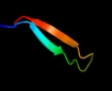
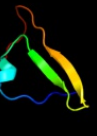
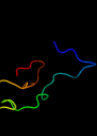
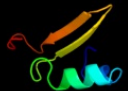
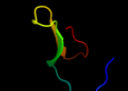
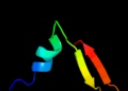


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1eb0A_	 Alignment		52.7	11	PDB header: chaperone Chain: A: PDB Molecule: urease accessory protein uree; PDBTitle: crystal structure of bacillus pasteurii uree at 1.85 a,2 phased by siras. type i crystal form.
2	c2kk8A_	 Alignment		46.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at4g05270; PDBTitle: nmr solution structure of a putative uncharacterized protein2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3449a
3	c1gmuB_	 Alignment		45.8	29	PDB header: metallochaperone Chain: B: PDB Molecule: uree; PDBTitle: structure of uree
4	d1earal	 Alignment		45.7	11	Fold: Urease metallochaperone UreE, N-terminal domain Superfamily: Urease metallochaperone UreE, N-terminal domain Family: Urease metallochaperone UreE, N-terminal domain
5	d1v61a_	 Alignment		40.0	14	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
6	d1omwa2	 Alignment		40.0	29	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
7	d1gmua1	 Alignment		38.7	28	Fold: Urease metallochaperone UreE, N-terminal domain Superfamily: Urease metallochaperone UreE, N-terminal domain Family: Urease metallochaperone UreE, N-terminal domain
8	c3q3fA_	 Alignment		36.5	30	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: ribonuclease/ubiquitin chimeric protein; PDBTitle: engineering domain-swapped binding interfaces by mutually exclusive2 folding: insertion of ubiquitin into position 103 of barnase
9	c3ny0D_	 Alignment		31.3	23	PDB header: metal binding protein Chain: D: PDB Molecule: urease accessory protein uree; PDBTitle: crystal structure of uree from helicobacter pylori (ni2+ bound form)
10	c2kdiA_	 Alignment		28.1	29	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin, vacuolar protein sorting-associated PDBTitle: solution structure of a ubiquitin/uim fusion protein
11	c2kzkA_	 Alignment		25.5	29	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein yol083w; PDBTitle: solution structure of alpha-mannosidase binding domain of atg34

12	c2ltmA_	Alignment		25.1	21	PDB header: electron transport Chain: A: PDB Molecule: nfu1 iron-sulfur cluster scaffold homolog, mitochondrial; PDBTitle: solution nmr structure of nfu1 iron-sulfur cluster scaffold homolog2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr2876b
13	c3a8qB_	Alignment		24.1	17	PDB header: signaling protein Chain: B: PDB Molecule: t-lymphoma invasion and metastasis-inducing PDBTitle: low-resolution crystal structure of the tiam2 phccex domain
14	c2kzbA_	Alignment		22.3	26	PDB header: protein transport Chain: A: PDB Molecule: autophagy-related protein 19; PDBTitle: solution structure of alpha-mannosidase binding domain of atg19
15	d1ttna1	Alignment		22.0	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
16	c1ttnA_	Alignment		22.0	30	PDB header: signaling protein Chain: A: PDB Molecule: dendritic cell-derived ubiquitin-like protein; PDBTitle: solution structure of the ubiquitin-like domain of human dc-2 ubp from dendritic cells
17	c2fwkB_	Alignment		16.1	17	PDB header: dna binding protein Chain: B: PDB Molecule: u6 snrna-associated sm-like protein lsm5; PDBTitle: crystal structure of cryptosporidium parvum u6 snrna-associated sm-2 like protein lsm5
18	d2q22a1	Alignment		15.7	18	Fold: Ava3019-like Superfamily: Ava3019-like Family: Ava3019-like
19	c2kcjA_	Alignment		12.5	14	PDB header: membrane protein Chain: A: PDB Molecule: pleckstrin homology domain-containing family a PDBTitle: solution structure of fapp1 ph domain
20	d1w1ha_	Alignment		12.2	21	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
21	d2fwka1	Alignment	not modelled	11.9	16	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
22	c3swnA_	Alignment	not modelled	11.7	24	PDB header: rna binding protein Chain: A: PDB Molecule: u6 snrna-associated sm-like protein lsm5; PDBTitle: structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
23	c2d9xA_	Alignment	not modelled	11.4	23	PDB header: lipid transport Chain: A: PDB Molecule: oxysterol binding protein-related protein 11; PDBTitle: solution structure of the ph domain of oxysterol binding2 protein-related protein 11 from human
24	c3a8nA_	Alignment	not modelled	10.9	22	PDB header: signaling protein Chain: A: PDB Molecule: t-lymphoma invasion and metastasis-inducing PDBTitle: crystal structure of the tiam1 phccex domain
25	d2ffma1	Alignment	not modelled	9.4	10	Fold: Hypothetical protein SAV1430 Superfamily: Hypothetical protein SAV1430 Family: Hypothetical protein SAV1430
26	d2h7aa1	Alignment	not modelled	9.4	64	Fold: YcgL-like Superfamily: YcgL-like Family: YcgL-like
27	c2auwB_	Alignment	not modelled	9.1	12	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
28	d1wiaa_	Alignment	not modelled	9.0	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

29	d1b33n_	Alignment	not modelled	8.5	36	Fold: Allophycocyanin linker chain (domain) Superfamily: Allophycocyanin linker chain (domain) Family: Allophycocyanin linker chain (domain)
30	d1zaka2	Alignment	not modelled	8.1	25	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
31	d1oqya4	Alignment	not modelled	8.0	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
32	c1cq0A_	Alignment	not modelled	7.3	75	PDB header: de novo protein Chain: A: PDB Molecule: protein (new hypothalamic neuropeptide/orexin- PDBTitle: solution structure of a human hypocretin-2/orexin-2 b'solution structure of a human hypocretin-2/orexin-b '
33	d1baka_	Alignment	not modelled	7.0	27	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
34	c2ojrA_	Alignment	not modelled	6.7	26	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin; PDBTitle: structure of ubiquitin solved by sad using the lanthanide-2 binding tag
35	c3qwmA_	Alignment	not modelled	6.6	11	PDB header: signaling protein Chain: A: PDB Molecule: iq motif and sec7 domain-containing protein 1; PDBTitle: crystal structure of gep100, the plextrin homology domain of iq motif2 and sec7 domain-containing protein 1 isoform a
36	c2z4dA_	Alignment	not modelled	6.5	50	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: nmr structures of yeast proteasome component rpn13
37	d1droa_	Alignment	not modelled	6.4	34	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
38	c2o4wA_	Alignment	not modelled	6.1	29	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: t4 lysozyme circular permutant
39	d1d3ba_	Alignment	not modelled	5.9	20	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
40	c2p0fA_	Alignment	not modelled	5.8	34	PDB header: ligand binding protein Chain: A: PDB Molecule: rho gtpase-activating protein 9; PDBTitle: arhgap9 ph domain in complex with ins(1,3,5)p3
41	c2kzrA_	Alignment	not modelled	5.7	21	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin thioesterase otu1; PDBTitle: solution nmr structure of ubiquitin thioesterase otu1 (ec 3.1.2.-)2 from mus musculus, northeast structural genomics consortium target3 mmt2a
42	d1o6wa1	Alignment	not modelled	5.6	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
43	d1ogwa_	Alignment	not modelled	5.5	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
44	d1iyfa_	Alignment	not modelled	5.4	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
45	c1z2mA_	Alignment	not modelled	5.3	23	PDB header: signaling protein Chain: A: PDB Molecule: interferon, alpha-inducible protein (clone ifi- PDBTitle: crystal structure of isg15, the interferon-induced2 ubiquitin cross reactive protein