Phyre2

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Description	P0AB26
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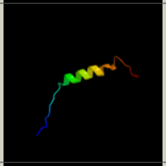
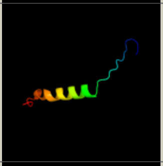
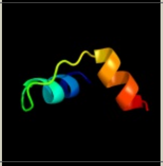
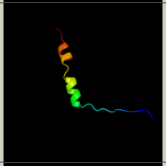
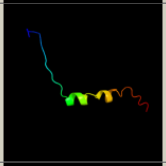
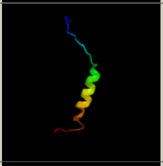
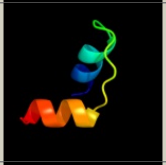
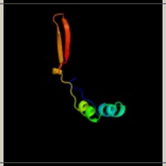
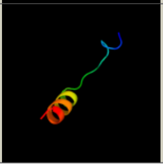
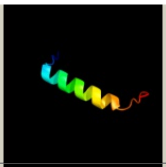
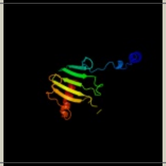
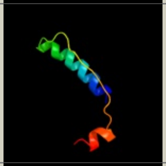
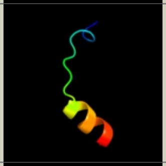
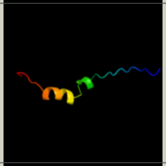
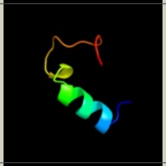
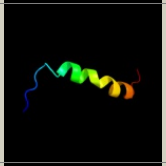
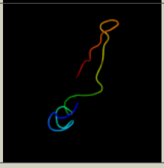
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eyrA_	Alignment		100.0	96	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yceb; **PDBTitle:** crystal structure of the uncharacterized lipoprotein yceb2 from e. coli at the resolution 2.0a. northeast structural3 genomics consortium target er542
2	d3d85d2	Alignment		26.7	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
3	d1t11a2	Alignment		22.6	21	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
4	d1w26a2	Alignment		22.2	20	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
5	d3bz6a1	Alignment		21.8	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PSPTO2686-like
6	d1p9ya_	Alignment		21.0	21	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
7	c1w26B_	Alignment		20.7	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
8	c1t11A_	Alignment		20.6	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
9	c3bz6A_	Alignment		18.7	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0502 protein pspto_2686; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000
10	c2im5C_	Alignment		15.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
11	d1vq0a2	Alignment		15.6	35	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like

12	c2nscA_	Alignment		11.4	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritima
13	d1p32a_	Alignment		9.4	13	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
14	c1wd6B_	Alignment		9.1	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
15	d1vzya2	Alignment		9.1	28	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
16	c3gtyX_	Alignment		8.1	21	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
17	d1ex2a_	Alignment		7.4	22	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**Maf-like
18	c3alzB_	Alignment		7.3	16	**PDB header:**viral protein/membrane protein **Chain:** B: **PDB Molecule:**cdw150; **PDBTitle:** crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (form i)
19	c2d3o1_	Alignment		7.2	19	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**trigger factor; **PDBTitle:** structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
20	c2k78A_	Alignment		6.9	24	**PDB header:**heme-binding protein **Chain:** A: **PDB Molecule:**iron-regulated surface determinant protein c; **PDBTitle:** solution structure of the isdc neat domain bound to zinc2 protoporphyrin
21	d2cpja1	Alignment	not modelled	6.6	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
22	c3evyB_	Alignment	not modelled	6.5	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative type i restriction enzyme r protein; **PDBTitle:** crystal structure of a fragment of a putative type i2 restriction enzyme r protein from bacteroides fragilis
23	d1rgya_	Alignment	not modelled	6.0	30	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
24	d2o6pa1	Alignment	not modelled	5.8	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**NEAT domain-like **Family:**NEAT domain
25	c3n3fB_	Alignment	not modelled	5.8	6	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**collagen alpha-1(xv) chain; **PDBTitle:** crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
26	c2o6pA_	Alignment	not modelled	5.6	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-regulated surface determinant protein c; **PDBTitle:** crystal structure of the heme-isdc complex