Phyre^2

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Description	P32703
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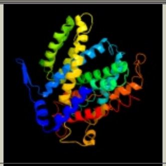
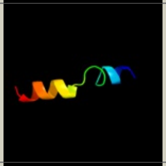
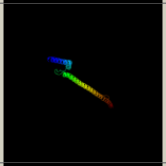
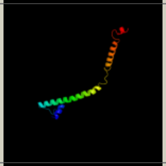
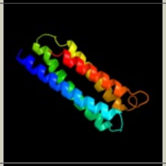
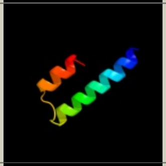
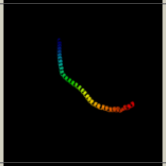
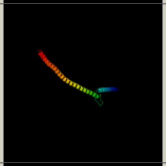
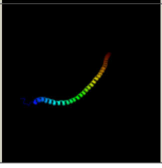
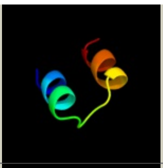
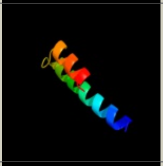
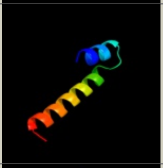
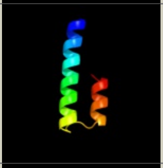
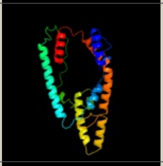
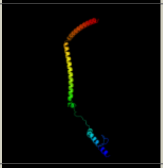
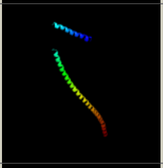
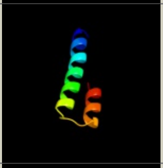
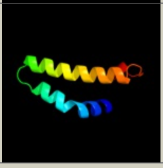
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zcdA_	Alignment		99.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na(+)/h(+) antiporter 1; **PDBTitle:** crystal structure of the na+/h+ antiporter nhaa
2	c2l0eA_	Alignment		93.7	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger
3	c2kbvA_	Alignment		84.4	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger
4	c3ojaB_	Alignment		43.8	11	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
5	d1f6ga_	Alignment		37.9	14	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
6	c3hzsA_	Alignment		33.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monofunctional glycosyltransferase; **PDBTitle:** s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
7	c1y4cA_	Alignment		32.4	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
8	d1vqop1	Alignment		29.1	19	**Fold:**Ribosomal protein L19 (L19e) **Superfamily:**Ribosomal protein L19 (L19e) **Family:**Ribosomal protein L19 (L19e)
9	c2zv4O_	Alignment		28.0	11	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
10	c3ojaA_	Alignment		25.2	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
11	c3dtpA_	Alignment		24.0	11	**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

12	d2csba1	Alignment		22.4	14	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
13	c4a1cO_	Alignment		22.3	16	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rpl19; **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.
14	c3exmA_	Alignment		20.6	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase sc4828; **PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
15	c2zkrp_	Alignment		20.6	19	**PDB header:**ribosomal protein/rna **Chain:** P: **PDB Molecule:**rna expansion segment es31 part i; **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
16	d2nwwa1	Alignment		19.8	19	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
17	c1i84V_	Alignment		19.7	15	**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.
18	c2dfsA_	Alignment		16.9	13	**PDB header:**contractile protein/transport protein **Chain:** A: **PDB Molecule:**myosin-5a; **PDBTitle:** 3-d structure of myosin-v inhibited state
19	c3iz5T_	Alignment		15.7	14	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l19 (l19e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
20	c3h36A_	Alignment		15.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyribonucleotide nucleotidyltransferase; **PDBTitle:** structure of an uncharacterized domain in polyribonucleotide2 nucleotidyltransferase from streptococcus mutans ua159
21	d2c0sa1	Alignment	not modelled	14.0	15	**Fold:**ROP-like **Superfamily:**BAS1536-like **Family:**BAS1536-like
22	c2v0pA_	Alignment	not modelled	13.7	8	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**type 2a phosphatase-associated protein 42; **PDBTitle:** the structure of tap42 alpha4 subunit
23	c1y4eA_	Alignment	not modelled	13.3	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
24	d2oqoa1	Alignment	not modelled	12.1	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
25	c3rl0j_	Alignment	not modelled	11.5	17	**PDB header:**membrane protein/exocytosis **Chain:** J: **PDB Molecule:**syntaxin-1a; **PDBTitle:** truncated snare complex with complexin (p1)
26	d1rkla_	Alignment	not modelled	11.2	21	**Fold:**Single transmembrane helix **Superfamily:**Oligosaccharyltransferase subunit ost4p **Family:**Oligosaccharyltransferase subunit ost4p
27	d2bzba1	Alignment	not modelled	10.5	22	**Fold:**ROP-like **Superfamily:**BAS1536-like **Family:**BAS1536-like
28	c3layF_	Alignment	not modelled	9.9	19	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
						PDB header:membrane protein

29	c1kilE_	Alignment	not modelled	9.7	14	**Chain:** E: **PDB Molecule:**complexin i snare-complex binding region; **PDBTitle:** three-dimensional structure of the complexin/snare complex
30	d1jkva_	Alignment	not modelled	9.4	24	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
31	c2l2lA_	Alignment	not modelled	9.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional repressor p66-alpha; **PDBTitle:** solution structure of the coiled-coil complex between mbd2 and2 p66alpha
32	c2akfA_	Alignment	not modelled	9.3	42	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
33	c2akfC_	Alignment	not modelled	9.3	42	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
34	c2akfB_	Alignment	not modelled	9.3	42	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
35	c3f1iH_	Alignment	not modelled	9.2	18	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
36	c2kncA_	Alignment	not modelled	9.1	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
37	c3lt7D_	Alignment	not modelled	8.9	25	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**adhesin yada; **PDBTitle:** a transition from strong right-handed to canonical left-handed2 supercoiling in a conserved coiled coil segment of trimeric3 autotransporter adhesins - the m3 mutant structure
38	c1ei3C_	Alignment	not modelled	8.8	9	**PDB header:** **PDB COMPND:**
39	c1nh2D_	Alignment	not modelled	8.7	21	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia small chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
40	c3dinD_	Alignment	not modelled	8.7	25	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
41	d2olua1	Alignment	not modelled	8.6	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
42	c2pfmA_	Alignment	not modelled	8.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
43	c2x7aB_	Alignment	not modelled	8.0	27	**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
44	d1v9va1	Alignment	not modelled	8.0	11	**Fold:**Bromodomain-like **Superfamily:**MAST3 pre-PK domain-like **Family:**MAST3 pre-PK domain-like
45	d2oeza1	Alignment	not modelled	8.0	20	**Fold:**YacF-like **Superfamily:**YacF-like **Family:**YacF-like
46	d1zk8a2	Alignment	not modelled	7.9	5	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
47	c3rkoF_	Alignment	not modelled	7.9	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
48	c2j9wB_	Alignment	not modelled	7.9	22	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vps28-prov protein; **PDBTitle:** structural insight into the escrt-i-ii link and its role in2 mvb trafficking
49	c1y66D_	Alignment	not modelled	7.7	27	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
50	d1c3ca_	Alignment	not modelled	7.6	13	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
51	d2j9ua1	Alignment	not modelled	7.5	22	**Fold:**Four-helical up-and-down bundle **Superfamily:**VPS28 C-terminal domain-like **Family:**VPS28 C-terminal domain-like
52	d2fcwa1	Alignment	not modelled	7.4	18	**Fold:**RAP domain-like **Superfamily:**RAP domain-like **Family:**RAP domain
53	c2qc7A_	Alignment	not modelled	7.4	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmic reticulum protein erp29; **PDBTitle:** crystal structure of the protein-disulfide isomerase related chaperone2 erp29
54	c1q90R_	Alignment	not modelled	7.2	16	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii

55	d1q90r_	Alignment	not modelled	7.2	16	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
56	c2qdqA_	Alignment	not modelled	7.2	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** crystal structure of the talin dimerisation domain
57	c2yvxD_	Alignment	not modelled	7.1	8	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
58	c3no7A_	Alignment	not modelled	7.1	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative plasmid related protein; **PDBTitle:** crystal structure of the centromere-binding protein parb from plasmid2 pcxc100
59	d1i0aa_	Alignment	not modelled	7.0	15	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
60	c1e3hA_	Alignment	not modelled	6.9	12	**PDB header:**polyribonucleotide transferase **Chain:** A: **PDB Molecule:**guanosine pentaphosphate synthetase; **PDBTitle:** semet derivative of streptomyces antibioticus pnpase/gpsi2 enzyme
61	c1oy8A_	Alignment	not modelled	6.8	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
62	d1kx5c_	Alignment	not modelled	6.8	27	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
63	d1iwga8	Alignment	not modelled	6.7	7	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
64	d1nh2d1	Alignment	not modelled	6.7	18	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
65	d2p12a1	Alignment	not modelled	6.5	12	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
66	d2oi8a2	Alignment	not modelled	6.5	11	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
67	c3qh9A_	Alignment	not modelled	6.4	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
68	c2e9fC_	Alignment	not modelled	6.3	24	**PDB header:**lyase **Chain:** C: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
69	c3zs9C_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
70	d1q90g_	Alignment	not modelled	6.3	18	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
71	c1q90G_	Alignment	not modelled	6.3	18	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**cytochrome b6f complex subunit petg; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
72	c3sjdE_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase/transport protein **Chain:** E: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain
73	c3c8tA_	Alignment	not modelled	6.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarate lyase; **PDBTitle:** crystal structure of fumarate lyase from mesorhizobium sp. bnc1
74	d1id3c_	Alignment	not modelled	6.3	27	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
75	d1eqza_	Alignment	not modelled	6.2	27	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
76	c2p90B_	Alignment	not modelled	6.2	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
77	c2w6aB_	Alignment	not modelled	6.2	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
78	d2ftua1	Alignment	not modelled	6.1	18	**Fold:**RAP domain-like **Superfamily:**RAP domain-like **Family:**RAP domain
79	c3q5dA_	Alignment	not modelled	6.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atlastin-1; **PDBTitle:** crystal structure of human atlastin-1 (residues 1-447) bound to gdp,2 crystal form 1
80	d1nvpd1	Alignment	not modelled	6.0	15	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
81	c1s5lL_	Alignment	not modelled	6.0	13	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center

82	c3a0bl_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
83	c3kziL_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
84	c3prqL_	Alignment	not modelled	6.0	13	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
85	c3prrL_	Alignment	not modelled	6.0	13	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
86	c3a0hl_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
87	c3arcL_	Alignment	not modelled	6.0	13	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
88	c3a0hL_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
89	c3a0bL_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
90	c1s5ll_	Alignment	not modelled	6.0	13	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
91	c2axtL_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
92	c2axtl_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
93	c3bz2L_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
94	c3bz1L_	Alignment	not modelled	6.0	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
95	d2axtl1	Alignment	not modelled	6.0	13	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
96	c3epvB_	Alignment	not modelled	6.0	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
97	d1q5na_	Alignment	not modelled	5.9	11	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
98	d1tj7a_	Alignment	not modelled	5.9	15	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
99	c3gaaB_	Alignment	not modelled	5.9	2	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ta1441; **PDBTitle:** the crystal structure of the protein with unknown function from2 thermoplasma acidophilum