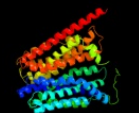
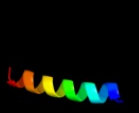
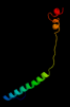
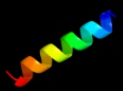


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0CE45
Date	Thu Jan 5 11:30:13 GMT 2012
Unique Job ID	6bb8930fbc257fae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pv7a_	 Alignment		99.9	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
2	d1pw4a_	 Alignment		99.9	13	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
3	c2gfpA_	 Alignment		99.8	12	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
4	c3o7pA_	 Alignment		99.8	13	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	c2xutC_	 Alignment		99.8	11	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	d2f23a1	 Alignment		62.4	10	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
7	d1grja1	 Alignment		50.2	24	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
8	c3qngD_	 Alignment		49.6	14	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
9	c1zxaB_	 Alignment		32.9	19	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
10	c1by0A_	 Alignment		29.6	28	PDB header: rna binding protein Chain: A: PDB Molecule: protein (hepatitis delta antigen); PDBTitle: n-terminal leucine-repeat region of hepatitis delta antigen
11	c2q7cC_	 Alignment		25.0	22	PDB header: viral protein Chain: C: PDB Molecule: fusion protein between yeast variant gcn4 and PDBTitle: crystal structure of iqn17

12	d1f6ga_	Alignment		24.9	13	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
13	c3hd6A_	Alignment		23.7	7	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
14	d1oqwa_	Alignment		20.4	13	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
15	d1xmpa_	Alignment		19.7	10	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
16	d2h8aa1	Alignment		17.4	7	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
17	d2pila_	Alignment		17.1	9	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
18	c3jqhA_	Alignment		13.8	24	PDB header: sugar binding protein Chain: A: PDB Molecule: c-type lectin domain family 4 member m; PDBTitle: structure of the neck region of the glycan-binding receptor2 dc-signr
19	d1ji6a3	Alignment		13.3	14	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain
20	c2hjmB_	Alignment		12.8	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein pf1176; PDBTitle: crystal structure of a singleton protein pf1176 from p. furiosus
21	d2ce7a1	Alignment	not modelled	12.0	13	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
22	c1a92B_	Alignment	not modelled	11.8	29	PDB header: leucine zipper Chain: B: PDB Molecule: delta antigen; PDBTitle: oligomerization domain of hepatitis delta antigen
23	c1m46B_	Alignment	not modelled	11.7	29	PDB header: cell cycle protein Chain: B: PDB Molecule: iq4 motif from myo2p, a class v myosin; PDBTitle: crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
24	c2nuxB_	Alignment	not modelled	11.5	35	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
25	c2oqqB_	Alignment	not modelled	11.5	16	PDB header: transcription Chain: B: PDB Molecule: transcription factor hy5; PDBTitle: crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
26	c3eh0C_	Alignment	not modelled	10.4	8	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli
27	d1u69a_	Alignment	not modelled	9.6	27	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
28	c2wl2B_	Alignment	not modelled	9.2	11	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of n-terminal domain of gyra with the2

					antibiotic simocyclinone d8 PDB header: oxidoreductase Chain: A: PDB Molecule: thymine dioxygenase jbp1; PDBTitle: the structural basis for recognition of j-base containing2 dna by a novel dna-binding domain in jbp1
29	c2xseA_	Alignment	not modelled	9.2	21
30	c1c94B_	Alignment	not modelled	8.8	15
31	c2kncA_	Alignment	not modelled	8.8	13
32	c1l4aE_	Alignment	not modelled	8.7	22
33	c3s2xB_	Alignment	not modelled	8.5	23
34	d2ia9a1	Alignment	not modelled	8.5	7
35	d1ab4a_	Alignment	not modelled	8.4	13
36	c2l5gA_	Alignment	not modelled	8.3	9
37	c1ji6A_	Alignment	not modelled	8.1	14
38	d2oara1	Alignment	not modelled	8.1	18
39	c3sokB_	Alignment	not modelled	7.9	17
40	d1ez4a2	Alignment	not modelled	7.6	23
41	d1ykhb1	Alignment	not modelled	7.4	8
42	c2novD_	Alignment	not modelled	7.4	21
43	c2kluA_	Alignment	not modelled	7.3	10
44	c1tj1D_	Alignment	not modelled	7.2	0
45	c2rdcA_	Alignment	not modelled	7.1	10
46	c2kwyA_	Alignment	not modelled	7.1	19
47	c3iz5K_	Alignment	not modelled	7.1	11
48	c3onoA_	Alignment	not modelled	7.1	14
49	c2kmfA_	Alignment	not modelled	7.1	16
50	c2y6xA_	Alignment	not modelled	7.0	20
51	d1lotsa_	Alignment	not modelled	6.9	13
52	c2w8aC_	Alignment	not modelled	6.7	8
53	d2cqea1	Alignment	not modelled	6.7	10
54	c2jo8B_	Alignment	not modelled	6.6	25

55	d2ba0d2	Alignment	not modelled	6.6	15	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
56	c2zxrA	Alignment	not modelled	6.5	12	PDB header: hydrolase Chain: A: PDB Molecule: single-stranded dna specific exonuclease recj; PDBTitle: crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
57	d1fx0a1	Alignment	not modelled	6.4	11	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
58	d2jf2a1	Alignment	not modelled	6.4	13	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
59	c1onvB	Alignment	not modelled	6.1	22	PDB header: transcription Chain: B: PDB Molecule: serine phosphatase fcp1a; PDBTitle: nmr structure of a complex containing the tfiif subunit2 rap74 and the rnap ii ctd phosphatase fcp1
60	d2b5ua2	Alignment	not modelled	6.1	17	Fold: Cloacin translocation domain Superfamily: Cloacin translocation domain Family: Cloacin translocation domain
61	d1h41a2	Alignment	not modelled	6.0	20	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: alpha-D-glucuronidase, N-terminal domain
62	d1hya2	Alignment	not modelled	5.9	10	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
63	c2q9qC	Alignment	not modelled	5.8	7	PDB header: replication Chain: C: PDB Molecule: dna replication complex gins protein psf1; PDBTitle: the crystal structure of full length human gins complex
64	c2l16A	Alignment	not modelled	5.8	15	PDB header: protein transport Chain: A: PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
65	c2rpaA	Alignment	not modelled	5.8	24	PDB header: hydrolase Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a1; PDBTitle: the solution structure of n-terminal domain of microtubule severing2 enzyme
66	c2xzaA	Alignment	not modelled	5.7	21	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
67	c2inrA	Alignment	not modelled	5.7	24	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 4 subunit a; PDBTitle: crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
68	c2k6iA	Alignment	not modelled	5.7	18	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein mj0223; PDBTitle: the domain features of the peripheral stalk subunit h of the2 methanogenic a1ao atp synthase and the nmr solution3 structure of h1-47
69	c1zvua	Alignment	not modelled	5.6	18	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit a; PDBTitle: structure of the full-length e. coli parc subunit
70	c1unyA	Alignment	not modelled	5.6	9	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
71	c2c5qE	Alignment	not modelled	5.4	23	PDB header: structural genomics,unknown function Chain: E: PDB Molecule: rraa-like protein yer010c; PDBTitle: crystal structure of yeast yer010cp
72	c3izcK	Alignment	not modelled	5.4	21	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein rpl16 (l13p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
73	c2hw2A	Alignment	not modelled	5.4	7	PDB header: transferase Chain: A: PDB Molecule: rifampin adp-ribosyl transferase; PDBTitle: crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
74	c2rddB	Alignment	not modelled	5.3	15	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
75	d2e9xa1	Alignment	not modelled	5.3	7	Fold: GINS helical bundle-like Superfamily: GINS helical bundle-like Family: PSF1 N-terminal domain-like
76	c3gb8B	Alignment	not modelled	5.3	4	PDB header: transport protein Chain: B: PDB Molecule: snurportin-1; PDBTitle: crystal structure of crml1/snurportin-1 complex
77	c1nohB	Alignment	not modelled	5.3	14	PDB header: viral protein Chain: B: PDB Molecule: head morphogenesis protein; PDBTitle: the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
78	c3ei1A	Alignment	not modelled	5.3	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna damage-binding protein 1; PDBTitle: structure of hsddb1-drddb2 bound to a 14 bp 6-42 photoproduct containing dna-duplex
79	c1ij3B	Alignment	not modelled	5.3	8	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position

80	c1ij3C_	Alignment	not modelled	5.3	8	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
81	c3ilwA_	Alignment	not modelled	5.3	11	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: structure of dna gyrase subunit a n-terminal domain
82	d1i9za_	Alignment	not modelled	5.3	22	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
83	d2fgea3	Alignment	not modelled	5.3	15	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
84	c3eb7B_	Alignment	not modelled	5.2	18	PDB header: toxin Chain: B: PDB Molecule: insecticidal delta-endotoxin cry8ea1; PDBTitle: crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution
85	d1gega_	Alignment	not modelled	5.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
86	d1k1xa1	Alignment	not modelled	5.2	11	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: 4-alpha-glucanotransferase, domain 2
87	c3jywM_	Alignment	not modelled	5.2	5	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l16(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
88	c1zi7C_	Alignment	not modelled	5.1	10	PDB header: lipid binding protein Chain: C: PDB Molecule: kes1 protein; PDBTitle: structure of truncated yeast oxysterol binding protein osh4
89	c3ifzA_	Alignment	not modelled	5.1	11	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
90	d1tsja_	Alignment	not modelled	5.1	18	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
91	c2yggA_	Alignment	not modelled	5.0	25	PDB header: metal binding protein/transport protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: complex of cambr and cam