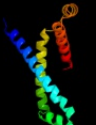
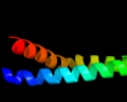
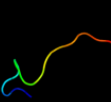
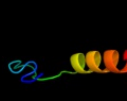
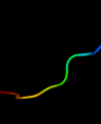
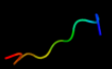


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nekc_	 Alignment		100.0	100	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
2	c1yq3C_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: succinate dehydrogenase cytochrome b, large subunit; PDBTitle: avian respiratory complex ii with oxaloacetate and ubiquinone
3	d1nekd_	 Alignment		98.7	18	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
4	d2bs2c1	 Alignment		97.6	9	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
5	d1kf6d_	 Alignment		96.2	17	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
6	d1kf6c_	 Alignment		92.6	17	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
7	c2hdeA_	 Alignment		19.9	20	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase complex subunit sap18; PDBTitle: solution structure of human sap18
8	d1qma2	 Alignment		17.7	14	Fold: IF3-like Superfamily: EPT/RTPC-like Family: RNA 3'-terminal phosphate cyclase, RTPC
9	c2vfyA_	 Alignment		15.3	13	PDB header: hydrolase Chain: A: PDB Molecule: akap18 delta; PDBTitle: akap18 delta central domain
10	c3c19A_	 Alignment		14.8	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
11	c3c25A_	 Alignment		14.4	30	PDB header: hydrolase/dna Chain: A: PDB Molecule: noti restriction endonuclease; PDBTitle: crystal structure of noti restriction endonuclease bound to cognate2 dna

12	c2ww9Q_	Alignment		14.0	36	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l39; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
13	d1iuha_	Alignment		13.3	17	Fold: LigT-like Superfamily: LigT-like Family: 2'-5' RNA ligase LigT
14	c2f9jP_	Alignment		12.8	33	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
15	c2ojmA_	Alignment		12.3	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: moronecidin; PDBTitle: solution structure and cell selectivity of piscidin 1 and2 its analogues
16	c3pqvD_	Alignment		11.5	21	PDB header: unknown function Chain: D: PDB Molecule: rc11 protein; PDBTitle: cyclase homolog
17	c4a1bB_	Alignment		9.1	36	PDB header: ribosome Chain: B: PDB Molecule: rpl39; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rna and3 proteins of molecule 3.
18	d2pu9b1	Alignment		8.5	27	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
19	c2zkr3_	Alignment		8.1	27	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
20	c2wfoA_	Alignment		7.7	50	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein 1; PDBTitle: crystal structure of machupo virus envelope glycoprotein2 gp1
21	d1rioA_	Alignment	not modelled	7.1	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
22	d1jh6a_	Alignment	not modelled	7.1	21	Fold: LigT-like Superfamily: LigT-like Family: tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase
23	c1qmiC_	Alignment	not modelled	6.9	14	PDB header: rna 3'-terminal phosphate cyclase Chain: C: PDB Molecule: rna 3'-terminal phosphate cyclase; PDBTitle: crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
24	c3dl8D_	Alignment	not modelled	6.7	33	PDB header: protein transport Chain: D: PDB Molecule: sece; PDBTitle: structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
25	d1eg3a2	Alignment	not modelled	6.3	29	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
26	c1jekA_	Alignment	not modelled	5.8	33	PDB header: viral protein Chain: A: PDB Molecule: env polyprotein; PDBTitle: visna tm core structure
27	c2d4gA_	Alignment	not modelled	5.8	0	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bsu11850; PDBTitle: structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis