Phyre^2

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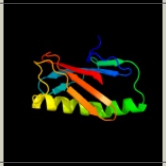
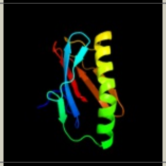
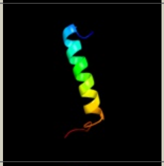
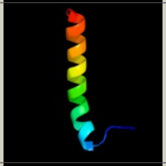
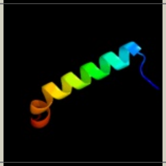
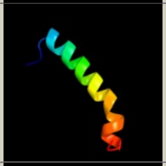
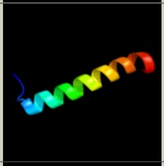
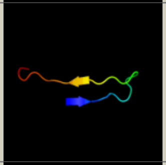
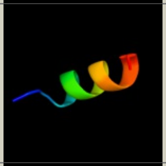
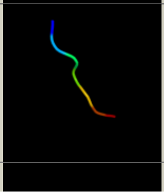
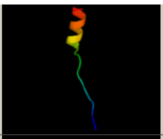
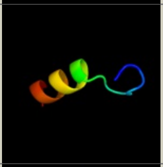
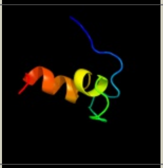
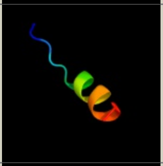
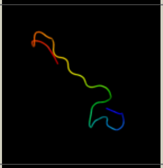
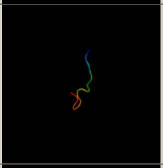
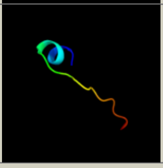
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ea9a1	Alignment		100.0	66	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
2	d2inwa1	Alignment		100.0	64	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
3	d2h28a1	Alignment		100.0	61	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
4	d1ryba_	Alignment		57.1	27	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
5	c2z2jA_	Alignment		48.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
6	c3neaA_	Alignment		34.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
7	c3v2iA_	Alignment		31.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
8	d2ptha_	Alignment		28.5	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
9	c3h3yF_	Alignment		24.5	29	**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
10	d1du0a_	Alignment		21.2	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
11	d1lpba2	Alignment		19.5	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like

12	c2yqkA_	Alignment		17.7	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
13	d1p7jb_	Alignment		16.8	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
14	d1mh3a1	Alignment		16.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
15	c3aqoD_	Alignment		16.3	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
16	d1s7ea1	Alignment		15.6	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
17	d1le8a_	Alignment		15.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
18	d1xv2a_	Alignment		15.5	27	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**Alpha-acetolactate decarboxylase-like
19	c1n8sC_	Alignment		14.9	43	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**colipase ii; **PDBTitle:** structure of the pancreatic lipase-colipase complex
20	c3d59B_	Alignment		13.9	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**platelet-activating factor acetylhydrolase; **PDBTitle:** crystal structure of human plasma platelet activating2 factor acetylhydrolase
21	d1e3oc1	Alignment	not modelled	13.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
22	d2e7ga1	Alignment	not modelled	13.6	16	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
23	d2d81a1	Alignment	not modelled	12.6	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PHB depolymerase-like
24	d1au7a1	Alignment	not modelled	11.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
25	c3a03A_	Alignment	not modelled	11.6	46	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
26	c3hruA_	Alignment	not modelled	11.4	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
27	d1p7ia_	Alignment	not modelled	10.9	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
28	d1f43a_	Alignment	not modelled	10.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
29	d2hrkb1	Alignment	not modelled	10.4	15	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Arc1p N-terminal domain-like

30	d1sana_	Alignment	not modelled	10.4	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
31	d1ftza_	Alignment	not modelled	10.0	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
32	c3fhkF_	Alignment	not modelled	9.9	28	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
33	d2hq2a1	Alignment	not modelled	9.8	26	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
34	d9anta_	Alignment	not modelled	9.7	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
35	d1jgga_	Alignment	not modelled	9.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
36	d1yz8p1	Alignment	not modelled	9.5	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
37	d1lfba_	Alignment	not modelled	9.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
38	d1fjla_	Alignment	not modelled	9.0	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
39	d2o5ha1	Alignment	not modelled	9.0	24	**Fold:**NMB0513-like **Superfamily:**NMB0513-like **Family:**NMB0513-like
40	c2dmqA_	Alignment	not modelled	9.0	25	**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
41	d1ocpa_	Alignment	not modelled	8.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
42	c2l9rA_	Alignment	not modelled	8.8	25	**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
43	d2craa1	Alignment	not modelled	8.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
44	d1wh5a_	Alignment	not modelled	8.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
45	d2hddb_	Alignment	not modelled	8.6	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
46	c2dmuA_	Alignment	not modelled	8.5	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
47	d1g3wa2	Alignment	not modelled	8.4	14	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
48	d2obba1	Alignment	not modelled	8.2	31	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
49	d1ijwc_	Alignment	not modelled	8.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
50	c2kp6A_	Alignment	not modelled	8.0	21	**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
51	c2da4A_	Alignment	not modelled	8.0	19	**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
52	d1b8ia_	Alignment	not modelled	7.9	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
53	d1gyxa_	Alignment	not modelled	7.8	17	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
54	c2da1A_	Alignment	not modelled	7.8	19	**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)
55	c1a31A_	Alignment	not modelled	7.7	23	**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
						Fold: Rubredoxin-like

56	d6rxna_	Alignment	not modelled	7.6	50	**Superfamily:**Rubredoxin-like **Family:**Rubredoxin
57	d1qcva_	Alignment	not modelled	7.5	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
58	d1ztra1	Alignment	not modelled	7.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
59	d1gt0c1	Alignment	not modelled	7.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
60	c2djnA_	Alignment	not modelled	7.3	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
61	d2dsxa1	Alignment	not modelled	7.3	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
62	d1b72a_	Alignment	not modelled	7.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
63	d1vnda_	Alignment	not modelled	7.2	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
64	d1zl8a1	Alignment	not modelled	7.1	17	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
65	c2dmsA_	Alignment	not modelled	7.1	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
66	d2rdva_	Alignment	not modelled	7.0	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
67	d1uhsa_	Alignment	not modelled	7.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
68	d1x93a1	Alignment	not modelled	7.0	40	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
69	c1x93B_	Alignment	not modelled	7.0	40	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical protein hp0222; **PDBTitle:** nmr structure of helicobacter pylori hp0222
70	d1h7va_	Alignment	not modelled	7.0	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
71	d1brfa_	Alignment	not modelled	6.8	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
72	c2hfpB_	Alignment	not modelled	6.7	83	**PDB header:**transcription **Chain:** B: **PDB Molecule:**src peptide fragment; **PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands
73	d1rb9a_	Alignment	not modelled	6.7	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
74	c1fm6E_	Alignment	not modelled	6.7	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.
75	c1fm9E_	Alignment	not modelled	6.7	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.
76	c1k74E_	Alignment	not modelled	6.7	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.
77	c2ypnA_	Alignment	not modelled	6.6	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
78	d1iu5a_	Alignment	not modelled	6.6	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
79	c3kmgE_	Alignment	not modelled	6.6	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
80	c1fm6V_	Alignment	not modelled	6.6	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.
						PDB header:membrane protein/protein binding

81	c1p8dD_	Alignment	not modelled	6.6	83	**Chain:** D: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3; **PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol
82	d1iroa_	Alignment	not modelled	6.6	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
83	c1p8dC_	Alignment	not modelled	6.5	71	**PDB header:**membrane protein/protein binding **Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3; **PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol
84	c1k7lF_	Alignment	not modelled	6.5	71	**PDB header:**transcription **Chain:** F: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
85	c1k7lD_	Alignment	not modelled	6.5	71	**PDB header:**transcription **Chain:** D: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
86	c1k7lH_	Alignment	not modelled	6.5	71	**PDB header:**transcription **Chain:** H: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
87	c1k7lB_	Alignment	not modelled	6.5	71	**PDB header:**transcription **Chain:** B: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
88	d1hdpa_	Alignment	not modelled	6.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
89	c1s7eA_	Alignment	not modelled	6.5	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 6; **PDBTitle:** solution structure of hnf-6
90	c1s24A_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
91	d1s24a_	Alignment	not modelled	6.5	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
92	d4rxna_	Alignment	not modelled	6.4	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
93	d2e1oa1	Alignment	not modelled	6.3	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	c2lcgA_	Alignment	not modelled	6.3	13	**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
95	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
96	c2dmtA_	Alignment	not modelled	6.3	31	**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
97	c2v3bB_	Alignment	not modelled	6.3	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
98	d1dx8a_	Alignment	not modelled	6.1	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
99	c3a01A_	Alignment	not modelled	6.1	31	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna