








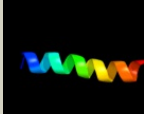



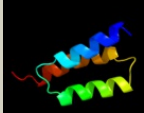



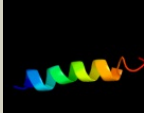


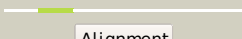
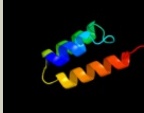
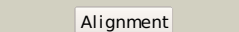





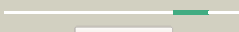
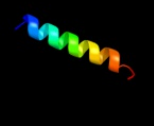










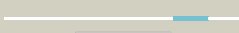
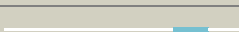







# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P02976
Date	Tue Jul 17 17:05:03 BST 2012
Unique Job ID	85d469624602092c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1gjsa_</a>	 Alignment		90.4	9	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> GA module, an albumin-binding domain
2	<a href="#">c2fs1A_</a>	 Alignment		88.7	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> psd-1; <b>PDBTitle:</b> solution structure of psd-1
3	<a href="#">d1edla_</a>	 Alignment		87.4	100	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> Immunoglobulin-binding protein A modules
4	<a href="#">c2jp3A_</a>	 Alignment		84.7	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fyxd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
5	<a href="#">c2jo1A_</a>	 Alignment		83.7	36	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
6	<a href="#">d1lp1a_</a>	 Alignment		83.6	55	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> Immunoglobulin-binding protein A modules
7	<a href="#">d2jwda1</a>	 Alignment		75.8	74	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> Immunoglobulin-binding protein A modules
8	<a href="#">c3kdpH_</a>	 Alignment		74.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
9	<a href="#">c3kdpG_</a>	 Alignment		74.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
10	<a href="#">d1lp1b_</a>	 Alignment		70.0	73	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> Immunoglobulin-binding protein A modules
11	<a href="#">d1deeg_</a>	 Alignment		65.6	84	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> Immunoglobulin-binding protein A modules

12	<a href="#">d1ppjw_</a>	 Alignment		55.2	14	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
13	<a href="#">d3cx5l_</a>	 Alignment		48.8	10	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
14	<a href="#">d1fc2c_</a>	 Alignment		47.6	74	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> Immunoglobulin-binding protein A modules
15	<a href="#">c2zxeG_</a>	 Alignment		46.2	9	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
16	<a href="#">c2ariA_</a>	 Alignment		43.4	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope polyprotein gp160; <b>PDBTitle:</b> solution structure of micelle-bound fusion domain of hiv-12 gp41
17	<a href="#">c2k1lB_</a>	 Alignment		41.1	31	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
18	<a href="#">c2k1lA_</a>	 Alignment		41.1	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
19	<a href="#">c2k1kA_</a>	 Alignment		41.1	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
20	<a href="#">c2k1kB_</a>	 Alignment		41.1	31	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
21	<a href="#">c3n23E_</a>	 Alignment	not modelled	35.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
22	<a href="#">c2j5dA_</a>	 Alignment	not modelled	30.3	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> nmr structure of bnp3 transmembrane domain in lipid2 bicelles
23	<a href="#">c2lonA_</a>	 Alignment	not modelled	21.6	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1b; <b>PDBTitle:</b> backbone structure of human membrane protein higd1b
24	<a href="#">c1spfA_</a>	 Alignment	not modelled	18.3	44	<b>PDB header:</b> lipoprotein(surface film) <b>Chain:</b> A: <b>PDB Molecule:</b> pulmonary surfactant-associated polypeptide c; <b>PDBTitle:</b> the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix
25	<a href="#">c2ka2A_</a>	 Alignment	not modelled	18.2	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
26	<a href="#">c2ka1B_</a>	 Alignment	not modelled	18.2	27	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
27	<a href="#">c2ka1A_</a>	 Alignment	not modelled	18.2	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting

						<b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
28	<a href="#">c2ka2B</a>	Alignment	not modelled	18.2	27	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bc12/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
29	<a href="#">c2ks1B</a>	Alignment	not modelled	17.9	41	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
30	<a href="#">d2j5ya1</a>	Alignment	not modelled	17.6	15	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> GA module, an albumin-binding domain
31	<a href="#">c1zdbA</a>	Alignment	not modelled	15.4	54	<b>PDB header:</b> igg binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> mini protein a domain, z38; <b>PDBTitle:</b> phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
32	<a href="#">c3g2eA</a>	Alignment	not modelled	15.3	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oorc subunit of 2-oxoglutarate:acceptor oxidoreductase; <b>PDBTitle:</b> structure of putative oorc subunit of 2-oxoglutarate:acceptor2 oxidoreductase from campylobacter jejuni
33	<a href="#">c3of4A</a>	Alignment	not modelled	15.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a fnm/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
34	<a href="#">c2y69Z</a>	Alignment	not modelled	14.2	30	<b>PDB header:</b> electron transport <b>Chain:</b> Z: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 8h; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
35	<a href="#">d2frea1</a>	Alignment	not modelled	11.0	20	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
36	<a href="#">c2k9yA</a>	Alignment	not modelled	10.2	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
37	<a href="#">c2k9yB</a>	Alignment	not modelled	10.2	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
38	<a href="#">c2kluA</a>	Alignment	not modelled	9.5	25	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
39	<a href="#">d1bkja</a>	Alignment	not modelled	9.3	40	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
40	<a href="#">d1f5va</a>	Alignment	not modelled	9.2	30	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
41	<a href="#">c3eofB</a>	Alignment	not modelled	9.1	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
42	<a href="#">c2h0uA</a>	Alignment	not modelled	8.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
43	<a href="#">d2igga</a>	Alignment	not modelled	8.7	5	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
44	<a href="#">c2e76D</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome b6-f complex iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
45	<a href="#">c3n2sD</a>	Alignment	not modelled	8.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh-dependent nitro/flavin reductase; <b>PDBTitle:</b> structure of nfra1 nitroreductase from b. subtilis
46	<a href="#">c2wqfA</a>	Alignment	not modelled	8.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> copper induced nitroreductase d; <b>PDBTitle:</b> crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fnm
47	<a href="#">d1v54m</a>	Alignment	not modelled	8.1	27	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
48	<a href="#">d2ifaa1</a>	Alignment	not modelled	8.0	50	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
49	<a href="#">c2lomA</a>	Alignment	not modelled	7.7	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1a; <b>PDBTitle:</b> backbone structure of human membrane protein higd1a
50	<a href="#">d1pj3a1</a>	Alignment	not modelled	7.7	55	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
51	<a href="#">c2kpeA</a>	Alignment	not modelled	7.4	30	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
52	<a href="#">c2kpeB</a>	Alignment	not modelled	7.4	30	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin-a;

52	<a href="#">c2kpeB</a>	Alignment	not modelled	7.4	30	<b>PDBTitle:</b> refined structure of glycoporin a transmembrane segment dimer in dpc2 micelles
53	<a href="#">dlzcha1</a>	Alignment	not modelled	7.2	30	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
54	<a href="#">c2zt9F</a>	Alignment	not modelled	7.2	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 7; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
55	<a href="#">d1o0sa1</a>	Alignment	not modelled	7.1	55	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
56	<a href="#">c3kwaA</a>	Alignment	not modelled	7.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
57	<a href="#">c1kqfB</a>	Alignment	not modelled	6.9	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur <b>PDBTitle:</b> formate dehydrogenase n from e. coli
58	<a href="#">d2igda</a>	Alignment	not modelled	6.8	4	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
59	<a href="#">d1f1sa3</a>	Alignment	not modelled	6.8	36	<b>Fold:</b> Hyaluronate lyase-like, C-terminal domain <b>Superfamily:</b> Hyaluronate lyase-like, C-terminal domain <b>Family:</b> Hyaluronate lyase-like, C-terminal domain
60	<a href="#">d1tula</a>	Alignment	not modelled	6.7	38	<b>Fold:</b> beta-clip <b>Superfamily:</b> Tlp20, baculovirus telokin-like protein <b>Family:</b> Tlp20, baculovirus telokin-like protein
61	<a href="#">d1n7oa2</a>	Alignment	not modelled	6.7	45	<b>Fold:</b> Hyaluronate lyase-like, C-terminal domain <b>Superfamily:</b> Hyaluronate lyase-like, C-terminal domain <b>Family:</b> Hyaluronate lyase-like, C-terminal domain
62	<a href="#">d1vl6a1</a>	Alignment	not modelled	6.7	36	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
63	<a href="#">c2w2hB</a>	Alignment	not modelled	6.3	26	<b>PDB header:</b> rna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclin-t1; <b>PDBTitle:</b> structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from eiav
64	<a href="#">c3e39A</a>	Alignment	not modelled	6.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (dde_0787) from desulfovibrio desulfuricans subsp. at 1.70 a3 resolution
65	<a href="#">d1rz4a1</a>	Alignment	not modelled	6.2	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
66	<a href="#">c1ww8A</a>	Alignment	not modelled	6.1	55	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate oxidoreductase; <b>PDBTitle:</b> crystal structure of malic enzyme from pyrococcus2 horikoshii ot3
67	<a href="#">d1gq2a1</a>	Alignment	not modelled	6.1	55	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
68	<a href="#">c2e1mA</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
69	<a href="#">c1tt9B</a>	Alignment	not modelled	5.8	32	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> formimidoyl transferase-cyclodeaminase <b>PDBTitle:</b> structure of the bifunctional and golgi associated2 formimino transferase cyclodeaminase octamer
70	<a href="#">c2pvjA</a>	Alignment	not modelled	5.8	39	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> solution structure of hiv-1 gp41 fusion domain bound to dpc2 micelle
71	<a href="#">d2e74g1</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
72	<a href="#">d1ps9a3</a>	Alignment	not modelled	5.7	31	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
73	<a href="#">c2hayD</a>	Alignment	not modelled	5.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas
74	<a href="#">d1vf5g</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
75	<a href="#">c1vf5G</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> protein pet g; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
76	<a href="#">d1vfra</a>	Alignment	not modelled	5.6	33	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
77	<a href="#">d1v54d</a>	Alignment	not modelled	5.5	31	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
						<b>PDB header:</b> immune system

78	<a href="#">c2rpvA_</a>	Alignment	not modelled	5.5	8	<b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin g-binding protein g; <b>PDBTitle:</b> solution structure of gb1 with lbt probe
79	<a href="#">c1erfA_</a>	Alignment	not modelled	5.4	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane glycoprotein; <b>PDBTitle:</b> conformational mapping of the n-terminal fusion peptide of2 hiv-1 gp41 using 13c-enhanced fourier transform infrared3 spectroscopy (ftir)
80	<a href="#">d1vkwa_</a>	Alignment	not modelled	5.3	30	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> Putative nitroreductase TM1586
81	<a href="#">c3ge6B_</a>	Alignment	not modelled	5.2	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exigobacterium sibiricum 255-15 at 1.85 a3 resolution
82	<a href="#">c4f43A_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protelomerase; <b>PDBTitle:</b> protelomerase tela mutant r255a complexed with caag hairpin dna
83	<a href="#">c3m5kA_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (bdi_1728) from parabacteroides distasonis atcc 85033 at 1.86 a resolution
84	<a href="#">d1m56d_</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Bacterial aa3 type cytochrome c oxidase subunit IV <b>Family:</b> Bacterial aa3 type cytochrome c oxidase subunit IV
85	<a href="#">c2lp1A_</a>	Alignment	not modelled	5.2	47	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> c99; <b>PDBTitle:</b> the solution nmr structure of the transmembrane c-terminal domain of2 the amyloid precursor protein (c99)
86	<a href="#">c1sazA_</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable butyrate kinase 2; <b>PDBTitle:</b> membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
87	<a href="#">d1fd6a_</a>	Alignment	not modelled	5.0	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
88	<a href="#">c1gz3B_</a>	Alignment	not modelled	5.0	55	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent malic enzyme; <b>PDBTitle:</b> molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate