


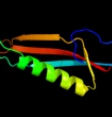
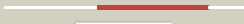




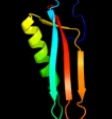

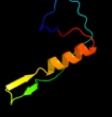
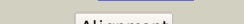


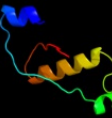



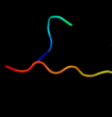




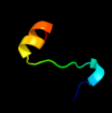
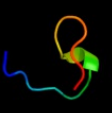



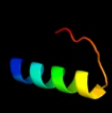



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P69411
Date	Thu Jan 5 12:11:31 GMT 2012
Unique Job ID	3c43b9e04178fec6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y1bA_	 Alignment		100.0	100	PDB header: membrane protein Chain: A: PDB Molecule: putative outer membrane protein, signal; PDBTitle: crystal structure of the e. coli outer membrane lipoprotein2 rcsf
2	d1vr4a1	 Alignment		97.1	24	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
3	c3qkbB_	 Alignment		96.8	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
4	c1y2iC_	 Alignment		96.4	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein s0862; PDBTitle: crystal structure of mcsg target apc27401 from shigella2 flexneri
5	d1y2ia_	 Alignment		96.3	16	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
6	c2jz7A_	 Alignment		42.6	22	PDB header: selenium-binding protein Chain: A: PDB Molecule: selenium binding protein; PDBTitle: solution nmr structure of selenium-binding protein from2 methanococcus vanniellii
7	d2qk3a1	 Alignment		16.7	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
8	d2jnaa1	 Alignment		16.6	10	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
9	c2kxhB_	 Alignment		12.0	28	PDB header: protein binding Chain: B: PDB Molecule: peptide of far upstream element-binding protein 1; PDBTitle: solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
10	d1nlia1	 Alignment		11.4	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
11	d1oblcl	 Alignment		10.6	31	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)

12	d1b9wa1	Alignment		10.4	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
13	d2cr9a1	Alignment		7.9	19	Fold: WGR domain-like Superfamily: WGR domain-like Family: WGR domain
14	d1eyfa_	Alignment		7.3	30	Fold: Ada DNA repair protein, N-terminal domain (N-Ada 10) Superfamily: Ada DNA repair protein, N-terminal domain (N-Ada 10) Family: Ada DNA repair protein, N-terminal domain (N-Ada 10)
15	c2stbl_	Alignment		6.9	24	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: protein (trypsin inhibitor); PDBTitle: anionic salmon trypsin in complex with squash seed2 inhibitor (cucurbita pepo trypsin inhibitor ii)
16	c2stal_	Alignment		6.3	29	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: protein (trypsin inhibitor); PDBTitle: anionic salmon trypsin in complex with squash seed2 inhibitor (cucurbita maxima trypsin inhibitor i)
17	d2btci_	Alignment		6.1	24	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant inhibitors of proteinases and amylases Family: Plant inhibitors of proteinases and amylases
18	c2btcl_	Alignment		6.1	24	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: protein (trypsin inhibitor); PDBTitle: bovine trypsin in complex with squash seed inhibitor2 (cucurbita pepo trypsin inhibitor ii)
19	d2noca1	Alignment		5.9	30	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
20	c2ctiA_	Alignment		5.6	29	PDB header: proteinase inhibitor (trypsin) Chain: A: PDB Molecule: trypsin inhibitor; PDBTitle: determination of the complete three-dimensional structure2 of the trypsin inhibitor from squash seeds in aqueous3 solution by nuclear magnetic resonance and a combination4 of distance geometry and dynamical simulated annealing
21	c1ctiA_	Alignment	not modelled	5.6	29	PDB header: proteinase inhibitor (trypsin) Chain: A: PDB Molecule: trypsin inhibitor; PDBTitle: determination of the complete three-dimensional structure2 of the trypsin inhibitor from squash seeds in aqueous3 solution by nuclear magnetic resonance and a combination4 of distance geometry and dynamical simulated annealing
22	c1ppe1_	Alignment	not modelled	5.6	29	PDB header: hydrolase(serine proteinase) Chain: I: PDB Molecule: trypsin inhibitor cmti-i; PDBTitle: the refined 2.0 angstroms x-ray crystal structure of the2 complex formed between bovine beta-trypsin and cmti-i, a3 trypsin inhibitor from squash seeds (cucurbita maxima):4 topological similarity of the squash seed inhibitors with5 the carboxypeptidase a inhibitor from potatoes
23	c3ctiA_	Alignment	not modelled	5.6	29	PDB header: proteinase inhibitor (trypsin) Chain: A: PDB Molecule: trypsin inhibitor; PDBTitle: relaxation matrix refinement of the solution structure of2 squash trypsin inhibitor
24	d1mi8a_	Alignment	not modelled	5.4	30	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
25	c3rhtB_	Alignment	not modelled	5.2	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus