
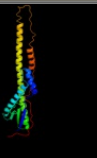



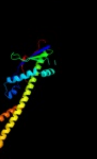

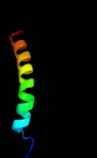



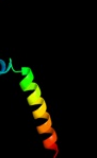



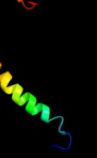

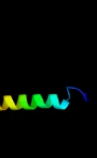




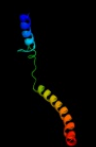
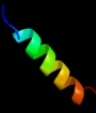



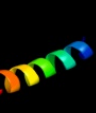

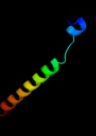



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76372
Date	Thu Jan 5 12:22:26 GMT 2012
Unique Job ID	3521ed868d64930c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3b8pa1	 Alignment		99.7	70	Fold: Ferredoxin-like Superfamily: Bacterial polysaccharide co-polymerase-like Family: FepE-like
2	d3b8ma1	 Alignment		99.6	19	Fold: Ferredoxin-like Superfamily: Bacterial polysaccharide co-polymerase-like Family: FepE-like
3	d3b8oa1	 Alignment		99.3	24	Fold: Ferredoxin-like Superfamily: Bacterial polysaccharide co-polymerase-like Family: FepE-like
4	c2qtsA	 Alignment		60.8	13	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
5	c2rmzA	 Alignment		56.3	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
6	c2yl4A	 Alignment		46.2	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
7	c2k1kA	 Alignment		42.2	31	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
8	c2k1lB	 Alignment		42.2	31	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
9	c2k1kB	 Alignment		42.2	31	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
10	c2k1lA	 Alignment		42.0	38	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	d2hyda2	 Alignment		41.8	19	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region

12	d1rhzb_	Alignment		35.3	15	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
13	c3ij4A_	Alignment		33.4	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
14	c3hd7A_	Alignment		33.0	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
15	d1pf4a2	Alignment		30.7	15	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
16	c2hydB_	Alignment		29.1	19	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
17	c2kncA_	Alignment		25.5	9	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
18	d1v54d_	Alignment		25.0	13	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
19	c2y69Q_	Alignment		24.4	13	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
20	c3g5uB_	Alignment		22.0	6	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
21	d3b60a2	Alignment	not modelled	21.4	19	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
22	c1vf5R_	Alignment	not modelled	20.1	22	PDB header: photosynthesis Chain: R: PDB Molecule: protein petI; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
23	c2e74E_	Alignment	not modelled	20.1	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
24	c2e75E_	Alignment	not modelled	20.1	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
25	d2e74e1	Alignment	not modelled	20.1	22	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
26	c2e76E_	Alignment	not modelled	20.1	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
27	d1nwaa_	Alignment	not modelled	19.5	31	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
28	c1nwaA_	Alignment	not modelled	19.5	31	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

29	c2y69Z_	Alignment	not modelled	19.0	27	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	c2yvxD_	Alignment	not modelled	18.5	3	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
31	c1vf5E_	Alignment	not modelled	18.3	24	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
32	d2axth1	Alignment	not modelled	18.3	27	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like
33	d1v54m_	Alignment	not modelled	17.9	27	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) Family: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
34	d1v54l_	Alignment	not modelled	16.5	19	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIla) Family: Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIla)
35	c2j89A_	Alignment	not modelled	15.8	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
36	c3bqhA_	Alignment	not modelled	15.1	31	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)
37	c3k07A_	Alignment	not modelled	14.8	0	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
38	d2r6gf1	Alignment	not modelled	14.4	12	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
39	c3b5wE_	Alignment	not modelled	13.2	16	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
40	c1fvaA_	Alignment	not modelled	13.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of bovine methionine sulfoxide reductase
41	d1ff3c_	Alignment	not modelled	12.4	38	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
42	d1xrda1	Alignment	not modelled	11.9	15	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
43	d1ff3a_	Alignment	not modelled	11.3	35	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
44	c3pilA_	Alignment	not modelled	11.1	31	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
45	c2o01L_	Alignment	not modelled	10.5	20	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
46	d1fvga_	Alignment	not modelled	10.3	35	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
47	c2kncB_	Alignment	not modelled	10.2	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
48	c1qcrD_	Alignment	not modelled	10.2	12	PDB header: PDB COMPND:
49	c2k21A_	Alignment	not modelled	10.2	14	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
50	c3b5xB_	Alignment	not modelled	10.2	16	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
51	c3e0mB_	Alignment	not modelled	10.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
52	c3cwbQ_	Alignment	not modelled	9.9	9	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
53	d2e74d2	Alignment	not modelled	9.3	22	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
54	c1kveA_	Alignment	not modelled	8.8	27	PDB header: toxin Chain: A: PDB Molecule: smk toxin; PDBTitle: killer toxin from halotolerant yeast

55	c2k1aA	Alignment	not modelled	8.8	25	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
56	c1ps9A	Alignment	not modelled	8.7	20	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
57	c1zrtD	Alignment	not modelled	8.6	18	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
58	c1m2zE	Alignment	not modelled	8.0	44	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
59	c1p84D	Alignment	not modelled	8.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
60	d1rh5b	Alignment	not modelled	7.8	18	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
61	c2y69Y	Alignment	not modelled	7.7	17	PDB header: electron transport Chain: Y: PDB Molecule: cytochrome c oxidase subunit 7c; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
62	d1pw4a	Alignment	not modelled	7.4	8	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
63	d1ylfa1	Alignment	not modelled	7.3	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
64	c1m2zB	Alignment	not modelled	7.2	44	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	d1xmec1	Alignment	not modelled	7.2	32	Fold: Single transmembrane helix Superfamily: Bacterial ba3 type cytochrome c oxidase subunit IIa Family: Bacterial ba3 type cytochrome c oxidase subunit IIa
66	d1jb0L	Alignment	not modelled	7.1	8	Fold: Photosystem I reaction center subunit XI, PsaL Superfamily: Photosystem I reaction center subunit XI, PsaL Family: Photosystem I reaction center subunit XI, PsaL
67	c3ipdB	Alignment	not modelled	7.1	15	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
68	d2e74g1	Alignment	not modelled	7.1	23	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
69	c3ixzB	Alignment	not modelled	7.1	25	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
70	c1vf5G	Alignment	not modelled	7.0	23	PDB header: photosynthesis Chain: G: PDB Molecule: protein pet g; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
71	d1vf5g	Alignment	not modelled	7.0	23	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
72	c2l2tA	Alignment	not modelled	7.0	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
73	c3p5nA	Alignment	not modelled	7.0	18	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	d1xd7a	Alignment	not modelled	6.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
75	c1ql1A	Alignment	not modelled	6.8	11	PDB header: virus Chain: A: PDB Molecule: pf1 bacteriophage coat protein b; PDBTitle: inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
76	c3m9bK	Alignment	not modelled	6.7	27	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
77	d1kqfb2	Alignment	not modelled	6.6	17	Fold: Single transmembrane helix Superfamily: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor Family: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
78	c2klua	Alignment	not modelled	6.6	24	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
79	c3b8eB	Alignment	not modelled	6.6	27	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump

80	d1otsa_	Alignment	not modelled	6.5	13	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
81	c3lwfD_	Alignment	not modelled	6.5	44	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
82	c2lbgA_	Alignment	not modelled	6.5	27	PDB header: membrane protein Chain: A: PDB Molecule: major prion protein; PDBTitle: structure of the chr of the prion protein in dpc micelles
83	c2kb1A_	Alignment	not modelled	6.5	6	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 kcsa
84	c3ghfA_	Alignment	not modelled	6.3	13	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
85	c3k69A_	Alignment	not modelled	6.2	21	PDB header: transcription Chain: A: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
86	c2ht2B_	Alignment	not modelled	6.2	13	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
87	c2y75F_	Alignment	not modelled	6.2	25	PDB header: transcription Chain: F: PDB Molecule: hth-type transcriptional regulator cymr; PDBTitle: the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
88	d2nr9a1	Alignment	not modelled	6.1	23	Fold: Rhomboid-like Superfamily: Rhomboid-like Family: Rhomboid-like
89	c2wscL_	Alignment	not modelled	6.1	15	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem i reaction center subunit xi, PDBTitle: improved model of plant photosystem i
90	c1amlA_	Alignment	not modelled	6.0	44	PDB header: serine protease inhibitor Chain: A: PDB Molecule: amyloid a4; PDBTitle: the alzheimer`s disease amyloid a4 peptide (residues 1-40)
91	c3n4xB_	Alignment	not modelled	5.9	6	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
92	d2yvxa3	Alignment	not modelled	5.9	3	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
93	d1reoa1	Alignment	not modelled	5.8	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
94	c3mp7A_	Alignment	not modelled	5.7	18	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase subunit secy; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
95	c2onkC_	Alignment	not modelled	5.7	6	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
96	d2onkc1	Alignment	not modelled	5.7	6	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
97	d1fftb2	Alignment	not modelled	5.6	13	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
98	c3a0hX_	Alignment	not modelled	5.6	33	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
99	c3a0hx_	Alignment	not modelled	5.6	33	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex