

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ej5a_	 Alignment		28.1	25	Fold: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Superfamily: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Family: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
2	c2p22C_	 Alignment		20.9	19	PDB header: transport protein Chain: C: PDB Molecule: protein srn2; PDBTitle: structure of the yeast escrt-i heterotetramer core
3	c2k42A_	 Alignment		16.5	25	PDB header: signaling protein Chain: A: PDB Molecule: wiscott-aldrich syndrome protein; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehcc effector
4	d1gvda_	 Alignment		15.0	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
5	d1guua_	 Alignment		14.0	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
6	c1guuA_	 Alignment		14.0	33	PDB header: transcription Chain: A: PDB Molecule: myb proto-oncogene protein; PDBTitle: crystal structure of c-myb r1
7	d1ea0a1	 Alignment		13.3	31	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
8	c2d9aA_	 Alignment		12.7	20	PDB header: transcription Chain: A: PDB Molecule: myb-related protein b; PDBTitle: solution structure of rsg1 ruh-050, a myb dna-binding2 domain in mouse cdna
9	c1fsdA_	 Alignment		12.1	17	PDB header: novel sequence Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
10	c1fsvA_	 Alignment		12.1	17	PDB header: beta beta alpha motif Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
11	c2l1kA_	 Alignment		10.3	27	PDB header: cell cycle, transcription Chain: A: PDB Molecule: cyclin-d-binding myb-like transcription factor 1; PDBTitle: solution nmr structure of the n-terminal myb-like 1 domain of the2 human cyclin-d-binding transcription factor 1 (hdmp1), northeast3 structural genomics consortium (nesg) target id hr8011a

12	d1chka_		Alignment		10.2	13	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Chitosanase
13	d1gv2a2		Alignment		9.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
14	d1w0ta_		Alignment		9.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: DNA-binding domain of telomeric protein
15	d1a5ja1		Alignment		9.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
16	d1zrra1		Alignment		9.5	35	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
17	c2cazF_		Alignment		9.1	21	PDB header: protein transport Chain: F; PDB Molecule: protein srn2; PDBTitle: escrt-i core
18	c1q0wA_		Alignment		8.2	64	PDB header: transport protein Chain: A; PDB Molecule: vacuolar protein sorting-associated protein PDBTitle: solution structure of vps27 amino-terminal uim-ubiquitin2 complex
19	d1h8ac1		Alignment		7.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
20	c3gh1A_		Alignment		7.7	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted nucleotide-binding protein; PDBTitle: crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
21	d1jw3a_		Alignment	not modelled	7.7	13	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
22	d1ofda1		Alignment	not modelled	7.7	25	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
23	d1w0ua_		Alignment	not modelled	7.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: DNA-binding domain of telomeric protein
24	c1zzaA_		Alignment	not modelled	7.0	21	PDB header: membrane protein Chain: A; PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
25	c2r9aA_		Alignment	not modelled	6.9	31	PDB header: protein binding Chain: A; PDB Molecule: non-homologous end-joining factor 1; PDBTitle: crystal structure of human xlf
26	d1vr3a1		Alignment	not modelled	6.8	30	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
27	c2kp6A_		Alignment	not modelled	6.4	29	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein cv0237 from chromobacterium2 violaceum. northeast structural genomics consortium (nesg) target3 cvt1
28	d1ldda_		Alignment	not modelled	6.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
							Fold: PR-1-like

29	d1rc9a1	Alignment	not modelled	6.2	15	Superfamily: PR-1-like Family: PR-1-like
30	d2f66c1	Alignment	not modelled	6.1	17	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VP537 C-terminal domain-like
31	c2k7rA_	Alignment	not modelled	5.9	11	PDB header: replication Chain: A: PDB Molecule: primosomal protein dnai; PDBTitle: n-terminal domain of the bacillus subtilis helicase-loading2 protein dnai
32	c3hslX_	Alignment	not modelled	5.8	25	PDB header: replication Chain: X: PDB Molecule: orf59; PDBTitle: the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
33	c3u5cM_	Alignment	not modelled	5.7	15	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s12; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
34	c1htrP_	Alignment	not modelled	5.7	23	PDB header: aspartyl protease Chain: P: PDB Molecule: progastricsin (pro segment); PDBTitle: crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
35	d1xg1a1	Alignment	not modelled	5.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: DNA-binding domain of telomeric protein
36	d1n6za_	Alignment	not modelled	5.2	36	Fold: Hypothetical protein Yml108w Superfamily: Hypothetical protein Yml108w Family: Hypothetical protein Yml108w