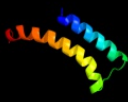
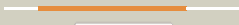
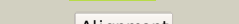
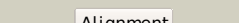
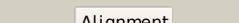
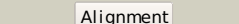
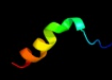
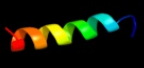
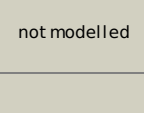


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l0lh_	 Alignment		84.9	10	Fold: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
2	d1ppjh_	 Alignment		83.2	10	Fold: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
3	c3cx5F_	 Alignment		82.4	13	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome b-c1 complex subunit 6; PDBTitle: structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer.
4	d3cx5f1	 Alignment		82.4	13	Fold: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
5	d1u97a_	 Alignment		67.0	29	Fold: Cysteine alpha-hairpin motif Superfamily: Cysteine alpha-hairpin motif Family: COX17-like
6	c2rnbA_	 Alignment		65.0	38	PDB header: metal transport Chain: A: PDB Molecule: cytochrome c oxidase copper chaperone; PDBTitle: solution structure of human cu(i)cox17
7	c2k3iA_	 Alignment		60.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: mitochondrial intermembrane space import and PDBTitle: the solution structure of human mia40
8	c2q00B_	 Alignment		42.8	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: orf c02003 protein; PDBTitle: crystal structure of the p95883_sulso protein from2 sulfobolus solfataricus. nesg target ssr10.
9	c2p22D_	 Alignment		27.5	50	PDB header: transport protein Chain: D: PDB Molecule: hypothetical 12.0 kda protein in ade3-ser2 PDBTitle: structure of the yeast escrt-i heterotetramer core
10	d2nn6b2	 Alignment		17.0	10	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
11	d2joda1	 Alignment		15.7	14	Fold: Hormone receptor domain Superfamily: Hormone receptor domain Family: Hormone receptor domain

12	d2nn6f2	Alignment		13.9	14	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
13	d1c55a_	Alignment		12.2	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
14	c4ab7C_	Alignment		11.4	9	PDB header: transferase Chain: C: PDB Molecule: protein arg5,6, mitochondrial; PDBTitle: crystal structure of a tetrameric acetylglutamate kinase2 from saccharomyces cerevisiae complexed with its substrate3 n-acetylglutamate
15	c3fybA_	Alignment		10.0	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function (duf1244); PDBTitle: crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
16	c2o35A_	Alignment		9.8	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf1244; PDBTitle: protein of unknown function (duf1244) from sinorhizobium meliloti
17	d2o35a1	Alignment		9.8	44	Fold: SMc04008-like Superfamily: SMc04008-like Family: SMc04008-like
18	d1wgna_	Alignment		8.8	45	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
19	d1b33n_	Alignment		7.3	29	Fold: Allophycocyanin linker chain (domain) Superfamily: Allophycocyanin linker chain (domain) Family: Allophycocyanin linker chain (domain)
20	c3fdqB_	Alignment		7.2	16	PDB header: dna binding protein/dna Chain: B: PDB Molecule: motility gene repressor mogr; PDBTitle: recognition of at-rich dna binding sites by the mogr2 repressor
21	c3picB_	Alignment	not modelled	6.9	32	PDB header: hydrolase Chain: B: PDB Molecule: cip2; PDBTitle: glucuronoyl esterase catalytic domain (cip2_ge) from hypocrea jecorina
22	c2r17C_	Alignment	not modelled	6.9	29	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein sorting-associated protein 35; PDBTitle: functional architecture of the retromer cargo-recognition complex
23	d1gbsa_	Alignment	not modelled	6.8	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme
24	c3s7yX_	Alignment	not modelled	6.6	13	PDB header: transferase Chain: X: PDB Molecule: n-acetylglutamate kinase / n-acetylglutamate synthase; PDBTitle: crystal structure of mnags in space group p3121 at 4.3 a resolution
25	c2kfvA_	Alignment	not modelled	6.6	27	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 3; PDBTitle: structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a
26	c2olsA_	Alignment	not modelled	6.2	17	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
27	c3fshC_	Alignment	not modelled	5.9	21	PDB header: ligase Chain: C: PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78

28	dlu7ka_	Alignment	not modelled	5.9	8	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
29	dlf3va_	Alignment	not modelled	5.7	23	Fold: Ferredoxin-like Superfamily: TRADD, N-terminal domain Family: TRADD, N-terminal domain
30	dlpkxa1	Alignment	not modelled	5.4	22	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
31	dlr2za1	Alignment	not modelled	5.3	21	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins