Phyre2

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Description	P33361
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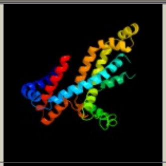
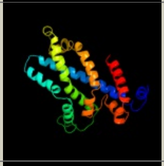
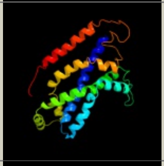
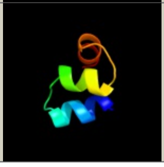
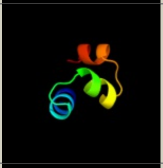
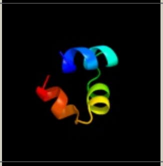
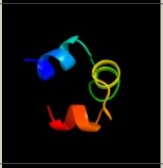
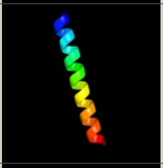
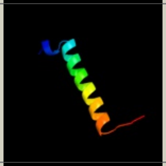
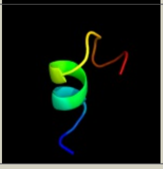
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3d31c1	Alignment		99.9	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	c3d31D_	Alignment		99.9	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
3	c2onkC_	Alignment		99.9	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
4	d2onkc1	Alignment		99.9	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	d3dhwa1	Alignment		99.8	25	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c2r6gF_	Alignment		99.8	15	**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
7	d2r6gf2	Alignment		99.8	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	c3fh6F_	Alignment		99.8	15	**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
9	d2r6gg1	Alignment		99.6	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d1ntca_	Alignment		42.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
11	d1umqa_	Alignment		35.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

12	c1umqA_	Alignment		35.4	19	**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
13	c3e7lD_	Alignment		24.1	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
14	d1fipa_	Alignment		23.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
15	d1etob_	Alignment		23.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	d1etxa_	Alignment		19.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	d1g2ha_	Alignment		15.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	c2jwaA_	Alignment		15.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
19	d1jb0j_	Alignment		12.6	27	**Fold:**Single transmembrane helix **Superfamily:**Subunit IX of photosystem I reaction centre, PsaJ **Family:**Subunit IX of photosystem I reaction centre, PsaJ
20	c2cw1A_	Alignment		11.4	28	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
21	c2k21A_	Alignment	not modelled	11.2	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
22	d2auwa1	Alignment	not modelled	10.7	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
23	c1ciiA_	Alignment	not modelled	10.2	25	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
24	d2ns0a1	Alignment	not modelled	9.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
25	c3hzqA_	Alignment	not modelled	9.1	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
26	d1i3ja_	Alignment	not modelled	9.0	19	**Fold:**DNA-binding domain of intron-encoded endonucleases **Superfamily:**DNA-binding domain of intron-encoded endonucleases **Family:**DNA-binding domain of intron-encoded endonucleases
27	d1t1ra3	Alignment	not modelled	8.8	50	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	d1rutx4	Alignment	not modelled	8.8	63	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

29	c2ka2B_	Alignment	not modelled	8.8	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
30	c2ka2A_	Alignment	not modelled	8.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
31	c2ka1B_	Alignment	not modelled	8.8	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
32	c2ka1A_	Alignment	not modelled	8.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
33	c2auwB_	Alignment	not modelled	8.4	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
34	d2phcb1	Alignment	not modelled	8.3	16	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
35	c3mmlD_	Alignment	not modelled	8.0	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
36	d1cf7a_	Alignment	not modelled	7.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
37	c2kr6A_	Alignment	not modelled	7.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit
38	c2d7dB_	Alignment	not modelled	7.8	23	**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
39	d1kqfb2	Alignment	not modelled	7.8	22	**Fold:**Single transmembrane helix **Superfamily:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor **Family:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
40	c1vf5E_	Alignment	not modelled	7.7	21	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
41	c2e75E_	Alignment	not modelled	7.7	21	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
42	c1vf5R_	Alignment	not modelled	7.7	21	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
43	c2e74E_	Alignment	not modelled	7.7	21	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
44	d2e74e1	Alignment	not modelled	7.7	21	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
45	c2e76E_	Alignment	not modelled	7.7	21	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
46	c2voyB_	Alignment	not modelled	7.5	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
47	c2zp2B_	Alignment	not modelled	7.2	15	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
48	d2nwua1	Alignment	not modelled	7.1	29	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
49	c2hx6A_	Alignment	not modelled	7.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
50	d1a9xa1	Alignment	not modelled	7.0	21	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
51	c2kwvA_	Alignment	not modelled	7.0	21	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
52	d2pzza1	Alignment	not modelled	6.8	43	**Fold:**RL5-like **Superfamily:**RL5-like

						Family:SSO1042-like
53	c3c9gB_	Alignment	not modelled	6.8	14	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**upf0200/upf0201 protein af_1395; **PDBTitle:** crystal structure of uncharacterized upf0201 protein af_135
54	c2j5dA_	Alignment	not modelled	6.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
55	c2k1lA_	Alignment	not modelled	6.6	35	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
56	c2k1lB_	Alignment	not modelled	6.6	35	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
57	c2k1kB_	Alignment	not modelled	6.6	35	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
58	c2k1kA_	Alignment	not modelled	6.6	35	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
59	c1pyuD_	Alignment	not modelled	6.6	40	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
60	d1st6a6	Alignment	not modelled	6.5	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
61	c3d7aB_	Alignment	not modelled	6.3	8	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0201 protein ph1010; **PDBTitle:** crystal structure of duf54 family protein ph1010 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
62	d3cx5c1	Alignment	not modelled	6.3	7	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
63	c1twcF_	Alignment	not modelled	6.2	36	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 23 **PDBTitle:** rna polymerase ii complexed with gtp
64	d1ppjc1	Alignment	not modelled	6.2	12	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
65	d1twff_	Alignment	not modelled	6.2	36	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
66	c2vn2B_	Alignment	not modelled	6.1	14	**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
67	c2phcB_	Alignment	not modelled	6.1	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
68	c2pmzW_	Alignment	not modelled	6.1	29	**PDB header:**translation, transferase **Chain:** W: **PDB Molecule:**dna-directed rna polymerase subunit k; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
69	c2rnoA_	Alignment	not modelled	6.1	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** solution structure of the n-terminal sap domain of sumo e3 ligases2 from oryza sativa
70	d1rh5b_	Alignment	not modelled	6.0	14	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
71	c3mkuA_	Alignment	not modelled	6.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
72	c2nq2A_	Alignment	not modelled	5.9	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**hypothetical abc transporter permease protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
73	d1i1ga1	Alignment	not modelled	5.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
74	d2cyya1	Alignment	not modelled	5.6	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
75	d1quba5	Alignment	not modelled	5.6	14	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
76	d1c1za5	Alignment	not modelled	5.6	15	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain

77	d2hwna1	Alignment	not modelled	5.6	32	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
78	c3skqA_	Alignment	not modelled	5.5	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**mitochondrial distribution and morphology protein 38; **PDBTitle:** mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
79	d1bccc2	Alignment	not modelled	5.4	11	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
80	d1qkla_	Alignment	not modelled	5.4	36	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
81	c1vc3B_	Alignment	not modelled	5.4	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
82	c3s1bA_	Alignment	not modelled	5.4	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mini-z; **PDBTitle:** the development of peptide-based tools for the analysis of2 angiogenesis
83	c3gucB_	Alignment	not modelled	5.3	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
84	c3iwcD_	Alignment	not modelled	5.2	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with s-adenosylmethionine2 methyl ester
85	d1jhfa1	Alignment	not modelled	5.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
86	d1pgja1	Alignment	not modelled	5.1	7	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
87	d1nvma1	Alignment	not modelled	5.1	6	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
88	d2pgda1	Alignment	not modelled	5.1	9	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
89	c2ijlB_	Alignment	not modelled	5.0	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**molybdenum-binding transcriptional repressor; **PDBTitle:** the structure of a putative mode from agrobacterium tumefaciens.
90	d1ui5a2	Alignment	not modelled	5.0	16	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
91	c3h0gF_	Alignment	not modelled	5.0	36	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
92	d1oxwa_	Alignment	not modelled	5.0	29	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Patatin