Phyre^2

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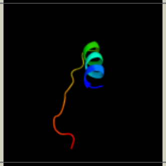
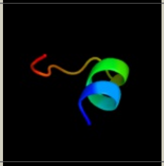
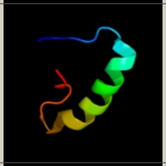
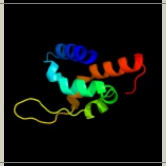
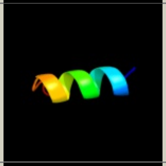
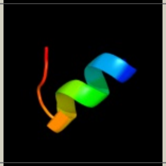
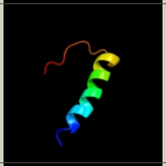
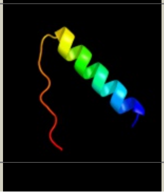
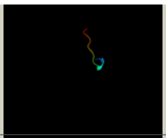
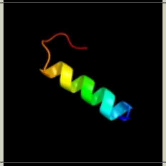
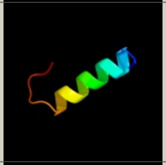
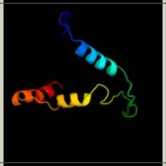
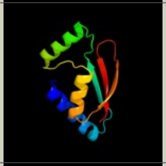
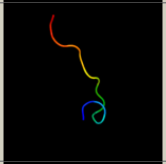
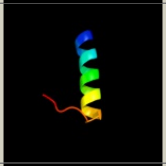
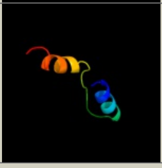
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pc6a_	Alignment		100.0	17	**Fold:**NinB **Superfamily:**NinB **Family:**NinB
2	c2kg4A_	Alignment		32.6	4	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible protein **PDBTitle:** three-dimensional structure of human gadd45alpha in2 solution by nmr
3	c2jxjA_	Alignment		31.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1a; **PDBTitle:** nmr structure of the arid domain from the histone h3k42 demethylase rbp2
4	c2kngA_	Alignment		23.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
5	c2lm1A_	Alignment		17.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**lysine-specific demethylase lid; **PDBTitle:** solution nmr structure of lysine-specific demethylase lid from2 drosophila melanogaster, northeast structural genomics consortium3 target fr824d
6	d2e1fa1	Alignment		16.7	10	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
7	c3cg6A_	Alignment		14.8	6	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible 45 gamma; **PDBTitle:** crystal structure of gadd45 gamma
8	d1oi1a2	Alignment		13.8	27	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
9	d1wh7a_	Alignment		12.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
10	d1kkxa_	Alignment		11.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
11	d1ax8a_	Alignment		11.4	15	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines

12	c1oz3C_	Alignment		11.2	43	**PDB header:**transcription **Chain:** C: **PDB Molecule:**lethal(3)malignant brain tumor-like protein; **PDBTitle:** crystal structure of 3-mbt repeats of lethal (3) malignant brain tumor2 (native-i) at 1.85 angstrom
13	d1eysc_	Alignment		11.1	35	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
14	c1eysC_	Alignment		11.1	35	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
15	d1j20a1	Alignment		11.0	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
16	d1bvp11	Alignment		11.0	19	**Fold:**A virus capsid protein alpha-helical domain **Superfamily:**A virus capsid protein alpha-helical domain **Family:**Orbivirus capsid
17	c3gwzB_	Alignment		10.9	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mmcr; **PDBTitle:** structure of the mitomycin 7-o-methyltransferase mmcr
18	d1oi1a1	Alignment		10.8	21	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
19	d1jhga_	Alignment		10.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
20	c2ztgA_	Alignment		9.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
21	c2eqyA_	Alignment	not modelled	9.8	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji, at rich interactive domain 1b; **PDBTitle:** solution structure of the arid domain of jarid1b protein
22	d1wjra_	Alignment	not modelled	9.7	14	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
23	d1wjsa_	Alignment	not modelled	9.3	23	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
24	c3ut1A_	Alignment	not modelled	9.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like protein 3; **PDBTitle:** crystal structure of the 3-mbt repeat domain of l3mbtl3
25	c2yqeA_	Alignment	not modelled	9.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji/arid domain-containing protein 1d; **PDBTitle:** solution structure of the arid domain of jarid1d protein
26	d1oz2a2	Alignment	not modelled	9.0	43	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
27	d2gtaa1	Alignment	not modelled	8.4	8	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
28	c3frwF_	Alignment	not modelled	8.2	5	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
29	d2cb2a1	Alignment	not modelled	7.8	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**SOR-like

30	d1miua4	Alignment	not modelled	7.7	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
31	c2wvsD_	Alignment	not modelled	7.6	15	**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	c3lwzC_	Alignment	not modelled	7.5	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
33	d2ahma1	Alignment	not modelled	7.3	0	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Coronavirus NSP7-like **Family:**Coronavirus NSP7-like
34	d2gtad1	Alignment	not modelled	7.0	8	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
35	d2aj6a1	Alignment	not modelled	6.9	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
36	d1rfma_	Alignment	not modelled	6.8	13	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
37	d1oz2a1	Alignment	not modelled	6.6	29	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
38	d1trra_	Alignment	not modelled	6.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
39	d1oz2a3	Alignment	not modelled	6.4	31	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
40	c1yycA_	Alignment	not modelled	6.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein; **PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
41	c3ebrA_	Alignment	not modelled	5.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
42	d1hl9a2	Alignment	not modelled	5.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
43	c1vl2C_	Alignment	not modelled	5.6	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
44	d1wjqa_	Alignment	not modelled	5.6	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
45	d2ezha_	Alignment	not modelled	5.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain