Phyre2

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Description	P61320
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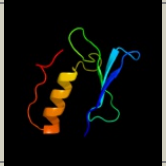
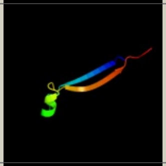
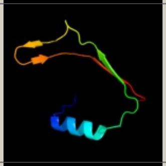
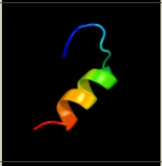
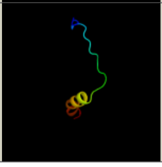
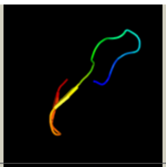
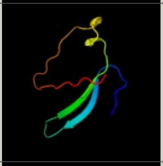
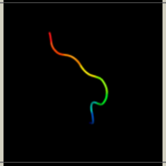
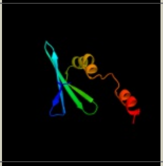
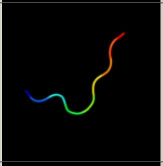
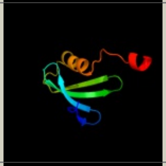
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iwma_	Alignment		100.0	97	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**Outer membrane lipoprotein receptor LolB
2	c3buuB_	Alignment		76.7	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized lola superfamily protein ne2245; **PDBTitle:** crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea
3	d1ekga_	Alignment		39.7	15	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
4	c2w7qB_	Alignment		35.9	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**outer-membrane lipoprotein carrier protein; **PDBTitle:** structure of pseudomonas aeruginosa lola
5	d2cc3a1	Alignment		25.1	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**VirB8-like
6	d1tp6a_	Alignment		24.8	10	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PA1314-like
7	d1iwla_	Alignment		24.2	10	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**Outer-membrane lipoproteins carrier protein LolA
8	d1vpka2	Alignment		16.8	15	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
9	d1ttza_	Alignment		15.8	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
10	c2fgyA_	Alignment		14.3	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxysome shell polypeptide; **PDBTitle:** beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
11	c3ls1A_	Alignment		13.6	19	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+

12	c3gf8A_	Alignment		13.6	10	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**putative polysaccharide binding proteins (duf1812); **PDBTitle:** crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
13	c3d0jA_	Alignment		11.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497; **PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
14	d1jb7b_	Alignment		11.9	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
15	c2i0qB_	Alignment		11.9	22	**PDB header:**structural protein/dna **Chain:** B: **PDB Molecule:**telomere-binding protein beta subunit; **PDBTitle:** crystal structure of a telomere single-strand dna-protein2 complex from o. nova with full-length alpha and beta3 telomere proteins
16	c3f10A_	Alignment		11.9	9	**PDB header:**hydrolase, lyase **Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase; **PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
17	c1otcB_	Alignment		10.3	22	**PDB header:**protein/dna **Chain:** B: **PDB Molecule:**protein (telomere-binding protein beta subunit); **PDBTitle:** the o. nova telomere end binding protein complexed with2 single strand dna
18	c2yh5A_	Alignment		9.6	25	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
19	d2noha2	Alignment		8.9	18	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**DNA repair glycosylase, N-terminal domain
20	d2hiya1	Alignment		8.3	15	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
21	d1p8ja1	Alignment	not modelled	8.2	24	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Proprotein convertase P-domain
22	d1zy9a1	Alignment	not modelled	7.8	18	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**YicI N-terminal domain-like
23	d1ew4a_	Alignment	not modelled	7.0	9	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
24	c3bmbB_	Alignment	not modelled	6.7	11	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
25	c2pn0D_	Alignment	not modelled	6.5	22	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
26	d2id4a1	Alignment	not modelled	6.4	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Proprotein convertase P-domain
27	c3ot2B_	Alignment	not modelled	6.2	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein;

28	c3ot2A_	Alignment	not modelled	6.2	10	**PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
29	c2xetB_	Alignment	not modelled	6.2	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly