






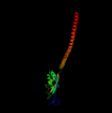





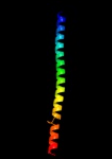

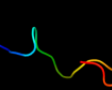

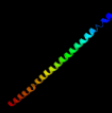



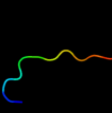







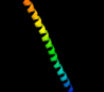
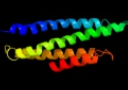


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bk6C_	 Alignment		99.9	25	PDB header: membrane protein Chain: C: PDB Molecule: ph stomatin; PDBTitle: crystal structure of a core domain of stomatin from2 pyrococcus horikoshii
2	c2rpbA_	 Alignment		99.8	25	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical membrane protein; PDBTitle: the solution structure of membrane protein
3	dlwina_	 Alignment		99.7	14	Fold: EF-Ts domain-like Superfamily: Band 7/SPFH domain Family: Band 7/SPFH domain
4	c2zv4O_	 Alignment		98.1	20	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
5	c2kk7A_	 Alignment		80.5	26	PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase subunit e; PDBTitle: nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii
6	c2k88A_	 Alignment		51.3	29	PDB header: hydrolase Chain: A: PDB Molecule: vacuolar proton pump subunit g; PDBTitle: association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase
7	dl12pa_	 Alignment		49.5	28	Fold: Single transmembrane helix Superfamily: F1F0 ATP synthase subunit B, membrane domain Family: F1F0 ATP synthase subunit B, membrane domain
8	c2kepA_	 Alignment		44.4	41	PDB header: transport protein Chain: A: PDB Molecule: general secretion pathway protein g; PDBTitle: solution structure of xcpt, the main component of the type 22 secretion system of pseudomonas aeruginosa
9	c3k5bE_	 Alignment		43.5	13	PDB header: hydrolase Chain: E: PDB Molecule: v-type atp synthase subunit e; PDBTitle: crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
10	c3u5gB_	 Alignment		33.8	17	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s1-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution
11	c1wd6B_	 Alignment		27.9	42	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli

12	d1t92a_	Alignment		25.9	29	Fold: Pili subunits Superfamily: Pili subunits Family: Pseudopilin
13	c2i7uA_	Alignment		25.0	36	PDB header: de novo protein/ligand binding protein Chain: A: PDB Molecule: four-alpha-helix bundle; PDBTitle: structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
14	c3fu1B_	Alignment		19.2	24	PDB header: protein transport Chain: B: PDB Molecule: general secretion pathway protein g; PDBTitle: crystal structure of the major pseudopilin from the type 2 secretion2 system of vibrio cholerae
15	c2xzm4_	Alignment		18.9	14	PDB header: ribosome Chain: 4: PDB Molecule: 40s ribosomal protein s3a; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
16	c2vgpD_	Alignment		12.8	33	PDB header: transferase Chain: D: PDB Molecule: inner centromere protein a; PDBTitle: crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
17	d2hiqa1	Alignment		12.6	42	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YdHR
18	d1tf5a1	Alignment		11.3	23	Fold: Pre-protein crosslinking domain of SecA Superfamily: Pre-protein crosslinking domain of SecA Family: Pre-protein crosslinking domain of SecA
19	c3k5bB_	Alignment		11.0	22	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase, subunit (vapc-therm); PDBTitle: crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
20	c1tt9B_	Alignment		10.9	14	PDB header: transferase, lyase Chain: B: PDB Molecule: formimidoyltransferase-cyclodeaminase PDBTitle: structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
21	c3kdpD_	Alignment	not modelled	10.5	18	PDB header: hydrolase Chain: D: PDB Molecule: sodium/potassium-transporting atpase subunit beta-1; PDBTitle: crystal structure of the sodium-potassium pump
22	d1htjf_	Alignment	not modelled	9.1	15	Fold: Regulator of G-protein signaling, RGS Superfamily: Regulator of G-protein signaling, RGS Family: Regulator of G-protein signaling, RGS
23	c1htjF_	Alignment	not modelled	9.1	15	PDB header: signaling protein Chain: F: PDB Molecule: kiaa0380; PDBTitle: structure of the rgs-like domain from pdz-rhogef
24	c3swfA_	Alignment	not modelled	8.2	40	PDB header: transport protein Chain: A: PDB Molecule: cgmp-gated cation channel alpha-1; PDBTitle: cnga1 621-690 containing clz domain
25	d5ruba2	Alignment	not modelled	7.3	25	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
26	c1jsuC_	Alignment	not modelled	7.1	32	PDB header: complex (transferase/cyclin/inhibitor) Chain: C: PDB Molecule: p27; PDBTitle: p27(kip1)/cyclin a/cdk2 complex
27	c2w2hD_	Alignment	not modelled	6.8	32	PDB header: rna-binding protein Chain: D: PDB Molecule: protein tat; PDBTitle: structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from eiav
28	d1wuua1	Alignment	not modelled	6.8	10	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
29	c3s93B_	Alignment	not modelled	6.5	11	PDB header: transcription Chain: B: PDB Molecule: tudor domain-containing protein 5;

					PDBTitle: crystal structure of conserved motif in tdrd5
30	d1wmda1	Alignment	not modelled	6.4	11 Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Proprotein convertase P-domain
31	c2jp3A	Alignment	not modelled	6.4	36 PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
32	c2ptnA	Alignment	not modelled	6.4	10 PDB header: transport protein Chain: A: PDB Molecule: hyperpolarization-activated (ih) channel; PDBTitle: structure and rearrangements in the carboxy-terminal region of spih2 channels
33	c2jo1A	Alignment	not modelled	6.3	24 PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
34	d2o4ta1	Alignment	not modelled	6.3	6 Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
35	d1o5ha	Alignment	not modelled	6.1	19 Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like
36	d2ozla1	Alignment	not modelled	6.0	20 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
37	c1y4cA	Alignment	not modelled	5.8	15 PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
38	c2kncB	Alignment	not modelled	5.7	13 PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
39	d1fft2	Alignment	not modelled	5.7	7 Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
40	d1nkt1	Alignment	not modelled	5.5	14 Fold: Pre-protein crosslinking domain of SecA Superfamily: Pre-protein crosslinking domain of SecA Family: Pre-protein crosslinking domain of SecA
41	c1o7fA	Alignment	not modelled	5.5	17 PDB header: regulation Chain: A: PDB Molecule: camp-dependent rap1 guanine-nucleotide exchange PDBTitle: crystal structure of the regulatory domain of epac2
42	c2k6iA	Alignment	not modelled	5.5	34 PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein mj0223; PDBTitle: the domain features of the peripheral stalk subunit h of the2 methanogenic a1ao atp synthase and the nmr solution3 structure of h1-47
43	c2zxeB	Alignment	not modelled	5.4	21 PDB header: hydrolase/transport protein Chain: B: PDB Molecule: na+,k+-atpase beta subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
44	d1ykwa2	Alignment	not modelled	5.4	21 Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
45	c3nngA	Alignment	not modelled	5.3	21 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the f5/8 type c domain of q5lfr2_bacfn protein2 from bacteroides fragilis. northeast structural genomics consortium3 target bfr258e
46	d1e3pa2	Alignment	not modelled	5.3	39 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
47	c9paiB	Alignment	not modelled	5.3	15 PDB header: hydrolase inhibitor Chain: B: PDB Molecule: protein (plasminogen activator inhibitor-1) residues 365- PDBTitle: cleaved substrate variant of plasminogen activator inhibitor-1
48	c2axcA	Alignment	not modelled	5.3	18 PDB header: hydrolase Chain: A: PDB Molecule: colicin e7; PDBTitle: crystal structure of cole7 translocation domain
49	c3i24B	Alignment	not modelled	5.1	17 PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
50	d2hsga1	Alignment	not modelled	5.1	21 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator