




















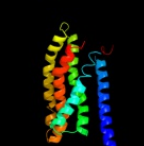
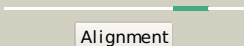
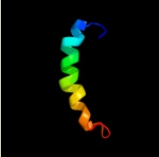

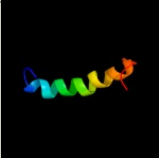
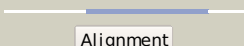
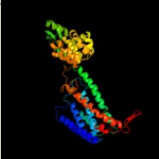
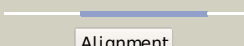
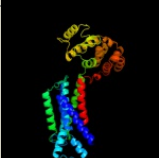


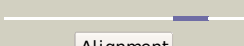

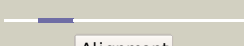
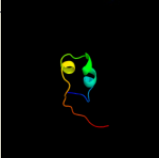
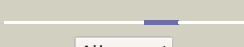



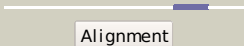
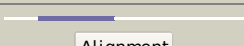
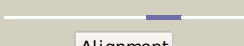
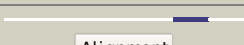


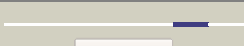



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0AV02
Date	Wed Jun 6 09:26:36 BST 2012
Unique Job ID	2cf7aaf7c591a056

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4djiA_	 Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
2	c3giaA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
3	c3lrcC_	 Alignment		100.0	16	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
4	c2jlnA_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
5	c2xq2A_	 Alignment		97.6	12	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsglT
6	d2a65a1	 Alignment		97.3	12	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
7	c3dh4A_	 Alignment		97.2	9	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
8	c2w8aC_	 Alignment		96.7	14	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
9	c4ainB_	 Alignment		90.8	13	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
10	c3hfxA_	 Alignment		74.8	13	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
11	c1oy8A_	 Alignment		43.8	8	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrB multidrug efflux pump

12	c2djbB_	 Alignment		41.3	24	PDB header: biosynthetic protein Chain: B: PDB Molecule: redy-like protein; PDBTitle: crystal structure of hapk from hahella chejuensis
13	c2yl4A_	 Alignment		30.2	13	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
14	c4djhA_	 Alignment		29.1	11	PDB header: hormone receptor/antagonist Chain: A: PDB Molecule: kappa-type opioid receptor, lysozyme; PDBTitle: structure of the human kappa opioid receptor in complex with jdtic
15	c2rb1A_	 Alignment		27.0	10	PDB header: membrane protein / hydrolase Chain: A: PDB Molecule: beta-2-adrenergic receptor/t4-lysozyme chimera; PDBTitle: high resolution crystal structure of human b2-adrenergic g protein-2 coupled receptor.
16	c2kr6A_	 Alignment		26.5	14	PDB header: hydrolase Chain: A: PDB Molecule: presenilin-1; PDBTitle: solution structure of presenilin-1 ctf subunit
17	c3qf4A_	 Alignment		17.4	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
18	d1jb7a3	 Alignment		15.3	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
19	c2vgqA_	 Alignment		12.1	13	PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card
20	c2lpdA_	 Alignment		11.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b
21	d2hyda2	 Alignment	not modelled	10.8	21	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
22	c2w2eA_	 Alignment	not modelled	10.4	20	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
23	c2w9jB_	 Alignment	not modelled	10.4	38	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle subunit srp14; PDBTitle: the crystal structure of srp14 from the schizosaccharomyces2 pombe signal recognition particle
24	c3g5uB_	 Alignment	not modelled	8.5	19	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
25	c3b5wE_	 Alignment	not modelled	8.4	19	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
26	c3cvoA_	 Alignment	not modelled	8.2	33	PDB header: transferase Chain: A: PDB Molecule: methyltransferase-like protein of unknown function; PDBTitle: crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
27	c3qf4B_	 Alignment	not modelled	8.1	13	PDB header: transport protein Chain: B: PDB Molecule: uncharacterized abc transporter atp-binding protein PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
		 Alignment				Fold: Multi drug efflux transporter AcrB transmembrane domain

