Phyre2

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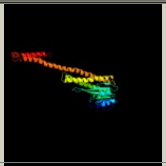
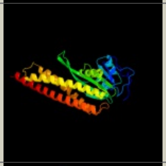
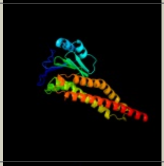
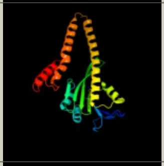
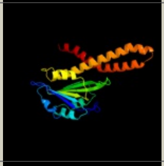
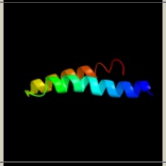
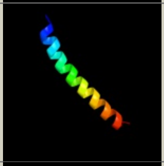
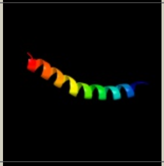
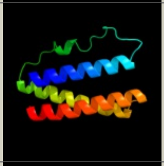
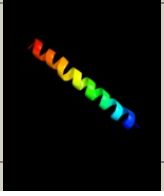
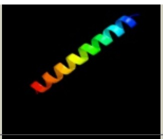
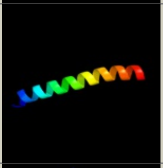
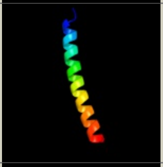
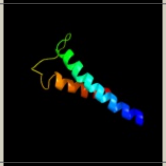
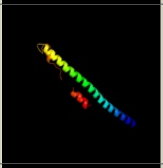
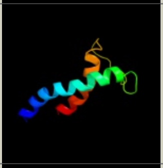
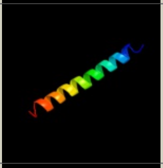
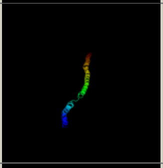
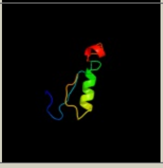
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bbjB_	Alignment		100.0	15	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
2	c3nwiC_	Alignment		100.0	90	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the soluble domain structure of the zntb zn2+ efflux system
3	d2iuba1	Alignment		100.0	15	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
4	c3ck6E_	Alignment		100.0	18	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**putative membrane transport protein; **PDBTitle:** crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
5	c2hn1A_	Alignment		100.0	16	**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	d2bbha1	Alignment		100.0	17	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
7	d2iuba2	Alignment		99.4	18	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
8	d3cx5d2	Alignment		64.2	13	**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
9	d1ppjd2	Alignment		63.2	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
10	c3fseB_	Alignment		33.0	9	**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
11	c1qcrD_	Alignment		29.7	19	**PDB header:** **PDB COMPND:**

12	c3cwbQ_	Alignment		27.8	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
13	c1p84D_	Alignment		27.3	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
14	c2yiuE_	Alignment		27.2	6	**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
15	c3dl8H_	Alignment		26.6	13	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
16	c1eboE_	Alignment		25.1	16	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**ebola virus envelope protein chimera consisting **PDBTitle:** crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
17	c3j01A_	Alignment		24.7	18	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
18	c2fynH_	Alignment		23.7	6	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
19	c3ghgK_	Alignment		21.7	10	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
20	c3tu8A_	Alignment		21.7	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**burkholderia lethal factor 1 (blf1); **PDBTitle:** crystal structure of the burkholderia lethal factor 1 (blf1)
21	c1zrtD_	Alignment	not modelled	20.7	9	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
22	c3mkuA_	Alignment	not modelled	18.7	13	**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
23	c1s1iJ_	Alignment	not modelled	18.6	43	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l11; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
24	c2akiY_	Alignment	not modelled	17.9	18	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
25	c4a1cD_	Alignment	not modelled	16.0	44	**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.
26	d1iwga8	Alignment	not modelled	15.2	11	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
27	c3rfuC_	Alignment	not modelled	15.2	10	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
						Fold: Long alpha-hairpin

28	d1e52a_	Alignment	not modelled	14.8	27	**Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
29	d2d69a2	Alignment	not modelled	14.7	20	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
30	c1dkgB_	Alignment	not modelled	14.4	18	**PDB header:**complex (hsp24/hsp70) **Chain:** B: **PDB Molecule:**nucleotide exchange factor grpe; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
31	c1oy8A_	Alignment	not modelled	13.6	24	**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
32	d1svda2	Alignment	not modelled	12.8	33	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
33	c1ei3E_	Alignment	not modelled	12.8	11	**PDB header:** **PDB COMPND:**
34	c2ks1B_	Alignment	not modelled	12.7	29	**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
35	c2cpbA_	Alignment	not modelled	12.4	9	**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
36	c2akfC_	Alignment	not modelled	11.6	12	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
37	c2akfB_	Alignment	not modelled	11.6	12	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
38	c2akfA_	Alignment	not modelled	11.6	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
39	d1bxna2	Alignment	not modelled	11.5	13	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
40	d1tqga_	Alignment	not modelled	11.5	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
41	d1i6za_	Alignment	not modelled	10.7	6	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
42	d1wh5a_	Alignment	not modelled	9.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
43	d2p61a1	Alignment	not modelled	9.6	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**TM1646-like **Family:**TM1646-like
44	c2xzm7_	Alignment	not modelled	9.4	20	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**plectin/s10 domain containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
45	c3qthA_	Alignment	not modelled	9.3	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical dinb-like protein (cps_3021) from2 colwellia psychrerythraea 34h at 2.20 a resolution
46	c2p61A_	Alignment	not modelled	9.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein tm_1646; **PDBTitle:** crystal structure of protein tm1646 from thermotoga2 maritima, pfam duf327
47	c3dinF_	Alignment	not modelled	8.8	18	**PDB header:**membrane protein, protein transport **Chain:** F: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
48	c2zqpY_	Alignment	not modelled	8.8	16	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
49	c1w5kB_	Alignment	not modelled	8.6	24	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
50	c1w5kC_	Alignment	not modelled	8.6	24	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
51	c1w5kA_	Alignment	not modelled	8.6	24	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
52	c1w5kD_	Alignment	not modelled	8.6	24	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
53	c3kyiA_	Alignment	not modelled	8.6	14	**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
						Fold: Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H,

54	d1rzhh2	Alignment	not modelled	8.5	36	transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
55	d2c2aa1	Alignment	not modelled	8.5	5	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
56	c2qupA_	Alignment	not modelled	8.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh1478 protein; **PDBTitle:** crystal structure of uncharacterized protein bh1478 from bacillus2 halodurans
57	c3u5gK_	Alignment	not modelled	8.1	16	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**40s ribosomal protein s10-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
58	d1l9bh2	Alignment	not modelled	7.9	36	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
59	c2oszA_	Alignment	not modelled	7.9	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
60	d1oe4a_	Alignment	not modelled	7.9	43	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
61	d1qoja_	Alignment	not modelled	7.7	28	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
62	c1htjF_	Alignment	not modelled	7.6	12	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**kiaa0380; **PDBTitle:** structure of the rgs-like domain from pdz-rhogef
63	d1htjf_	Alignment	not modelled	7.6	12	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
64	d1wpga4	Alignment	not modelled	7.6	8	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
65	c2oltB_	Alignment	not modelled	7.6	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution
66	d1wi3a_	Alignment	not modelled	7.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
67	c2y69Y_	Alignment	not modelled	7.6	13	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**cytochrome c oxidase subunit 7c; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
68	c3c0uA_	Alignment	not modelled	7.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yaeq; **PDBTitle:** crystal structure of e.coli yaeq protein
69	d1u5pa1	Alignment	not modelled	7.4	14	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
70	d1mh3a1	Alignment	not modelled	7.4	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
71	c3ixzA_	Alignment	not modelled	7.3	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
72	c2dceA_	Alignment	not modelled	7.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1915 protein; **PDBTitle:** solution structure of the swirm domain of human kiaa19152 protein
73	d1i5na_	Alignment	not modelled	7.3	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
74	c2lchA_	Alignment	not modelled	7.2	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or38; **PDBTitle:** solution nmr structure of a protein with a redesigned hydrophobic2 core, northeast structural genomics consortium target or38
75	c1s94A_	Alignment	not modelled	7.2	11	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**s-syntaxin; **PDBTitle:** crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
76	d1s94a_	Alignment	not modelled	7.2	11	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
77	d1h9aa2	Alignment	not modelled	7.2	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
78	c1kmiZ_	Alignment	not modelled	7.2	9	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
79	c3qnqD_	Alignment	not modelled	7.1	20	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific

						phosphotransferase system
80	c2wwbA_	Alignment	not modelled	7.1	11	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**protein transport protein sec61 subunit alpha isoform 1; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
81	c3r1fO_	Alignment	not modelled	7.1	11	**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
82	d1uhsa_	Alignment	not modelled	7.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
83	d9anta_	Alignment	not modelled	7.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
84	d1e3oc1	Alignment	not modelled	6.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	d1s35a2	Alignment	not modelled	6.9	8	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
86	d1d6za4	Alignment	not modelled	6.8	25	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
87	d8ruca2	Alignment	not modelled	6.8	13	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
88	c2vi6F_	Alignment	not modelled	6.7	17	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
89	d2rcrh2	Alignment	not modelled	6.7	36	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
90	c1nfoA_	Alignment	not modelled	6.7	4	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein e2; **PDBTitle:** apolipoprotein e2 (apoe2, d154a mutation)
91	c3movB_	Alignment	not modelled	6.7	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
92	c3b8eC_	Alignment	not modelled	6.6	13	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
93	d1eysh2	Alignment	not modelled	6.6	25	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
94	c1gk4A_	Alignment	not modelled	6.5	19	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
95	d1riqa1	Alignment	not modelled	6.5	12	**Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
96	d1le8a_	Alignment	not modelled	6.4	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	c3a7pB_	Alignment	not modelled	6.4	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
98	c2l2tA_	Alignment	not modelled	6.4	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
99	d1du0a_	Alignment	not modelled	6.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain