










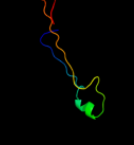

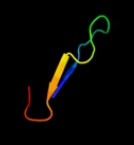

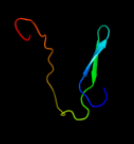

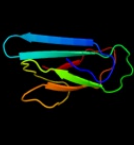

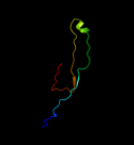

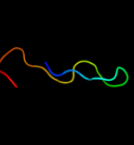
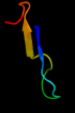
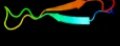
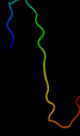


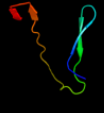

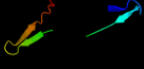



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xska_</a>	 Alignment		100.0	98	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> csgc; <b>PDBTitle:</b> e. coli curli protein csgc - secys
2	<a href="#">d1x9la_</a>	 Alignment		42.4	19	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> DR1885-like metal-binding protein <b>Family:</b> DR1885-like metal-binding protein
3	<a href="#">d1x99a_</a>	 Alignment		42.1	16	<b>Fold:</b> Cytolysin/lectin <b>Superfamily:</b> Cytolysin/lectin <b>Family:</b> Fungal fruit body lectin
4	<a href="#">c2ofeA_</a>	 Alignment		33.1	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sclerotium rolfsii lectin; <b>PDBTitle:</b> the crystal structure of sclerotium rolfsii lectin in complex with n-2 acetyl-d-glucosamine
5	<a href="#">c2k6za_</a>	 Alignment		30.9	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1943; <b>PDBTitle:</b> solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
6	<a href="#">c2yhga_</a>	 Alignment		16.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose-binding protein; <b>PDBTitle:</b> ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
7	<a href="#">d1dkia_</a>	 Alignment		16.1	23	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
8	<a href="#">d1ex0a1</a>	 Alignment		15.5	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Transglutaminase N-terminal domain
9	<a href="#">c2wdaA_</a>	 Alignment		15.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted lyase; <b>PDBTitle:</b> the x-ray structure of the streptomyces coelicolor a32 chondroitin ac lyase in complex with chondroitin sulphate
10	<a href="#">c2e7mA_</a>	 Alignment		13.7	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein kiaa0319; <b>PDBTitle:</b> solution structure of the pkd domain (329-428) from human2 kiaa0319
11	<a href="#">d1pvja_</a>	 Alignment		13.7	23	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like

12	<a href="#">c3bb7A_</a>	Alignment		12.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interpain a; <b>PDBTitle:</b> structure of prevotella intermedia prointerpain a fragment 39-3592 (mutant c154a)
13	<a href="#">c2kj6A_</a>	Alignment		12.2	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin folding cofactor b; <b>PDBTitle:</b> nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a
14	<a href="#">d1w8oa1</a>	Alignment		12.2	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
15	<a href="#">c2ys4A_</a>	Alignment		11.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hydrocephalus-inducing protein homolog; <b>PDBTitle:</b> solution structure of the n-terminal papd-like domain of2 hydin protein from human
16	<a href="#">d1vjja1</a>	Alignment		10.4	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Transglutaminase N-terminal domain
17	<a href="#">d2q3za1</a>	Alignment		10.3	36	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Transglutaminase N-terminal domain
18	<a href="#">d1z8ga2</a>	Alignment		10.0	20	<b>Fold:</b> SRCR-like <b>Superfamily:</b> SRCR-like <b>Family:</b> Hepsin, N-terminal domain
19	<a href="#">c2ezvA_</a>	Alignment		8.3	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> type ii restriction enzyme sfii; <b>PDBTitle:</b> crystal structure of tetrameric restriction endonuclease2 sfii bound to cognate dna.
20	<a href="#">d1ekra_</a>	Alignment		7.8	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Molybdenum cofactor biosynthesis protein C, MoaC <b>Family:</b> Molybdenum cofactor biosynthesis protein C, MoaC
21	<a href="#">c3h8dC_</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> motor protein/signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin-vi; <b>PDBTitle:</b> crystal structure of myosin vi in complex with dab2 peptide
22	<a href="#">c2ideE_</a>	Alignment	not modelled	7.4	31	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> E: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis protein c; <b>PDBTitle:</b> crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus thermophilus hb8
23	<a href="#">c2xr4A_</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lectin; <b>PDBTitle:</b> c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
24	<a href="#">d2zkmx2</a>	Alignment	not modelled	6.7	23	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
25	<a href="#">d1g0da1</a>	Alignment	not modelled	5.7	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Transglutaminase N-terminal domain
26	<a href="#">c2zq0B_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase (alpha-glucosidase subb); <b>PDBTitle:</b> crystal structure of subb complexed with acarbose
27	<a href="#">c2jnzA_</a>	Alignment	not modelled	5.2	9	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> phl p 3 allergen; <b>PDBTitle:</b> solution structure of phl p 3, a major allergen from2 timothy grass pollen
28	<a href="#">d1v7wa2</a>	Alignment	not modelled	5.1	18	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Glycosyltransferase family 36 N-terminal domain

29 [c2emcA](#)

Alignment

not modelled

5.1

64

**PDB header:**transcription  
**Chain:** A: **PDB Molecule:**zinc finger protein 473;  
**PDBTitle:** solution structure of the c2h2 type zinc finger (region 641-2 673) of human zinc finger protein 473