Phyre^2

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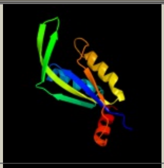
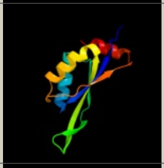
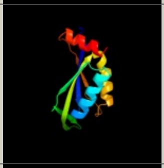
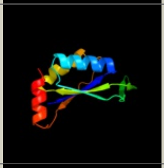
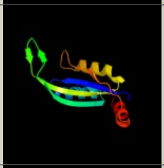
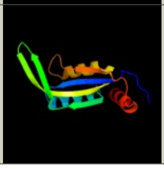
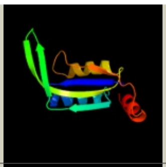
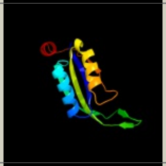
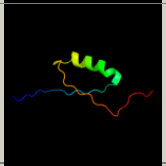
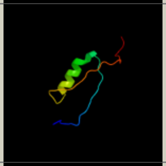
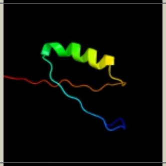
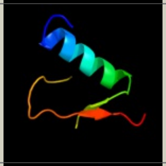
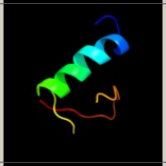
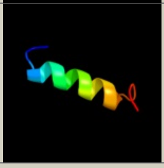
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1naqa_	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
2	c2zomC_	Alignment		100.0	41	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**protein cuta, chloroplast, putative, expressed; **PDBTitle:** crystal structure of cuta1 from oryza sativa
3	c2zfhA_	Alignment		100.0	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cuta; **PDBTitle:** crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
4	c1xk8A_	Alignment		100.0	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**divalent cation tolerant protein cuta; **PDBTitle:** divalent cation tolerant protein cuta from homo sapiens2 o60888
5	d2zfha1	Alignment		100.0	37	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
6	c3ahpA_	Alignment		100.0	28	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cuta1; **PDBTitle:** crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
7	c2nuhA_	Alignment		100.0	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**periplasmic divalent cation tolerance protein; **PDBTitle:** crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
8	d1ukua_	Alignment		100.0	37	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
9	d1p1la_	Alignment		100.0	32	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
10	d1kr4a_	Alignment		100.0	34	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
11	d1osce_	Alignment		100.0	37	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)

12	d1nzaa_	Alignment		100.0	39	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
13	d1vhfa_	Alignment		100.0	35	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
14	c2gx8B_	Alignment		90.7	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
15	d2gx8a1	Alignment		90.2	22	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
16	c2nydB_	Alignment		72.8	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
17	d1v3fa_	Alignment		71.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
18	d2csoa1	Alignment		62.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
19	d1w4ma_	Alignment		36.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
20	d1fsha_	Alignment		35.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
21	d1uhwa_	Alignment	not modelled	35.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
22	d1b4ba_	Alignment	not modelled	28.7	16	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
23	c2pbiA_	Alignment	not modelled	28.6	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 9; **PDBTitle:** the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
24	c3cagF_	Alignment	not modelled	25.0	12	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
25	d1gr0a1	Alignment	not modelled	22.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
26	d1nkta4	Alignment	not modelled	22.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
27	d1o7fa1	Alignment	not modelled	22.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
28	c2ysrA_	Alignment	not modelled	21.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dep domain-containing protein 1; **PDBTitle:** solution structure of the dep domain from human dep domain-2 containing protein 1

29	c3tl6B_	Alignment	not modelled	18.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
30	c1b4aA_	Alignment	not modelled	17.7	16	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
31	d1iznb_	Alignment	not modelled	17.6	27	**Fold:**Subunits of heterodimeric actin filament capping protein Capz **Superfamily:**Subunits of heterodimeric actin filament capping protein Capz **Family:**Capz beta-1 subunit
32	c3lk2B_	Alignment	not modelled	17.5	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**f-actin-capping protein subunit beta isoforms 1 and 2; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
33	c3ml6D_	Alignment	not modelled	17.2	25	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**chimeric complex between protein dishevlled2 homolog dvl-2 **PDBTitle:** a complex between dishevlled2 and clathrin adaptor ap-2
34	c3ereD_	Alignment	not modelled	17.1	12	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
35	c1vytF_	Alignment	not modelled	13.8	33	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid
36	c1t0jC_	Alignment	not modelled	13.7	33	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
37	d1u9ya1	Alignment	not modelled	12.8	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
38	c3qmlC_	Alignment	not modelled	12.1	21	**PDB header:**chaperone/protein transport **Chain:** C: **PDB Molecule:**nucleotide exchange factor sil1; **PDBTitle:** the structural analysis of sil1-bip complex reveals the mechanism for2 sil1 to function as a novel nucleotide exchange factor
39	c2v3sB_	Alignment	not modelled	12.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase osr1; **PDBTitle:** structural insights into the recognition of substrates and2 activators by the osr1 kinase
40	c2l23A_	Alignment	not modelled	11.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25; **PDBTitle:** nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
41	d1i1ga2	Alignment	not modelled	11.6	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
42	d2ixma1	Alignment	not modelled	10.9	18	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
43	c2e1aD_	Alignment	not modelled	10.6	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
44	d2cfxa2	Alignment	not modelled	10.4	8	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
45	d1vyua1	Alignment	not modelled	10.4	18	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
46	d1wjwa_	Alignment	not modelled	10.1	29	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
47	c2zbcH_	Alignment	not modelled	9.7	24	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
48	d1dkua1	Alignment	not modelled	9.7	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
49	c1vytE_	Alignment	not modelled	9.3	33	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid
50	c3n5bB_	Alignment	not modelled	9.1	25	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**asr0485 protein; **PDBTitle:** the complex of pii and pipx from anabaena
51	c2g62A_	Alignment	not modelled	9.0	18	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**protein phosphatase 2a, regulatory subunit b' (pr 53); **PDBTitle:** crystal structure of human ptpa
52	c2xg8D_	Alignment	not modelled	8.9	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**pipx; **PDBTitle:** structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942

53	c1ca0C_	Alignment	not modelled	8.0	25	**PDB header:**complex (serine protease/inhibitor) **Chain:** C: **PDB Molecule:**bovine chymotrypsin; **PDBTitle:** bovine chymotrypsin complexed to appi
54	c2fugC_	Alignment	not modelled	7.7	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
55	d1tf5a4	Alignment	not modelled	7.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
56	c2djwF_	Alignment	not modelled	7.6	18	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
57	d1orfa_	Alignment	not modelled	7.6	13	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
58	c2cy8A_	Alignment	not modelled	7.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-phenylglycine aminotransferase; **PDBTitle:** crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
59	d1xhna1	Alignment	not modelled	7.2	24	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
60	d2p5ma1	Alignment	not modelled	7.1	14	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
61	c3jx9B_	Alignment	not modelled	7.0	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
62	d1fuja_	Alignment	not modelled	6.9	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
63	d1pfxc_	Alignment	not modelled	6.7	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
64	d1j6wa_	Alignment	not modelled	6.5	24	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
65	c3h4wA_	Alignment	not modelled	6.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatidylinositol-specific phospholipase c1; **PDBTitle:** structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus
66	d1eufa_	Alignment	not modelled	6.2	40	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
67	d2ac7a1	Alignment	not modelled	6.1	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
68	d1m9ua_	Alignment	not modelled	6.1	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
69	d1vjea_	Alignment	not modelled	6.0	41	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
70	c2r0lA_	Alignment	not modelled	6.0	33	**PDB header:**hydrolase, immune system **Chain:** A: **PDB Molecule:**hepatocyte growth factor activator; **PDBTitle:** short form hgfa with inhibitory fab75
71	d1fmca_	Alignment	not modelled	6.0	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	c1md7A_	Alignment	not modelled	5.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**c1r complement serine protease; **PDBTitle:** monomeric structure of the zymogen of complement protease2 c1r
73	c1x60A_	Alignment	not modelled	5.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
74	d1os8a_	Alignment	not modelled	5.8	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
75	d1xx9a_	Alignment	not modelled	5.8	20	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
76	c1aksB_	Alignment	not modelled	5.6	20	**PDB header:**serine protease **Chain:** B: **PDB Molecule:**alpha trypsin; **PDBTitle:** crystal structure of the first active autolysate form of2 the porcine alpha trypsin
77	d1xe0a_	Alignment	not modelled	5.5	32	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Nucleoplasmin-like core domain **Family:**Nucleoplasmin-like core domain
78	d1qd1a2	Alignment	not modelled	5.4	8	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.

						Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
79	d1rfna_	Alignment	not modelled	5.3	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Eukaryotic proteases
80	d2cyya2	Alignment	not modelled	5.2	22	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain