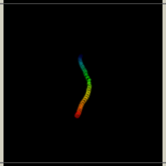
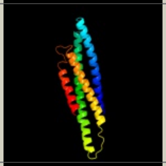
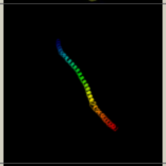
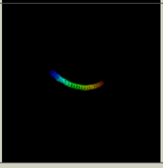
Description	P77338
Date	Thu Jan 5 12:28:00 GMT 2012
Unique Job ID	c6a9fdb8c192fa4a

Detailed template information

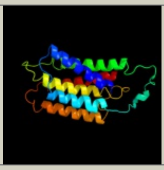
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vv5D_	Alignment		100.0	22	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
2	d2vv5a2	Alignment		99.8	20	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
3	d2vv5a1	Alignment		99.6	33	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
4	d2vv5a3	Alignment		99.1	18	**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		99.0	14	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
6	c1c1gA_	Alignment		98.3	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	c1sjjB_	Alignment		98.1	11	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**actinin; **PDBTitle:** cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
8	c1bf5A_	Alignment		97.9	13	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
9	c1yvlB_	Alignment		97.8	6	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
10	c3ojaB_	Alignment		97.6	8	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
11	c1bg1A_	Alignment		97.5	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex

12	c2efrB_	Alignment		97.4	8	**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
13	c3dtpA_	Alignment		97.4	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
14	c2oevA_	Alignment		97.3	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
15	c1ei3C_	Alignment		97.3	8	**PDB header:** **PDB COMPND:**
16	c3ghgK_	Alignment		97.3	9	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
17	c2d3eD_	Alignment		97.2	13	**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
18	c3cwgA_	Alignment		97.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
19	c1ei3E_	Alignment		97.1	10	**PDB header:** **PDB COMPND:**
20	c2fxmB_	Alignment		96.9	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
21	c1hciB_	Alignment	not modelled	96.9	8	**PDB header:**triple-helix coiled coil **Chain:** B: **PDB Molecule:**alpha-actinin 2; **PDBTitle:** crystal structure of the rod domain of alpha-actinin
22	c3na7A_	Alignment	not modelled	96.8	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
23	c1f5nA_	Alignment	not modelled	96.7	11	**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.
24	c3hizB_	Alignment	not modelled	96.7	9	**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
25	c3ojaA_	Alignment	not modelled	96.6	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
26	c1jchC_	Alignment	not modelled	96.5	11	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
27	c2oexB_	Alignment	not modelled	96.5	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** structure of alix/aip1 v domain
28	c3u59C_	Alignment	not modelled	96.4	15	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin

						beta
29	c1deqO_	Alignment	not modelled	96.4	9	**PDB header:** **PDB COMPND:**
30	c1y4cA_	Alignment	not modelled	96.3	10	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
31	c3r6nA_	Alignment	not modelled	96.1	11	**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
32	c1deqF_	Alignment	not modelled	96.1	7	**PDB header:** **PDB COMPND:**
33	c3o0zD_	Alignment	not modelled	96.0	8	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human rock i
34	c1g8xB_	Alignment	not modelled	95.9	8	**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
35	c2y3aB_	Alignment	not modelled	95.7	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
36	c2b9cA_	Alignment	not modelled	95.4	8	**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
37	c3l9oA_	Alignment	not modelled	94.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
38	c3ol1A_	Alignment	not modelled	94.7	18	**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
39	c2gl2B_	Alignment	not modelled	93.9	11	**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
40	c4a55B_	Alignment	not modelled	93.7	9	**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
41	c3ipkA_	Alignment	not modelled	92.9	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
42	c2ch7A_	Alignment	not modelled	92.5	12	**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
43	c2v1yB_	Alignment	not modelled	92.5	11	**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
44	c2zv4O_	Alignment	not modelled	91.6	12	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
45	c2v71A_	Alignment	not modelled	90.4	15	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
46	c3hnwB_	Alignment	not modelled	90.2	10	**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
47	c2rd0B_	Alignment	not modelled	89.4	6	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a human p110alpha/p85alpha complex
48	c2v66C_	Alignment	not modelled	88.7	9	**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	c1l8dB_	Alignment	not modelled	88.3	9	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
50	c2wpqA_	Alignment	not modelled	87.8	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)
51	c2zkrt_	Alignment	not modelled	86.7	21	**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
52	c2e7sM_	Alignment	not modelled	86.1	14	**PDB header:**endocytosis/exocytosis **Chain:** M: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the yeast sec2p gef domain

53	c2i1jA_	Alignment	not modelled	85.0	12	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
54	c1deqD_	Alignment	not modelled	84.5	12	**PDB header:** **PDB COMPND:**
55	c2dq3A_	Alignment	not modelled	84.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
56	c2j69D_	Alignment	not modelled	81.6	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
57	d2hqha1	Alignment	not modelled	81.5	38	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
58	c2qihA_	Alignment	not modelled	81.3	5	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein uspa1; **PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
59	d2cqaa1	Alignment	not modelled	79.5	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
60	d1nz9a_	Alignment	not modelled	79.3	27	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
61	c1i84V_	Alignment	not modelled	79.0	11	**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.
62	c3u1aC_	Alignment	not modelled	78.8	12	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
63	c2xgjA_	Alignment	not modelled	77.8	10	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
64	d1nppa2	Alignment	not modelled	77.2	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
65	c2jvvA_	Alignment	not modelled	76.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
66	c2kvqG_	Alignment	not modelled	76.5	15	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
67	c2e6zA_	Alignment	not modelled	71.6	18	**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
68	c2dfsA_	Alignment	not modelled	71.6	11	**PDB header:**contractile protein/transport protein **Chain:** A: **PDB Molecule:**myosin-5a; **PDBTitle:** 3-d structure of myosin-v inhibited state
69	d1vqoq1	Alignment	not modelled	71.4	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
70	c2p22C_	Alignment	not modelled	69.3	10	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein srn2; **PDBTitle:** structure of the yeast escrt-i heterotetramer core
71	d2cp6a1	Alignment	not modelled	69.0	39	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
72	c2v4hA_	Alignment	not modelled	68.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
73	d2plsa1	Alignment	not modelled	66.9	24	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
74	c2vfyA_	Alignment	not modelled	66.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
75	d2ap3a1	Alignment	not modelled	66.6	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**MW0975(SA0943)-like **Family:**MW0975(SA0943)-like
76	c1quuA_	Alignment	not modelled	66.1	10	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**human skeletal muscle alpha-actinin 2; **PDBTitle:** crystal structure of two central spectrin-like repeats from2 alpha-actinin
77	d1t9ha1	Alignment	not modelled	64.6	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
78	c3g67A_	Alignment	not modelled	63.8	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima

79	c3qo8A_	Alignment	not modelled	63.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
80	d1whka_	Alignment	not modelled	62.3	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
81	c4a1cS_	Alignment	not modelled	60.3	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.
82	c2jeeA_	Alignment	not modelled	60.3	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
83	d1whma_	Alignment	not modelled	59.9	32	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
84	d1yeza1	Alignment	not modelled	59.9	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
85	d1vqot1	Alignment	not modelled	59.5	32	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
86	c3iz5Y_	Alignment	not modelled	57.7	29	**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
87	d2coya1	Alignment	not modelled	57.5	36	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
88	c2rcnA_	Alignment	not modelled	57.3	31	**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.
89	c2k52A_	Alignment	not modelled	57.1	18	**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
90	d2gvha1	Alignment	not modelled	57.0	36	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
91	c2no2A_	Alignment	not modelled	56.3	11	**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
92	d2cp2a1	Alignment	not modelled	56.0	25	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
93	c2eqbC_	Alignment	not modelled	55.8	8	**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
94	c3a7pB_	Alignment	not modelled	55.4	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
95	c3n4xB_	Alignment	not modelled	55.2	10	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
96	d2cp5a1	Alignment	not modelled	55.0	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
97	d1y7ua1	Alignment	not modelled	55.0	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
98	c3iz5U_	Alignment	not modelled	55.0	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
99	c1q46A_	Alignment	not modelled	54.7	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
100	d2coza1	Alignment	not modelled	54.6	32	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
101	c2zvnF_	Alignment	not modelled	54.3	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
102	d1whja_	Alignment	not modelled	53.2	33	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
103	c4a1aP_	Alignment	not modelled	53.2	21	**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.
104	d2p13a1	Alignment	not modelled	53.1	10	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like

						Family: CorC/HlyC domain-like
105	c3b7kA_	Alignment	not modelled	52.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
106	c2gvhC_	Alignment	not modelled	52.6	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**agr_l_2016p; **PDBTitle:** crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
107	c3izcU_	Alignment	not modelled	51.8	24	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
108	d2e3ha1	Alignment	not modelled	51.2	35	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
109	c1mhsA_	Alignment		51.2	9	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
110	c2zkrq_	Alignment	not modelled	50.8	27	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **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
111	d2e3ia1	Alignment	not modelled	50.7	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
112	d1h6za2	Alignment	not modelled	50.5	38	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
113	d1vpma_	Alignment	not modelled	50.3	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
114	c3m9bK_	Alignment	not modelled	49.4	22	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
115	c2yv5A_	Alignment	not modelled	49.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
116	d1yvca1	Alignment	not modelled	49.0	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
117	d2o1ra1	Alignment	not modelled	48.8	18	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
118	c3qh9A_	Alignment	not modelled	48.8	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
119	d1ylia1	Alignment	not modelled	48.8	29	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
120	c2z0wA_	Alignment	not modelled	48.4	25	**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