





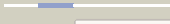
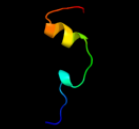



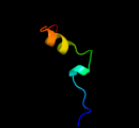

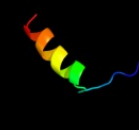




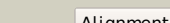

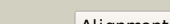


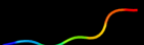
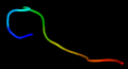
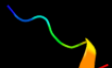
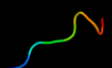



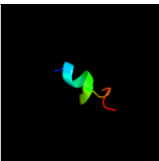


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ptjA_	 Alignment		98.1	8	PDB header: hydrolase Chain: A: PDB Molecule: upf0603 protein at1g54780, chloroplastic; PDBTitle: structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein attip18.3
2	c2kw7A_	 Alignment		97.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
3	c2kptA_	 Alignment		62.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative secreted protein; PDBTitle: solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a
4	c2y69S_	 Alignment		22.8	32	PDB header: electron transport Chain: S: PDB Molecule: cytochrome c oxidase subunit 5b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
5	d1q90n_	 Alignment		18.4	64	Fold: Single transmembrane helix Superfamily: PetN subunit of the cytochrome b6f complex Family: PetN subunit of the cytochrome b6f complex
6	d1v54f_	 Alignment		15.8	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Cytochrome c oxidase Subunit F
7	d1pprm2	 Alignment		13.2	25	Fold: Peridinin-chlorophyll protein Superfamily: Peridinin-chlorophyll protein Family: Peridinin-chlorophyll protein
8	c3ismC_	 Alignment		12.3	64	PDB header: hydrolase inhibitor/hydrolase Chain: C: PDB Molecule: cg4930; PDBTitle: crystal structure of the endog/endogi complex: mechanism of endog2 inhibition
9	c3mpoD_	 Alignment		11.7	22	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
10	d1wr8a_	 Alignment		10.3	23	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
11	c3sviA_	 Alignment		8.4	60	PDB header: signaling protein Chain: A: PDB Molecule: type iii effector hopab2; PDBTitle: structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion

12	d2axtm1	Alignment		8.3	50	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein M, PsbM Family: PsbM-like
13	d1dwna_	Alignment		6.7	100	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
14	c2wnmA_	Alignment		6.4	38	PDB header: hydrolase Chain: A: PDB Molecule: gene 2; PDBTitle: solution structure of gp2
15	d2apja1	Alignment		6.2	56	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxylen esterase-like
16	d1zmba1	Alignment		6.2	44	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxylen esterase-like
17	d1gkpa1	Alignment		5.8	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
18	c2r5vA_	Alignment		5.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pcza361.1; PDBTitle: hydroxymandelate synthase crystal structure
19	c1f20A_	Alignment		5.3	33	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.

20	c2kneB_	Alignment		5.3	54	PDB header: metal transport Chain: B: PDB Molecule: atpase, ca++ transporting, plasma membrane 4; PDBTitle: calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
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