28	d1iwga7	Alignment	not modelled	8.1	8	Supersfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
29	d1olpa2	Alignment	not modelled	8.0	30	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Alpha-toxin, C-terminal domain
30	c2hg5D_	Alignment	not modelled	7.9	14	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
31	d1x6fa1	Alignment	not modelled	7.8	26	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
32	c3k07A_	Alignment	not modelled	7.6	11	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
33	c3uonA_	Alignment	not modelled	7.6	12	PDB header: signaling protein/antagonist Chain: A: PDB Molecule: human m2 muscarinic acetylcholine receptor t4 lysozyme PDBTitle: structure of the human m2 muscarinic acetylcholine receptor bound to2 an antagonist
34	d1kf6c_	Alignment	not modelled	7.6	8	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
35	d1kf6d_	Alignment	not modelled	7.6	20	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
36	c1dsjA_	Alignment	not modelled	7.5	41	PDB header: viral peptide Chain: A: PDB Molecule: vpr protein; PDBTitle: nmr solution structure of vpr50_75, 20 structures
37	c2hydB_	Alignment	not modelled	7.2	21	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
38	d1iwga8	Alignment	not modelled	7.0	8	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
39	d2cjrA1	Alignment	not modelled	6.9	27	Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Coronavirus nucleocapsid protein
40	d1khoa2	Alignment	not modelled	6.8	18	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Alpha-toxin, C-terminal domain
41	c3aqpB_	Alignment	not modelled	6.8	13	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
42	d1ca1a2	Alignment	not modelled	6.8	30	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Alpha-toxin, C-terminal domain
43	c2rajA_	Alignment	not modelled	6.7	17	PDB header: structural protein Chain: A: PDB Molecule: sorting nexin-9; PDBTitle: so4 bound px-bar membrane remodeling unit of sorting nexin 9
44	d1jeqa1	Alignment	not modelled	6.7	22	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
45	c3emlA_	Alignment	not modelled	6.5	9	PDB header: membrane protein, receptor Chain: A: PDB Molecule: human adenosine a2a receptor/t4 lysozyme chimera; PDBTitle: the 2.6 a crystal structure of a human a2a adenosine2 receptor bound to zm241385.
46	c1ciiA_	Alignment	not modelled	6.5	18	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
47	d1f0la3	Alignment	not modelled	6.5	18	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
48	c2kpeB_	Alignment	not modelled	6.4	25	PDB header: membrane protein Chain: B: PDB Molecule: glycophorin-a; PDBTitle: refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
49	c2kpeA_	Alignment	not modelled	6.4	25	PDB header: membrane protein Chain: A: PDB Molecule: glycophorin-a; PDBTitle: refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
50	d2o4aa1	Alignment	not modelled	6.3	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
51	c2khrA_	Alignment	not modelled	6.2	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: protein mbth; PDBTitle: solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
52	c3kdpD_	Alignment	not modelled	6.2	7	PDB header: hydrolase Chain: D: PDB Molecule: sodium/potassium-transporting atpase subunit beta-1; PDBTitle: crystal structure of the sodium-potassium pump
53	c1zkaA_	Alignment	not modelled	6.1	29	PDB header: transcription Chain: A: PDB Molecule: transcription factor relb; PDBTitle: nf-kb relb forms an intertwined homodimer, y300s mutant

54	c2l9bA_	Alignment	not modelled	6.0	22	PDB header: transcription Chain: A: PDB Molecule: mrna 3'-end-processing protein rna15; PDBTitle: heterodimer between rna14p monkeytail domain and rna15p hinge domain2 of the yeast cf ia complex
55	d1exta2	Alignment	not modelled	5.9	23	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
56	d2yvxa3	Alignment	not modelled	5.9	14	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
57	c3v2yA_	Alignment	not modelled	5.8	9	PDB header: hydrolase Chain: A: PDB Molecule: sphingosine 1-phosphate receptor 1, lysozyme chimera; PDBTitle: crystal structure of a lipid g protein-coupled receptor at 2.80a
58	c3c8vA_	Alignment	not modelled	5.7	16	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
59	d1v54d_	Alignment	not modelled	5.6	17	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
60	c2hu9B_	Alignment	not modelled	5.5	20	PDB header: metal transport Chain: B: PDB Molecule: mercuric transport protein periplasmic component; PDBTitle: x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
61	c2y69Q_	Alignment	not modelled	5.4	17	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
62	c1jrrA_	Alignment	not modelled	5.4	28	PDB header: dna binding protein Chain: A: PDB Molecule: thyroid autoantigen; PDBTitle: the three-dimensional structure of the c-terminal dna2 binding domain of human ku70
63	d1nria_	Alignment	not modelled	5.2	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
64	c1nriA_	Alignment	not modelled	5.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
65	d1gjia1	Alignment	not modelled	5.1	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain