

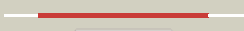






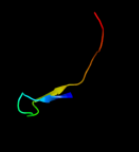

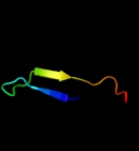



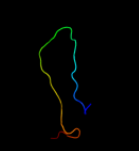

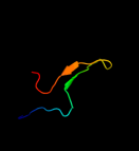



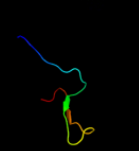
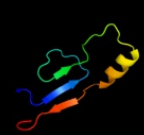






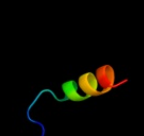
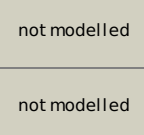


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fsuA_	 Alignment		100.0	95	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein phnh; PDBTitle: crystal structure of the phnh protein from escherichia coli
2	d2fsua1	 Alignment		100.0	95	Fold: PLP-dependent transferase-like Superfamily: PhnH-like Family: PhnH-like
3	dli4aa_	 Alignment		47.6	24	Fold: Annexin Superfamily: Annexin Family: Annexin
4	c1w3wA_	 Alignment		25.6	24	PDB header: coagulation Chain: A: PDB Molecule: annexin a8; PDBTitle: the 2.1 angstrom resolution structure of annexin a8
5	c3s9xA_	 Alignment		24.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asch domain; PDBTitle: high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
6	d1t62a_	 Alignment		23.5	48	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical protein EF3133
7	d1qjwa_	 Alignment		22.3	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
8	d2c7fa1	 Alignment		21.4	9	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
9	c3fdfA_	 Alignment		19.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fr253; PDBTitle: crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
10	d1dd1a_	 Alignment		18.7	11	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
11	c3o2qB_	 Alignment		18.7	17	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex

12	dlygsa_	Alignment		14.9	11	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
13	dlhm6a_	Alignment		14.4	15	Fold: Annexin Superfamily: Annexin Family: Annexin
14	c3o2sB_	Alignment		14.2	17	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72 complex
15	dlhvda_	Alignment		12.7	20	Fold: Annexin Superfamily: Annexin Family: Annexin
16	dlaina_	Alignment		12.0	18	Fold: Annexin Superfamily: Annexin Family: Annexin
17	dlavca1	Alignment		11.4	25	Fold: Annexin Superfamily: Annexin Family: Annexin
18	d2nn6h3	Alignment		11.3	29	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
19	dlm9ia1	Alignment		10.9	25	Fold: Annexin Superfamily: Annexin Family: Annexin
20	clavcA_	Alignment		10.7	31	PDB header: calcium/phospholipid-binding protein Chain: A: PDB Molecule: annexin vi; PDBTitle: bovine annexin vi (calcium-bound)
21	dlm9ia2	Alignment	not modelled	10.5	20	Fold: Annexin Superfamily: Annexin Family: Annexin
22	c2hjhB_	Alignment	not modelled	10.5	26	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
23	dlaxna_	Alignment	not modelled	10.0	20	Fold: Annexin Superfamily: Annexin Family: Annexin
24	d2pofa1	Alignment	not modelled	9.9	16	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
25	c3c8oB_	Alignment	not modelled	9.3	5	PDB header: hydrolase regulator Chain: B: PDB Molecule: regulator of ribonuclease activity a; PDBTitle: the crystal structure of rraa from pao1
26	dlalaa_	Alignment	not modelled	8.3	20	Fold: Annexin Superfamily: Annexin Family: Annexin
27	dlavca2	Alignment	not modelled	8.0	20	Fold: Annexin Superfamily: Annexin Family: Annexin
28	dlm5a_	Alignment	not modelled	7.2	15	Fold: Annexin Superfamily: Annexin Family: Annexin
29	dlkhxa_	Alignment	not modelled	6.9	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain

					Family: SMAD domain
30	c1kxhA_	Alignment	not modelled	6.9	17 PDB header: transcription Chain: A: PDB Molecule: smad2; PDBTitle: crystal structure of a phosphorylated smad2
31	c1q46A_	Alignment	not modelled	6.1	10 PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
32	c2kl7A_	Alignment	not modelled	6.0	44 PDB header: signaling protein, structural protein Chain: A: PDB Molecule: fibulin-4; PDBTitle: solution nmr structure of the egf-like 1 domain of human2 fibulin-4. northeast structural genomics target hr6275
33	d1w7ba_	Alignment	not modelled	6.0	20 Fold: Annexin Superfamily: Annexin Family: Annexin
34	d2ie7a1	Alignment	not modelled	5.8	20 Fold: Annexin Superfamily: Annexin Family: Annexin