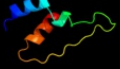
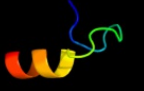


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dw3A_	 Alignment		54.1	30	PDB header: photosynthesis Chain: A: PDB Molecule: intrinsic membrane protein pufx; PDBTitle: solution structure of the rhodobacter sphaeroides pufx2 membrane protein
2	d1ysga1	 Alignment		19.0	29	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
3	d1g5ma_	 Alignment		16.3	24	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
4	d2ponb1	 Alignment		14.4	29	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
5	d1kl7a_	 Alignment		12.7	26	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
6	d1s4ka_	 Alignment		12.5	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
7	c1lflA_	 Alignment		11.2	46	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),3 if1 and ike
8	c2k9yB_	 Alignment		10.3	38	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
9	c2k9yA_	 Alignment		10.3	38	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
10	c2wvrC_	 Alignment		9.7	20	PDB header: replication Chain: C: PDB Molecule: dna replication factor cdt1; PDBTitle: human cdt1:geminin complex
11	c2bolA_	 Alignment		9.0	19	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small12 heat shock protein

12	dli7qb_	Alignment		9.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	dlxrxal	Alignment		8.6	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
14	clxrxD_	Alignment		8.6	33	PDB header: replication inhibitor Chain: D: PDB Molecule: sega protein; PDBTitle: crystal structure of a dna-binding protein
15	d2p7tc1	Alignment		8.4	36	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
16	clwloA_	Alignment		8.2	4	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: safe protein; PDBTitle: solution structure of the hypothetical protein from thermus2 thermophilus hb8
17	d2j6ba1	Alignment		7.1	21	Fold: STIV B116-like Superfamily: STIV B116-like Family: STIV B116-like
18	c2x4iA_	Alignment		6.6	25	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein 114; PDBTitle: orf 114a from sulfolobus islandicus rudivirus 1
19	c3fmtF_	Alignment		6.1	33	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein sega; PDBTitle: crystal structure of sega bound to dna
20	dli1qb_	Alignment		6.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	c3e15D_	Alignment	not modelled	5.9	17	PDB header: hydrolase Chain: D: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: 6-phosphogluconolactonase from plasmodium vivax
22	d1t57a_	Alignment	not modelled	5.2	27	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like