Phyre^2

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Description	P31549
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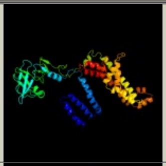
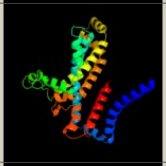
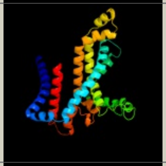
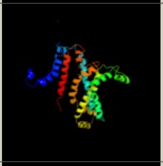
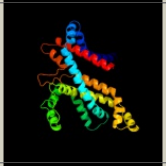
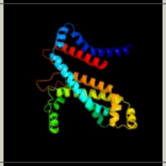
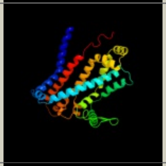
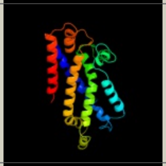
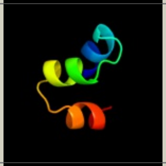
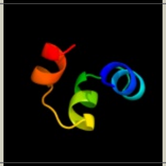
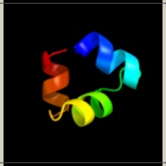
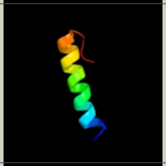
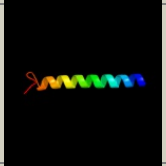
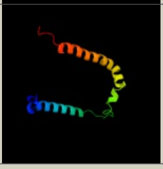
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r6gF_	Alignment		100.0	13	**PDB header:**hydrolase/transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** the crystal structure of the e. coli maltose transporter
2	c3d31D_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
3	d3d31c1	Alignment		100.0	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	c3fh6F_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
5	d2onkc1	Alignment		100.0	22	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c2onkC_	Alignment		100.0	22	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
7	d2r6gf2	Alignment		100.0	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	d2r6gg1	Alignment		99.9	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3dhwa1	Alignment		99.8	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c1umqA_	Alignment		49.9	16	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
11	d1umqa_	Alignment		49.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

12	d1ntca_	Alignment		48.9	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
13	d1fipa_	Alignment		41.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	c3e7lD_	Alignment		34.6	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
15	d1etob_	Alignment		34.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	d1etxa_	Alignment		30.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	c2hx6A_	Alignment		29.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
18	d1g2ha_	Alignment		25.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	c2jwaA_	Alignment		14.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
20	c3rkoF_	Alignment		12.0	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
21	c2cw1A_	Alignment	not modelled	9.6	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
22	c3mk7F_	Alignment	not modelled	8.6	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
23	d2diia1	Alignment	not modelled	8.5	11	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
24	c1pyuD_	Alignment	not modelled	8.4	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
25	d1cf7a_	Alignment	not modelled	8.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
26	c3s1bA_	Alignment	not modelled	8.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mini-z; **PDBTitle:** the development of peptide-based tools for the analysis of2 angiogenesis
27	c1loiA_	Alignment	not modelled	8.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclic 3',5'-amp specific phosphodiesterase rd1; **PDBTitle:** n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
28	c2diiA_	Alignment	not modelled	8.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih

						basal2 transcription factor complex p62 subunit
29	d1v54g_	Alignment	not modelled	7.8	9	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
30	c2d7dB_	Alignment	not modelled	7.7	13	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**40-mer from uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
31	d1pf4a2	Alignment	not modelled	7.5	14	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
32	d1st6a6	Alignment	not modelled	7.4	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
33	c1twcF_	Alignment	not modelled	7.3	29	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 23 **PDBTitle:** rna polymerase ii complexed with gtp
34	d1twff_	Alignment	not modelled	7.3	29	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
35	d1v54c_	Alignment	not modelled	7.3	11	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
36	c2pmzW_	Alignment	not modelled	7.1	14	**PDB header:**translation, transferase **Chain:** W: **PDB Molecule:**dna-directed rna polymerase subunit k; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
37	c2kncA_	Alignment	not modelled	6.7	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
38	d2ns0a1	Alignment	not modelled	6.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
39	c1vc3B_	Alignment	not modelled	6.5	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
40	d1qkla_	Alignment	not modelled	6.5	29	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
41	d2axtj1	Alignment	not modelled	6.2	30	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
42	d1d5ya2	Alignment	not modelled	6.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
43	c2l0kA_	Alignment	not modelled	6.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
44	d2oy9a1	Alignment	not modelled	6.1	9	**Fold:**BH2638-like **Superfamily:**BH2638-like **Family:**BH2638-like
45	c3plxB_	Alignment	not modelled	6.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
46	c3h0gF_	Alignment	not modelled	6.0	29	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
47	d1v54m_	Alignment	not modelled	6.0	24	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
48	c3lk3T_	Alignment	not modelled	5.9	30	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** crystal structure of capz bound to the cpi and csi uncapping2 motifs from carmil
49	c2l2tA_	Alignment	not modelled	5.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
50	d1sjpa1	Alignment	not modelled	5.7	13	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**GroEL chaperone, ATPase domain
51	c2oviA_	Alignment	not modelled	5.6	4	**PDB header:**ligand binding protein, metal transport **Chain:** A: **PDB Molecule:**hypothetical protein chux; **PDBTitle:** structure of the heme binding protein chux
52	d2auwa1	Alignment	not modelled	5.6	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
53	d1h6gb1	Alignment	not modelled	5.5	4	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
54	c2jz1A_	Alignment	not modelled	5.5	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein doublesex; **PDBTitle:** dsx_long
						Fold: Double psi beta-barrel

55	d1ppya_	Alignment	not modelled	5.5	15	**Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
56	c2vn2B_	Alignment	not modelled	5.4	8	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
57	d1q3qa1	Alignment	not modelled	5.4	15	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**Group II chaperonin (CCT, TRIC), ATPase domain
58	c1pt1B_	Alignment	not modelled	5.4	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
59	c2lhuA_	Alignment	not modelled	5.4	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
60	c2ks1B_	Alignment	not modelled	5.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
61	d3fapb_	Alignment	not modelled	5.3	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) **Family:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
62	c2kvlA_	Alignment	not modelled	5.2	9	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
63	c3qkbB_	Alignment	not modelled	5.2	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
64	c2l37A_	Alignment	not modelled	5.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribosome-inactivating protein luffin p1; **PDBTitle:** 3d solution structure of arginine/glutamate-rich polypeptide luffin p12 from the seeds of sponge gourd (luffa cylindrical)
65	c1ql1A_	Alignment	not modelled	5.1	12	**PDB header:**virus **Chain:** A: **PDB Molecule:**pf1 bacteriophage coat protein b; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
66	c1uheA_	Alignment	not modelled	5.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
67	c2rddB_	Alignment	not modelled	5.0	17	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
68	c2fomA_	Alignment	not modelled	5.0	17	**PDB header:**viral protein/protease **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** dengue virus ns2b/ns3 protease
69	d1ku7a_	Alignment	not modelled	5.0	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
70	c2e19A_	Alignment	not modelled	5.0	9	**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