Phyre²

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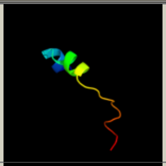
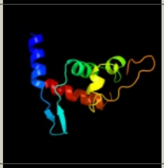
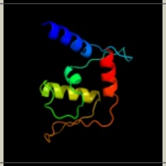
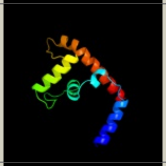
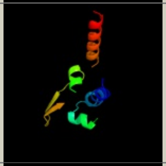
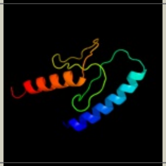
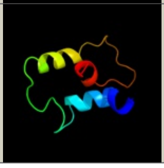
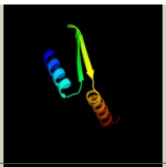
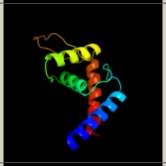
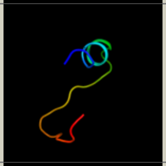
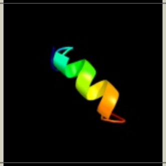
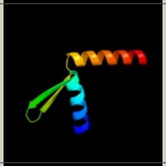
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1htrP_	Alignment		46.3	26	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
2	c2wa1A_	Alignment		38.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**non-structural protein 5; **PDBTitle:** structure of the methyltransferase domain from modoc virus,2 a flavivirus with no known vector (nkv)
3	d2d1ha1	Alignment		35.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
4	c1hsjA_	Alignment		32.3	14	**PDB header:**transcription/sugar binding protein **Chain:** A: **PDB Molecule:**fusion protein consisting of staphylococcus **PDBTitle:** sarr mbp fusion structure
5	d2frha1	Alignment		31.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
6	d2etha1	Alignment		24.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
7	d1stza1	Alignment		22.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
8	d1sfxa_	Alignment		22.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
9	d1jhfa1	Alignment		20.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
10	c2px2B_	Alignment		20.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**genome polyprotein [contains: capsid protein c **PDBTitle:** crystal structure of the murray valley encephalitis virus2 ns5 2'-o methyltransferase domain in complex with sah3 (monoclinic form 1)
11	d1u61a_	Alignment		20.3	19	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like

12	c3ctaA_	Alignment		19.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
13	d1lnwa_	Alignment		18.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
14	c1stzB_	Alignment		16.8	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
15	c2colA_	Alignment		16.1	17	**PDB header:**lyase/metal binding protein **Chain:** A: **PDB Molecule:**bifunctional hemolysin-adenylate cyclase; **PDBTitle:** crystal structure analysis of cyaa/c-cam with pyrophosphate
16	d1s58a_	Alignment		15.7	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
17	d1ub9a_	Alignment		15.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
18	c1ykuB_	Alignment		14.8	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pxo2-61; **PDBTitle:** crystal structure of a sensor domain homolog
19	d1t3la2	Alignment		14.1	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
20	d1p4xa2	Alignment		12.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
21	d2fbha1	Alignment	not modelled	12.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
22	c1z1cA_	Alignment	not modelled	12.3	24	**PDB header:**virus/dna **Chain:** A: **PDB Molecule:**coat protein vp2; **PDBTitle:** structural determinants of tissue tropism and in vivo2 pathogenicity for the parvovirus minute virus of mice
23	d1nava_	Alignment	not modelled	12.3	11	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
24	c3da5A_	Alignment	not modelled	11.5	42	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**argonaute; **PDBTitle:** crystal structure of piwi/argonaute/zwille(paz) domain from2 thermococcus thioreducens
25	c3h8dE_	Alignment	not modelled	11.3	42	**PDB header:**motor protein/signaling protein **Chain:** E: **PDB Molecule:**disabled homolog 2; **PDBTitle:** crystal structure of myosin vi in complex with dab2 peptide
26	c3u5gK_	Alignment	not modelled	11.0	21	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**40s ribosomal protein s10-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
27	d1mvma_	Alignment	not modelled	10.8	24	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
28	d1k3va_	Alignment	not modelled	10.7	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
						PDB header:virus

29	c1k3vA_	Alignment	not modelled	10.7	33	**Chain:** A: **PDB Molecule:**capsid protein vp2; **PDBTitle:** porcine parvovirus capsid
30	c3cjnA_	Alignment	not modelled	10.5	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
31	d2gmga1	Alignment	not modelled	10.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
32	c3nttA_	Alignment	not modelled	10.3	18	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis
33	d1hsja1	Alignment	not modelled	10.2	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
34	d1k8ta_	Alignment	not modelled	10.0	13	**Fold:**Adenylylcyclase toxin (the edema factor) **Superfamily:**Adenylylcyclase toxin (the edema factor) **Family:**Adenylylcyclase toxin (the edema factor)
35	c3dkxA_	Alignment	not modelled	9.9	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein repb; **PDBTitle:** crystal structure of the replication initiator protein2 encoded on plasmid pmv158 (repb), trigonal form, to 2.7 ang3 resolution
36	c2xzm7_	Alignment	not modelled	9.8	14	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**plectin/s10 domain containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
37	d1c8da_	Alignment	not modelled	9.6	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
38	c3kieF_	Alignment	not modelled	9.6	12	**PDB header:**virus **Chain:** F: **PDB Molecule:**capsid protein vp1; **PDBTitle:** crystal structure of adeno-associated virus serotype 3b
39	d1lp3a_	Alignment	not modelled	9.6	12	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
40	c2j8pA_	Alignment	not modelled	9.1	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
41	c2g8gA_	Alignment	not modelled	9.0	12	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid; **PDBTitle:** structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4
42	c4a5mH_	Alignment	not modelled	8.7	22	**PDB header:**transcription **Chain:** H: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yybr; **PDBTitle:** redox regulator hypr in its oxidized form
43	c3bjaA_	Alignment	not modelled	8.5	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
44	c2jtvA_	Alignment	not modelled	7.9	18	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
45	c3pmdA_	Alignment	not modelled	7.3	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
46	c1xfzA_	Alignment	not modelled	7.2	13	**PDB header:**lyase/metal binding protein **Chain:** A: **PDB Molecule:**calmodulin-sensitive adenylate cyclase; **PDBTitle:** crystal structure of anthrax edema factor (ef) in complex2 with calmodulin in the presence of 1 millimolar3 exogenously added calcium chloride
47	c1xfuE_	Alignment	not modelled	7.2	13	**PDB header:**lyase/metal binding protein **Chain:** E: **PDB Molecule:**calmodulin-sensitive adenylate cyclase; **PDBTitle:** crystal structure of anthrax edema factor (ef) truncation2 mutant, ef-delta 64 in complex with calmodulin
48	c2gslE_	Alignment	not modelled	7.2	15	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein; **PDBTitle:** x-ray crystal structure of protein fn1578 from fusobacterium2 nucleatum. northeast structural genomics consortium target nr1.
49	d2i9ca1	Alignment	not modelled	6.9	8	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**RPA1889-like
50	d1bh9b_	Alignment	not modelled	6.6	33	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
51	d2j5pa1	Alignment	not modelled	6.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
52	c2oqgA_	Alignment	not modelled	6.5	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
53	d1okra_	Alignment	not modelled	6.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor

54	c3obhA_	Alignment	not modelled	6.2	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
55	d1dmga_	Alignment	not modelled	6.2	13	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
56	c2qenA_	Alignment	not modelled	6.2	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**walker-type atpase; **PDBTitle:** the walker-type atpase paby2304 of pyrococcus abyssi
57	d2b50a1	Alignment	not modelled	6.1	12	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
58	c3f6oB_	Alignment	not modelled	6.1	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
59	c2w9yA_	Alignment	not modelled	5.9	14	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**fatty acid/retinol binding protein protein 7, **PDBTitle:** the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
60	d1y88a1	Alignment	not modelled	5.9	23	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**Hypothetical protein AF1548, C-terminal domain
61	c1fpvA_	Alignment	not modelled	5.9	22	**PDB header:**virus **Chain:** A: **PDB Molecule:**feline panleukopenia virus (strain b) viral **PDBTitle:** structure determination of feline panleukopenia virus empty2 particles
62	c2b1wA_	Alignment	not modelled	5.8	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**caspase recruitment domain protein 4; **PDBTitle:** solution structure of the nod1 caspase activating and recruitment2 domain
63	c3g3zA_	Alignment	not modelled	5.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
64	d1q3ma_	Alignment	not modelled	5.8	44	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
65	d1q8ha_	Alignment	not modelled	5.7	44	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
66	c1q8hA_	Alignment	not modelled	5.7	44	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**osteocalcin; **PDBTitle:** crystal structure of porcine osteocalcin
67	d2olua1	Alignment	not modelled	5.7	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
68	d1un2a_	Alignment	not modelled	5.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
69	d1pq9a_	Alignment	not modelled	5.4	11	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
70	c3elkA_	Alignment	not modelled	5.3	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator ta0346; **PDBTitle:** crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum
71	c2nyxB_	Alignment	not modelled	5.3	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis