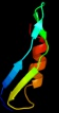
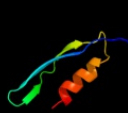
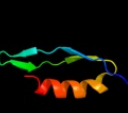
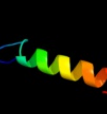
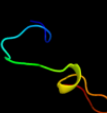
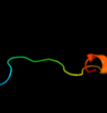


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lwxA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:ubiquinone oxidoreductase, na translocating, PDBTitle: crystal structure of na(+)-translocating nadh-quinone2 reductase subunit c (yp_001302508.1) from parabacteroides3 distasonis atcc 8503 at 1.10 a resolution
2	c3o6uB_	 Alignment		99.2	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein cpe2226; PDBTitle: crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
3	c2kzxA_	 Alignment		99.1	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
4	c3dczA_	 Alignment		98.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative rnfg subunit of electron transport complex; PDBTitle: crystal structure of a putative rnfg subunit of electron transport2 complex (tm0246) from thermotoga maritima at 1.65 a resolution
5	d1u07a_	 Alignment		76.4	9	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
6	d1ihra_	 Alignment		75.9	9	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
7	d2gskb1	 Alignment		72.3	9	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
8	c2k9kA_	 Alignment		71.8	18	PDB header: metal transport Chain: A: PDB Molecule: tonb2; PDBTitle: molecular characterization of the tonb2 protein from vibrio2 anguillarum
9	c1xx3A_	 Alignment		66.2	9	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
10	d1wfza_	 Alignment		43.3	16	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
11	c2grxC_	 Alignment		42.5	9	PDB header: metal transport Chain: C: PDB Molecule: protein tonb; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferriochrome

12	d1lr0a_	Alignment		37.9	16	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TolA
13	c2z7eB_	Alignment		19.7	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: nifu-like protein; PDBTitle: crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
14	d1r9pa_	Alignment		13.8	17	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
15	c1gr0A_	Alignment		12.6	26	PDB header: isomerase Chain: A: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc.
16	d1fusa_	Alignment		11.1	21	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Fungal ribonucleases
17	c2k5tA_	Alignment		10.0	16	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein yhhk; PDBTitle: solution nmr structure of putative n-acetyl transferase2 yhhk from e. coli bound to coenzyme a: northeast3 structural genomics consortium target et106
18	d1rdsa_	Alignment		7.1	9	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Fungal ribonucleases
19	c1d4cB_	Alignment		6.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
20	d1szwa_	Alignment		6.6	16	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: tRNA pseudouridine synthase TruD
21	c2koeA_	Alignment	not modelled	6.5	18	PDB header: membrane protein, signaling protein Chain: A: PDB Molecule: human cannabinoid receptor 1 - helix 7/8 peptide; PDBTitle: human cannabinoid receptor 1 - helix 7/8 peptide
22	c1x5dA_	Alignment	not modelled	6.5	19	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a6; PDBTitle: the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6
23	d1gr0a2	Alignment	not modelled	6.5	40	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
24	c3dinD_	Alignment	not modelled	6.5	6	PDB header: membrane protein, protein transport Chain: D: PDB Molecule: preprotein translocase subunit sece; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
25	d2bv3a3	Alignment	not modelled	6.1	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
26	d3c0na1	Alignment	not modelled	5.7	36	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Aerolysin/Pertussis toxin (APT) domain
27	d1vjpa1	Alignment	not modelled	5.6	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain