Phyre^2

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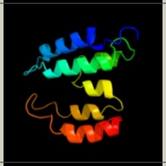
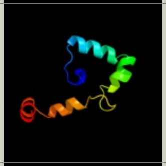
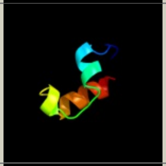
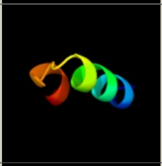
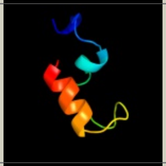
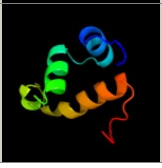
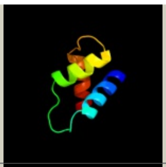
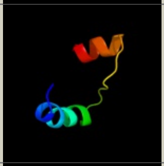
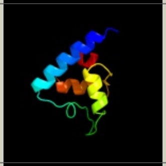
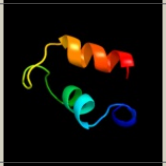
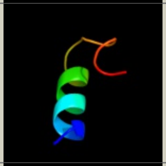
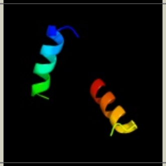
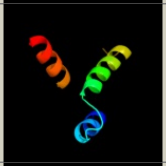
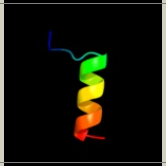
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ou3a1	Alignment		99.6	17	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**COG3793-like
2	c2jxuA_	Alignment		98.7	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**terb; **PDBTitle:** nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
3	d1z67a1	Alignment		86.5	18	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
4	c3hugJ_	Alignment		56.3	23	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
5	d1aisb2	Alignment		56.1	8	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
6	d1ln4a_	Alignment		47.6	30	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
7	d2p7vb1	Alignment		42.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
8	d1yzma1	Alignment		39.3	25	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
9	d1z0kb1	Alignment		38.9	25	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
10	d1ku7a_	Alignment		37.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
11	c3fymA_	Alignment		36.9	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus

12	c3ol4B_	Alignment		35.3	6	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
13	d1rq8a_	Alignment		34.9	25	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
14	c2iv1J_	Alignment		34.4	10	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
15	d1ttya_	Alignment		33.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
16	d1z0jb1	Alignment		33.4	42	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
17	d1jo0a_	Alignment		33.2	25	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
18	c3obkH_	Alignment		32.9	20	**PDB header:**lyase **Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase; **PDBTitle:** crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
19	d1ctda_	Alignment		32.4	33	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
20	d1vkeb_	Alignment		32.4	11	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
21	c2l27B_	Alignment	not modelled	32.2	12	**PDB header:**membrane protein, peptide binding protei **Chain:** B: **PDB Molecule:**peptide agonist; **PDBTitle:** nmr structure of the ecd1 of crf-r1 in complex with a peptide agonist
22	c2rmfA_	Alignment	not modelled	30.6	21	**PDB header:**hormone **Chain:** A: **PDB Molecule:**urocortin; **PDBTitle:** human urocortin 1
23	c3m3hA_	Alignment	not modelled	30.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
24	d1msza_	Alignment	not modelled	30.5	6	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
25	c1mszA_	Alignment	not modelled	30.5	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
26	c2wusR_	Alignment	not modelled	30.5	9	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
27	d1dwka1	Alignment	not modelled	26.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
28	d1vola2	Alignment	not modelled	24.6	11	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain

29	d2gyqa1	Alignment	not modelled	23.9	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**YciF-like
30	d1d5ya1	Alignment	not modelled	22.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
31	c3t72o_	Alignment	not modelled	22.4	18	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
32	c2k29A_	Alignment	not modelled	22.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
33	c3oi8B_	Alignment	not modelled	21.8	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
34	d1ku3a_	Alignment	not modelled	20.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
35	d1ufma_	Alignment	not modelled	19.4	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
36	c2k9lA_	Alignment	not modelled	18.5	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
37	c3beyC_	Alignment	not modelled	18.1	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
38	c2a6eF_	Alignment	not modelled	17.8	18	**PDB header:**transferase **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** crystal structure of the t. thermophilus rna polymerase2 holoenzyme
39	c1p8cD_	Alignment	not modelled	17.7	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
40	c3hjlA_	Alignment	not modelled	16.1	11	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
41	d2gtia2	Alignment	not modelled	16.0	9	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
42	c2zetD_	Alignment	not modelled	15.2	10	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**melanophilin; **PDBTitle:** crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
43	d1hqva_	Alignment	not modelled	15.1	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Penta-EF-hand proteins
44	c2i7aA_	Alignment	not modelled	14.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calpain 13; **PDBTitle:** domain iv of human calpain 13
45	d1l6sa_	Alignment	not modelled	14.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
46	d1vola1	Alignment	not modelled	13.6	6	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
47	d1bl0a1	Alignment	not modelled	13.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
48	c1l9uH_	Alignment	not modelled	13.1	24	**PDB header:**transcription **Chain:** H: **PDB Molecule:**sigma factor siga; **PDBTitle:** thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
49	d2c1ha1	Alignment	not modelled	12.9	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
50	d1w8ia_	Alignment	not modelled	12.7	37	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
51	c1y66D_	Alignment	not modelled	12.4	20	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
52	c2rhbD_	Alignment	not modelled	11.7	27	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**uridylate-specific endoribonuclease; **PDBTitle:** crystal structure of nsp15-h234a mutant- hexamer in2 asymmetric unit
53	d1h7na_	Alignment	not modelled	11.5	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
54	d1ojra_	Alignment	not modelled	11.3	13	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
						PDB header:apoptosis

55	c2ib1A_	Alignment	not modelled	11.0	11	**Chain:** A: **PDB Molecule:**death domain containing membrane protein nradd; **PDBTitle:** solution structure of p45 death domain
56	d2e74g1	Alignment	not modelled	11.0	20	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
57	d2q0ta1	Alignment	not modelled	10.9	23	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
58	d1lmb3_	Alignment	not modelled	10.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
59	d1bi5a2	Alignment	not modelled	10.7	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
60	d2ozka2	Alignment	not modelled	10.6	27	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
61	c1vf5G_	Alignment	not modelled	10.5	20	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**protein pet g; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
62	d1vf5g_	Alignment	not modelled	10.5	20	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
63	d2cyya1	Alignment	not modelled	10.4	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
64	d1mkma1	Alignment	not modelled	10.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
65	c2lfcA_	Alignment	not modelled	9.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
66	c3bh1A_	Alignment	not modelled	9.8	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0371 protein dip2346; **PDBTitle:** crystal structure of protein dip2346 from corynebacterium diphtheriae
67	d2h85a2	Alignment	not modelled	9.8	27	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
68	d2hf5a1	Alignment	not modelled	9.8	29	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
69	d1ngra_	Alignment	not modelled	9.6	15	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
70	c2ev2B_	Alignment	not modelled	9.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
71	d2p90a1	Alignment	not modelled	9.6	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Cgl1923-like **Family:**Cgl1923-like
72	c2of5K_	Alignment	not modelled	9.5	15	**PDB header:**apoptosis **Chain:** K: **PDB Molecule:**leucine-rich repeat and death domain-containing **PDBTitle:** oligomeric death domain complex
73	d1rp3a1	Alignment	not modelled	9.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
74	d2tpta1	Alignment	not modelled	9.2	21	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
75	c1ichA_	Alignment	not modelled	9.1	15	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
76	d1icha_	Alignment	not modelled	9.1	15	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
77	d1tw3a1	Alignment	not modelled	8.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
78	d2bida_	Alignment	not modelled	8.8	25	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
79	d1o17a1	Alignment	not modelled	8.8	19	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
80	c2gtiA_	Alignment	not modelled	8.5	9	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** mutation of mhv coronavirus non-structural protein nsp15 (f307l)
						Fold: Methionine synthase domain-like **Superfamily:**Nucleoside

81	d1khda1	Alignment	not modelled	8.5	9	phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
82	c1wxpA_	Alignment	not modelled	8.2	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tho complex subunit 1; **PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84
83	d2ofya1	Alignment	not modelled	8.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
84	c2cpmA_	Alignment	not modelled	8.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sperm-associated antigen 7; **PDBTitle:** solution structure of the r3h domain of human sperm-2 associated antigen 7
85	c2p90B_	Alignment	not modelled	8.1	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
86	c2wvsD_	Alignment	not modelled	7.9	24	**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
87	c1gpmD_	Alignment	not modelled	7.9	14	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
88	c2z2sD_	Alignment	not modelled	7.9	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**anti-sigma factor chrr, transcriptional activator chrr; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
89	d2gf5a1	Alignment	not modelled	7.8	30	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
90	c3omtA_	Alignment	not modelled	7.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
91	c2vn2B_	Alignment	not modelled	7.7	15	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
92	d1brwa1	Alignment	not modelled	7.7	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
93	d1or7a1	Alignment	not modelled	7.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
94	d1t07a_	Alignment	not modelled	7.7	14	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
95	d1u0ua2	Alignment	not modelled	7.7	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
96	c3t98A_	Alignment	not modelled	7.6	33	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup54; **PDBTitle:** molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
97	d1ee0a2	Alignment	not modelled	7.6	25	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
98	c2yqfA_	Alignment	not modelled	7.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
99	c3e35A_	Alignment	not modelled	7.5	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco1997; **PDBTitle:** actinobacteria-specific protein of unknown function, sco1997