Phyre2

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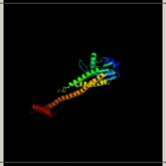
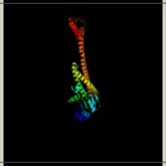
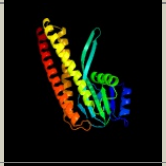
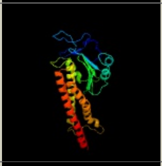
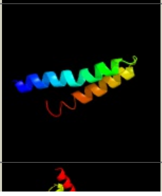
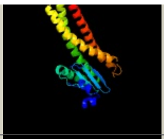
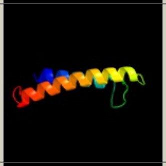
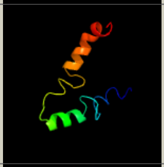
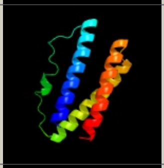
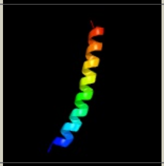
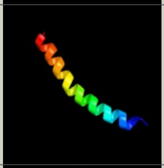
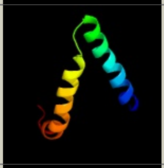
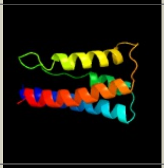
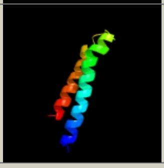
Description	RVBD1239c_(corA)_1381948_1383048
Date	Wed Jul 31 22:05:33 BST 2019
Unique Job ID	4511745b02595aff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bbjB_	Alignment		100.0	27	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
2	c5n9yB_	Alignment		100.0	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the full-length structure of zntb
3	c4ev6E_	Alignment		100.0	18	**PDB header:**metal transport **Chain:** E: **PDB Molecule:**magnesium transport protein cora; **PDBTitle:** the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
4	d2iuba1	Alignment		100.0	24	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
5	c2hn1A_	Alignment		100.0	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**magnesium and cobalt transporter; **PDBTitle:** crystal structure of a cora soluble domain from a. fulgidus in complex2 with co2+
6	c5n77A_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**magnesium transport protein cora; **PDBTitle:** crystal structure of the cytosolic domain of the cora magnesium2 channel from escherichia coli in complex with magnesium
7	c4egwB_	Alignment		100.0	14	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**magnesium transport protein cora; **PDBTitle:** the structure of the soluble domain of cora from methanocaldococcus2 jannaschii
8	c3nwiC_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the soluble domain structure of the zntb zn2+ efflux system
9	d2bbha1	Alignment		100.0	24	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
10	c3ck6E_	Alignment		100.0	11	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**putative membrane transport protein; **PDBTitle:** crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
11	d2iuba2	Alignment		99.4	30	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
						

12	c3rkgA_	Alignment		95.9	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**magnesium transporter mrs2, mitochondrial; **PDBTitle:** structural and functional characterization of the yeast mg2+ channel2 mrs2
13	c6adqP_	Alignment		84.5	9	**PDB header:**electron transport **Chain:** P: **PDB Molecule:**prokaryotic respiratory supercomplex associate factor 1 **PDBTitle:** respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
14	c6o7ua_	Alignment		58.4	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:** **PDBTitle:** saccharomyces cerevisiae v-atpase stv1-vo
15	c3fseB_	Alignment		57.1	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
16	d3cx5d2	Alignment		53.8	19	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
17	d1ppjd2	Alignment		52.8	25	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
18	c5voxb_	Alignment		50.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type proton atpase subunit b; **PDBTitle:** yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
19	c3kyiA_	Alignment		40.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative histidine protein kinase; **PDBTitle:** crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
20	c6akfC_	Alignment		35.8	11	**PDB header:**membrane protein/toxin **Chain:** C: **PDB Molecule:**claudin-3; **PDBTitle:** crystal structure of mouse claudin-3 p134a mutant in complex with c-2 terminal fragment of clostridium perfringens enterotoxin
21	d1iyka1	Alignment	not modelled	31.4	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
22	c6gcsD_	Alignment	not modelled	30.9	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nimm subunit; **PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica
23	c5sv0C_	Alignment	not modelled	30.8	9	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**biopolymer transport protein exbb; **PDBTitle:** structure of the exbb/exbd complex from e. coli at ph 7.0
24	d1u5pa1	Alignment	not modelled	30.5	9	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
25	c1p84D_	Alignment	not modelled	29.8	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
26	c3j01A_	Alignment	not modelled	29.7	7	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
27	c1qcrD_	Alignment	not modelled	29.3	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ubiquinol cytochrome c oxidoreductase; **PDBTitle:** crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
28	c3cwbQ_	Alignment	not modelled	29.2	19	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
29	c4nxuA	Alignment	not modelled	27.8	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**bipolar kinesin krp-130;

29	c4pxuA_	Alignment	not modelled	27.8	15	**PDBTitle:** structural basis for the assembly of the mitotic motor kinesin-5 into2 bipolar tetramers
30	c2yiuE_	Alignment	not modelled	27.8	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
31	c2fynH_	Alignment	not modelled	27.8	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
32	c3dl8H_	Alignment	not modelled	27.1	5	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
33	c2gtlO_	Alignment	not modelled	25.3	28	**PDB header:**oxygen storage/transport **Chain:** O: **PDB Molecule:**extracellular hemoglobin linker l3 subunit; **PDBTitle:** lumbricus erythrocruorin at 3.5a resolution
34	c5dirD_	Alignment	not modelled	25.0	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lipoprotein signal peptidase; **PDBTitle:** membrane protein at 2.8 angstroms
35	d1gqea_	Alignment	not modelled	23.2	14	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
36	d1iica1	Alignment	not modelled	23.1	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
37	c1zrtD_	Alignment	not modelled	23.1	22	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
38	c4cadF_	Alignment	not modelled	22.9	8	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**ras and a-factor converting enzyme 1, rce1; **PDBTitle:** mechanism of farnesylated caax protein processing by the integral2 membrane protease rce1
39	c1xyr6_	Alignment	not modelled	22.5	28	**PDB header:**virus **Chain:** 6: **PDB Molecule:**genome polyprotein, coat protein vp3; **PDB Fragment:**residues 620-630 **PDBTitle:** poliovirus 135s cell entry intermediate
40	c5aymA_	Alignment	not modelled	21.9	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 39 (iron-regulated transporter); **PDBTitle:** crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
41	c3rfuC_	Alignment	not modelled	21.8	18	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
42	c1iicA_	Alignment	not modelled	21.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**peptide n-myristoyltransferase; **PDBTitle:** crystal structure of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoylcoa
43	d1tqga_	Alignment	not modelled	21.0	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
44	c2wuuA_	Alignment	not modelled	20.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-myristoyltransferase; **PDBTitle:** structure of n-myristoyltransferase from l. donovani
45	c2akiY_	Alignment	not modelled	20.3	7	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a translocating2 secyeg protein-conducting channel into the cryo-em map of a secyeg-3 nascent chain-70s ribosome complex from e. coli
46	d1wh5a_	Alignment	not modelled	20.2	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
47	c3d5cX_	Alignment	not modelled	19.4	9	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
48	c3mkuA_	Alignment	not modelled	19.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
49	c4a95B_	Alignment	not modelled	18.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** plasmodium vivax n-myristoyltransferase with quinoline inhibitor
50	c6mjpG_	Alignment	not modelled	17.9	20	**PDB header:**lipid transport **Chain:** G: **PDB Molecule:**lps export abc transporter permease lptg; **PDBTitle:** lptb(e163q)fgc from vibrio cholerae
51	c5ijpA_	Alignment	not modelled	17.8	12	**PDB header:**inositol phosphate binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the spx domain of chaetomium thermophilum vtc4 in2 complex with inositol hexakisphosphate (insp6).
52	c3ci9B_	Alignment	not modelled	17.7	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
53	c4w6vA_	Alignment	not modelled	17.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**di-/tripeptide transporter; **PDBTitle:** crystal structure of a peptide transporter from yersinia2

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54	d1cuna2	Alignment	not modelled	17.4	10	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
55	d1s35a1	Alignment	not modelled	17.4	7	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
56	c4djiA_	Alignment	not modelled	17.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable glutamate/gamma-aminobutyrate antiporter; **PDBTitle:** structure of glutamate-gaba antiporter gadc
57	d1e52a_	Alignment	not modelled	16.8	14	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
58	c3nvtA_	Alignment	not modelled	16.8	13	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
59	c3ednB_	Alignment	not modelled	16.6	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein, phzf family; **PDBTitle:** crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family
60	d1s35a2	Alignment	not modelled	16.5	9	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
61	c5l75G_	Alignment	not modelled	16.3	17	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**fig000906: predicted permease; **PDBTitle:** a protein structure
62	c1s1iJ_	Alignment	not modelled	15.9	71	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l11; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
63	c3r1fO_	Alignment	not modelled	15.8	16	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
64	c2p6fA_	Alignment	not modelled	15.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** crystal structures of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoyl-coa and inhibitors
65	c4lunU_	Alignment	not modelled	15.5	3	**PDB header:**rna binding protein **Chain:** U: **PDB Molecule:**nonsense-mediated mrna decay protein 2; **PDBTitle:** structure of the n-terminal mif4g domain from s. cerevisiae upf2, a2 protein involved in the degradation of mrnas containing premature3 stop codons
66	c2lp4A_	Alignment	not modelled	15.4	8	**PDB header:**transferase/signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** solution structure of p1-chey/p2 complex in bacterial chemotaxis
67	c5ir6B_	Alignment	not modelled	15.2	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bd-type quinol oxidase subunit ii; **PDBTitle:** the structure of bd oxidase from geobacillus thermodenitrificans
68	c2m20B_	Alignment	not modelled	14.9	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
69	d1e3oc1	Alignment	not modelled	14.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
70	c5x62A_	Alignment	not modelled	14.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnosine n-methyltransferase; **PDBTitle:** crystal structure of a carnosine n-methyltransferase bound by adohcy
71	c3bunB_	Alignment	not modelled	14.6	15	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its binding motif2 in sprouty4
72	c4cadC_	Alignment	not modelled	14.5	8	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**ras and a-factor converting enzyme 1, rce1; **PDBTitle:** mechanism of farnesylated caax protein processing by the integral2 membrane protease rce1
73	d1i6za_	Alignment	not modelled	14.4	12	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
74	c5go2D_	Alignment	not modelled	14.2	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**protein aroa(g); **PDBTitle:** crystal structure of chorismate mutase like domain of bifunctional2 dahp synthase of bacillus subtilis in complex with citrate
75	c4cawA_	Alignment	not modelled	14.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** crystal structure of aspergillus fumigatus n-myristoyl2 transferase in complex with myristoyl coa and a pyrazole3 sulphonamide ligand
76	c2xdjF_	Alignment	not modelled	13.9	10	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
77	c2cblA_	Alignment	not modelled	13.7	15	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2

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78	c2cpbA_	Alignment	not modelled	13.6	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**m13 major coat protein; **PDBTitle:** solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
79	c5fv8B_	Alignment	not modelled	13.6	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**fosw; **PDBTitle:** structure of cjun-fosw coiled coil complex.
80	c5tj5A_	Alignment	not modelled	13.5	11	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**v-type proton atpase subunit a; **PDBTitle:** atomic model for the membrane-embedded motor of a eukaryotic v-atpase
81	c6k1hF_	Alignment	not modelled	13.5	6	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**pts system mannose-specific eiid component; **PDBTitle:** structure of membrane protein
82	c2akfA_	Alignment	not modelled	13.4	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
83	c2akfC_	Alignment	not modelled	13.4	15	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
84	c2akfB_	Alignment	not modelled	13.4	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
85	c5fv8A_	Alignment	not modelled	13.4	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**fosw; **PDBTitle:** structure of cjun-fosw coiled coil complex.
86	c3uunA_	Alignment	not modelled	13.4	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**dystrophin; **PDBTitle:** crystal structure of n-terminal first spectrin repeat of dystrophin
87	c2ks1B_	Alignment	not modelled	13.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
88	c1qoyA_	Alignment	not modelled	13.2	16	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin e; **PDBTitle:** e.coli hemolysin e (hlye, clya, shea)
89	c4pguA_	Alignment	not modelled	13.0	14	**PDB header:**membrance protein **Chain:** A: **PDB Molecule:**uncharacterized protein yetj; **PDBTitle:** crystal structure of yetj from bacillus subtilis at ph 7 by soaking
90	c4a1cD_	Alignment	not modelled	12.9	56	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l11; **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.
91	c1ytrA_	Alignment	not modelled	12.9	29	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bacteriocin plantaricin a; **PDBTitle:** nmr structure of plantaricin a in dpc micelles, 202 structures
92	d1o4xa1	Alignment	not modelled	12.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
93	c3zf7L_	Alignment	not modelled	12.7	86	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l11, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
94	c5ue8B_	Alignment	not modelled	12.7	9	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**protein unc-13 homolog a; **PDBTitle:** the crystal structure of munc13-1 c1c2bmun domain
95	c5mg3D_	Alignment	not modelled	12.6	8	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**protein translocase subunit secd; **PDBTitle:** em fitted model of bacterial holo-translocon
96	d1wpga4	Alignment	not modelled	12.2	10	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
97	c3ixzA_	Alignment	not modelled	12.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
98	d1uhsa_	Alignment	not modelled	12.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
99	c3okqA_	Alignment	not modelled	11.9	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6