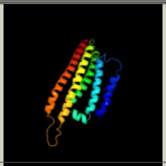
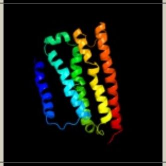
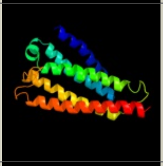
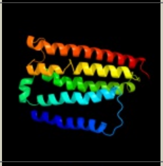
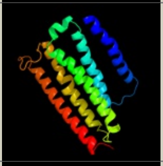
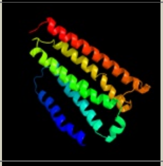
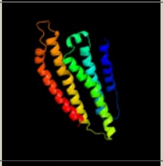
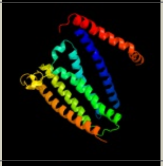
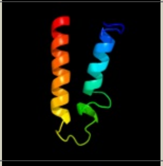
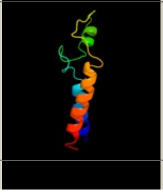
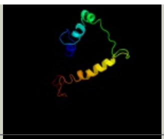
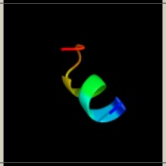
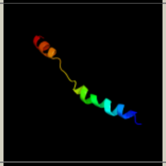
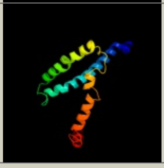
Email	l.a.kelley@imperial.ac.uk
Description	P26459
Date	Thu Jan 5 11:42:55 GMT 2012
Unique Job ID	374fbf11f079fe07

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mk7K_	Alignment		96.7	14	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit n; **PDBTitle:** the structure of cbb3 cytochrome oxidase
2	d1ffta_	Alignment		91.8	18	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
3	c1fftF_	Alignment		91.8	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
4	d1ar1a_	Alignment		79.7	17	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
5	d3dtua1	Alignment		76.8	18	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
6	c1m56G_	Alignment		76.1	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
7	d1v54a_	Alignment		75.7	15	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
8	c3o0rB_	Alignment		40.0	10	**PDB header:**immune system/oxidoreductase **Chain:** B: **PDB Molecule:**nitric oxide reductase subunit b; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
9	d1xmea1	Alignment		31.0	19	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
10	c3kp9A_	Alignment		29.1	16	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
11	c2bbjB_	Alignment		17.1	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter

12	c3lw52_	Alignment		16.2	21	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from photosystem i; **PDB Fragment:**residues 81-246; **PDBTitle:** improved model of plant photosystem i
13	d2p3ha1	Alignment		14.1	7	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
14	d2r2za1	Alignment		13.5	36	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
15	d3deda1	Alignment		11.5	36	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
16	d2o3ga1	Alignment		11.0	29	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
17	c3fh6F_	Alignment		10.3	8	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
18	c3dedB_	Alignment		9.5	36	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable hemolysin; **PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum
19	c1hgvA_	Alignment		9.1	23	**PDB header:**virus **Chain:** A: **PDB Molecule:**ph75 inovirus major coat protein; **PDBTitle:** filamentous bacteriophage ph75
20	d2a65a1	Alignment		8.2	15	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
21	d2gz4a1	Alignment	not modelled	8.2	12	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
22	d2oaia1	Alignment	not modelled	7.9	43	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
23	c3lemA_	Alignment	not modelled	7.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructosyltransferase; **PDBTitle:** crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose
24	d2nqwa1	Alignment	not modelled	7.5	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
25	c2l9uA_	Alignment	not modelled	7.3	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
26	d2plsa1	Alignment	not modelled	6.9	29	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
27	c3mepC_	Alignment	not modelled	6.5	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein eca2234; **PDBTitle:** crystal structure of eca2234 protein from erwinia2 carotovora, northeast structural genomics consortium target3 ewr44
28	d2rk5a1	Alignment	not modelled	6.5	36	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
29	c3kopB_	Alignment	not modelled	6.4	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein with a cyclophilin-like fold2

						(yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
30	c3k11A_	Alignment	not modelled	6.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
31	c3eh4A_	Alignment	not modelled	5.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase subunit 1; **PDBTitle:** structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
32	c3llbA_	Alignment	not modelled	5.8	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
33	d2axta1	Alignment	not modelled	5.5	18	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
34	d2o1ra1	Alignment	not modelled	5.1	14	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like