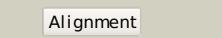


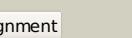
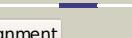
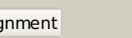
Phyre²

Email	I.a.kelley@imperial.ac.uk
Description	P39270
Date	Thu Jan 5 11:58:41 GMT 2012
Unique Job ID	c22e1a7e45e51274

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3shpA			55.1	56	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sthe_0691; PDBTitle: crystal structure of putative acetyltransferase from sphaerobacter2 thermophilus dsm 20745
2	c1ceuA			26.4	17	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
3	d2d9ra1			14.6	24	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: PG0164-like
4	c1ifIA			10.2	10	PDB header: virus Chain: A: PDB Molecule: inovirus; PDBTitle: molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13), if1 and ifke
5	c2df7H			10.2	50	PDB header: virus like particle Chain: H: PDB Molecule: structural polyprotein vp2; PDBTitle: crystal structure of infectious bursal disease virus vp2 subviral2 particle
6	c2k6IA			10.0	38	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the solution structure of xacb0070 from xanthomonas2 axonopodis pv citri reveals this new protein is a member of3 the rh family of transcriptional repressors
7	d2df7a1			9.7	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Birnaviridae-like VP
8	c1m8IA			9.6	13	PDB header: viral protein Chain: A: PDB Molecule: vpr protein; PDBTitle: nmr structure of the hiv-1 regulatory protein vpr
9	d1yu8x1			9.4	17	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
10	c3nqzB			9.4	23	PDB header: hydrolase Chain: B: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
11	d1lunda			9.4	17	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain

12	d1unca_			9.0	11	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
13	clyqlA_			8.8	14	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: structural genomics of caenorhabditis elegans: glutathione2 s-transferase
14	d1t0za_			8.7	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
15	d1u4ga_			8.0	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
16	d1b33n_			7.8	33	Fold: Allophycocyanin linker chain (domain) Superfamily: Allophycocyanin linker chain (domain) Family: Allophycocyanin linker chain (domain)
17	c3ideD_			7.6	29	PDB header: virus like particle Chain: D: PDB Molecule: capsid protein vp2; PDBTitle: structure of ipnv subviral particle
18	d1xcr1			7.5	50	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: PTD012-like
19	c1zdbA_			7.2	29	PDB header: IgG binding domain Chain: A: PDB Molecule: mini protein a domain, z38; PDBTitle: phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
20	d1s28a_			7.1	36	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
21	c2h2wA_		not modelled	7.0	24	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
22	c2k6nA_		not modelled	6.9	22	PDB header: structural protein Chain: A: PDB Molecule: supervillin; PDBTitle: solution structure of human supervillin headpiece, minimized2 average
23	c3zqoK_		not modelled	6.6	29	PDB header: dna-binding protein Chain: K: PDB Molecule: terminase small subunit; PDBTitle: crystal structure of the small terminase oligomerization2 core domain from a spp1-like bacteriophage (crystal form 3)
24	d1oz9a_		not modelled	6.4	21	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
25	c3nixF_		not modelled	6.4	20	PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
26	d1kqfc_		not modelled	6.2	12	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit
27	d1oqva_		not modelled	6.0	11	Fold: Pili subunits Superfamily: Pili subunits Family: TcpA-like pilin
28	c2cj0A_		not modelled	5.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: chloroperoxidase; PDBTitle: chloroperoxidase complexed with nitrate

29	d1qzpa		Alignment	not modelled	5.9	17	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
30	d1n2fa		Alignment	not modelled	5.9	19	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
31	d1ujsa		Alignment	not modelled	5.7	20	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
32	d1yu5x1		Alignment	not modelled	5.7	17	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
33	c213xa		Alignment	not modelled	5.6	39	PDB header: protein binding Chain: A: PDB Molecule: ablim2 protein; PDBTitle: villin head piece domain of human ablim2
34	c2jmhA		Alignment	not modelled	5.5	57	PDB header: allergen Chain: A: PDB Molecule: mite allergen blo t 5; PDBTitle: nmr solution structure of blo t 5, a major mite allergen2 from blomia tropicalis
35	c1vjqB		Alignment	not modelled	5.5	21	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
36	d2d8ca1		Alignment	not modelled	5.2	33	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
37	c3gd9A		Alignment	not modelled	5.1	38	PDB header: hydrolase Chain: A: PDB Molecule: laminaripentose-producing beta-1,3-guluaose PDBTitle: crystal structure of laminaripentose-producing beta-1,3-2 glucanase in complex with laminaritetroose
38	d1leda		Alignment	not modelled	5.1	29	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules