Phyre^2

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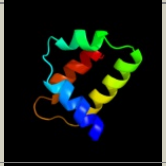
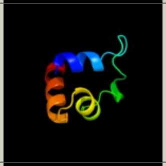
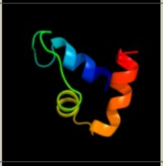
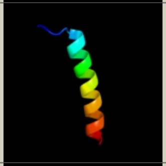
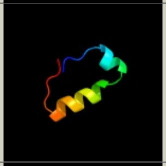
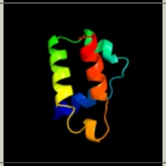
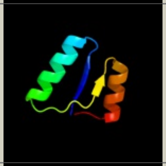
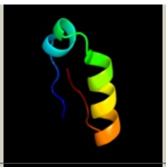
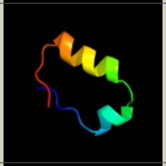
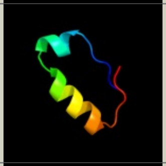
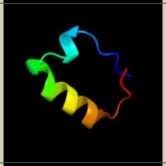
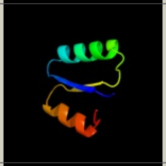
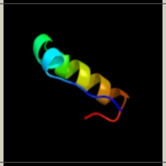
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xn7a_	Alignment		58.5	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
2	d1k8kg_	Alignment		58.1	23	**Fold:**alpha-alpha superhelix **Superfamily:**Arp2/3 complex 16 kDa subunit ARPC5 **Family:**Arp2/3 complex 16 kDa subunit ARPC5
3	d1ylfa1	Alignment		48.9	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
4	c3k69A_	Alignment		44.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
5	d1vcta1	Alignment		41.2	8	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
6	d1xqoa_	Alignment		40.8	11	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
7	d2ihta1	Alignment		40.5	55	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
8	c3dwlG_	Alignment		40.4	20	**PDB header:**structural protein **Chain:** G: **PDB Molecule:**actin-related protein 2/3 complex subunit 5; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
9	d1s8na_	Alignment		37.1	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
10	d1xd7a_	Alignment		33.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
11	d1ufma_	Alignment		32.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)

12	d1t9ba1	Alignment		29.9	33	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
13	d2ji7a1	Alignment		29.7	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
14	d1q6za1	Alignment		29.6	28	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
15	d1zpda1	Alignment		28.0	28	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
16	d1ozha1	Alignment		27.7	31	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
17	c3c3mA_	Alignment		26.1	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
18	c2vbgB_	Alignment		24.4	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**branched-chain alpha-ketoacid decarboxylase; **PDBTitle:** the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
19	d1pvda1	Alignment		23.2	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
20	d1p6qa_	Alignment		23.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
21	c2y75F_	Alignment	not modelled	20.9	7	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
22	d1u0sy_	Alignment	not modelled	20.5	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
23	c3t6kB_	Alignment	not modelled	20.4	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
24	d1jbea_	Alignment	not modelled	19.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
25	c3h1gA_	Alignment	not modelled	17.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
26	d1ovma1	Alignment	not modelled	17.2	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
27	c3c5tB_	Alignment	not modelled	16.9	26	**PDB header:**signaling protein/signaling protein **Chain:** B: **PDB Molecule:**exendin-4; **PDBTitle:** crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain
28	c3hzhA_	Alignment	not modelled	16.8	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis response regulator (chey-3); **PDBTitle:** crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi

29	c3khtA_	Alignment	not modelled	16.8	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
30	d1ny5a1	Alignment	not modelled	16.7	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	c1ojhK_	Alignment	not modelled	16.2	19	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**nbla; **PDBTitle:** crystal structure of nbla from pcc 7120
32	d2pl1a1	Alignment	not modelled	16.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	c2qxyB_	Alignment	not modelled	16.0	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
34	c2zwmA_	Alignment	not modelled	15.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
35	c3i42A_	Alignment	not modelled	15.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
36	c1zpdA_	Alignment	not modelled	15.7	28	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
37	c3grcD_	Alignment	not modelled	15.6	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
38	d2fug21	Alignment	not modelled	15.6	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
39	d1ojha_	Alignment	not modelled	15.5	19	**Fold:**NblA-like **Superfamily:**NblA-like **Family:**NblA-like
40	d1zgza1	Alignment	not modelled	15.3	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c3txmA_	Alignment	not modelled	15.3	18	**PDB header:**hydrolase, protein binding **Chain:** A: **PDB Molecule:**26s proteasome regulatory complex subunit p42b; **PDBTitle:** crystal structure of rpn6 from drosophila melanogaster, gd(3+) complex
42	c3cg4A_	Alignment	not modelled	15.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey-like); **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
43	c3c97A_	Alignment	not modelled	14.8	13	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
44	c3hv2B_	Alignment	not modelled	13.5	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator/hd domain protein; **PDBTitle:** crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
45	d1mvoa_	Alignment	not modelled	13.4	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	c3cf4G_	Alignment	not modelled	13.3	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
47	d1ybha1	Alignment	not modelled	13.3	30	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
48	c1jrjA_	Alignment	not modelled	13.1	29	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
49	d1ig6a_	Alignment	not modelled	13.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
50	c2j48A_	Alignment	not modelled	12.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
51	c3a0rB_	Alignment	not modelled	12.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
52	d1kgsa2	Alignment	not modelled	12.1	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
53	c1ozhD_	Alignment	not modelled	12.0	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**acetolactate synthase, catabolic; **PDBTitle:** the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.

54	d2ayxa1	Alignment	not modelled	11.7	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
55	d1bgpa_	Alignment	not modelled	11.6	26	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
56	d1ys7a2	Alignment	not modelled	11.5	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c1d0rA_	Alignment	not modelled	10.9	22	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
58	d2ez9a1	Alignment	not modelled	10.9	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
59	c3cixA_	Alignment	not modelled	10.8	26	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
60	d1yioa2	Alignment	not modelled	10.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c2rohA_	Alignment	not modelled	10.4	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**telomere binding protein-1; **PDBTitle:** the dna binding domain of rtbp1
62	c3rceA_	Alignment	not modelled	10.3	26	**PDB header:**transferase/peptide **Chain:** A: **PDB Molecule:**oligosaccharide transferase to n-glycosylate proteins; **PDBTitle:** bacterial oligosaccharyltransferase pglb
63	c2qzjC_	Alignment	not modelled	10.2	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
64	d2a9pa1	Alignment	not modelled	10.2	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
65	c2rjnA_	Alignment	not modelled	9.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
66	c2jrzA_	Alignment	not modelled	9.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1c; **PDBTitle:** solution structure of the bright/arid domain from the human2 jarid1c protein.
67	c2ji6B_	Alignment	not modelled	9.7	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
68	d1dbwa_	Alignment	not modelled	9.5	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	c2hqoA_	Alignment	not modelled	9.5	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
70	c3j08A_	Alignment	not modelled	9.5	19	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
71	d1q3ma_	Alignment	not modelled	9.3	29	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
72	c3lwfD_	Alignment	not modelled	9.2	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
73	c3gl9B_	Alignment	not modelled	9.2	24	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
74	c2bpbB_	Alignment	not modelled	9.1	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
75	c2jxjA_	Alignment	not modelled	9.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1a; **PDBTitle:** nmr structure of the arid domain from the histone h3k42 demethylase rbp2
76	c3r0jA_	Alignment	not modelled	8.8	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
77	d1w36d1	Alignment	not modelled	8.8	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
78	c3f6cB_	Alignment	not modelled	8.7	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
79	c3b2nA_	Alignment	not modelled	8.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr

						family, from2 staphylococcus aureus
80	c3hdgE_	Alignment	not modelled	8.6	11	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
81	c2panF_	Alignment	not modelled	8.6	21	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
82	c1xmeB_	Alignment	not modelled	8.5	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
83	c1k8vA_	Alignment	not modelled	8.5	43	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**neuropeptide f; **PDBTitle:** the nmr-derived conformation of neuropeptide f from2 moniezia expansa
84	c3eodA_	Alignment	not modelled	8.4	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
85	d1heya_	Alignment	not modelled	8.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	c3hdlA_	Alignment	not modelled	8.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**royal palm tree peroxidase; **PDBTitle:** crystal structure of highly glycosylated peroxidase from royal palm2 tree
87	c2nxwB_	Alignment	not modelled	8.2	31	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phenyl-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
88	d1xg7a_	Alignment	not modelled	8.1	7	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
89	d1qh8a_	Alignment	not modelled	8.1	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
90	d1pa2a_	Alignment	not modelled	8.0	26	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**CCP-like
91	d1o6ea_	Alignment	not modelled	8.0	19	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
92	c1hr6C_	Alignment	not modelled	7.9	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mitochondrial processing peptidase alpha subunit; **PDBTitle:** yeast mitochondrial processing peptidase
93	c3cg0A_	Alignment	not modelled	7.6	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase **PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
94	c3mmnA_	Alignment	not modelled	7.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
95	d2djia1	Alignment	not modelled	7.5	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
96	c2pgnA_	Alignment	not modelled	7.5	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclohexane-1,2-dione hydrolase (cdh); **PDBTitle:** the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
97	d1qkka_	Alignment	not modelled	7.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
98	c1fp2A_	Alignment	not modelled	7.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoflavone o-methyltransferase; **PDBTitle:** crystal structure analysis of isoflavone o-methyltransferase
99	d2ev0a1	Alignment	not modelled	7.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein