

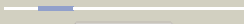






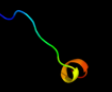

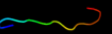

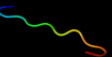



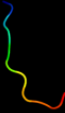

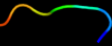




Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jb0a_	 Alignment		23.6	33	Fold: Photosystem I subunits PsaA/PsaB Superfamily: Photosystem I subunits PsaA/PsaB Family: Photosystem I subunits PsaA/PsaB
2	d1jb0b_	 Alignment		21.2	33	Fold: Photosystem I subunits PsaA/PsaB Superfamily: Photosystem I subunits PsaA/PsaB Family: Photosystem I subunits PsaA/PsaB
3	c2l61A_	 Alignment		19.6	35	PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle.
4	c3d0fA_	 Alignment		16.7	6	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
5	c2vsaA_	 Alignment		14.3	27	PDB header: toxin Chain: A: PDB Molecule: mosquitocidal toxin; PDBTitle: structure and mode of action of a mosquitocidal holotoxin
6	d3e9va1	 Alignment		12.8	33	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
7	d2z15a1	 Alignment		11.8	33	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
8	c2ktrA_	 Alignment		9.2	11	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
9	d1q90c_	 Alignment		9.0	0	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
10	c2jvyA_	 Alignment		8.7	38	PDB header: metal binding protein Chain: A: PDB Molecule: nf-kappa-b essential modulator; PDBTitle: solution structure of the eda-id-related c417f mutant of2 human nemo zinc finger
11	c2aapA_	 Alignment		8.4	38	PDB header: toxin Chain: A: PDB Molecule: jingzhaotoxin-vii; PDBTitle: solution structure of jingzhaotoxin-vii

12	c1e1hC_	Alignment		8.2	19	PDB header: hydrolase Chain: C: PDB Molecule: botulinum neurotoxin type a light chain; PDBTitle: crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase.
13	d1wmha_	Alignment		8.0	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
14	c3k3qB_	Alignment		7.8	19	PDB header: immune system Chain: B: PDB Molecule: botulinum neurotoxin type a; PDBTitle: crystal structure of a llama antibody complexed with the c.2 botulinum neurotoxin serotype a catalytic domain
15	c1ymzA_	Alignment		7.6	17	PDB header: unknown function Chain: A: PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
16	c2iyjA_	Alignment		7.6	13	PDB header: isomerase Chain: A: PDB Molecule: thiol disulfide interchange protein dsbc; PDBTitle: crystal structure of the n-terminal dimer domain of e.coli2 dsbc
17	c3ic3C_	Alignment		7.2	0	PDB header: oxidoreductase Chain: C: PDB Molecule: putative pyruvate dehydrogenase; PDBTitle: structure of a putative pyruvate dehydrogenase from the photosynthetic2 bacterium rhodospseudomonas palustris cga009
18	c1e0mA_	Alignment		7.1	21	PDB header: de novo protein Chain: A: PDB Molecule: wwprototype; PDBTitle: prototype ww domain
19	d1rfsa_	Alignment		7.0	9	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
20	d1cewi_	Alignment		7.0	9	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Cystatins
21	c2j4mA_	Alignment	not modelled	7.0	24	PDB header: protein binding Chain: A: PDB Molecule: endoglucanase 45a; PDBTitle: double dockerin from piromyces equi cel45a
22	c2wwaj_	Alignment	not modelled	6.8	33	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l19; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
23	d1p90a_	Alignment	not modelled	6.6	26	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: Nitrogenase accessory factor
24	d1hc1a3	Alignment	not modelled	6.6	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arthropod hemocyanin, C-terminal domain
25	d2jmfa1	Alignment	not modelled	6.4	13	Fold: WW domain-like Superfamily: WW domain Family: WW domain
26	d1plqa2	Alignment	not modelled	6.3	15	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
27	d2rm0w1	Alignment	not modelled	6.0	21	Fold: WW domain-like Superfamily: WW domain Family: WW domain
28	c2kykA_	Alignment	not modelled	5.8	20	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: the sandwich region between two Imp2a py motif regulates the2 interaction between aip4ww2domain and py motif Fold: SufE/NifU

29	d1mzga_	Alignment	not modelled	5.7	16	Superfamily: SufE/NifU Family: SufE-like
30	d1t3ba2	Alignment	not modelled	5.6	13	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
31	c2djyA_	Alignment	not modelled	5.2	13	PDB header: ligase/signaling protein Chain: A: PDB Molecule: smad ubiquitination regulatory factor 2; PDBTitle: solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
32	d1pqsa_	Alignment	not modelled	5.1	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
33	d1r46a2	Alignment	not modelled	5.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain