Phyre^2

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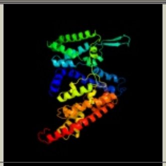
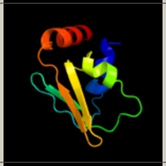
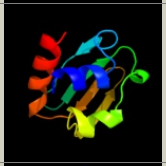
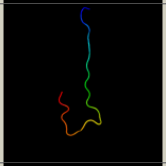
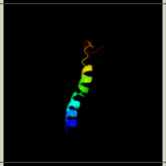
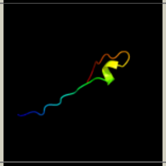
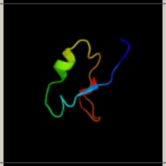
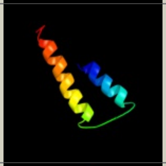
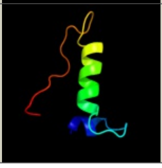
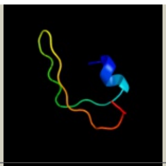
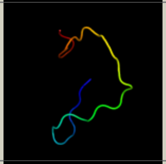
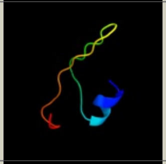
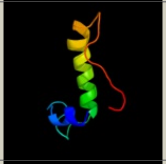
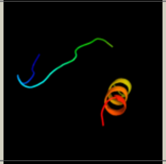
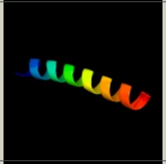
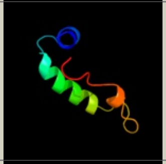
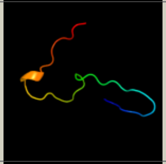
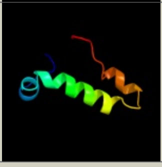
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	 Alignment		100.0	14	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	c3ipjB_	 Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, iiabc component; **PDBTitle:** the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
3	c1ibaA_	 Alignment		99.9	32	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
4	d3bp8c1	 Alignment		99.9	32	**Fold:**Homing endonuclease-like **Superfamily:**Glucose permease domain IIB **Family:**Glucose permease domain IIB
5	c3sy6A_	 Alignment		46.3	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbrial protein bf1861; **PDBTitle:** crystal structure of a fimbrial protein bf1861 [bacteroides fragilis2 nctc 9343] (bf1861) from bacteroides fragilis nctc 9343 at 1.90 a3 resolution
6	c2kncA_	 Alignment		42.4	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
7	c3t2lA_	 Alignment		39.0	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative cell adhesion protein; **PDBTitle:** crystal structure of a putative cell adhesion protein (bf1858) from2 bacteroides fragilis nctc 9343 at 2.33 a resolution
8	c2janD_	 Alignment		34.8	29	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
9	d1i1ga2	 Alignment		19.7	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
10	c2bbjB_	 Alignment		15.7	20	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
11	c2hqnA_	 Alignment		15.4	12	**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

12	d1ffgb_	Alignment		14.7	13	**Fold:**Ferredoxin-like **Superfamily:**CheY-binding domain of CheA **Family:**CheY-binding domain of CheA
13	c2wshC_	Alignment		14.5	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
14	c1a0oH_	Alignment		14.1	13	**PDB header:**chemotaxis **Chain:** H: **PDB Molecule:**chea; **PDBTitle:** chey-binding domain of chea in complex with chey
15	c2pmuD_	Alignment		13.6	21	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
16	d1vgga_	Alignment		13.5	26	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
17	c2xv4S_	Alignment		13.3	19	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc3; **PDBTitle:** structure of human rpc62 (partial)
18	d1gxqa_	Alignment		12.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
19	d1ciya1	Alignment		12.7	19	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
20	d1kgsa1	Alignment		12.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
21	c2oarA_	Alignment	not modelled	11.7	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
22	c1vbkA_	Alignment	not modelled	10.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
23	d2bgwa1	Alignment	not modelled	10.3	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
24	d1ji6a1	Alignment	not modelled	10.3	23	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
25	d1wlqc_	Alignment	not modelled	9.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA replication factor Cdt1
26	c3ufiA_	Alignment	not modelled	9.1	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**hypothetical protein bacova_04980; **PDBTitle:** crystal structure of a hypothetical protein2 bacova_04980(zp_02067969.1) from bacteroides ovatus atcc 8483 at 2.183 a resolution
27	c1p68A_	Alignment	not modelled	9.1	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein s-824; **PDBTitle:** solution structure of s-824, a de novo designed four helix2 bundle
28	c2ekmC_	Alignment	not modelled	8.0	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of st1219 protein from sulfolobus tokodaii

29	c2voyB_	Alignment	not modelled	8.0	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
30	d2oara1	Alignment	not modelled	7.9	10	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
31	c1m6yA_	Alignment	not modelled	7.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
32	d2cfua2	Alignment	not modelled	7.7	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
33	c2ht2B_	Alignment	not modelled	7.6	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
34	d1ngka_	Alignment	not modelled	7.3	26	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
35	c2gl0A_	Alignment	not modelled	7.3	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of pae2307 in complex with adenosine
36	c3ksiA_	Alignment	not modelled	7.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
37	c2d16B_	Alignment	not modelled	7.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph1918; **PDBTitle:** crystal structure of ph1918 protein from pyrococcus horikoshii ot3
38	c2djwF_	Alignment	not modelled	7.0	13	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
39	c2cfuA_	Alignment	not modelled	6.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
40	c2jzyA_	Alignment	not modelled	6.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
41	c1oy8A_	Alignment	not modelled	6.2	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
42	c2ketA_	Alignment	not modelled	6.2	29	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**cathelicidin-6; **PDBTitle:** solution structure of bmap-27
43	c1lkzB_	Alignment	not modelled	6.1	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
44	c1dlcA_	Alignment	not modelled	6.0	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
45	d1fzda_	Alignment	not modelled	6.0	30	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
46	c2kscA_	Alignment	not modelled	6.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
47	c3ibwA_	Alignment	not modelled	5.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
48	c3aq8A_	Alignment	not modelled	5.8	22	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
49	d2cfxa2	Alignment	not modelled	5.7	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
50	c3k8hA_	Alignment	not modelled	5.5	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**30klp; **PDBTitle:** structure of crystal form i of tp0453
51	d2cg4a2	Alignment	not modelled	5.5	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
52	d1vbka2	Alignment	not modelled	5.5	12	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
53	d1p2fa1	Alignment	not modelled	5.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
						Fold: Globin-like

54	d1s69a_	Alignment	not modelled	5.3	19	**Superfamily:**Globin-like **Family:**Truncated hemoglobin
55	c2j61B_	Alignment	not modelled	5.3	39	**PDB header:**lectin **Chain:** B: **PDB Molecule:**ficolin-2; **PDBTitle:** l-ficolin complexed to n-acetylglucosamine (forme c)
56	d1m1jc1	Alignment	not modelled	5.1	30	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
57	d1x0pa1	Alignment	not modelled	5.1	21	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
58	d1lwub1	Alignment	not modelled	5.1	22	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like