Phyre2

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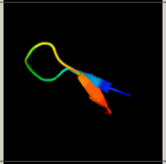
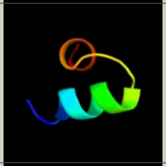
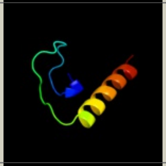
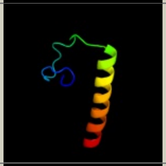
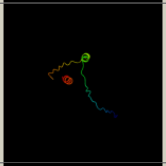
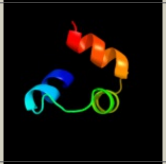
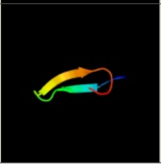
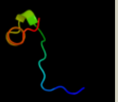
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sg7a1	Alignment		49.3	46	**Fold:**ChaB-like **Superfamily:**ChaB-like **Family:**ChaB-like
2	c1sg7A_	Alignment		49.3	46	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cation transport regulator chab; **PDBTitle:** nmr solution structure of the putative cation transport2 regulator chab
3	d1lq1a_	Alignment		45.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**Spo0A
4	d1fc3a_	Alignment		44.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**Spo0A
5	d2ikba1	Alignment		26.3	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
6	c2l9yA_	Alignment		22.3	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
7	d2nr7a1	Alignment		21.7	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
8	d2jnaa1	Alignment		18.0	15	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
9	c2k9iB_	Alignment		17.3	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
10	c2cg4B_	Alignment		17.1	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
11	c2bw2A_	Alignment		16.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bypass of forespore c; **PDBTitle:** bofc from bacillus subtilis

12	d1ttya_	Alignment		14.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
13	c1rk8C_	Alignment		14.4	22	**PDB header:**translation **Chain:** C: **PDB Molecule:**within the bgcn gene intron protein; **PDBTitle:** structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
14	d1rk8c_	Alignment		14.4	22	**Fold:**WW domain-like **Superfamily:**Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain **Family:**Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
15	c3lpeF_	Alignment		14.4	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
16	d1qqha_	Alignment		13.8	27	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
17	c1mgtA_	Alignment		13.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (o6-methylguanine-dna methyltransferase); **PDBTitle:** crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
18	d1gzsb_	Alignment		12.5	17	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
19	d2cg4a1	Alignment		12.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
20	d2cyya1	Alignment		11.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
21	c2ysaA_	Alignment	not modelled	11.7	50	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6; **PDBTitle:** solution structure of the zinc finger cchc domain from the2 human retinoblastoma-binding protein 6 (retinoblastoma-3 binding q protein 1, rbq-1)
22	d1tueb_	Alignment	not modelled	11.6	27	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
23	c2o8xA_	Alignment	not modelled	11.6	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
24	d1ku7a_	Alignment	not modelled	11.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
25	d1r6ea_	Alignment	not modelled	11.3	19	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
26	c1tueG_	Alignment	not modelled	10.9	27	**PDB header:**replication **Chain:** G: **PDB Molecule:**regulatory protein e2; **PDBTitle:** the x-ray structure of the papillomavirus helicase in2 complex with its molecular matchmaker e2
27	c3frwF_	Alignment	not modelled	10.5	16	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
28	d2ilaa_	Alignment	not modelled	10.4	27	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)

29	c2c5kP_	Alignment	not modelled	9.8	21	**PDB header:**protein transport **Chain:** P: **PDB Molecule:**vacuolar protein sorting protein 51; **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51
30	c1l0oC_	Alignment	not modelled	9.6	12	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
31	d1l0oc_	Alignment	not modelled	9.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
32	d1rp3a1	Alignment	not modelled	9.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
33	c3korD_	Alignment	not modelled	9.4	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
34	c2dbbA_	Alignment	not modelled	9.1	23	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
35	c2fgtA_	Alignment	not modelled	8.8	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component system yycf/yycg regulatory **PDBTitle:** crystal structure of yych from bacillus subtilis
36	c2e1cA_	Alignment	not modelled	8.6	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
37	c3h8dC_	Alignment	not modelled	8.4	21	**PDB header:**motor protein/signaling protein **Chain:** C: **PDB Molecule:**myosin-vi; **PDBTitle:** crystal structure of myosin vi in complex with dab2 peptide
38	d1qmha1	Alignment	not modelled	8.4	13	**Fold:**Thioredoxin fold **Superfamily:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain **Family:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain
39	c2c5iP_	Alignment	not modelled	8.2	21	**PDB header:**protein transport **Chain:** P: **PDB Molecule:**vacuolar protein sorting protein 51; **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
40	c2bcmB_	Alignment	not modelled	7.9	27	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**f1845 fimbrial protein; **PDBTitle:** daae adhesin
41	d1e0ga_	Alignment	not modelled	7.8	22	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
42	d1z67a1	Alignment	not modelled	7.7	18	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
43	d1jhga_	Alignment	not modelled	7.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
44	d1pn0a2	Alignment	not modelled	7.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
45	c1or7A_	Alignment	not modelled	7.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
46	c2ia0A_	Alignment	not modelled	7.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
47	d1ut1a_	Alignment	not modelled	7.1	27	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Dr-family adhesin
48	d1i1ga1	Alignment	not modelled	7.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
49	d1h54a2	Alignment	not modelled	7.1	25	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
50	c1i1gA_	Alignment	not modelled	7.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
51	d2joka1	Alignment	not modelled	6.8	40	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
52	c2djpA_	Alignment	not modelled	6.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
53	d1mgta1	Alignment	not modelled	6.6	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain **Family:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain
54	d1ofcx1	Alignment	not modelled	6.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Myb/SANT domain
55	d2a7wa1	Alignment	not modelled	6.4	13	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
56	c2a7wF_	Alignment	not modelled	6.4	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
57	c2opkC_	Alignment	not modelled	6.1	27	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
58	d1s6la1	Alignment	not modelled	5.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
59	d2vera1	Alignment	not modelled	5.8	20	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Dr-family adhesin
60	c2vbzA_	Alignment	not modelled	5.5	23	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
61	c2krcA_	Alignment	not modelled	5.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta; **PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
62	c2l4aA_	Alignment	not modelled	5.4	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
63	d1or7a1	Alignment	not modelled	5.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
64	d2cfxa1	Alignment	not modelled	5.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain