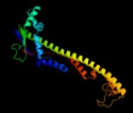
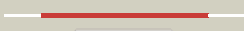
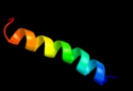
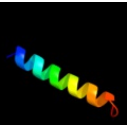
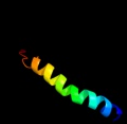
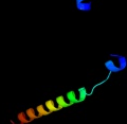


Phyre2

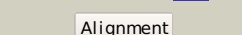
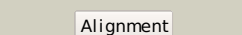
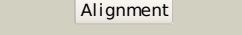
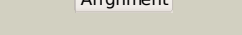
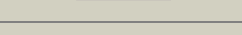
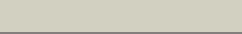
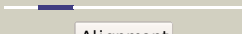
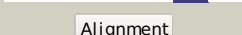
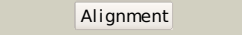
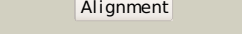
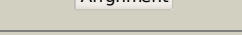
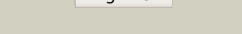
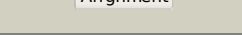
Email	I.a.kelley@imperial.ac.uk
Description	P26266
Date	Thu Jan 5 11:42:50 GMT 2012
Unique Job ID	1d20f32957d51675

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3b8ma1	 Alignment		99.8	97	Fold: Ferredoxin-like Superfamily: Bacterial polysaccharide co-polymerase-like Family: FepE-like
2	d3b8oa1	 Alignment		99.2	19	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		63.4	9	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	c2rmzA_	 Alignment		61.7	29	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
6	c2klua_	 Alignment		56.6	13	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
7	c2qtsA_	 Alignment		54.2	4	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
8	d2hyda2	 Alignment		50.5	9	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
9	c2k1kA_	 Alignment		48.9	20	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
10	c2k1lA_	 Alignment		48.9	20	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
11	c2k1lB_	 Alignment		48.9	20	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

12	c2k1kB_	Alignment		48.9	20	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
13	c2k21A_	Alignment		43.3	10	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
14	c2hydB_	Alignment		36.5	9	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
15	d1pf4a2	Alignment		35.8	9	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
16	c2kncA_	Alignment		33.2	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
17	c3hd7A_	Alignment		29.6	15	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
18	c3g5uB_	Alignment		28.5	11	PDB header: membrane protein Chain: B: PDB Molecule: multi-drug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
19	d1v54d_	Alignment		27.7	8	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
20	c2y69Q_	Alignment		27.3	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
21	d3b60a2	Alignment	not modelled	26.5	13	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
22	d1rhzb_	Alignment	not modelled	22.9	13	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
23	c3ij4A_	Alignment	not modelled	22.7	13	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
24	c2l34B_	Alignment	not modelled	21.6	21	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
25	c2l34A_	Alignment	not modelled	21.6	21	PDB header: protein binding Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
26	d1y5ic1	Alignment	not modelled	19.9	11	Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain
27	c3b5wE_	Alignment	not modelled	17.5	13	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
28	d1v54m_	Alignment	not modelled	17.1	17	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) Family: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)

29	c2y69Z_	Alignment	not modelled	16.5	17	PDB header: electron transport Chain: Z: PDB Molecule: cytochrome c oxidase polypeptide 8h; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
30	c3sc0A_	Alignment	not modelled	16.1	32	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
31	c1vf5R_	Alignment	not modelled	15.4	22	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
32	d2e74e1	Alignment	not modelled	15.4	22	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
33	c1vf5E_	Alignment	not modelled	15.4	22	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
34	c2e74E_	Alignment	not modelled	15.4	22	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
35	c2e75E_	Alignment	not modelled	15.4	22	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
36	c2e76E_	Alignment	not modelled	15.4	22	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
37	d1v54q_	Alignment	not modelled	15.0	8	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
38	c3k07A_	Alignment	not modelled	13.1	13	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
39	d2r6gf1	Alignment	not modelled	12.0	10	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
40	c3b5xB_	Alignment	not modelled	11.2	9	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
41	c2l35B_	Alignment	not modelled	10.5	13	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
42	c2l2tA_	Alignment	not modelled	10.4	15	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
43	c2k1aA_	Alignment	not modelled	10.4	9	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: bicelle-embedded integrin alpha(iiib) transmembrane segment
44	d1v54l_	Alignment	not modelled	10.3	11	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIla) Family: Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIla)
45	c2l35A_	Alignment	not modelled	10.2	21	PDB header: protein binding Chain: A: PDB Molecule: dap12-nkg2c tm; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
46	c2yvxD_	Alignment	not modelled	9.5	0	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
47	d1xrda1	Alignment	not modelled	9.4	19	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
48	d1pw4a_	Alignment	not modelled	9.2	16	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
49	c1kqfB_	Alignment	not modelled	8.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
50	d1rh5b_	Alignment	not modelled	8.5	14	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
51	c2ht2B_	Alignment	not modelled	8.3	9	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
52	c2y69Y_	Alignment	not modelled	8.3	10	PDB header: electron transport Chain: Y: PDB Molecule: cytochrome c oxidase subunit 7c; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
53	c2kb1A_	Alignment	not modelled	8.0	13	PDB header: membrane protein Chain: A: PDB Molecule: wsk3; PDBTitle: nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsc
54	d1lotsa_	Alignment	not modelled	7.8	9	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel

55	c2wwbC_	 Alignment	not modelled	7.5	22	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	c2wwbB_	 Alignment	not modelled	7.5	16	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
57	c1m2zE_	 Alignment	not modelled	7.3	25	PDB header: hormone/hormone activator Chain: E: PDB Molecule: nuclear receptor coactivator 2; PDBTitle: crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif
58	c1ps9A_	 Alignment	not modelled	7.1	17	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
59	c2jwaA_	 Alignment	not modelled	6.9	20	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
60	d2e74d2	 Alignment	not modelled	6.9	13	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
61	d1o73a_	 Alignment	not modelled	6.7	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
62	c3ipdB_	 Alignment	not modelled	6.7	12	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
63	c2kvlA_	 Alignment	not modelled	6.6	19	PDB header: viral protein Chain: A: PDB Molecule: major outer capsid protein vp7; PDBTitle: nmr structure of the c-terminal domain of vp7
64	c1m2zB_	 Alignment	not modelled	6.6	25	PDB header: hormone/hormone activator Chain: B: PDB Molecule: nuclear receptor coactivator 2; PDBTitle: crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif
65	c2k9yA_	 Alignment	not modelled	6.5	14	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
66	c2k9yB_	 Alignment	not modelled	6.5	14	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
67	c1xl6B_	 Alignment	not modelled	6.5	13	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
68	c2j7aC_	 Alignment	not modelled	6.5	5	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c quinol dehydrogenase nrhf; PDBTitle: crystal structure of cytochrome c nitrite reductase nrha2 complex from desulfovibrio vulgaris
69	c1ijA_	 Alignment	not modelled	6.4	13	PDB header: signaling protein Chain: A: PDB Molecule: erbb-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbb-2 membrane spanning2 segment
70	d1nwaa_	 Alignment	not modelled	6.3	13	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
71	c1nwaA_	 Alignment	not modelled	6.3	13	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
72	c2o01L_	 Alignment	not modelled	6.3	13	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
73	c3p5nA_	 Alignment	not modelled	6.1	8	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
74	d2yvxa3	 Alignment	not modelled	6.1	8	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
75	d1fftb2	 Alignment	not modelled	6.0	10	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
76	c2ks1B_	 Alignment	not modelled	6.0	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
77	c1fvaA_	 Alignment	not modelled	5.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of bovine methionine sulfoxide reductase
78	c2gqcA_	 Alignment	not modelled	5.7	31	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
79	c3a0hx_	Alignment	not modelled	5.7	11	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex

80	c3a0bX_	Alignment	not modelled	5.7	11	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
81	c3a0hX_	Alignment	not modelled	5.7	11	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
82	c3a0bx_	Alignment	not modelled	5.7	11	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
83	c1q2iA_	Alignment	not modelled	5.7	26	PDB header: antitumor protein Chain: A: PDB Molecule: pnc27; PDBTitle: nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
84	d1kqfb2	Alignment	not modelled	5.7	6	Fold: Single transmembrane helix Superfamily: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor Family: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
85	c3jycA_	Alignment	not modelled	5.5	7	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
86	c3ghfA_	Alignment	not modelled	5.5	9	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
87	c2h4bC_	Alignment	not modelled	5.4	29	PDB header: de novo protein Chain: C: PDB Molecule: pancreatic hormone; PDBTitle: cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
88	c2h3sB_	Alignment	not modelled	5.4	29	PDB header: de novo protein Chain: B: PDB Molecule: pancreatic hormone; PDBTitle: cis-azobenzene-avian pancreatic polypeptide bound to dpc2 micelles
89	c2h4bD_	Alignment	not modelled	5.4	29	PDB header: de novo protein Chain: D: PDB Molecule: pancreatic hormone; PDBTitle: cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
90	d1q90d_	Alignment	not modelled	5.4	14	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
91	c2j89A_	Alignment	not modelled	5.4	38	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
92	d1reoa1	Alignment	not modelled	5.4	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
93	c2kncB_	Alignment	not modelled	5.4	18	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfa iib-beta3 transmembrane-cytoplasmic2 heterocomplex
94	c1xopA_	Alignment	not modelled	5.3	30	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
95	c1s5lx_	Alignment	not modelled	5.3	11	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii psbx protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
96	c3bqhA_	Alignment	not modelled	5.3	13	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)
97	d3cmna1	Alignment	not modelled	5.2	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Caur0242-like
98	d1lfma_	Alignment	not modelled	5.2	8	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
99	d2pila_	Alignment	not modelled	5.2	6	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin