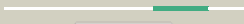
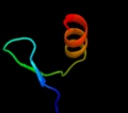
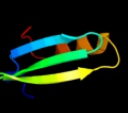
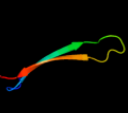
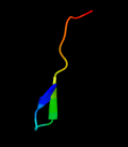
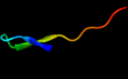
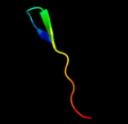


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1aopa2	 Alignment		59.6	16	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
2	c2gj2A_	 Alignment		41.3	21	PDB header: metal binding protein Chain: A: PDB Molecule: wsv230; PDBTitle: crystal structure of vp9 from white spot syndrome virus
3	c3gypA_	 Alignment		35.1	15	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone rtt106; PDBTitle: rtt106p
4	d2nptb1	 Alignment		26.4	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
5	d2c60a1	 Alignment		25.7	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
6	c2c60A_	 Alignment		25.0	33	PDB header: transferase Chain: A: PDB Molecule: human mitogen-activated protein kinase kinase PDBTitle: crystal structure of human mitogen-activated protein kinase2 kinase kinase 3 isoform 2 phox domain at 1.25 a resolution
7	d2cu1a1	 Alignment		24.3	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
8	c2bolA_	 Alignment		22.8	33	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
9	d1t77a2	 Alignment		21.8	6	Fold: PH domain-like barrel Superfamily: PH domain-like Family: PreBEACH PH-like domain
10	c3fssA_	 Alignment		21.6	16	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone rtt106; PDBTitle: structure of the tandem ph domains of rtt106
11	d2p7ja1	 Alignment		20.6	23	Fold: Profilin-like Superfamily: Sensory domain-like Family: Ykul C-terminal domain-like

12	c2klrA	Alignment		19.2	40	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin b chain; PDBTitle: solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
13	c3q9qB	Alignment		18.8	29	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
14	c2wj5A	Alignment		18.2	40	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein beta-6; PDBTitle: rat alpha crystallin domain
15	d1kcxal	Alignment		15.5	29	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
16	d2gc1a1	Alignment		12.8	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: SSRP1-like
17	c2x8nA	Alignment		12.4	35	PDB header: structural genomics Chain: A: PDB Molecule: cv0863; PDBTitle: solution nmr structure of uncharacterized protein cv08632 from chromobacterium violaceum. northeast structural3 genomics target (nesg) target cvt3. ocsf4 target cv0863.
18	c3qlaA	Alignment		11.4	32	PDB header: chaperone Chain: A: PDB Molecule: low molecular weight heat shock protein; PDBTitle: crystal structure of the hspa from xanthomonas axonopodis
19	c2ai4A	Alignment		10.1	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so1698; PDBTitle: structure of protein of unknown function so1698 from shewanella2 oneidensis
20	d2ftwa1	Alignment		8.9	27	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
21	c1in0B	Alignment	not modelled	8.8	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
22	c2wj7D	Alignment	not modelled	8.8	55	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alphab crystallin
23	c3l1eA	Alignment	not modelled	8.4	33	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin a chain; PDBTitle: bovine alphaa crystallin zinc bound
24	c3flvA	Alignment	not modelled	7.8	15	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa-binding domain-containing protein 5; PDBTitle: the crystal structure of human acyl-coenzyme a binding domain2 containing 5
25	c2copA	Alignment	not modelled	7.2	18	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coenzyme a binding domain containing 6; PDBTitle: solution structure of rsgi ruh-040, an acbp domain from2 human cdna
26	c1st7A	Alignment	not modelled	6.8	15	PDB header: transport protein Chain: A: PDB Molecule: acyl-coa-binding protein; PDBTitle: solution structure of acyl coenzyme a binding protein from2 yeast
27	d2ooda1	Alignment	not modelled	6.6	30	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
28	c3fp5A	Alignment	not modelled	6.4	12	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa binding protein; PDBTitle: crystal structure of acbp from monilophthora pernicioso

29	d1hb6a_	Alignment	not modelled	6.4	15	Fold: Acyl-CoA binding protein-like Superfamily: Acyl-CoA binding protein Family: Acyl-CoA binding protein
30	d1gtfa_	Alignment	not modelled	6.4	55	Fold: Double-stranded beta-helix Superfamily: TRAP-like Family: Trp RNA-binding attenuation protein (TRAP)
31	d1in0a2	Alignment	not modelled	6.1	19	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
32	d2pv4a1	Alignment	not modelled	6.1	41	Fold: Sama2622-like Superfamily: Sama2622-like Family: Sama2622-like
33	d1pxza_	Alignment	not modelled	5.9	17	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Pectate lyase-like
34	d1wapa_	Alignment	not modelled	5.8	55	Fold: Double-stranded beta-helix Superfamily: TRAP-like Family: Trp RNA-binding attenuation protein (TRAP)
35	c2zxyA_	Alignment	not modelled	5.3	13	PDB header: oxygen binding, transport protein Chain: A: PDB Molecule: cytochrome c552; PDBTitle: crystal structure of cytochrome c555 from aquifex aeolicus