








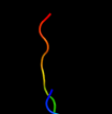

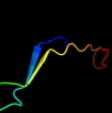


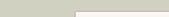








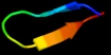

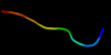
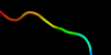






Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q9Z3A0
Date	Thu Jan 5 12:38:31 GMT 2012
Unique Job ID	1be3331859e83b7c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dw8B_	 Alignment		22.0	15	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: serine/threonine-protein phosphatase 2a 55 kda regulatory PDBTitle: structure of a protein phosphatase 2a holoenzyme with b55 subunit
2	d1jl3a_	 Alignment		18.7	38	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
3	c3nctC_	 Alignment		17.3	32	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
4	c2krcA_	 Alignment		16.2	35	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit delta; PDBTitle: solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
5	d2noca1	 Alignment		14.8	25	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
6	c2pxgA_	 Alignment		9.2	13	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein; PDBTitle: nmr solution structure of omla
7	c2jv5A_	 Alignment		8.5	33	PDB header: protein binding Chain: A: PDB Molecule: reticulon-4; PDBTitle: nogo54
8	c2kxxA_	 Alignment		6.7	24	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
9	d2igia1	 Alignment		6.6	40	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
10	c1y8aA_	 Alignment		6.5	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
11	c2ko2A_	 Alignment		6.4	33	PDB header: membrane protein Chain: A: PDB Molecule: reticulon-4; PDBTitle: nogo66

12	c1x9dA_	Alignment		6.4	55	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum mannosyl-oligosaccharide 1, PDBTitle: crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
13	d1x9da1	Alignment		6.4	55	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
14	c2kerA_	Alignment		6.0	50	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-amylase inhibitor z-2685; PDBTitle: alpha-amylase inhibitor parvulostat (z-2685) from2 streptomyces parvulus
15	d1ok0a_	Alignment		5.9	50	Fold: alpha-Amylase inhibitor tendamistat Superfamily: alpha-Amylase inhibitor tendamistat Family: alpha-Amylase inhibitor tendamistat
16	c3asiA_	Alignment		5.8	63	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-1-alpha; PDBTitle: alpha-neurexin-1 ectodomain fragment; lns5-egf3-lns6
17	d1hcua_	Alignment		5.5	33	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
18	c3d3rA_	Alignment		5.5	55	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
19	d1p2za2	Alignment		5.2	53	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
20	d1hnfa2	Alignment		5.2	78	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
21	d2b5ib1	Alignment	not modelled	5.1	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
22	c3cxjB_	Alignment	not modelled	5.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus