Phyre^2

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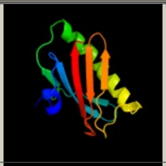
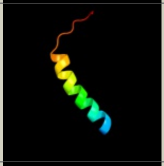
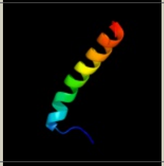
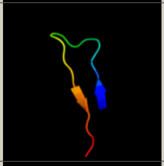
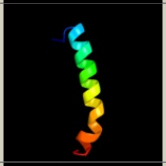
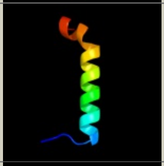
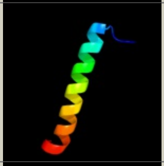
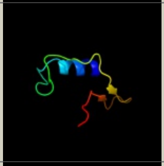
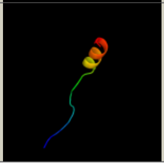
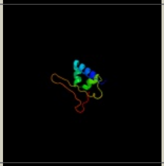
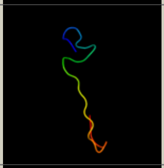
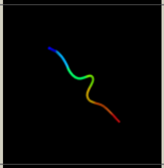
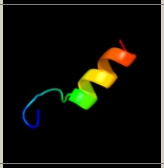
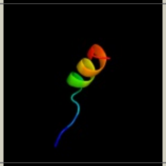
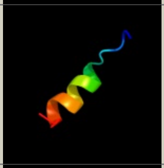
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ea9a1	Alignment		100.0	83	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
2	d2h28a1	Alignment		100.0	61	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
3	d2inwa1	Alignment		100.0	63	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
4	d1ryba_	Alignment		56.8	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
5	c2z2jA_	Alignment		47.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
6	c3h3yF_	Alignment		47.5	33	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**baseplate structural protein gp6; **PDBTitle:** fitting of the gp6 crystal structure into 3d cryo-em2 reconstruction of bacteriophage t4 star-shaped baseplate
7	c3v2iA_	Alignment		31.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
8	c3neaA_	Alignment		30.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
9	d2ptha_	Alignment		29.4	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
10	d2e7ga1	Alignment		25.2	17	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
11	c2yqkA_	Alignment		21.8	9	**PDB header:**transcription/apoptosis **Chain:** A: **PDB Molecule:**arginine-glutamic acid dipeptide repeats protein; **PDBTitle:** solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats

12	d1du0a_	Alignment		18.6	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
13	d2qdya1	Alignment		17.6	24	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
14	d1xv2a_	Alignment		17.1	23	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**Alpha-acetolactate decarboxylase-like
15	d1lpba2	Alignment		15.8	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
16	d1mh3a1	Alignment		15.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
17	d1le8a_	Alignment		14.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
18	d1s7ea1	Alignment		14.7	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
19	c3aqoD_	Alignment		14.2	32	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** structure and function of a membrane component secdf that enhances2 protein export
20	d1p7jb_	Alignment		14.0	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
21	d1e3oc1	Alignment	not modelled	12.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
22	d1au7a1	Alignment	not modelled	11.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
23	c3hruA_	Alignment	not modelled	11.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
24	c3a03A_	Alignment	not modelled	11.0	31	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
25	c1n8sC_	Alignment	not modelled	10.9	43	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**colipase ii; **PDBTitle:** structure of the pancreatic lipase-colipase complex
26	d2d81a1	Alignment	not modelled	10.2	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PHB depolymerase-like
27	d1g3wa2	Alignment	not modelled	9.9	14	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
28	d1p7ia_	Alignment	not modelled	9.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
29	d1f43a_	Alignment	not modelled	9.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Homeodomain
30	d1sana_	Alignment	not modelled	9.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
31	d1yz8p1	Alignment	not modelled	9.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
32	d2hrkb1	Alignment	not modelled	9.5	15	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Arc1p N-terminal domain-like
33	c1a31A_	Alignment	not modelled	9.5	27	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**protein (topoisomerase i); **PDBTitle:** human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
34	d1ftza_	Alignment	not modelled	9.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
35	d1lfba_	Alignment	not modelled	9.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
36	c2lcgA_	Alignment	not modelled	9.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
37	d1ocpa_	Alignment	not modelled	8.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
38	d9anta_	Alignment	not modelled	8.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
39	d1jgga_	Alignment	not modelled	8.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
40	d1wh5a_	Alignment	not modelled	8.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
41	c3fhkF_	Alignment	not modelled	8.7	22	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
42	d2hddb_	Alignment	not modelled	8.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
43	c2jobA_	Alignment	not modelled	8.6	3	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
44	d1gyxa_	Alignment	not modelled	8.6	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
45	c2dmqA_	Alignment	not modelled	8.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**lim/homeobox protein lhx9; **PDBTitle:** solution structure of the homeobox domain of lim/homeobox2 protein lhx9
46	d2craa1	Alignment	not modelled	8.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
47	d1qcva_	Alignment	not modelled	8.4	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
48	d6rxna_	Alignment	not modelled	8.3	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
49	d1fjla_	Alignment	not modelled	8.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
50	c2da1A_	Alignment	not modelled	8.1	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
51	c2l9rA_	Alignment	not modelled	8.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
52	d2dsxa1	Alignment	not modelled	8.0	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
53	c2kp6A_	Alignment	not modelled	7.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
54	c2dmuA_	Alignment	not modelled	7.8	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
55	d2rdva_	Alignment	not modelled	7.7	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like

						Family: Rubredoxin
56	c2da4A_	Alignment	not modelled	7.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
57	d1bcoa1	Alignment	not modelled	7.7	35	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
58	d2obba1	Alignment	not modelled	7.6	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
59	d1h7va_	Alignment	not modelled	7.6	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
60	d1zl8a1	Alignment	not modelled	7.6	25	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
61	d1ijwc_	Alignment	not modelled	7.5	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
62	d1brfa_	Alignment	not modelled	7.5	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
63	d1x93a1	Alignment	not modelled	7.5	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
64	c1x93B_	Alignment	not modelled	7.5	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical protein hp0222; **PDBTitle:** nmr structure of helicobacter pylori hp0222
65	d1b8ia_	Alignment	not modelled	7.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
66	d1rb9a_	Alignment	not modelled	7.3	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
67	d1iu5a_	Alignment	not modelled	7.3	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
68	d1s24a_	Alignment	not modelled	7.2	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
69	c1s24A_	Alignment	not modelled	7.2	50	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
70	d1iroa_	Alignment	not modelled	7.1	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
71	c2djnA_	Alignment	not modelled	7.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein dlx-5; **PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein dlx-5
72	d1b72a_	Alignment	not modelled	6.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
73	c2v3bB_	Alignment	not modelled	6.8	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
74	d4rxna_	Alignment	not modelled	6.8	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
75	d1dx8a_	Alignment	not modelled	6.8	67	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
76	d1gvda_	Alignment	not modelled	6.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
77	d1ztra1	Alignment	not modelled	6.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
78	c2dmsA_	Alignment	not modelled	6.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
79	d2o5ha1	Alignment	not modelled	6.6	21	**Fold:**NMB0513-like **Superfamily:**NMB0513-like **Family:**NMB0513-like
80	c2ypnA_	Alignment	not modelled	6.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
81	d1hcra_	Alignment	not modelled	6.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
82	d1qasa3	Alignment	not modelled	6.4	83	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC

83	c1s7eA_	Alignment	not modelled	6.4	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 6; **PDBTitle:** solution structure of hnf-6
84	d1vnda_	Alignment	not modelled	6.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	c3eq1A_	Alignment	not modelled	6.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
86	d1y74a1	Alignment	not modelled	6.3	25	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
87	d1eexa_	Alignment	not modelled	6.3	47	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit
88	d1p91a_	Alignment	not modelled	6.3	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
89	c2da2A_	Alignment	not modelled	6.2	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
90	c2dmtA_	Alignment	not modelled	6.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein barh-like 1; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein barh-like 1
91	d1hdpa_	Alignment	not modelled	6.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
92	d1q8la_	Alignment	not modelled	6.1	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
93	d2zkmx4	Alignment	not modelled	6.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
94	c3a01A_	Alignment	not modelled	5.9	25	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
95	c2hfpB_	Alignment	not modelled	5.8	83	**PDB header:**transcription **Chain:** B: **PDB Molecule:**src peptide fragment; **PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands
96	c1fm6E_	Alignment	not modelled	5.8	83	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
97	c1fm9E_	Alignment	not modelled	5.8	83	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and gi262570 and co-activator peptides.
98	c1k74E_	Alignment	not modelled	5.8	83	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.3 angstrom resolution crystal structure of the2 heterodimer of the human ppargamma and rxralpha ligand3 binding domains respectively bound with gw409544 and 9-cis4 retinoic acid and co-activator peptides.
99	c3kmgE_	Alignment	not modelled	5.7	83	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator-1; **PDBTitle:** the x-ray crystal structure of ppar-gamma in complex with an indole2 derivative modulator, gsk538, and an src-1 peptide