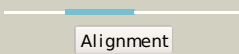
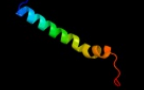
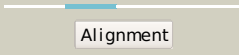
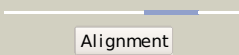
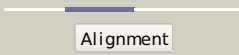
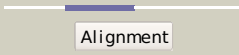
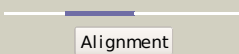
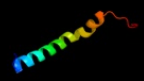
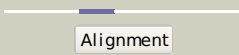
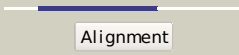
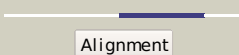
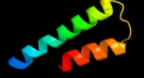
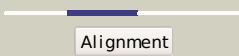
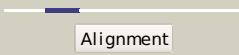
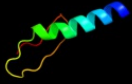
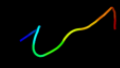
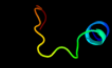


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AAY1
Date	Thu Jan 5 11:14:06 GMT 2012
Unique Job ID	bc24d20703254808

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w07a2	 Alignment		33.1	8	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: acyl-CoA oxidase C-terminal domains
2	d2ddha2	 Alignment		33.0	7	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: acyl-CoA oxidase C-terminal domains
3	c3iz5K_	 Alignment		20.2	22	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l13a (l13p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
4	c2ddhA_	 Alignment		15.4	8	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa oxidase; PDBTitle: crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
5	c1w07A_	 Alignment		14.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa oxidase; PDBTitle: arabidopsis thaliana acyl-coa oxidase 1
6	c2fonA_	 Alignment		12.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal acyl-coa oxidase 1a; PDBTitle: x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato)
7	c3hm5A_	 Alignment		11.7	44	PDB header: transcription Chain: A: PDB Molecule: dna methyltransferase 1-associated protein 1; PDBTitle: sant domain of human dna methyltransferase 1 associated2 protein 1
8	c4acoA_	 Alignment		9.1	30	PDB header: dna binding protein Chain: A: PDB Molecule: centromere dna-binding protein complex cbf3 subunit a; PDBTitle: structure of the budding yeast ndc10 n-terminal domain
9	c3ag5A_	 Alignment		9.0	22	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
10	d2a6qb1	 Alignment		8.9	15	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
11	c2js5B_	 Alignment		8.8	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1

12	d1r5ta_	Alignment		8.6	13	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
13	c3lasA_	Alignment		8.5	23	PDB header: lyase Chain: A: PDB Molecule: putative carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
14	c4a1a1_	Alignment		8.5	22	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l13a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
15	d1iyjb2	Alignment		7.4	40	Fold: BRCA2 tower domain Superfamily: BRCA2 tower domain Family: BRCA2 tower domain
16	d1efva2	Alignment		7.3	29	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
17	c2jtvA_	Alignment		7.1	30	PDB header: structural genomics Chain: A: PDB Molecule: protein of unknown function; PDBTitle: solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
18	d1qvea_	Alignment		7.1	33	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
19	d1v65a_	Alignment		7.0	31	Fold: KRAB domain (Kruppel-associated box) Superfamily: KRAB domain (Kruppel-associated box) Family: KRAB domain (Kruppel-associated box)
20	d2fy8a1	Alignment		6.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
21	d1efpa2	Alignment	not modelled	6.0	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
22	d1poca_	Alignment	not modelled	5.1	39	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Insect phospholipase A2