Phyre^2

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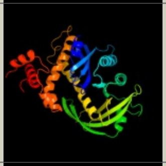
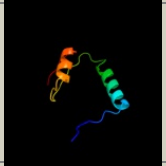
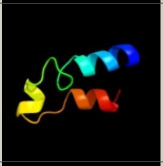
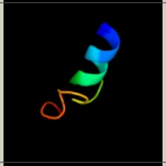
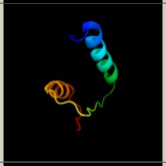
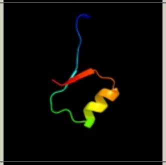
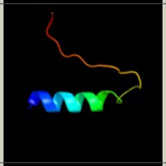
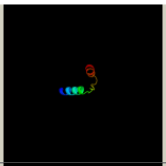
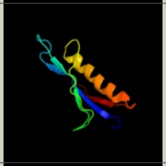
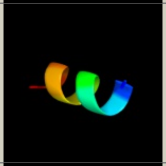
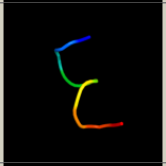
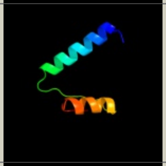
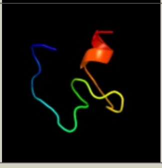
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		100.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		100.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d1ovma1	Alignment		25.6	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
4	d1y76b1	Alignment		20.4	34	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
5	d2bgwa2	Alignment		20.2	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
6	d1j1la_	Alignment		16.1	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
7	d1zpda1	Alignment		13.1	8	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
8	d2csfa1	Alignment		12.4	38	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
9	c2ziuA_	Alignment		11.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
10	c1skoA_	Alignment		11.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase 1 **PDBTitle:** mp1-p14 complex
11	d1ttya_	Alignment		11.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain

12	c2uvpB_	Alignment		9.8	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hoba; **PDBTitle:** crystal structure of hoba (hp1230)from helicobacter pylori
13	c2qkkI_	Alignment		9.8	8	**PDB header:**hydrolase/dna/rna **Chain:** I: **PDB Molecule:**ribonuclease h1; **PDBTitle:** human rnase h catalytic domain mutant d210n in complex with2 14-mer rna/dna hybrid
14	d2aq0a1	Alignment		9.0	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
15	d1tc3c_	Alignment		8.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
16	d2gpia1	Alignment		8.5	45	**Fold:**Shew3726-like **Superfamily:**Shew3726-like **Family:**Shew3726-like
17	c1smzA_	Alignment		8.2	56	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transportan in bicellar solution with **PDBTitle:** structure of transportan in phospholipid bicellar solution
18	d1pvda1	Alignment		8.1	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
19	c2zyzA_	Alignment		8.1	58	**PDB header:**splicing **Chain:** A: **PDB Molecule:**putative uncharacterized protein pae0789; **PDBTitle:** pyrobaculum aerophilum splicing endonuclease
20	d2qklb1	Alignment		7.6	36	**Fold:**Dcp2 domain-like **Superfamily:**Dcp2 domain-like **Family:**Dcp2 box A domain
21	c2ixsB_	Alignment	not modelled	7.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sdai restriction endonuclease; **PDBTitle:** structure of sdai restriction endonuclease
22	d1yioa1	Alignment	not modelled	7.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
23	c2rpiA_	Alignment	not modelled	7.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
24	d1st6a5	Alignment	not modelled	6.8	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
25	c3e5bB_	Alignment	not modelled	6.7	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
26	d3cpta1	Alignment	not modelled	6.7	20	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
27	d1qwia_	Alignment	not modelled	6.5	13	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
28	d1vf6c_	Alignment	not modelled	6.2	31	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
29	c1vf6C	Alignment	not modelled	6.2	31	**PDB header:**protein binding/protein transport **Chain:** C: **PDB Molecule:**maguk p55 subfamily member 5;

29	c1vf6C_	Alignment	not modelled	6.2	31	**PDBTitle:** 2.1 angstrom crystal structure of the pals-1-l27n and patj2 l27 heterodimer complex
30	d2hs5a2	Alignment	not modelled	6.1	18	**Fold:**GntR ligand-binding domain-like **Superfamily:**GntR ligand-binding domain-like **Family:**GntR ligand-binding domain-like
31	c2ejsA_	Alignment	not modelled	5.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**autocrine motility factor receptor, isoform 2; **PDBTitle:** solution structure of ruh-076, a human cue domain
32	c2hnhA_	Alignment	not modelled	5.8	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
33	d1st6a3	Alignment	not modelled	5.7	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
34	d1y7la1	Alignment	not modelled	5.6	10	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
35	c1kyqC_	Alignment	not modelled	5.6	19	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
36	c3qp5C_	Alignment	not modelled	5.6	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
37	c2zixA_	Alignment	not modelled	5.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** crystal structure of the mus81-eme1 complex
38	d1y1pa1	Alignment	not modelled	5.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	d1weya_	Alignment	not modelled	5.5	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
40	d1xsva_	Alignment	not modelled	5.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
41	d1ftha_	Alignment	not modelled	5.4	12	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
42	d1e3oc2	Alignment	not modelled	5.3	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
43	d2fefa1	Alignment	not modelled	5.2	21	**Fold:**Bromodomain-like **Superfamily:**PA2201 N-terminal domain-like **Family:**PA2201 N-terminal domain-like
44	c3sztB_	Alignment	not modelled	5.1	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone