Phyre^2

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Description	P58006
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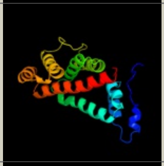
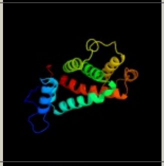
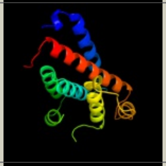
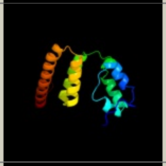
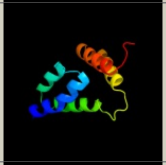
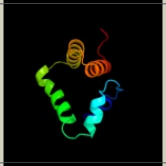
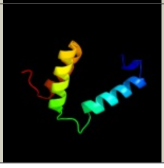
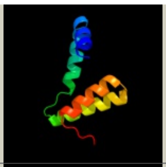
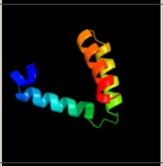
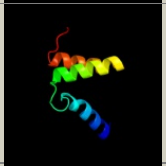
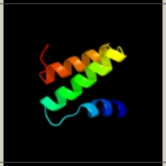
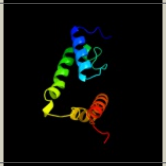
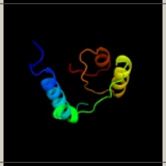
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pfxa1	Alignment		99.9	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
2	c3c1lB_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative antioxidant defense protein mlr4105; **PDBTitle:** crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
3	d2oyoa1	Alignment		99.8	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
4	d2prra1	Alignment		99.8	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
5	c3lvyB_	Alignment		99.8	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
6	d2o4da1	Alignment		99.2	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
7	d2ouwa1	Alignment		99.0	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
8	d2gmya1	Alignment		98.9	18	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
9	c2qeuA_	Alignment		97.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
10	d2cwqa1	Alignment		97.6	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
11	c3beyC_	Alignment		97.0	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217

12	c1p8cD_	Alignment		97.0	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
13	c3d7iB_	Alignment		96.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family protein; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
14	d1vkea_	Alignment		96.1	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
15	d1vkeb_	Alignment		95.7	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
16	d2q0ta1	Alignment		94.3	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
17	c4g9qA_	Alignment		81.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of a 4-carboxymuconolactone decarboxylase
18	c2r8rB_	Alignment		58.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
19	d2af7a1	Alignment		56.9	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
20	d1knca_	Alignment		44.9	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
21	c1ckxA_	Alignment	not modelled	37.4	40	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cystic fibrosis transmembrane conductance **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
22	c2dgxA_	Alignment	not modelled	27.2	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rna recognition motif in kiaa04302 protein
23	c3ntsB_	Alignment	not modelled	20.3	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**vsdc; **PDBTitle:** catalytic domain of vsdc from aeromonas hydrophila
24	c1ckwA_	Alignment	not modelled	18.0	31	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (cystic fibrosis transmembrane **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
25	c2ly8A_	Alignment	not modelled	16.2	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**budding yeast chaperone scm3; **PDBTitle:** the budding yeast chaperone scm3 recognizes the partially unfolded2 dimer of the centromere-specific cse4/h4 histone variant
26	c3c18B_	Alignment	not modelled	16.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
27	c2d9gA_	Alignment	not modelled	15.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yy1-associated factor 2; **PDBTitle:** solution structure of the zf-ranbp domain of yy1-associated2 factor 2

28	d1id3b_	Alignment	not modelled	14.3	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
29	d1kx5b_	Alignment	not modelled	14.2	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
30	d2k3ka1	Alignment	not modelled	13.7	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
31	c2l5aA_	Alignment	not modelled	12.7	18	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
32	c3pgwP_	Alignment	not modelled	12.6	15	**PDB header:**splicing/dna/rna **Chain:** P: **PDB Molecule:**u1-a; **PDBTitle:** crystal structure of human u1 snrnp
33	c2a3jA_	Alignment	not modelled	11.9	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u1 small nuclear ribonucleoprotein a; **PDBTitle:** structure of urndesign, a complete computational redesign2 of human u1a protein
34	c3btpA_	Alignment	not modelled	11.9	35	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
35	d1hw8c2	Alignment	not modelled	10.8	24	**Fold:**Substrate-binding domain of HMG-CoA reductase **Superfamily:**Substrate-binding domain of HMG-CoA reductase **Family:**Substrate-binding domain of HMG-CoA reductase
36	c2pehA_	Alignment	not modelled	10.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**splicing factor 45; **PDBTitle:** crystal structure of the uhm domain of human spf45 in complex with2 sf3b155-ulm5
37	d1zpya1	Alignment	not modelled	10.3	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**half-ferritin
38	d1rg6a_	Alignment	not modelled	9.7	22	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
39	d1zk8a2	Alignment	not modelled	9.0	12	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
40	c3bjxB_	Alignment	not modelled	8.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**halocarboxylic acid dehalogenase dehi; **PDBTitle:** structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
41	d1auda_	Alignment	not modelled	8.8	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
42	c1ponB_	Alignment	not modelled	8.5	38	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr
43	d1rz4a1	Alignment	not modelled	8.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
44	c1zzaA_	Alignment	not modelled	8.1	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
45	d1hrti_	Alignment	not modelled	8.0	35	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
46	c3thfA_	Alignment	not modelled	7.7	27	**PDB header:**actin-binding protein/protein binding **Chain:** A: **PDB Molecule:**protein shroom; **PDBTitle:** crystal structure of the sd2 domain from drosophila shroom
47	d2huec1	Alignment	not modelled	7.4	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
48	c3kx6C_	Alignment	not modelled	7.3	35	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
49	d4htci_	Alignment	not modelled	7.1	35	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
50	c3k1tA_	Alignment	not modelled	7.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
51	d1wj7a1	Alignment	not modelled	6.9	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
52	d1nu4a_	Alignment	not modelled	6.5	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
53	c3odnA_	Alignment	not modelled	6.5	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dally-like protein; **PDBTitle:** the crystal structure of drosophila dally-like protein core domain
						PDB header:virus

54	c1bev4_	Alignment	not modelled	6.4	29	**Chain:** 4: **PDB Molecule:**bovine enterovirus coat proteins vp1 to vp4; **PDBTitle:** bovine enterovirus vg-5-27
55	c2eapA_	Alignment	not modelled	6.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lymphocyte cytosolic protein 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
56	c2qb0D_	Alignment	not modelled	6.4	23	**PDB header:**hydrolase regulator **Chain:** D: **PDB Molecule:**telsam domain - lysozyme chimera; **PDBTitle:** structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
57	d1jmxa2	Alignment	not modelled	6.2	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
58	c3ol4B_	Alignment	not modelled	6.2	46	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
59	d1jmsa4	Alignment	not modelled	6.2	27	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
60	c1rue4_	Alignment	not modelled	6.0	40	**PDB header:**virus **Chain:** 4: **PDB Molecule:**rhinovirus 14; **PDBTitle:** rhinovirus 14 site directed mutant n1219a complexed with2 antiviral compound win 52035
61	c3ajfA_	Alignment	not modelled	5.8	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
62	d1iooa_	Alignment	not modelled	5.7	17	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
63	d1sxja1	Alignment	not modelled	5.7	31	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
64	d1ussa_	Alignment	not modelled	5.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
65	d2vana2	Alignment	not modelled	5.4	9	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
66	c2krcA_	Alignment	not modelled	5.2	25	**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
67	c3i3nA_	Alignment	not modelled	5.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**kelch-like protein 11; **PDBTitle:** crystal structure of the btb-back domains of human klhl11
68	c1hwjB_	Alignment	not modelled	5.1	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hmg-coa reductase; **PDBTitle:** complex of the catalytic portion of human hmg-coa reductase2 with cerivastatin