Phyre2

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Description	P76119
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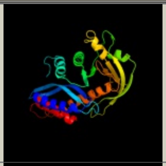
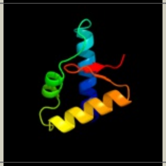
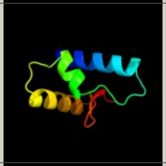
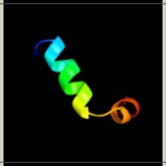
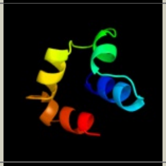
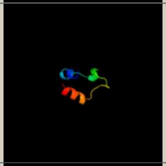
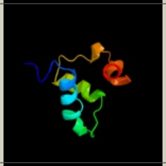
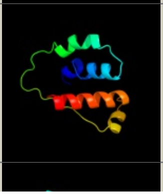
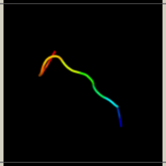
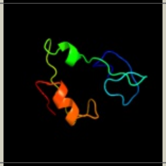
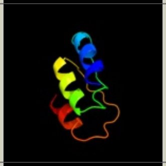
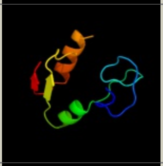
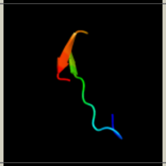
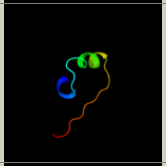
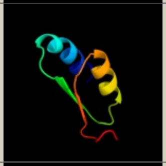
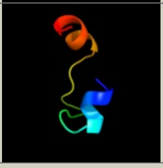
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b7ea_	Alignment		98.1	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1musa_	Alignment		98.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d2v9va2	Alignment		79.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
4	c2v9vA_	Alignment		66.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
5	d2ezha_	Alignment		52.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
6	d2ezia_	Alignment		49.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
7	c3hefB_	Alignment		39.9	17	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
8	c6paxA_	Alignment		36.1	27	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
9	c2kzvA_	Alignment		29.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
10	c2vp8A_	Alignment		24.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
11	d1osna_	Alignment		20.4	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases

12	c2plyB_	Alignment		19.1	16	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
13	c3nswA_	Alignment		17.5	70	**PDB header:**immune system **Chain:** A: **PDB Molecule:**excretory-secretory protein 2; **PDBTitle:** crystal structure of ancylostoma ceylanicum excretory-secretory2 protein 2
14	c3a52A_	Alignment		17.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
15	d1ajza_	Alignment		16.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
16	c3e2dB_	Alignment		15.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
17	c3mx7A_	Alignment		15.3	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
18	d3orca_	Alignment		14.4	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
19	c2y5sA_	Alignment		14.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
20	d1pdnc_	Alignment		13.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
21	d1iyxa1	Alignment	not modelled	13.3	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
22	c3r1iB_	Alignment	not modelled	13.1	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
23	c1hj0A_	Alignment	not modelled	12.2	25	**PDB header:**actin binding peptide **Chain:** A: **PDB Molecule:**thymosin beta9; **PDBTitle:** thymosin beta9
24	d1eyea_	Alignment	not modelled	11.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
25	d1dlwa_	Alignment	not modelled	10.5	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
26	c2iucB_	Alignment	not modelled	10.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	d1uuza_	Alignment	not modelled	9.7	15	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
28	d1d1la_	Alignment	not modelled	9.6	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
29	d2hxja1	Alignment	not modelled	9.5	14	**Fold:**FinO-like **Superfamily:**FinO-like

						Family: FinO-like
30	d2gm3a1	Alignment	not modelled	9.5	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
31	c3rf7A_	Alignment	not modelled	9.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
32	c3emkA_	Alignment	not modelled	9.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
33	d2a22a1	Alignment	not modelled	9.1	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
34	d2fgga1	Alignment	not modelled	9.0	31	**Fold:**dsRBD-like **Superfamily:**Rv2632c-like **Family:**Rv2632c-like
35	c2kvcA_	Alignment	not modelled	8.8	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
36	d1mpga1	Alignment	not modelled	8.8	8	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
37	c3douA_	Alignment	not modelled	8.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase j; **PDBTitle:** crystal structure of methyltransferase involved in cell2 division from thermoplasma volcanicum gss1
38	c2pijB_	Alignment	not modelled	8.6	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
39	d4croa_	Alignment	not modelled	8.3	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
40	c3pk0B_	Alignment	not modelled	8.3	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
41	d1e8qa_	Alignment	not modelled	8.2	13	**Fold:**Cellulose docking domain, dockering **Superfamily:**Cellulose docking domain, dockering **Family:**Cellulose docking domain, dockering
42	d2ezla_	Alignment	not modelled	8.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
43	d1vi7a1	Alignment	not modelled	8.0	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
44	d1xb4a2	Alignment	not modelled	7.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
45	c2rfpA_	Alignment	not modelled	7.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
46	c3gk0H_	Alignment	not modelled	7.2	24	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
47	c2z1nA_	Alignment	not modelled	7.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
48	d3bpya1	Alignment	not modelled	7.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
49	d1s69a_	Alignment	not modelled	7.0	20	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
50	c2hxjF_	Alignment	not modelled	7.0	14	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein of unknown function nmb1681 from2 neisseria meningitidis mc58, possible nucleic acid binding protein
51	d1cyda_	Alignment	not modelled	7.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
52	d2c6ya1	Alignment	not modelled	6.8	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
53	d2ptza1	Alignment	not modelled	6.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
54	c3l1pA_	Alignment	not modelled	6.7	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pou domain, class 5, transcription factor 1;

						PDBTitle: pou protein:dna complex
55	c1c94B_	Alignment	not modelled	6.7	38	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper; **PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
56	c3aq8A_	Alignment	not modelled	6.5	13	**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
57	c3ol4B_	Alignment	not modelled	6.5	35	**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
58	c3ak4C_	Alignment	not modelled	6.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
59	c2wdzD_	Alignment	not modelled	6.4	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
60	d2czda1	Alignment	not modelled	6.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
61	c1e17A_	Alignment	not modelled	6.3	7	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
62	c3cxtA_	Alignment	not modelled	6.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
63	d1w6ta1	Alignment	not modelled	6.2	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
64	c3b9nB_	Alignment	not modelled	6.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
65	c2kl8A_	Alignment	not modelled	6.0	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
66	d1l1ya_	Alignment	not modelled	6.0	57	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
67	c1l2aD_	Alignment	not modelled	6.0	57	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
68	c1qcrD_	Alignment	not modelled	5.9	6	**PDB header:** **PDB COMPND:**
69	d1g31a_	Alignment	not modelled	5.8	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
70	c3gdfA_	Alignment	not modelled	5.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
71	d2abka_	Alignment	not modelled	5.4	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
72	c2o2sA_	Alignment	not modelled	5.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
73	d1m5wa_	Alignment	not modelled	5.4	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
74	c3cwbQ_	Alignment	not modelled	5.3	5	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
75	c1htrP_	Alignment	not modelled	5.3	20	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
76	d1un2a_	Alignment	not modelled	5.2	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
77	c3co7C_	Alignment	not modelled	5.2	11	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
78	d2giab1	Alignment	not modelled	5.2	50	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Guide RNA binding protein gBP
79	c2giaB_	Alignment	not modelled	5.2	50	**PDB header:**translation **Chain:** B: **PDB Molecule:**mitochondrial rna-binding protein 1;

							PDBTitle: crystal structures of trypanosoma bruciei mrp1/mrp2
80	d2i7pa1		Alignment	not modelled	5.2	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
81	c3gafF_		Alignment	not modelled	5.1	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
82	d2c4ka1		Alignment	not modelled	5.1	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
83	c3hluA_		Alignment	not modelled	5.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
84	c2bmbA_		Alignment	not modelled	5.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
85	d1gpqa_		Alignment	not modelled	5.1	16	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
86	d2o23a1		Alignment	not modelled	5.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
87	c2x4mD_		Alignment	not modelled	5.1	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
88	d1g9ga_		Alignment	not modelled	5.0	26	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain