



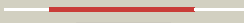






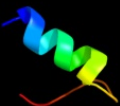

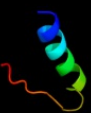

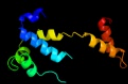





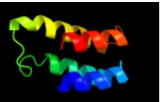

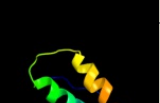

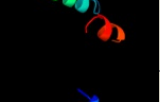






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3c4rC_</a>	 Alignment		100.0	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein encoded by 2 cryptic prophage
2	<a href="#">d2fi2a1</a>	 Alignment		93.8	21	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Retrovirus capsid dimerization domain-like <b>Family:</b> SCAN domain
3	<a href="#">c3lhrA_</a>	 Alignment		93.8	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 24; <b>PDBTitle:</b> crystal structure of the scan domain from human znf24
4	<a href="#">d1y7qa1</a>	 Alignment		93.0	19	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Retrovirus capsid dimerization domain-like <b>Family:</b> SCAN domain
5	<a href="#">d1nlna_</a>	 Alignment		52.0	23	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Adenain-like
6	<a href="#">c3ikmD_</a>	 Alignment		29.7	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase subunit gamma-1; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase2 holoenzyme
7	<a href="#">c2ek0B_</a>	 Alignment		22.0	31	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> stage v sporulation protein s (spovs) related protein; <b>PDBTitle:</b> stage v sporulation protein s (spovs) from thermus thermophilus zinc2 form
8	<a href="#">d2ao9a1</a>	 Alignment		22.0	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
9	<a href="#">d2nr5a1</a>	 Alignment		20.6	23	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> SO2669-like <b>Family:</b> SO2669-like
10	<a href="#">c2lkeA_</a>	 Alignment		19.4	36	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-m; <b>PDBTitle:</b> structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails
11	<a href="#">c2kngA_</a>	 Alignment		18.9	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein Isr2; <b>PDBTitle:</b> solution structure of c-domain of Isr2

12	<a href="#">c2lchA_</a>	Alignment		16.8	13	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein or38; <b>PDBTitle:</b> solution nmr structure of a protein with a redesigned hydrophobic2 core, northeast structural genomics consortium target or38
13	<a href="#">c2j8pA_</a>	Alignment		16.7	30	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage stimulation factor 64 kda subunit; <b>PDBTitle:</b> nmr structure of c-terminal domain of human cstf-64
14	<a href="#">c1pqvS_</a>	Alignment		15.2	16	<b>PDB header:</b> transferase/transcription <b>Chain:</b> S: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> rna polymerase ii-tfiis complex
15	<a href="#">c1y1yS_</a>	Alignment		15.2	16	<b>PDB header:</b> transferase/transcription/dna-rna hybrid <b>Chain:</b> S: <b>PDB Molecule:</b> transcription elongation factor s-ii; <b>PDBTitle:</b> rna polymerase ii-tfiis-dna/rna complex
16	<a href="#">c3pcqM_</a>	Alignment		13.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> photosystem i reaction center subunit xii; <b>PDBTitle:</b> femtosecond x-ray protein nanocrystallography
17	<a href="#">c2qxB_</a>	Alignment		12.7	50	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> enhancer of zeste homolog 2; <b>PDBTitle:</b> structural basis of ezh2 recognition by eed
18	<a href="#">c3ndqA_</a>	Alignment		11.6	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor a protein 1; <b>PDBTitle:</b> structure of human tfiis domain ii
19	<a href="#">d2ejqa1</a>	Alignment		11.5	16	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> TTHA0227-like
20	<a href="#">c2fs1A_</a>	Alignment		11.4	41	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> psd-1; <b>PDBTitle:</b> solution structure of psd-1
21	<a href="#">d1yqga1</a>	Alignment	not modelled	11.4	19	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> ProC C-terminal domain-like
22	<a href="#">d1tqga_</a>	Alignment	not modelled	11.1	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Chemotaxis protein CheA P1 domain
23	<a href="#">d2jn6a1</a>	Alignment	not modelled	10.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
24	<a href="#">c2ao9H_</a>	Alignment	not modelled	10.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> phage protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
25	<a href="#">c2dmeA_</a>	Alignment	not modelled	10.4	7	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 3; <b>PDBTitle:</b> solution structure of the tfiis domain ii of human phd2 finger protein 3
26	<a href="#">c2rodB_</a>	Alignment	not modelled	10.1	24	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> noxaa; <b>PDBTitle:</b> solution structure of mcl-1 complexed with noxaa
27	<a href="#">d1pula_</a>	Alignment	not modelled	9.3	16	<b>Fold:</b> Hypothetical protein MTH677 <b>Superfamily:</b> Hypothetical protein MTH677 <b>Family:</b> Hypothetical protein MTH677
28	<a href="#">d2fy9a1</a>	Alignment	not modelled	9.2	40	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> AbrB N-terminal domain-like
29	<a href="#">d1yfbal</a>	Alignment	not modelled	8.7	40	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> AbrB N-terminal domain-like

30	<a href="#">c3sohB_</a>	Alignment	not modelled	8.3	20	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar motor switch protein flig; <b>PDBTitle:</b> architecture of the flagellar rotor
31	<a href="#">c2ro5B_</a>	Alignment	not modelled	8.1	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> stage v sporulation protein t; <b>PDBTitle:</b> rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
32	<a href="#">c2jssA_</a>	Alignment	not modelled	8.0	12	<b>PDB header:</b> chaperone/nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of histone h2b.1 and histone h2a.z; <b>PDBTitle:</b> nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
33	<a href="#">c3fblA_</a>	Alignment	not modelled	7.7	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of orf132 of the archaeal virus acidianus2 filamentous virus 1 (afv1)
34	<a href="#">c1jb0M_</a>	Alignment	not modelled	7.7	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> photosystem 1 reaction centre subunit xii; <b>PDBTitle:</b> crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
35	<a href="#">d1jb0m_</a>	Alignment	not modelled	7.7	32	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XII of photosystem I reaction centre, PsaM <b>Family:</b> Subunit XII of photosystem I reaction centre, PsaM
36	<a href="#">d2ahra1</a>	Alignment	not modelled	7.6	17	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> ProC C-terminal domain-like
37	<a href="#">d1tp6a_</a>	Alignment	not modelled	7.3	24	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PA1314-like
38	<a href="#">d1l1aa1</a>	Alignment	not modelled	6.9	17	<b>Fold:</b> Hemocyanin, N-terminal domain <b>Superfamily:</b> Hemocyanin, N-terminal domain <b>Family:</b> Hemocyanin, N-terminal domain
39	<a href="#">c3bowC_</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> calpastatin; <b>PDBTitle:</b> structure of m-calpain in complex with calpastatin
40	<a href="#">d2obpa1</a>	Alignment	not modelled	6.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ReutB4095-like
41	<a href="#">c2xoaA_</a>	Alignment	not modelled	6.1	25	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
42	<a href="#">d1hc1a1</a>	Alignment	not modelled	6.1	20	<b>Fold:</b> Hemocyanin, N-terminal domain <b>Superfamily:</b> Hemocyanin, N-terminal domain <b>Family:</b> Hemocyanin, N-terminal domain
43	<a href="#">d1keaa_</a>	Alignment	not modelled	6.0	13	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
44	<a href="#">c3fidA_</a>	Alignment	not modelled	5.9	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative outer membrane protein (lpxr); <b>PDBTitle:</b> lpxr from salmonella typhimurium
45	<a href="#">d2r31a1</a>	Alignment	not modelled	5.9	15	<b>Fold:</b> ATP12-like <b>Superfamily:</b> ATP12-like <b>Family:</b> ATP12-like
46	<a href="#">c1whsB_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> serine carboxypeptidase <b>Chain:</b> B: <b>PDB Molecule:</b> serine carboxypeptidase ii; <b>PDBTitle:</b> structure of the complex of l-benzylsuccinate with wheat serine2 carboxypeptidase ii at 2.0 angstroms resolution
47	<a href="#">c1btqA_</a>	Alignment	not modelled	5.2	44	<b>PDB header:</b> anion transport <b>Chain:</b> A: <b>PDB Molecule:</b> band 3 anion transport protein; <b>PDBTitle:</b> the solution structures of the first and second2 transmembrane-spanning segments of band 3
48	<a href="#">c1btrA_</a>	Alignment	not modelled	5.2	44	<b>PDB header:</b> anion transport <b>Chain:</b> A: <b>PDB Molecule:</b> band 3 anion transport protein; <b>PDBTitle:</b> the solution structures of the first and second2 transmembrane-spanning segments of band 3
49	<a href="#">d1ouoa_</a>	Alignment	not modelled	5.1	21	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Endonuclease I
50	<a href="#">c2gqcA_</a>	Alignment	not modelled	5.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rhomboid intramembrane protease; <b>PDBTitle:</b> solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa