Phyre^2

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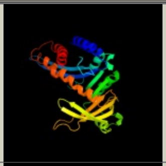
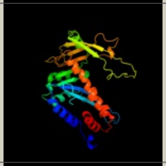
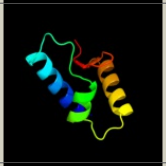
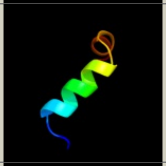
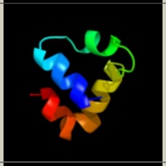
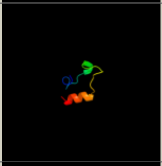
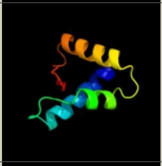
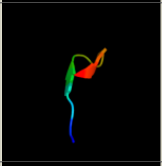
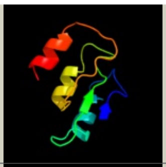
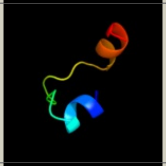
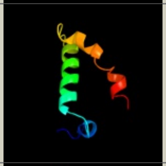
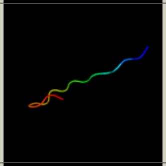
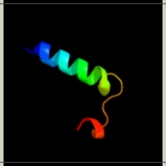
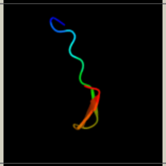
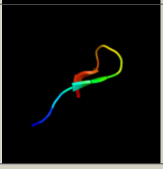
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b7ea_	Alignment		97.6	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1musa_	Alignment		97.6	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d2v9va2	Alignment		85.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
4	c2v9vA_	Alignment		74.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
5	d2ezha_	Alignment		49.3	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
6	d2ezia_	Alignment		47.5	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
7	c3hefB_	Alignment		42.3	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
8	c6paxA_	Alignment		38.6	22	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
9	c2plyB_	Alignment		30.0	11	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
10	d1e8qa_	Alignment		19.9	36	**Fold:**Cellulose docking domain, dockering **Superfamily:**Cellulose docking domain, dockering **Family:**Cellulose docking domain, dockering
11	c2pfsA_	Alignment		19.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea

12	c2vp8A_	Alignment		17.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
13	d1pdnc_	Alignment		17.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
14	d1dlwa_	Alignment		16.5	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
15	d1ajza_	Alignment		15.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
16	d2fgga1	Alignment		15.1	31	**Fold:**dsRBD-like **Superfamily:**Rv2632c-like **Family:**Rv2632c-like
17	c3qd7X_	Alignment		14.7	10	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
18	c2kvcA_	Alignment		13.0	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
19	c3mx7A_	Alignment		12.9	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
20	c2j4mA_	Alignment		11.8	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**endoglucanase 45a; **PDBTitle:** double dockerin from piromyces equi cel45a
21	c3aq8A_	Alignment	not modelled	11.7	4	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
22	d1mpga1	Alignment	not modelled	11.5	14	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
23	d1iyxa1	Alignment	not modelled	11.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
24	d1g9ga_	Alignment	not modelled	11.1	63	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
25	c2y5sA_	Alignment	not modelled	11.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
26	d1s69a_	Alignment	not modelled	10.9	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
27	c3ol4B_	Alignment	not modelled	10.9	26	**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
28	d2ezla_	Alignment	not modelled	10.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
29	d1osna_	Alignment	not modelled	10.6	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

29	d1osha_	Alignment	not modelled	10.6	9	hydrolases **Family:**Nucleotide and nucleoside kinases
30	c1qcrD_	Alignment	not modelled	9.8	8	**PDB header:** **PDB COMPND:**
31	d3bpya1	Alignment	not modelled	9.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
32	d1md6a_	Alignment	not modelled	9.1	17	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
33	c2rfpA_	Alignment	not modelled	9.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
34	c1l2aD_	Alignment	not modelled	9.0	50	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
35	d1l1ya_	Alignment	not modelled	9.0	50	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
36	c3r1iB_	Alignment	not modelled	8.8	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
37	d1idra_	Alignment	not modelled	8.7	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
38	c3gk0H_	Alignment	not modelled	8.4	20	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
39	c1hj0A_	Alignment	not modelled	8.3	19	**PDB header:**actin binding peptide **Chain:** A: **PDB Molecule:**thymosin beta9; **PDBTitle:** thymosin beta9
40	d2c6ya1	Alignment	not modelled	8.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
41	c2b99A_	Alignment	not modelled	8.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
42	c3cwbQ_	Alignment	not modelled	8.1	8	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
43	c2kzvA_	Alignment	not modelled	8.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
44	c1e17A_	Alignment	not modelled	7.8	9	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
45	c2vdaA_	Alignment	not modelled	7.7	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
46	c3rf7A_	Alignment	not modelled	7.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
47	d2abka_	Alignment	not modelled	7.6	11	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
48	c3co7C_	Alignment	not modelled	7.6	13	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
49	c2x4mD_	Alignment	not modelled	7.5	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
50	c3ny0D_	Alignment	not modelled	7.4	11	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**urease accessory protein uree; **PDBTitle:** crystal structure of uree from helicobacter pylori (ni2+ bound form)
51	c1p84D_	Alignment	not modelled	7.4	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
52	d1w6ta1	Alignment	not modelled	7.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
53	d2ptza1	Alignment	not modelled	7.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
54	c3hluA_	Alignment	not modelled	7.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in

						bacteria2 duf2179 from eubacterium ventriosum
55	c2kl8A_	Alignment	not modelled	7.0	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
56	d1g31a_	Alignment	not modelled	7.0	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
57	d1vi7a1	Alignment	not modelled	7.0	18	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
58	d2ilaa_	Alignment	not modelled	6.9	22	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
59	d1ogla_	Alignment	not modelled	6.8	18	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**Type II deoxyuridine triphosphatase
60	d1eyea_	Alignment	not modelled	6.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
61	d1un2a_	Alignment	not modelled	6.6	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
62	c2giaB_	Alignment	not modelled	6.6	63	**PDB header:**translation **Chain:** B: **PDB Molecule:**mitochondrial rna-binding protein 1; **PDBTitle:** crystal structures of trypanosoma bruciei mrp1/mrp2
63	d2giab1	Alignment	not modelled	6.6	63	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Guide RNA binding protein gBP
64	d1m5wa_	Alignment	not modelled	6.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
65	d1uuza_	Alignment	not modelled	6.4	20	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
66	c3a52A_	Alignment	not modelled	6.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
67	c2jpiA_	Alignment	not modelled	6.3	20	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
68	c3emkA_	Alignment	not modelled	6.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
69	c3nswA_	Alignment	not modelled	6.2	60	**PDB header:**immune system **Chain:** A: **PDB Molecule:**excretory-secretory protein 2; **PDBTitle:** crystal structure of ancylostoma ceylanicum excretory-secretory2 protein 2
70	c3k6qB_	Alignment	not modelled	6.2	14	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
71	c3e2dB_	Alignment	not modelled	6.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
72	c2iucB_	Alignment	not modelled	6.1	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
73	c2zqeA_	Alignment	not modelled	6.1	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
74	d1dlya_	Alignment	not modelled	6.0	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
75	c1dlyA_	Alignment	not modelled	6.0	12	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
76	d2a22a1	Alignment	not modelled	6.0	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
77	c2j66A_	Alignment	not modelled	6.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**btrk; **PDBTitle:** structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
78	c1gmuB_	Alignment	not modelled	6.0	9	**PDB header:**metallochaperone **Chain:** B: **PDB Molecule:**uree; **PDBTitle:** structure of uree
79	c3g73A_	Alignment	not modelled	5.9	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
80	c3pk0B_	Alignment	not modelled	5.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase

						sdr from2 mycobacterium smegmatis
81	d2o0ma1	Alignment	not modelled	5.9	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
82	c2o0mA_	Alignment	not modelled	5.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
83	d1pcna1	Alignment	not modelled	5.9	36	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
84	c1c94B_	Alignment	not modelled	5.8	63	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper; **PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
85	d2czda1	Alignment	not modelled	5.8	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
86	c3a44D_	Alignment	not modelled	5.8	0	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
87	d1xb4a2	Alignment	not modelled	5.8	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
88	d1ha7a_	Alignment	not modelled	5.7	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
89	d1d5va_	Alignment	not modelled	5.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
90	d1qpma_	Alignment	not modelled	5.7	14	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
91	c3i0oA_	Alignment	not modelled	5.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spectinomycin phosphotransferase; **PDBTitle:** crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomcyin
92	c2z1nA_	Alignment	not modelled	5.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
93	d1k92a2	Alignment	not modelled	5.6	36	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
94	d1yqea1	Alignment	not modelled	5.6	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
95	c3douA_	Alignment	not modelled	5.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase j; **PDBTitle:** crystal structure of methyltransferase involved in cell2 division from thermoplasma volcanicum gss1
96	c2l0eA_	Alignment	not modelled	5.5	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger
97	d1rh6a_	Alignment	not modelled	5.5	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
98	d1cyda_	Alignment	not modelled	5.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	d1xi8a3	Alignment	not modelled	5.4	23	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like