Phyre^2

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Description	P0AEK7
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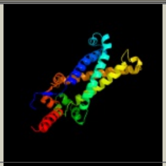
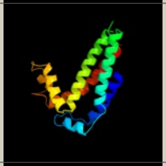
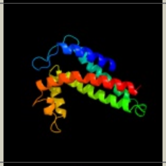
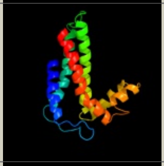
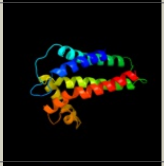
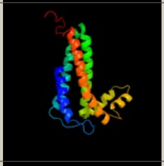
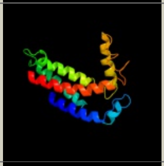
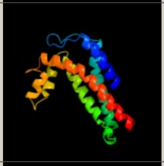
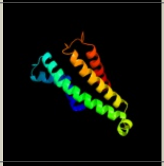
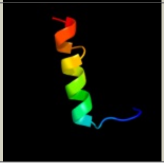
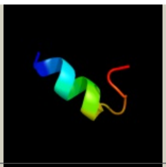
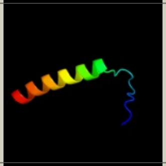
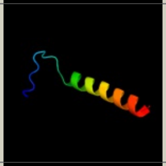
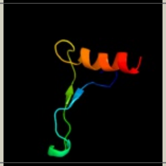
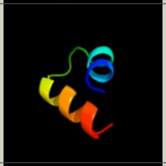
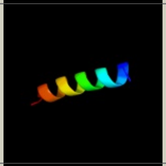
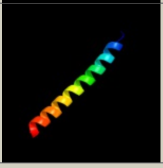
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kqfc_	Alignment		100.0	100	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Formate dehydrogenase N, cytochrome (gamma) subunit
2	d3cx5c2	Alignment		97.8	12	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
3	c2qjkM_	Alignment		97.7	14	**PDB header:**electron transport **Chain:** M: **PDB Molecule:**cytochrome b; **PDBTitle:** crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
4	d1q90b_	Alignment		97.6	11	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
5	d2e74a1	Alignment		97.6	14	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
6	c3cx5N_	Alignment		97.5	13	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**cytochrome b; **PDBTitle:** structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer.
7	d1ppjc2	Alignment		97.4	16	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
8	d1bccc3	Alignment		97.4	15	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
9	c3cwbC_	Alignment		97.3	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome b; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
10	d1y5ic1	Alignment		38.1	15	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain
11	c2kygC_	Alignment		16.4	23	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**protein cbfa2t1; **PDBTitle:** structure of the aml1-eto nervy domain - pka(riia) complex and its2 contribution to aml1-eto activity

12	c2levA_	Alignment		13.3	47	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ler; **PDBTitle:** structure of the dna complex of the c-terminal domain of ler
13	d1ecfa1	Alignment		11.1	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
14	c1fcuA_	Alignment		8.2	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
15	c1ecjB_	Alignment		7.8	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
16	c2xzn2_	Alignment		7.7	10	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**40s ribosomal protein s8; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
17	d1fcqa_	Alignment		7.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
18	c2pe4A_	Alignment		6.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
19	c3nrtC_	Alignment		6.0	21	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative ryanodine receptor; **PDBTitle:** the crystal strucutre of putative ryanodine receptor from bacteroides2 thetaiotaomicron vpi-5482
20	d1m56d_	Alignment		5.8	12	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
21	c2qfaC_	Alignment	not modelled	5.7	38	**PDB header:**cell cycle/cell cycle/cell cycle **Chain:** C: **PDB Molecule:**inner centromere protein; **PDBTitle:** crystal structure of a survivin-borealin-incenp core complex
22	c1v0dA_	Alignment	not modelled	5.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna fragmentation factor 40 kda subunit; **PDBTitle:** crystal structure of caspase-activated dnase (cad)
23	d1v0da_	Alignment	not modelled	5.4	21	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Caspase-activated DNase, CAD (DffB, DFF40)
24	d2ct5a1	Alignment	not modelled	5.4	26	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**BED zinc finger
25	c1rrzA_	Alignment	not modelled	5.3	20	**PDB header:**structural genomics,biosynthetic protein **Chain:** A: **PDB Molecule:**glycogen synthesis protein glgs; **PDBTitle:** solution structure of glgs protein from e. coli
26	d1rrza_	Alignment	not modelled	5.3	20	**Fold:**Spectrin repeat-like **Superfamily:**Glycogen synthesis protein GlgS **Family:**Glycogen synthesis protein GlgS