Phyre2

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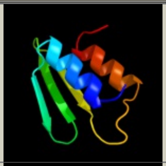
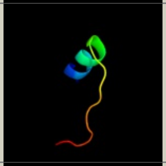
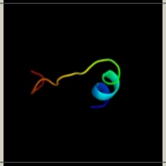
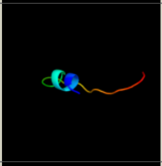
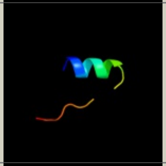
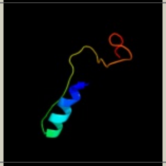
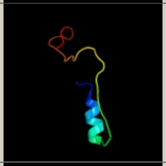
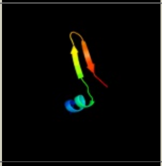
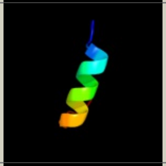
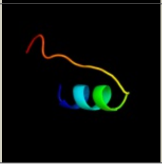
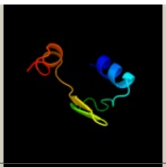
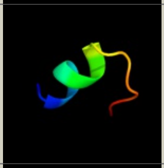
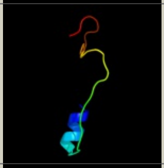
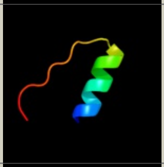
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1whza_	Alignment		99.7	28	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
2	c2wj0B_	Alignment		58.0	10	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**archaeal hjc; **PDBTitle:** crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
3	d1gefa_	Alignment		54.0	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
4	d1ob8a_	Alignment		49.8	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
5	d1hh1a_	Alignment		49.1	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
6	c3o2qB_	Alignment		37.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
7	c3o2sB_	Alignment		37.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
8	c2jugB_	Alignment		27.5	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
9	d1h3da1	Alignment		24.5	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
10	c3cf4A_	Alignment		17.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
11	d1ul7a_	Alignment		17.6	20	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1

12	d1nh8a1	Alignment		16.1	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
13	c2lciA_	Alignment		15.9	57	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
14	c1q1kA_	Alignment		15.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
15	c2vd3B_	Alignment		14.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
16	c1nh7A_	Alignment		13.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
17	c3fdfA_	Alignment		13.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fr253; **PDBTitle:** crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
18	d2doaa1	Alignment		13.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ELL N2 domain-like
19	d1k25a2	Alignment		12.4	5	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
20	d1o6wa2	Alignment		11.7	13	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
21	c2dcrA_	Alignment	not modelled	11.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fes/fps; **PDBTitle:** fully automated solution structure determination of the fes2 sh2 domain
22	c2v1nA_	Alignment	not modelled	10.8	31	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein kin homolog; **PDBTitle:** solution structure of the region 51-160 of human kin172 reveals a winged helix fold
23	c3jthA_	Alignment	not modelled	10.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
24	c2e5nA_	Alignment	not modelled	10.6	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase ii elongation factor ell2; **PDBTitle:** solution structure of the ell_n2 domain of target of rna2 polymerase ii elongation factor ell2
25	c2gjwC_	Alignment	not modelled	10.4	19	**PDB header:**hydrolase/rna **Chain:** C: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** rna recognition and cleavage by an splicing endonuclease
26	c3ieyA_	Alignment	not modelled	10.1	9	**PDB header:**hydrolase/rna binding protein **Chain:** A: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** crystal structure of the functional nanoarchaeum equitans trna2 splicing endonuclease
27	d1pyya2	Alignment	not modelled	9.4	0	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
28	c2zkrt_	Alignment	not modelled	9.2	23	**PDB header:**ribosomal protein/rna **Chain:** T: **PDB Molecule:**rna expansion segment es39 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within

						an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
29	d2fi0a1	Alignment	not modelled	9.1	29	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
30	c3g3zA_	Alignment	not modelled	9.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
31	c2it0A_	Alignment	not modelled	8.7	32	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
32	d2p5ka1	Alignment	not modelled	8.5	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
33	c2vd2A_	Alignment	not modelled	8.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the crystal structure of hisg from b. subtilis
34	d1f1ea_	Alignment	not modelled	7.5	29	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
35	d1rp5a2	Alignment	not modelled	7.4	0	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
36	d1b4aa1	Alignment	not modelled	7.4	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
37	c3a1yF_	Alignment	not modelled	7.4	37	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
38	d1r1ta_	Alignment	not modelled	7.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
39	c3hruA_	Alignment	not modelled	7.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
40	c2jscB_	Alignment	not modelled	7.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
41	c3eyiB_	Alignment	not modelled	7.0	30	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
42	c1zrjA_	Alignment	not modelled	6.9	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**e1b-55kda-associated protein 5 isoform c; **PDBTitle:** solution structure of the sap domain of human e1b-55kda-2 associated protein 5 isoform c
43	d1gyza_	Alignment	not modelled	6.8	22	**Fold:**PABP domain-like **Superfamily:**Ribosomal protein L20 **Family:**Ribosomal protein L20
44	c1g3wA_	Alignment	not modelled	6.8	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
45	c2bruC_	Alignment	not modelled	6.6	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
46	c1pt9B_	Alignment	not modelled	6.6	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
47	d1d4oa_	Alignment	not modelled	6.6	27	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
48	d1h1js_	Alignment	not modelled	6.6	7	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
49	c1b4aA_	Alignment	not modelled	6.6	28	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
50	c2do1A_	Alignment	not modelled	6.5	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nuclear protein hcc-1; **PDBTitle:** solution structure of the sap domain of human nuclear2 protein hcc-1
51	d2a2pa1	Alignment	not modelled	6.5	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
52	c3ereD_	Alignment	not modelled	6.5	28	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
53	d1i94m_	Alignment	not modelled	6.4	25	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
54	d1pnoa_	Alignment	not modelled	6.4	33	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)

55	c1keeH_	Alignment	not modelled	6.4	25	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
56	c3ieyB_	Alignment	not modelled	6.4	18	**PDB header:**hydrolase/rna binding protein **Chain:** B: **PDB Molecule:**neq261; **PDBTitle:** crystal structure of the functional nanoarchaeum equitans trna2 splicing endonuclease
57	d1xrsb2	Alignment	not modelled	6.3	21	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
58	d1ub9a_	Alignment	not modelled	6.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
59	d1g5qa_	Alignment	not modelled	6.3	12	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
60	c3pqkD_	Alignment	not modelled	6.3	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
61	d1zrja1	Alignment	not modelled	6.3	36	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
62	c1f5tA_	Alignment	not modelled	6.2	25	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
63	c2k4bA_	Alignment	not modelled	6.1	4	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
64	c1fx7C_	Alignment	not modelled	6.1	32	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
65	d1jqlb_	Alignment	not modelled	6.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
66	c2zkqm_	Alignment	not modelled	5.9	6	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
67	c2vb0A_	Alignment	not modelled	5.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polyprotein 3bcd; **PDBTitle:** crystal structure of coxsackievirus b3 proteinase 3c
68	c2qwwB_	Alignment	not modelled	5.7	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
69	d2fxaa1	Alignment	not modelled	5.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
70	d1p3y1_	Alignment	not modelled	5.3	12	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
71	d2d1ha1	Alignment	not modelled	5.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
72	c2kk6A_	Alignment	not modelled	5.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fer; **PDBTitle:** solution structure of sh2 domain of proto-oncogene tyrosine-2 protein kinase fer from homo sapiens, northeast structural3 genomics consortium (nesg) target hr3461d
73	d1p4xa1	Alignment	not modelled	5.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
74	d2frha1	Alignment	not modelled	5.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
75	c2kvuA_	Alignment	not modelled	5.1	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**mkl/myocardin-like protein 1; **PDBTitle:** solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e
76	d1f9na1	Alignment	not modelled	5.1	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
77	d2al3a1	Alignment	not modelled	5.1	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
78	d1g3wa1	Alignment	not modelled	5.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein