Phyre^2

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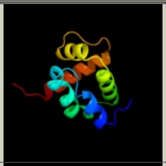
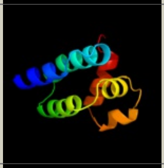
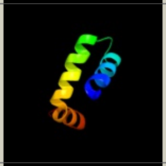
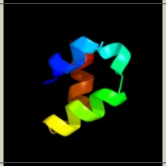
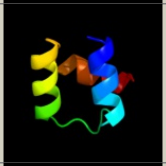
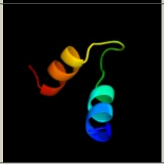
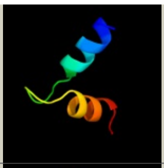
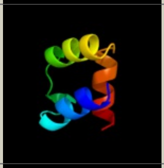
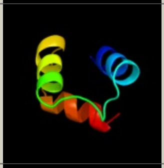
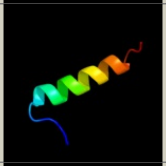
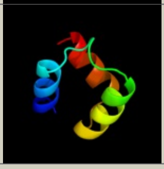
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x6iB_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ygfy; **PDBTitle:** crystal structure of ygfy from escherichia coli
2	c2jr5A_	Alignment		100.0	52	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0350 protein vc_2471; **PDBTitle:** solution structure of upf0350 protein vc_2471. northeast2 structural genomics target vcr36
3	d1puza_	Alignment		99.9	32	**Fold:**YgfY-like **Superfamily:**YgfY-like **Family:**YgfY-like
4	c2lm4A_	Alignment		99.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**succinate dehydrogenase assembly factor 2, mitochondrial; **PDBTitle:** solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a
5	c3ermD_	Alignment		54.7	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved protein with unknown function2 from pseudomonas syringae pv. tomato str. dc3000
6	d2cqxa1	Alignment		43.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
7	d1au7a1	Alignment		37.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
8	d1yrnb_	Alignment		30.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
9	c2da4A_	Alignment		30.1	13	**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
10	c2dmtA_	Alignment		29.8	20	**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
11	d1xrxa1	Alignment		28.3	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like

12	c1xrxD_	Alignment		28.3	17	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
13	d1ddfa_	Alignment		26.7	10	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
14	d1x2ma1	Alignment		25.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
15	d1wnaa1	Alignment		24.7	19	**Fold:**TTHA1528-like **Superfamily:**TTHA1528-like **Family:**TTHA1528-like
16	c2dmuA_	Alignment		24.7	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
17	d1ftta_	Alignment		23.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
18	c2e19A_	Alignment		20.9	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor 8; **PDBTitle:** solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
19	d1x4oa1	Alignment		20.1	21	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
20	d2e1oa1	Alignment		19.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
21	c2xcjB_	Alignment	not modelled	19.1	9	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
22	d1p7jb_	Alignment	not modelled	18.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
23	d1ig7a_	Alignment	not modelled	18.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
24	d1b8ia_	Alignment	not modelled	18.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
25	d2ecba1	Alignment	not modelled	18.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
26	c3bs3A_	Alignment	not modelled	17.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
27	c2wl8D_	Alignment	not modelled	17.7	10	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
28	d1ahdp_	Alignment	not modelled	17.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
29	d1rh2a_	Alignment	not modelled	17.3	11	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines

						Family: Interferons/interleukin-10 (IL-10)
30	d1ztra1	Alignment	not modelled	16.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
31	c2da2A_	Alignment	not modelled	16.7	24	**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)
32	d1uhsa_	Alignment	not modelled	16.7	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
33	c2lk2A_	Alignment	not modelled	16.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein tgif1; **PDBTitle:** solution nmr structure of homeobox domain (171-248) of human homeobox2 protein tgif1, northeast structural genomics consortium target3 hr4411b
34	c2djnA_	Alignment	not modelled	16.6	20	**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
35	d1ug0a_	Alignment	not modelled	16.2	27	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
36	c2da3A_	Alignment	not modelled	16.0	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the third homeobox domain of at-2 binding transcription factor 1 (atbf1)
37	d1au1a_	Alignment	not modelled	15.8	11	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
38	d1fjla_	Alignment	not modelled	15.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
39	c2da1A_	Alignment	not modelled	15.4	13	**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)
40	c3gxvA_	Alignment	not modelled	15.4	9	**PDB header:**hydrolase/replication **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
41	c2l9rA_	Alignment	not modelled	14.9	20	**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
42	d1p7ia_	Alignment	not modelled	14.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
43	d1jgga_	Alignment	not modelled	14.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
44	d1x2na1	Alignment	not modelled	14.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
45	c3omtA_	Alignment	not modelled	14.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
46	d1fkma2	Alignment	not modelled	13.5	17	**Fold:**Left-handed superhelix **Superfamily:**Ypt/Rab-GAP domain of gyp1p **Family:**Ypt/Rab-GAP domain of gyp1p
47	d1fjlb_	Alignment	not modelled	13.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
48	d2r5yb1	Alignment	not modelled	13.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
49	d1dzfa1	Alignment	not modelled	13.3	28	**Fold:**Restriction endonuclease-like **Superfamily:**Eukaryotic RPB5 N-terminal domain **Family:**Eukaryotic RPB5 N-terminal domain
50	d2r1jl1	Alignment	not modelled	13.1	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
51	d2hddb_	Alignment	not modelled	12.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
52	c3nauA_	Alignment	not modelled	12.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
53	d2icta1	Alignment	not modelled	12.1	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
54	d1lfup_	Alignment	not modelled	12.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain

55	d1x57a1	Alignment	not modelled	12.1	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
56	d1y7ya1	Alignment	not modelled	11.9	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
57	c3ocmB_	Alignment	not modelled	11.7	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
58	d1k61a_	Alignment	not modelled	11.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
59	c2dmnA_	Alignment	not modelled	10.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein tgif2lx; **PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein tgif2lx
60	d1gt0c1	Alignment	not modelled	10.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
61	d2d6fc2	Alignment	not modelled	10.3	14	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
62	c2da5A_	Alignment	not modelled	10.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
63	c3f52A_	Alignment	not modelled	10.2	8	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
64	d1le8b_	Alignment	not modelled	9.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
65	d1zq1c2	Alignment	not modelled	9.6	18	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
66	c3oq9C_	Alignment	not modelled	9.3	12	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** structure of the fas/fadd death domain assembly
67	c2da7A_	Alignment	not modelled	9.2	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
68	d1le8a_	Alignment	not modelled	8.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
69	d1bw5a_	Alignment	not modelled	8.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
70	c2ef8A_	Alignment	not modelled	8.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
71	d1hdpa_	Alignment	not modelled	8.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
72	c1jqsB_	Alignment	not modelled	8.3	8	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
73	d1adra_	Alignment	not modelled	8.2	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
74	d1octc1	Alignment	not modelled	8.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	c3fwcO_	Alignment	not modelled	8.1	17	**PDB header:**cell cycle, transcription **Chain:** O: **PDB Molecule:**protein sus1; **PDBTitle:** sac3:sus1:cdc31 complex
76	c3a4cA_	Alignment	not modelled	8.0	17	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
77	c2k40A_	Alignment	not modelled	7.8	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox expressed in es cells 1; **PDBTitle:** nmr structure of hesx-1 homeodomain double mutant r31l/e42l
78	c1s7eA_	Alignment	not modelled	7.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 6; **PDBTitle:** solution structure of hnf-6
79	d1ocpa_	Alignment	not modelled	7.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
80	d1ys7a1	Alignment	not modelled	7.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
81	d1llib_	Alignment	not modelled	7.5	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family: Phage repressors
82	c2dmsA_	Alignment	not modelled	7.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
83	d1utxa_	Alignment	not modelled	7.3	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
84	d2ecca1	Alignment	not modelled	7.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	c2k0sA_	Alignment	not modelled	7.3	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adp-ribosylation factor-like protein 2-binding **PDBTitle:** solution nmr structure of protein bc066483
86	d2cuea1	Alignment	not modelled	7.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
87	c3tgnA_	Alignment	not modelled	7.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
88	c3jw4C_	Alignment	not modelled	7.1	19	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, marr/emrr family; **PDBTitle:** the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
89	c3qwlA_	Alignment	not modelled	7.1	15	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**tbc1 domain family member 7; **PDBTitle:** crystal structure of human tbc1 domain family member 7
90	d1fexa_	Alignment	not modelled	7.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
91	d2fq4a2	Alignment	not modelled	7.0	16	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
92	c3fmtF_	Alignment	not modelled	7.0	18	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna
93	d2croa_	Alignment	not modelled	6.9	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
94	c2e8nA_	Alignment	not modelled	6.9	7	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
95	c3a01A_	Alignment	not modelled	6.9	22	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
96	d1pufb_	Alignment	not modelled	6.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	c3ecoB_	Alignment	not modelled	6.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
98	c2k6oA_	Alignment	not modelled	6.8	19	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cathelicidin antimicrobial peptide; **PDBTitle:** human ll-37 structure
99	d1vhqa_	Alignment	not modelled	6.7	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI