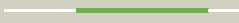
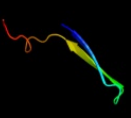
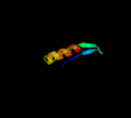
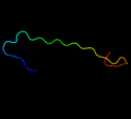
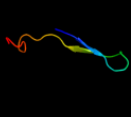
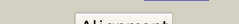
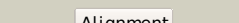
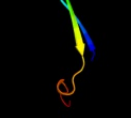
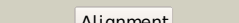
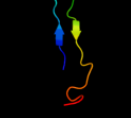
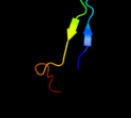
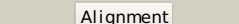


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s3aa1	 Alignment		99.3	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Mitochondrial ribosomal protein L51/S25/Cl-B8 domain
2	d2a2pa1	 Alignment		53.6	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
3	d2pnwa1	 Alignment		21.5	30	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
4	c3fhkF_	 Alignment		20.6	14	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
5	c3ks7D_	 Alignment		19.9	28	PDB header: hydrolase Chain: D: PDB Molecule: putative putative pngase f; PDBTitle: crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
6	d2g5da1	 Alignment		19.8	22	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
7	c2jroA_	 Alignment		19.3	3	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
8	c3czbA_	 Alignment		16.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transglycosylase; PDBTitle: crystal structure of putative transglycosylase from caulobacter2 crescentus
9	d2pi8a1	 Alignment		15.4	21	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
10	d2ae0x1	 Alignment		12.6	21	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
11	c2uveA_	 Alignment		12.1	13	PDB header: hydrolase Chain: A: PDB Molecule: exopolysaccharuronase; PDBTitle: structure of yersinia enterocolitica family 282 exopolysaccharuronase

12	c2eeiA	Alignment		11.6	14	PDB header: metal binding protein Chain: A: PDB Molecule: pdz domain-containing protein 1; PDBTitle: solution structure of second pdz domain of pdz domain2 containing protein 1
13	d1mp9a2	Alignment		10.5	15	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
14	c1vsvy7	Alignment		10.4	25	PDB header: hydrolase Chain: 7: PDB Molecule: proteasome activator blm10; PDBTitle: proteasome activator complex
15	d1cmia	Alignment		10.3	22	Fold: DLC Superfamily: DLC Family: DLC
16	d2dw4a3	Alignment		9.3	6	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
17	d1aisa1	Alignment		9.1	17	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
18	c3ol4B	Alignment		8.6	17	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
19	d1wlha	Alignment		8.5	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
20	c3iynO	Alignment		7.3	43	PDB header: virus Chain: O: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
21	c4ds1C	Alignment	not modelled	6.9	22	PDB header: structural protein/transport protein Chain: C: PDB Molecule: dynein light chain 1, cytoplasmic; PDBTitle: the structure of a yeast dyn2-nup159 complex and the molecular basis2 for the dynein light chain - nuclear pore interaction
22	d1g7oa2	Alignment	not modelled	6.8	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
23	c4a9zD	Alignment	not modelled	6.4	9	PDB header: transcription Chain: D: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of human p63 tetramerization domain
24	d1qnaa2	Alignment	not modelled	5.9	10	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
25	d1b6aa1	Alignment	not modelled	5.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
26	d2iida2	Alignment	not modelled	5.5	5	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
27	d1nh2a2	Alignment	not modelled	5.4	11	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain