Phyre2

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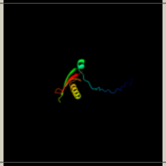
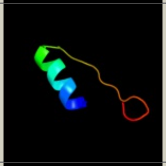
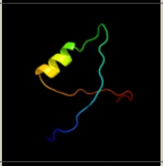
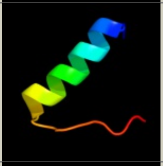
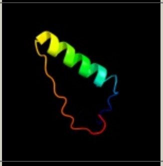
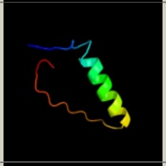
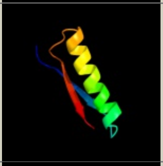
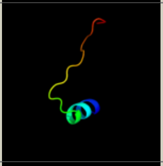
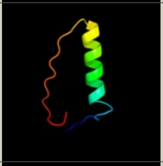
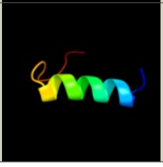
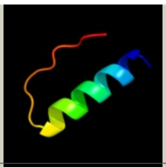
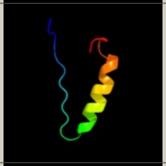
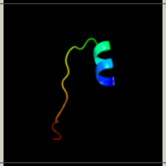
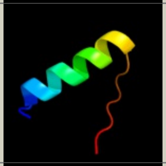
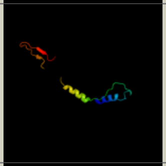
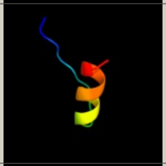
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2noca1	Alignment		100.0	73	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
2	d2jnaa1	Alignment		100.0	25	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
3	c3dfeA_	Alignment		39.0	19	**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		37.8	9	**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		29.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
6	c3lubE_	Alignment		27.2	24	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
7	c3no4A_	Alignment		23.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
8	c3rofA_	Alignment		18.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
9	c1hl8B_	Alignment		17.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
10	d1v7za_	Alignment		16.9	29	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
11	c3sdoB_	Alignment		14.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei

12	c2y1bA_	Alignment		13.9	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
13	d3etja1	Alignment		12.8	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
14	c3eypB_	Alignment		12.1	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
15	c3mo4B_	Alignment		11.5	17	**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
16	d1luca_	Alignment		11.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
17	c2btvB_	Alignment		10.8	11	**PDB header:**virus **Chain:** B: **PDB Molecule:**protein (vp3 core protein); **PDBTitle:** atomic model for bluetongue virus (btv) core
18	c3qkbB_	Alignment		10.6	44	**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
19	d1cdwa2	Alignment		10.4	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
20	d1lucb_	Alignment		10.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
21	d1mp9a2	Alignment	not modelled	9.0	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
22	d1txka2	Alignment	not modelled	8.9	14	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
23	d1hl9a2	Alignment	not modelled	8.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
24	c1txkA_	Alignment	not modelled	8.6	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
25	d1f07a_	Alignment	not modelled	8.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
26	c3eikB_	Alignment	not modelled	8.4	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
27	d1mp9a1	Alignment	not modelled	8.1	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
28	c2gi4A_	Alignment	not modelled	7.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
						PDB header:selenium-binding protein

29	c2jz7A_	Alignment	not modelled	7.9	29	**Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
30	d1nh2a2	Alignment	not modelled	7.7	9	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
31	c2wvsD_	Alignment	not modelled	7.4	21	**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
32	c1f02T_	Alignment	not modelled	7.4	23	**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
33	c1mp9B_	Alignment	not modelled	7.1	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
34	d1tqxa_	Alignment	not modelled	7.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
35	d1qnaa2	Alignment	not modelled	6.9	9	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
36	c1d3uA_	Alignment	not modelled	6.9	45	**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
37	c2z8uQ_	Alignment	not modelled	6.9	35	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
38	c2zfdB_	Alignment	not modelled	6.8	10	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
39	c3mp6A_	Alignment	not modelled	6.6	13	**PDB header:**histone binding protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, saga- **PDBTitle:** complex structure of sgf29 and dimethylated h3k4
40	c3cbnA_	Alignment	not modelled	6.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mth639; **PDBTitle:** crystal structure of a conserved protein (mth639) from2 methanobacterium thermoautotrophicum
41	c3ir9A_	Alignment	not modelled	6.6	23	**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.
42	c1ngmM_	Alignment	not modelled	6.5	10	**PDB header:**transcription/dna **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
43	c1rm1A_	Alignment	not modelled	6.5	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**tata-box binding protein; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
44	d1aisa2	Alignment	not modelled	6.3	39	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
45	d1nh2a1	Alignment	not modelled	6.0	26	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
46	c1z69D_	Alignment	not modelled	5.7	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
47	d1aisa1	Alignment	not modelled	5.6	22	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
48	d1nqka_	Alignment	not modelled	5.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
49	d2p1ra1	Alignment	not modelled	5.6	22	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
50	c3e15D_	Alignment	not modelled	5.5	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** 6-phosphogluconolactonase from plasmodium vivax
51	d1zjca1	Alignment	not modelled	5.2	11	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
52	d1fe0a_	Alignment	not modelled	5.2	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
53	c3ne8A_	Alignment	not modelled	5.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1