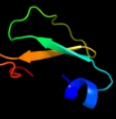
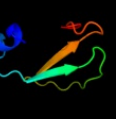
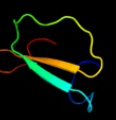


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4A9
Date	Sun Jul 8 11:45:06 BST 2012
Unique Job ID	cb512630c2bfffacc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tinA_	 Alignment		97.8	18	PDB header: serine protease inhibitor Chain: A: PDB Molecule: trypsin inhibitor v; PDBTitle: three-dimensional structure in solution of cucurbita maxima2 trypsin inhibitor-v determined by nmr spectroscopy
2	d1dwma_	 Alignment		97.8	34	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
3	c1vbwA_	 Alignment		97.8	20	PDB header: protein binding Chain: A: PDB Molecule: trypsin inhibitor bgit; PDBTitle: crystal structure of bitter gourd trypsin inhibitor
4	c2ci2I_	 Alignment		97.7	20	PDB header: proteinase inhibitor (chymotrypsin) Chain: I: PDB Molecule: chymotrypsin inhibitor 2; PDBTitle: crystal and molecular structure of the serine proteinase2 inhibitor ci-2 from barley seeds
5	c3rdyA_	 Alignment		97.7	25	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: bwi-1=protease inhibitor/trypsin inhibitor; PDBTitle: crystal structure of buckwheat trypsin inhibitor rbt1 at 1.84 angstrom2 resolution
6	d1ypci_	 Alignment		97.7	20	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
7	d1to2i_	 Alignment		97.7	20	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
8	d2snii_	 Alignment		97.7	20	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
9	d1csei_	 Alignment		97.6	20	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
10	d1legla_	 Alignment		97.6	20	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
11	c1ciqB_	 Alignment		32.9	30	PDB header: serine protease inhibitor Chain: B: PDB Molecule: chymotrypsin inhibitor 2; PDBTitle: complex of two fragments of ci2, residues 1-40 and 41-64

12	c1cq4B_	Alignment		19.5	32	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: protein (serine proteinase inhibitor 2); PDBTitle: ci 2 mutant with tetraglutamine (mgqqqqgm) replacing met59
13	c3h3hA_	Alignment		14.2	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ji0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
14	c2l55A_	Alignment		12.5	28	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
15	d1fxza2	Alignment		11.6	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
16	d3dxoa1	Alignment		10.6	23	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0744-like
17	c1hymB_	Alignment		9.3	26	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr2 structure)
18	c3ltiA_	Alignment		8.0	31	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta14 domains
19	d1qcsa2	Alignment		7.2	5	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
20	c2hx6A_	Alignment		6.6	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
21	c3msoA_	Alignment	not modelled	6.1	23	PDB header: isomerase Chain: A: PDB Molecule: steroid delta-isomerase; PDBTitle: crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
22	d2gp4a1	Alignment	not modelled	6.1	9	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
23	d2je6i2	Alignment	not modelled	6.0	15	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
24	c3kebB_	Alignment	not modelled	6.0	10	PDB header: oxidoreductase Chain: B: PDB Molecule: probable thiol peroxidase; PDBTitle: thiol peroxidase from chromobacterium violaceum
25	c3ac0B_	Alignment	not modelled	5.8	24	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
26	d2ba0a2	Alignment	not modelled	5.7	13	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
27	c1cauB_	Alignment	not modelled	5.7	2	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin; PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
28	d1edya_	Alignment	not modelled	5.6	16	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Alpha-macroglobulin receptor domain Family: Alpha-macroglobulin receptor domain
						PDB header: isomerase

29	c4dolA_	Alignment	not modelled	5.5	14	Chain: A: PDB Molecule: at1g53520; PDBTitle: crystal structure of arabidopsis thaliana fatty-acid binding protein2 at1g53520 (atfap3)
30	c3nrlB_	Alignment	not modelled	5.5	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rumgna_01417; PDBTitle: crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
31	c2kxxA_	Alignment	not modelled	5.2	19	PDB header: protein binding Chain: A: PDB Molecule: small protein a; PDBTitle: nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
32	d1uika2	Alignment	not modelled	5.1	9	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein