Phyre2

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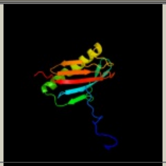
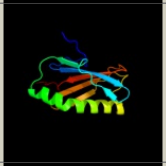
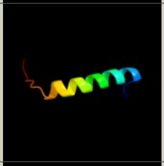
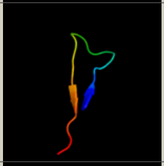
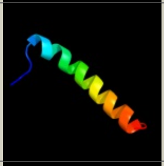
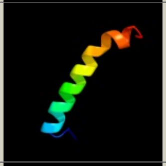
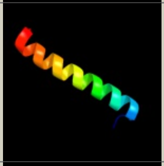
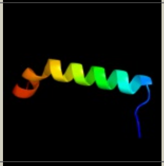
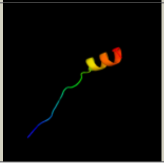
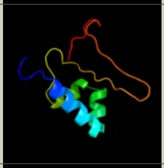
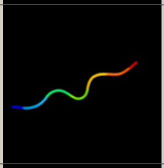
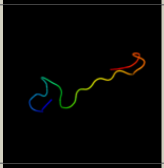
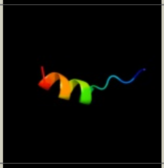
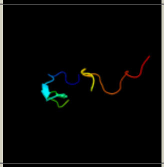
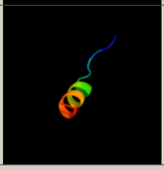
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2inwa1	Alignment		100.0	91	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
2	d2h28a1	Alignment		100.0	97	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
3	d2ea9a1	Alignment		100.0	65	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
4	d1ryba_	Alignment		52.1	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
5	c3h3yF_	Alignment		46.2	22	**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
6	c2z2jA_	Alignment		44.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
7	c3v2iA_	Alignment		25.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
8	d2e7ga1	Alignment		24.6	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
9	d2ptha_	Alignment		24.4	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
10	c3neaA_	Alignment		23.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
11	c2yqkA_	Alignment		20.9	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		19.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
13	d2qdya1	Alignment		17.7	21	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
14	d1lpba2	Alignment		16.7	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
15	d1xv2a_	Alignment		15.7	23	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**Alpha-acetolactate decarboxylase-like
16	d1p7jb_	Alignment		14.5	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
17	d1mh3a1	Alignment		14.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
18	d1s7ea1	Alignment		14.3	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
19	d1p91a_	Alignment		13.5	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
20	d1le8a_	Alignment		13.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
21	c3aqoD_	Alignment	not modelled	12.7	48	**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
22	c3hruA_	Alignment	not modelled	12.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
23	d2obba1	Alignment	not modelled	12.1	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
24	d1e3oc1	Alignment	not modelled	11.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
25	c3a03A_	Alignment	not modelled	10.6	31	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
26	c1ze2B_	Alignment	not modelled	10.5	16	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
27	c1n8sC_	Alignment	not modelled	10.2	43	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**colipase ii; **PDBTitle:** structure of the pancreatic lipase-colipase complex
28	d1au7a1	Alignment	not modelled	10.0	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
						PDB header:structural genomics, unknown function

29	c2lcgA_	Alignment	not modelled	9.9	13	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
30	d1g3wa2	Alignment	not modelled	9.8	16	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
31	d1sana_	Alignment	not modelled	8.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
32	d1k8ib2	Alignment	not modelled	8.9	19	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
33	d1p7ia_	Alignment	not modelled	8.8	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
34	d1f43a_	Alignment	not modelled	8.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
35	c2jobA_	Alignment	not modelled	8.4	0	**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
36	d1qcva_	Alignment	not modelled	8.2	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
37	d6rxna_	Alignment	not modelled	8.2	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
38	d1wh5a_	Alignment	not modelled	8.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
39	d9anta_	Alignment	not modelled	8.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
40	d1lfba_	Alignment	not modelled	7.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
41	d1ftza_	Alignment	not modelled	7.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
42	d2dsxa1	Alignment	not modelled	7.9	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
43	d1yz8p1	Alignment	not modelled	7.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
44	d1jgga_	Alignment	not modelled	7.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
45	d2hrkb1	Alignment	not modelled	7.8	30	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Arc1p N-terminal domain-like
46	d2hddb_	Alignment	not modelled	7.8	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
47	c2dmqA_	Alignment	not modelled	7.7	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
48	d1ocpa_	Alignment	not modelled	7.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
49	d2o5ha1	Alignment	not modelled	7.6	18	**Fold:**NMB0513-like **Superfamily:**NMB0513-like **Family:**NMB0513-like
50	d2rdva_	Alignment	not modelled	7.5	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
51	d1h7va_	Alignment	not modelled	7.4	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
52	d1brfa_	Alignment	not modelled	7.3	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
53	d1ijwc_	Alignment	not modelled	7.3	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
54	d2craa1	Alignment	not modelled	7.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
55	d1rb9a_	Alignment	not modelled	7.2	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein;

56	c2kp6A_	Alignment	not modelled	7.1	32	**PDBTitle:** solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
57	d1iu5a_	Alignment	not modelled	7.1	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
58	c2da1A_	Alignment	not modelled	7.0	31	**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)
59	d1iroa_	Alignment	not modelled	7.0	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
60	c1s24A_	Alignment	not modelled	6.9	33	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
61	d1s24a_	Alignment	not modelled	6.9	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
62	c1x93B_	Alignment	not modelled	6.9	40	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical protein hp0222; **PDBTitle:** nmr structure of helicobacter pylori hp0222
63	d1x93a1	Alignment	not modelled	6.9	40	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
64	d1fjla_	Alignment	not modelled	6.8	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
65	c2dmuA_	Alignment	not modelled	6.8	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
66	d4rxna_	Alignment	not modelled	6.7	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
67	c2v3bB_	Alignment	not modelled	6.7	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
68	c3fhkF_	Alignment	not modelled	6.7	25	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
69	d1dx8a_	Alignment	not modelled	6.6	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
70	c2da4A_	Alignment	not modelled	6.6	38	**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
71	c2l9rA_	Alignment	not modelled	6.5	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
72	d1b8ia_	Alignment	not modelled	6.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
73	d1b72a_	Alignment	not modelled	6.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	d1hcra_	Alignment	not modelled	6.3	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
75	c2djnA_	Alignment	not modelled	6.1	25	**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
76	d1qasa3	Alignment	not modelled	6.0	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
77	d1zl8a1	Alignment	not modelled	5.9	21	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
78	d1vnda_	Alignment	not modelled	5.9	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
79	c2dmsA_	Alignment	not modelled	5.9	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
80	c3eq1A_	Alignment	not modelled	5.8	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
81	c2dmtA_	Alignment	not modelled	5.7	25	**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
82	d2vzsa1	Alignment	not modelled	5.6	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain

						Family:beta-Galactosidase/glucuronidase domain
83	d1ztra1	Alignment	not modelled	5.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
84	c1a31A_	Alignment	not modelled	5.6	24	**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
85	c2kn9A_	Alignment	not modelled	5.5	33	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
86	d1gvda_	Alignment	not modelled	5.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
87	c1zcjA_	Alignment	not modelled	5.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase
88	c2da2A_	Alignment	not modelled	5.5	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)
89	d1nk3p_	Alignment	not modelled	5.4	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
90	d1uhsa_	Alignment	not modelled	5.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
91	d2cufa1	Alignment	not modelled	5.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
92	c2hfpB_	Alignment	not modelled	5.4	83	**PDB header:**transcription **Chain:** B: **PDB Molecule:**src peptide fragment; **PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands
93	c3a01A_	Alignment	not modelled	5.3	25	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
94	c1k74E_	Alignment	not modelled	5.3	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.
95	c1fm9E_	Alignment	not modelled	5.3	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.
96	c1fm6E_	Alignment	not modelled	5.3	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	c3kmgE_	Alignment	not modelled	5.3	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
98	c1fm6V_	Alignment	not modelled	5.3	83	**PDB header:**transcription **Chain:** V: **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.
99	d1hdpa_	Alignment	not modelled	5.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain