Phyre^2

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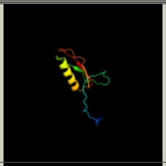
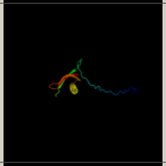
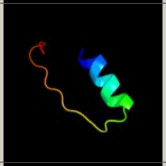
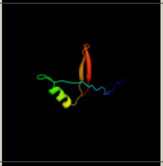
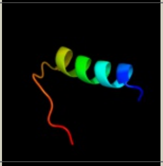
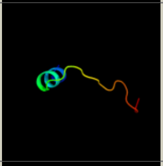
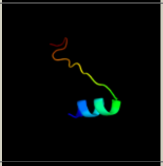
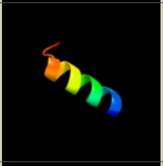
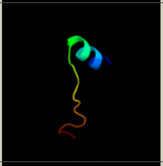
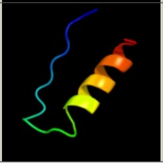
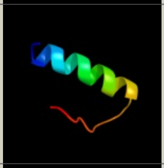
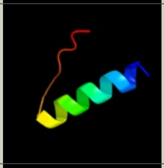
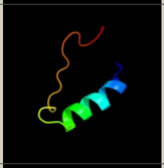
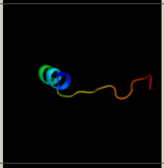
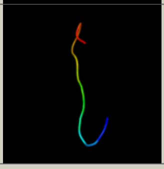
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2noca1	Alignment		100.0	36	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
2	d2jnaa1	Alignment		100.0	29	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
3	c3dfeA_	Alignment		37.9	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative pii-like signaling protein; **PDBTitle:** crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution
4	c2k4qA_	Alignment		28.9	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major tail protein v; **PDBTitle:** the solution structure of gpv, the major tail protein from2 bacteriophage lambda
5	c3b9nB_	Alignment		27.1	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
6	c1hl8B_	Alignment		18.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
7	c3sdoB_	Alignment		14.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
8	c3eypB_	Alignment		13.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
9	c3qkbB_	Alignment		13.4	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
10	c3mo4B_	Alignment		12.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
11	c2jz7A_	Alignment		10.8	22	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii

12	d1lucb_	Alignment		10.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
13	d1luca_	Alignment		10.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
14	c2y1bA_	Alignment		10.4	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
15	d1cdwa2	Alignment		9.9	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
16	d1f07a_	Alignment		9.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
17	d1txka2	Alignment		9.3	29	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
18	d1hl9a2	Alignment		9.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
19	c1f02T_	Alignment		9.1	47	**PDB header:**cell adhesion **Chain:** T: **PDB Molecule:**translocated intimin receptor; **PDBTitle:** crystal structure of c-terminal 282-residue fragment of2 intimin in complex with translocated intimin receptor3 (tir) intimin-binding domain
20	c1txkA_	Alignment		8.9	29	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
21	c2wvsD_	Alignment	not modelled	8.7	33	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
22	c2w1sB_	Alignment	not modelled	8.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** unique ligand binding specificity of a family 322 carbohydrate-binding module from the mu toxin produced by3 clostridium perfringens
23	d1mp9a2	Alignment	not modelled	7.6	5	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
24	d1nh2a2	Alignment	not modelled	6.8	9	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
25	c3ir9A_	Alignment	not modelled	6.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
26	d1qnaa2	Alignment	not modelled	6.7	9	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
27	c3eikB_	Alignment	not modelled	6.6	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
28	d1mp9a1	Alignment	not modelled	6.6	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain

29	c1z69D_	Alignment	not modelled	5.8	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**coenzyme f420-dependent n(5),n(10)- **PDBTitle:** crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
30	d1ycga1	Alignment	not modelled	5.7	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
31	c1mp9B_	Alignment	not modelled	5.7	5	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
32	c2z8uQ_	Alignment	not modelled	5.6	10	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
33	c2i7gA_	Alignment	not modelled	5.5	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
34	c1d3uA_	Alignment	not modelled	5.3	15	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**tata-binding protein; **PDBTitle:** tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
35	d1aisa2	Alignment	not modelled	5.2	13	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
36	d1nh2a1	Alignment	not modelled	5.2	9	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
37	c1rm1A_	Alignment	not modelled	5.2	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**tata-box binding protein; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
38	c1ngmM_	Alignment	not modelled	5.2	10	**PDB header:**transcription/dna **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
39	c3gzaB_	Alignment	not modelled	5.1	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution