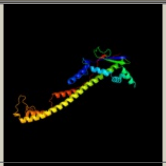
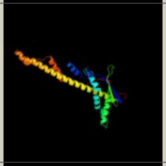
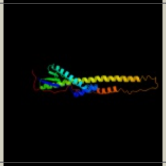
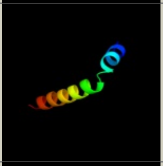
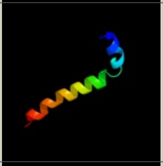
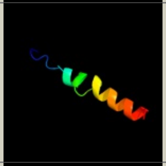
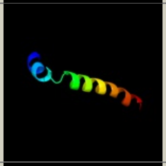
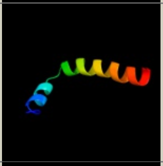
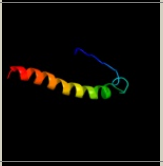
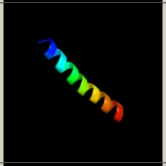
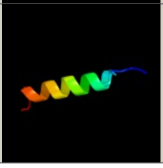
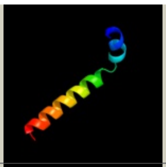
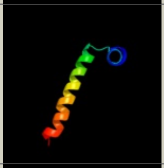
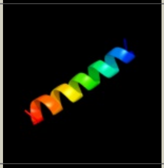
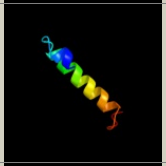
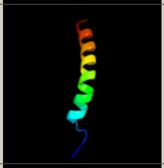
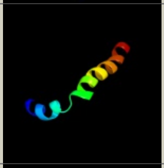
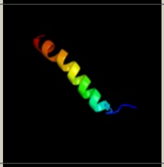
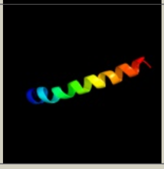
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AG00
Date	Thu Jan 5 11:27:42 GMT 2012
Unique Job ID	4018e5160322fa19

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3b8ma1	Alignment		99.7	18	**Fold:**Ferredoxin-like **Superfamily:**Bacterial polysaccharide co-polymerase-like **Family:**FepE-like
2	d3b8oa1	Alignment		99.6	94	**Fold:**Ferredoxin-like **Superfamily:**Bacterial polysaccharide co-polymerase-like **Family:**FepE-like
3	d3b8pa1	Alignment		99.2	26	**Fold:**Ferredoxin-like **Superfamily:**Bacterial polysaccharide co-polymerase-like **Family:**FepE-like
4	c2yl4A_	Alignment		67.4	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter, abcb10
5	d2hyda2	Alignment		60.3	9	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
6	c2rmzA_	Alignment		56.7	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
7	c2hydB_	Alignment		46.8	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
8	d1pf4a2	Alignment		43.5	18	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
9	d1pw4a_	Alignment		43.4	18	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
10	c3hd7A_	Alignment		39.0	19	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
11	c3ij4A_	Alignment		35.2	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amiloride-sensitive cation channel 2, neuronal; **PDBTitle:** cesium sites in the crystal structure of a functional acid2 sensing ion channel in the desensitized state

12	d3b60a2	Alignment		32.1	34	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
13	c3g5uB_	Alignment		29.8	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
14	c2kncA_	Alignment		27.8	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
15	d2r6gf1	Alignment		22.8	15	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
16	c2qtsA_	Alignment		21.1	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acid-sensing ion channel; **PDBTitle:** structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph
17	c3b5wE_	Alignment		21.1	34	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
18	c2y69Z_	Alignment		20.7	20	**PDB header:**electron transport **Chain:** Z: **PDB Molecule:**cytochrome c oxidase polypeptide 8h; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
19	d1v54m_	Alignment		20.4	20	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
20	c2yvxD_	Alignment		19.5	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
21	c2k21A_	Alignment	not modelled	16.5	19	**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
22	d1xrda1	Alignment	not modelled	16.5	16	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
23	d1rhzb_	Alignment	not modelled	15.9	15	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
24	c2e75E_	Alignment	not modelled	15.8	17	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
25	d2e74e1	Alignment	not modelled	15.8	17	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
26	c1vf5R_	Alignment	not modelled	15.8	17	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
27	c2e76E_	Alignment	not modelled	15.8	17	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
28	c2e74E_	Alignment	not modelled	15.8	17	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus

29	d1v54d_	Alignment	not modelled	15.1	5	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
30	c2y69Q_	Alignment	not modelled	14.8	5	**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
31	c3b5xB_	Alignment	not modelled	13.4	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
32	c1vf5E_	Alignment	not modelled	13.4	18	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
33	c3ixzB_	Alignment	not modelled	11.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
34	c2k1aA_	Alignment	not modelled	11.8	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
35	c3arct_	Alignment	not modelled	11.4	14	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
36	c3k07A_	Alignment	not modelled	11.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
37	d2alea1	Alignment	not modelled	10.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
38	d1ctja_	Alignment	not modelled	9.8	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
39	c3si5X_	Alignment	not modelled	9.8	25	**PDB header:**cell cycle **Chain:** X: **PDB Molecule:**protein casc5; **PDBTitle:** kinetochore-bubr1 kinase complex
40	c2kncB_	Alignment	not modelled	9.8	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
41	c2l2tA_	Alignment	not modelled	9.6	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
42	c2o01L_	Alignment	not modelled	9.2	27	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
43	d1c6ra_	Alignment	not modelled	8.8	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
44	d1v54g_	Alignment	not modelled	8.5	8	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
45	d1xmec1	Alignment	not modelled	8.4	21	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa
46	d1nwaa_	Alignment	not modelled	8.4	19	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
47	c1nwaA_	Alignment	not modelled	8.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
48	c2wwbB_	Alignment	not modelled	8.2	21	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
49	d1y5ic1	Alignment	not modelled	7.8	34	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain
50	c3b8eB_	Alignment	not modelled	7.7	20	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
51	c3sc0A_	Alignment	not modelled	7.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methylmalonic aciduria and homocystinuria type c protein; **PDBTitle:** crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
52	c1kqfB_	Alignment	not modelled	7.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
53	c3ghfA_	Alignment	not modelled	7.4	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
						PDB header:viral protein

54	c2kvlA_	Alignment	not modelled	7.3	11	**Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
55	c2wwbC_	Alignment	not modelled	7.3	16	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**protein transport protein sec61 subunit beta; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
56	c1fvaA_	Alignment	not modelled	7.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of bovine methionine sulfoxide reductase
57	c2j89A_	Alignment	not modelled	7.1	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine sulfoxide reductase a; **PDBTitle:** functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
58	c3bqhA_	Alignment	not modelled	7.1	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb; **PDBTitle:** structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
59	c2k1lA_	Alignment	not modelled	7.0	21	**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
60	c2k1kB_	Alignment	not modelled	7.0	21	**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
61	c2k1lB_	Alignment	not modelled	7.0	21	**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
62	c2k1kA_	Alignment	not modelled	7.0	21	**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
63	c2ht2B_	Alignment	not modelled	6.9	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
64	d1ff3c_	Alignment	not modelled	6.8	13	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
65	d1v54l_	Alignment	not modelled	6.7	19	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa) **Family:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)
66	d1fvga_	Alignment	not modelled	6.7	12	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
67	c1ps9A_	Alignment	not modelled	6.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
68	c1xl6B_	Alignment	not modelled	6.6	6	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**inward rectifier potassium channel; **PDBTitle:** intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
69	d1jr1a4	Alignment	not modelled	6.6	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
70	d1ff3a_	Alignment	not modelled	6.5	12	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
71	c1amlA_	Alignment	not modelled	6.5	33	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**amyloid a4; **PDBTitle:** the alzheimer`s disease amyloid a4 peptide (residues 1-40)
72	c3pilA_	Alignment	not modelled	6.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
73	d1cpca_	Alignment	not modelled	6.3	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
74	c3a0bx_	Alignment	not modelled	6.1	17	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
75	c3a0bX_	Alignment	not modelled	6.1	17	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
76	c3a0hX_	Alignment	not modelled	6.1	17	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
77	c3a0hx_	Alignment	not modelled	6.1	17	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
78	d1xk4c1	Alignment	not modelled	6.0	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
79	d1otsa_	Alignment	not modelled	6.0	22	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
						Fold: Globin-like

80	d1jboa_	Alignment	not modelled	6.0	5	**Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
81	c3dmiA_	Alignment	not modelled	5.9	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** crystallization and structural analysis of cytochrome c62 from the diatom phaeodactylum tricornutum at 1.5 a3 resolution
82	d2i5nh2	Alignment	not modelled	5.8	11	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
83	c2l9uA_	Alignment	not modelled	5.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
84	c2kluA_	Alignment	not modelled	5.7	15	**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
85	c2gqcA_	Alignment	not modelled	5.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rhomboid intramembrane protease; **PDBTitle:** solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
86	c1s5lx_	Alignment	not modelled	5.6	17	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
87	c1kveA_	Alignment	not modelled	5.6	31	**PDB header:**toxin **Chain:** A: **PDB Molecule:**smk toxin; **PDBTitle:** killer toxin from halotolerant yeast
88	c3kdpG_	Alignment	not modelled	5.6	25	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
89	c3kdpH_	Alignment	not modelled	5.6	25	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
90	c2k9yB_	Alignment	not modelled	5.6	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
91	c2k9yA_	Alignment	not modelled	5.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
92	c1ql1A_	Alignment	not modelled	5.5	26	**PDB header:**virus **Chain:** A: **PDB Molecule:**pf1 bacteriophage coat protein b; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
93	c1ronA_	Alignment	not modelled	5.5	19	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**neuropeptide y; **PDBTitle:** nmr solution structure of human neuropeptide y
94	d1f1fa_	Alignment	not modelled	5.4	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
95	c3e0mB_	Alignment	not modelled	5.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
96	d2guka1	Alignment	not modelled	5.3	38	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
97	d1gdva_	Alignment	not modelled	5.3	10	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
98	d1w36c3	Alignment	not modelled	5.3	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Exodeoxyribonuclease V beta chain (RecC), C-terminal domain
99	c3dr0B_	Alignment	not modelled	5.2	8	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002