














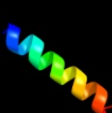



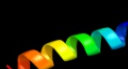







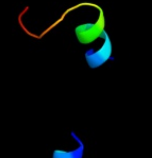


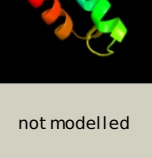


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		34.4	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
2	<a href="#">c3fo8D_</a>	 Alignment		34.1	75	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> tail sheath protein gp18; <b>PDBTitle:</b> crystal structure of the bacteriophage t4 tail sheath2 protein, protease resistant fragment gp18pr
3	<a href="#">d2nr9a1</a>	 Alignment		32.1	13	<b>Fold:</b> Rhomboid-like <b>Superfamily:</b> Rhomboid-like <b>Family:</b> Rhomboid-like
4	<a href="#">c2h3oA_</a>	 Alignment		26.4	30	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merft, a membrane protein with two trans-2 membrane helices
5	<a href="#">c2j5dA_</a>	 Alignment		23.8	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> nmr structure of bnip3 transmembrane domain in lipid2 bicelles
6	<a href="#">d1y5ic1</a>	 Alignment		21.1	15	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Respiratory nitrate reductase 1 gamma chain <b>Family:</b> Respiratory nitrate reductase 1 gamma chain
7	<a href="#">d3blhb2</a>	 Alignment		19.9	19	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
8	<a href="#">c2ka2A_</a>	 Alignment		18.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
9	<a href="#">c2ka2B_</a>	 Alignment		18.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
10	<a href="#">c2ka1A_</a>	 Alignment		18.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
11	<a href="#">c2ka1B_</a>	 Alignment		18.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles

12	<a href="#">dljkw1</a>	Alignment		15.9	19	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
13	<a href="#">dlpprm2</a>	Alignment		15.6	22	<b>Fold:</b> Peridinin-chlorophyll protein <b>Superfamily:</b> Peridinin-chlorophyll protein <b>Family:</b> Peridinin-chlorophyll protein
14	<a href="#">c1zp2A</a>	Alignment		13.3	29	<b>PDB header:</b> transcription/cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase ii holoenzyme cyclin-like subunit; <b>PDBTitle:</b> structure of the mediator subunit cyclin c
15	<a href="#">c2jplA</a>	Alignment		12.4	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit alpha; <b>PDBTitle:</b> lactococcin g-a in tfe
16	<a href="#">d1ehkb2</a>	Alignment		10.9	33	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
17	<a href="#">c1hfeT</a>	Alignment		9.7	27	<b>PDB header:</b> hydrogenase <b>Chain:</b> T: <b>PDB Molecule:</b> protein (fe-only hydrogenase (e.c.1.18.99.1) <b>PDBTitle:</b> 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
18	<a href="#">d1hfes</a>	Alignment		9.7	27	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Fe-only hydrogenase smaller subunit <b>Family:</b> Fe-only hydrogenase smaller subunit
19	<a href="#">d2pb9a1</a>	Alignment		8.9	57	<b>Fold:</b> AraD/HMP-PK domain-like <b>Superfamily:</b> AraD/HMP-PK domain-like <b>Family:</b> Phosphomethylpyrimidine kinase C-terminal domain-like
20	<a href="#">c2i53A</a>	Alignment		7.7	16	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cyclin k; <b>PDBTitle:</b> crystal structure of cyclin k
21	<a href="#">c1wazA</a>	Alignment	not modelled	7.6	33	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
22	<a href="#">c2cjqa</a>	Alignment	not modelled	7.1	22	<b>PDB header:</b> merfase <b>Chain:</b> A: <b>PDB Molecule:</b> rna-directed rna polymerase; <b>PDBTitle:</b> bovine viral diarrhea virus cp7-r12 rna-dependent rna2 polymerase
23	<a href="#">c2v1nA</a>	Alignment	not modelled	7.0	6	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein kin homolog; <b>PDBTitle:</b> solution structure of the region 51-160 of human kin172 reveals a winged helix fold
24	<a href="#">c3nd0A</a>	Alignment	not modelled	6.4	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sli0855 protein; <b>PDBTitle:</b> x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
25	<a href="#">d1xmeb2</a>	Alignment	not modelled	6.3	33	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
26	<a href="#">c1kxuA</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> regulatory protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclin h; <b>PDBTitle:</b> cyclin h, a positive regulatory subunit of cdk activating kinase
27	<a href="#">c1vk5A</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> expressed protein; <b>PDBTitle:</b> x-ray structure of gene product from arabidopsis thaliana at3g22680
28	<a href="#">d1vk5a</a>	Alignment	not modelled	6.2	29	<b>Fold:</b> Hypothetical protein At3g22680 <b>Superfamily:</b> Hypothetical protein At3g22680 <b>Family:</b> Hypothetical protein At3g22680

29	<a href="#">d2phpa1</a>	Alignment	not modelled	6.1	57	<b>Fold:</b> AraD/HMP-PK domain-like <b>Superfamily:</b> AraD/HMP-PK domain-like <b>Family:</b> Phosphomethylpyrimidine kinase C-terminal domain-like
30	<a href="#">d2ivxa1</a>	Alignment	not modelled	6.0	8	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
31	<a href="#">d2i53a1</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
32	<a href="#">c2joxA</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> churchill protein; <b>PDBTitle:</b> embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
33	<a href="#">d1m0da</a>	Alignment	not modelled	5.7	22	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Endonuclease I (Holliday junction resolvase)
34	<a href="#">c3hzqA</a>	Alignment	not modelled	5.7	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> structure of a tetrameric mscl in an expanded intermediate2 state
35	<a href="#">c2nysA</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> agr_c_3712p; <b>PDBTitle:</b> x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.
36	<a href="#">d2nysa1</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> AGR C 3712p-like
37	<a href="#">c2qasA</a>	Alignment	not modelled	5.2	30	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of caulobacter crescentus ssfb ortholog