Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
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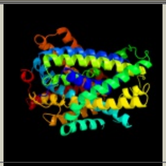
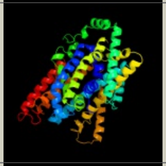
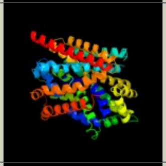
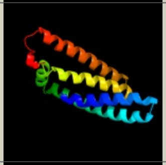
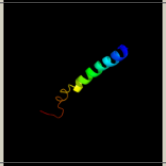
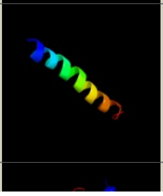
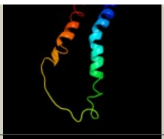
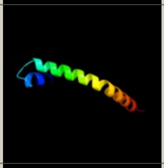
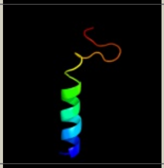
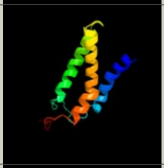
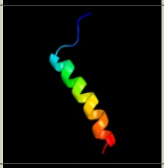
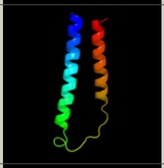
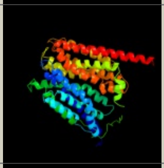
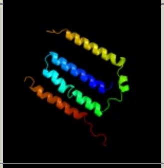
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
2	c3lrcC_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
3	c2jlnA_	Alignment		99.9	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	c2xq2A_	Alignment		99.3	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
5	c3dh4A_	Alignment		99.2	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	d2a65a1	Alignment		97.3	14	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
7	c2w8aC_	Alignment		96.1	10	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
8	c3hfxA_	Alignment		79.0	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
9	c3m7bA_	Alignment		57.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein teha homolog; **PDBTitle:** crystal structure of plant slac1 homolog teha
10	c2kncA_	Alignment		46.2	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
11	c2rddB_	Alignment		40.6	26	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.

12	d1fftb2	Alignment		37.8	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
13	c3qnqD_	Alignment		22.2	8	**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
14	c2kluA_	Alignment		21.6	14	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
15	c2qjkM_	Alignment		20.1	10	**PDB header:**electron transport **Chain:** M: **PDB Molecule:**cytochrome b; **PDBTitle:** crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
16	c2voyG_	Alignment		19.1	16	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
17	c1m57H_	Alignment		18.6	12	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
18	d1pw4a_	Alignment		17.4	11	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
19	c3rkoF_	Alignment		16.1	10	**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
20	c2jp3A_	Alignment		15.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
21	d3dtub2	Alignment	not modelled	15.3	12	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
22	d3ehbb2	Alignment	not modelled	15.0	19	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
23	c1qleB_	Alignment	not modelled	14.6	19	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
24	c1ar1B_	Alignment	not modelled	14.6	19	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
25	c1fftG_	Alignment	not modelled	14.3	9	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
26	c1ujlA_	Alignment	not modelled	13.9	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h **PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker
27	c2bbjB_	Alignment	not modelled	13.6	6	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
						Fold: MetI-like

28	d3dhwa1	Alignment	not modelled	13.3	12	**Superfamily:**MetI-like **Family:**MetI-like
29	d1jt8a_	Alignment	not modelled	13.2	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
30	c3cwbQ_	Alignment	not modelled	13.1	17	**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
31	c3aqpB_	Alignment	not modelled	13.0	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
32	d1iwga8	Alignment	not modelled	12.5	9	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
33	c3ixzA_	Alignment	not modelled	11.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
34	d2yvxa3	Alignment	not modelled	11.8	19	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
35	d1niga_	Alignment	not modelled	11.8	21	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238
36	d1pv7a_	Alignment	not modelled	11.4	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
37	c3rkoK_	Alignment	not modelled	11.3	12	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
38	c1qcrD_	Alignment	not modelled	11.2	17	**PDB header:** **PDB COMPND:**
39	c2e2sA_	Alignment	not modelled	11.1	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**agelenin; **PDBTitle:** solution structure of agelenin, an insecticidal peptide2 from the venom of agelena opulenta
40	c2k21A_	Alignment	not modelled	11.1	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
41	c2cpbA_	Alignment	not modelled	10.8	29	**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
42	c2k1kB_	Alignment	not modelled	10.8	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
43	c2k1lB_	Alignment	not modelled	10.8	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
44	c2k1lA_	Alignment	not modelled	10.8	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
45	c2k1kA_	Alignment	not modelled	10.8	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
46	c3aa0C_	Alignment	not modelled	10.0	38	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**21mer peptide from leucine-rich repeat-containing protein **PDBTitle:** crystal structure of actin capping protein in complex with the cp-2 binding motif derived from carmil
47	c2xutC_	Alignment	not modelled	9.9	7	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
48	c2jo1A_	Alignment	not modelled	9.9	11	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
49	c3b8eC_	Alignment	not modelled	9.7	8	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
50	c1p84D_	Alignment	not modelled	9.6	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
51	d1otsa_	Alignment	not modelled	9.5	22	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
52	d1zela1	Alignment	not modelled	9.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rv2827c N-terminal domain-like
						PDB header:lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yaji;

53	c2jwyA_	Alignment	not modelled	9.1	13	**PDBTitle:** solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540
54	d2iuba2	Alignment	not modelled	9.1	3	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
55	d1g2913	Alignment	not modelled	9.0	29	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
56	d2nr9a1	Alignment	not modelled	9.0	22	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like **Family:**Rhomboid-like
57	c3fh6F_	Alignment	not modelled	8.9	13	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
58	c1oy8A_	Alignment	not modelled	8.9	7	**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
59	c2dmpA_	Alignment	not modelled	8.9	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** solution structure of the third homeobox domain of zinc2 fingers and homeoboxes protein 2
60	c3njcA_	Alignment	not modelled	8.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yslb protein; **PDBTitle:** crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
61	d1v54d_	Alignment	not modelled	8.7	8	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
62	c2y69Q_	Alignment	not modelled	8.6	8	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
63	c2h3oA_	Alignment	not modelled	8.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
64	d2oara1	Alignment	not modelled	8.4	17	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
65	c2oarA_	Alignment	not modelled	8.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
66	c2k1aA_	Alignment	not modelled	8.2	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
67	c2l3hA_	Alignment	not modelled	8.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prostatic acid phosphatase; **PDBTitle:** nmr structure in a membrane environment reveals putative amyloidogenic2 regions of the sevi precursor peptide pap248-286
68	d1j9ia_	Alignment	not modelled	8.2	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
69	c3ixxE_	Alignment	not modelled	8.2	25	**PDB header:**virus **Chain:** E: **PDB Molecule:**peptide pr; **PDBTitle:** the pseudo-atomic structure of west nile immature virus in2 complex with fab fragments of the anti-fusion loop antibody3 e53
70	c3r7gB_	Alignment	not modelled	8.1	8	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**formin-2; **PDBTitle:** crystal structure of spire kind domain in complex with the tail of2 fmn2
71	c2jo8B_	Alignment	not modelled	8.1	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
72	d1rhzb_	Alignment	not modelled	8.0	18	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
73	c2cblA_	Alignment	not modelled	8.0	24	**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 on zap-70
74	d1zh5a1	Alignment	not modelled	8.0	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
75	c3bunB_	Alignment	not modelled	8.0	24	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
76	d1t98a2	Alignment	not modelled	7.9	21	**Fold:**STAT-like **Superfamily:**MukF C-terminal domain-like **Family:**MukF C-terminal domain-like
77	c1wazA_	Alignment	not modelled	7.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
						Fold: Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H,

78	d1eysh2	Alignment	not modelled	7.7	19	transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
79	c3lk2T_	Alignment	not modelled	7.7	50	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
80	c3c6eC_	Alignment	not modelled	7.7	43	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**prm; **PDBTitle:** crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the dengue 2 virus at neutral ph
81	c3mk7F_	Alignment	not modelled	7.7	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
82	c3opyJ_	Alignment	not modelled	7.6	18	**PDB header:**transferase **Chain:** J: **PDB Molecule:**6-phosphofructo-1-kinase gamma-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
83	c3opyL_	Alignment	not modelled	7.6	18	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6-phosphofructo-1-kinase gamma-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
84	c3p5nA_	Alignment	not modelled	7.6	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**riboflavin uptake protein; **PDBTitle:** structure and mechanism of the s component of a bacterial ecf2 transporter
85	c3hzqA_	Alignment	not modelled	7.6	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
86	c3c6rE_	Alignment	not modelled	7.5	43	**PDB header:**virus **Chain:** E: **PDB Molecule:**peptide pr; **PDBTitle:** low ph immature dengue virus
87	c2k9yB_	Alignment	not modelled	7.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
88	c2k9yA_	Alignment	not modelled	7.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
89	d2h8pc1	Alignment	not modelled	7.3	9	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
90	c3nauA_	Alignment	not modelled	7.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
91	d1zyba1	Alignment	not modelled	7.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
92	d1rh5b_	Alignment	not modelled	7.2	18	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
93	d2ecba1	Alignment	not modelled	7.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	c2zxeA_	Alignment	not modelled	7.2	11	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
95	d2e2ca_	Alignment	not modelled	7.2	14	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
96	c2l2tA_	Alignment	not modelled	7.1	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
97	c3iz5d_	Alignment	not modelled	7.0	19	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4 (l4p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
98	d1ubdc2	Alignment	not modelled	7.0	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
99	c3op0B_	Alignment	not modelled	7.0	18	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide