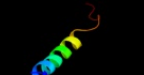
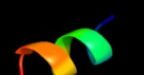
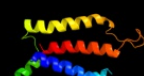
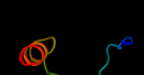
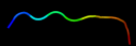
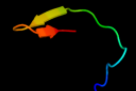
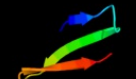


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	D6VTK4
Date	Mon Jul 2 19:10:02 BST 2012
Unique Job ID	1e960aed19b3fa90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k9pA_	 Alignment		99.9	95	PDB header: membrane protein Chain: A: PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles
2	c4dblB_	 Alignment		77.4	12	PDB header: transport protein Chain: B: PDB Molecule: vitamin b12 import system permease protein btuc; PDBTitle: crystal structure of e159q mutant of btucdf
3	d1l7va_	 Alignment		63.6	10	Fold: ABC transporter involved in vitamin B12 uptake, BtuC Superfamily: ABC transporter involved in vitamin B12 uptake, BtuC Family: ABC transporter involved in vitamin B12 uptake, BtuC
4	c2kncA_	 Alignment		24.2	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
5	c3gvzB_	 Alignment		19.9	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein cv2077; PDBTitle: crystal structure of the protein cv2077 from2 chromobacterium violaceum. northeast structural genomics3 consortium target cvr62
6	d2hkua2	 Alignment		19.0	50	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
7	c2cblA_	 Alignment		14.1	30	PDB header: complex (proto-oncogene/peptide) Chain: A: PDB Molecule: proto-oncogene cbl; PDBTitle: n-terminal domain of cbl in complex with its binding site2 on zap-70
8	c3bunB_	 Alignment		14.0	30	PDB header: ligase/signaling protein Chain: B: PDB Molecule: e3 ubiquitin-protein ligase cbl; PDBTitle: crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
9	c2k1aA_	 Alignment		13.5	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
10	c2nq2A_	 Alignment		13.1	14	PDB header: metal transport Chain: A: PDB Molecule: hypothetical abc transporter permease protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
11	c3pf6C_	 Alignment		12.3	28	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein pp-luz7_gp033; PDBTitle: the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.

12	c1u2pA_	Alignment		10.2	10	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
13	c3g4dB_	Alignment		8.9	16	PDB header: lyase Chain: B: PDB Molecule: (+)-delta-cadinene synthase isozyme xc1; PDBTitle: crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
14	c2jz2A_	Alignment		8.6	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ssl0352 protein; PDBTitle: solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
15	d2k57a1	Alignment		8.2	17	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
16	d1wfa1	Alignment		6.9	24	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
17	c3n0fA_	Alignment		6.8	21	PDB header: lyase Chain: A: PDB Molecule: isoprene synthase; PDBTitle: crystal structure of isoprene synthase from grey poplar leaves2 (populus x canescens)
18	c1hx9A_	Alignment		6.8	24	PDB header: lyase Chain: A: PDB Molecule: 5-epi-aristolochene synthase; PDBTitle: crystal structure of teas w273s form 1
19	d1mkea1	Alignment		6.4	50	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
20	c2ongA_	Alignment		6.2	21	PDB header: lyase Chain: A: PDB Molecule: 4s-limonene synthase; PDBTitle: crystal structure of of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp).
21	d1te7a_	Alignment	not modelled	6.1	17	Fold: PUA domain-like Superfamily: PUA domain-like Family: yqfB-like
22	d5easa1	Alignment	not modelled	6.1	24	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpenoid cyclase N-terminal domain
23	d1n1ba1	Alignment	not modelled	6.1	15	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpenoid cyclase N-terminal domain
24	c2k1kB_	Alignment	not modelled	5.9	40	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
25	c2k1lA_	Alignment	not modelled	5.9	40	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
26	c2k1lB_	Alignment	not modelled	5.9	40	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
27	c2k1kA_	Alignment	not modelled	5.9	40	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
28	c3saeA_	Alignment	not modelled	5.8	21	PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
						Fold: IHF-like DNA-binding proteins

29	d1b8za_	Alignment	not modelled	5.8	22	Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
30	d2o97b1	Alignment	not modelled	5.7	17	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
31	c3dgpA_	Alignment	not modelled	5.7	7	PDB header: transcription Chain: A: PDB Molecule: rna polymerase ii transcription factor b subunit 2; PDBTitle: crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
32	c3dhgB_	Alignment	not modelled	5.6	29	PDB header: oxidoreductase Chain: B: PDB Molecule: toluene 4-monooxygenase hydroxylase beta subunit; PDBTitle: crystal struture of toluene 4-monooxygenase hydroxylase
33	d1k3zb_	Alignment	not modelled	5.5	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
34	c2y69Y_	Alignment	not modelled	5.5	19	PDB header: electron transport Chain: Y: PDB Molecule: cytochrome c oxidase subunit 7c; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
35	d1p3qr_	Alignment	not modelled	5.5	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
36	d1nexa2	Alignment	not modelled	5.5	20	Fold: POZ domain Superfamily: POZ domain Family: BTB/POZ domain
37	c2ifsA_	Alignment	not modelled	5.2	50	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protien ineracting PDBTitle: structure of the n-wasp evh1 domain in complex with an2 extended wip peptide
38	d1pbya4	Alignment	not modelled	5.2	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5