Phyre²

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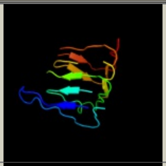
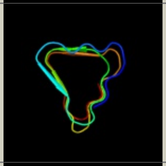
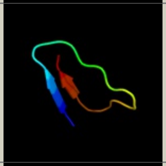
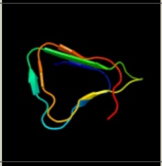
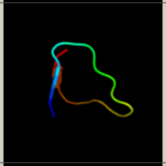
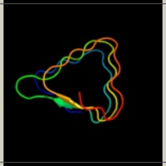
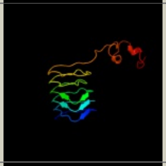
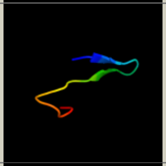
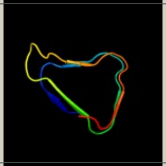
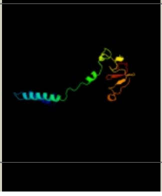
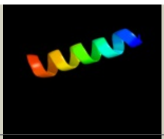
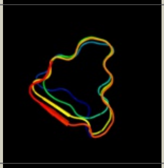
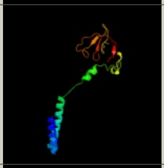
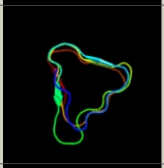
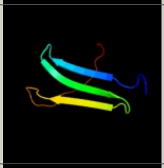
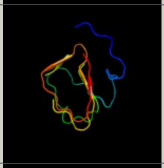
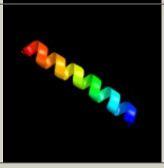
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f9ca1	Alignment		68.3	17	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
2	c1fwyA_	Alignment		54.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
3	c1hf2A_	Alignment		46.1	33	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
4	c2i5kB_	Alignment		43.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
5	d1hf2a1	Alignment		41.7	33	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
6	c3mc4A_	Alignment		36.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase **PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
7	c1hm8A_	Alignment		32.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase; **PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
8	d1o12a1	Alignment		30.5	24	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
9	d2icya1	Alignment		30.0	22	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
10	c2qkxA_	Alignment		28.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
11	c3b8eC_	Alignment		28.7	15	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump

12	c2i5nH_	Alignment		28.6	15	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**reaction center protein h chain; **PDBTitle:** 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
13	c3brkX_	Alignment		27.8	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
14	c3d98A_	Alignment		26.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
15	c2zxeA_	Alignment		25.3	13	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
16	c3f1xA_	Alignment		20.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
17	d1jk9b1	Alignment		20.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
18	c2z8gB_	Alignment		18.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isopullulanase; **PDBTitle:** aspergillus niger atcc9642 isopullulanase complexed with isopanose
19	d1ogmx2	Alignment		16.9	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Dextranase, catalytic domain
20	c3mk7F_	Alignment		15.6	25	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
21	c3jx8B_	Alignment	not modelled	15.1	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of putative lipid binding protein (yp_001304415.1)2 from parabacteroides distasonis atcc 8503 at 2.16 a resolution
22	c1t5eB_	Alignment	not modelled	14.8	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
23	c3gueB_	Alignment	not modelled	14.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp-glucose-1-phosphate uridylyltransferase 2; **PDBTitle:** crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
24	d1eysh2	Alignment	not modelled	14.1	26	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
25	c2q4jB_	Alignment	not modelled	14.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable utp-glucose-1-phosphate uridylyltransferase 2; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
26	c1k6nH_	Alignment	not modelled	12.1	32	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosynthetic reaction center h subunit; **PDBTitle:** e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
27	c1ogoX_	Alignment	not modelled	11.3	17	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**dextranase; **PDBTitle:** dex49a from penicillium minioluteum complex with isomaltose
						PDB header:hydrolase

28	c3kdpD_	Alignment	not modelled	9.1	12	**Chain:** D: **PDB Molecule:**sodium/potassium-transporting atpase subunit beta-1; **PDBTitle:** crystal structure of the sodium-potassium pump
29	c2v0hA_	Alignment	not modelled	8.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
30	c1eysH_	Alignment	not modelled	8.8	26	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
31	c3ixzA_	Alignment	not modelled	8.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
32	c2f1mA_	Alignment	not modelled	8.2	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
33	d1ua7a1	Alignment	not modelled	7.2	14	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
34	c2aklA_	Alignment	not modelled	6.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
35	d2axtm1	Alignment	not modelled	6.1	32	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein M, PsbM **Family:**PsbM-like
36	d2vnud3	Alignment	not modelled	5.7	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
37	d2akka1	Alignment	not modelled	5.7	19	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
38	d1srda_	Alignment	not modelled	5.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like