Phyre^2

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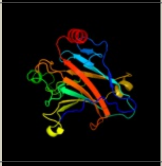
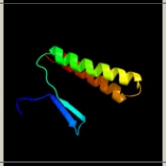
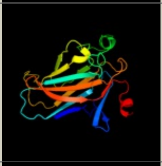
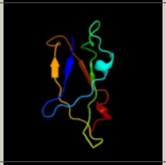
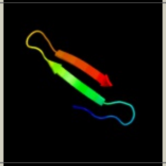
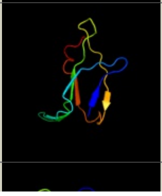
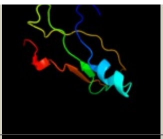
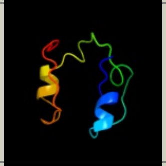
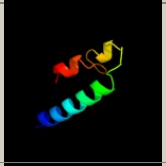
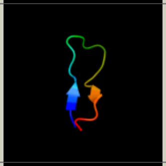
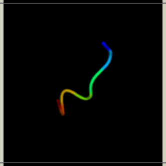
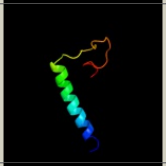
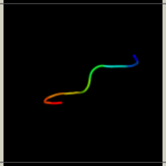
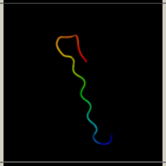
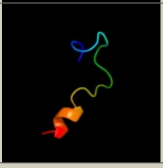
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xipA_	Alignment		100.0	27	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**tumour protein p73; **PDBTitle:** crystal structure of the dna binding domain of human tp732 refined at 1.8 a resolution
2	c2rmnA_	Alignment		100.0	24	**PDB header:**cell cycle, antitumor protein **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** the solution structure of the p63 dna-binding domain
3	c3q06B_	Alignment		100.0	28	**PDB header:**cell cycle/dna **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** an induced fit mechanism regulates p53 dna binding kinetics to confer2 sequence specificity
4	d2ac0a1	Alignment		100.0	26	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
5	c2j1xA_	Alignment		100.0	27	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** human p53 core domain mutant m133l-v203a-y220c-n239y-n268d
6	d1hu8a_	Alignment		100.0	29	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
7	c2rp4C_	Alignment		100.0	100	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription factor p53; **PDBTitle:** solution structure of the oligomerization domain in dmp53
8	d1t4wa_	Alignment		98.7	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
9	c3k2kA_	Alignment		38.4	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxypeptidase; **PDBTitle:** crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
10	c4gopB_	Alignment		21.8	26	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
11	c4a37A_	Alignment		21.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-carboxypeptidase; **PDBTitle:** metallo-carboxypeptidase from pseudomonas aeruginosa

12	c3l2nA_	Alignment		19.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m14, carboxypeptidase a; **PDBTitle:** crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution
13	c2kumA_	Alignment		18.6	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**c-c motif chemokine 27; **PDBTitle:** solution structure of the human chemokine ccl27
14	d2b5dx1	Alignment		18.6	18	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**AmyC C-terminal domain-like
15	c2l4nA_	Alignment		17.3	26	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**c-c motif chemokine 21; **PDBTitle:** solution structure of the chemokine ccl21
16	c3gycB_	Alignment		17.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
17	d1ufaa1	Alignment		15.3	13	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**AmyC C-terminal domain-like
18	c3cguB_	Alignment		15.0	33	**PDB header:**hormone/signaling protein **Chain:** B: **PDB Molecule:**protein giant-lens; **PDBTitle:** crystal structure of unliganded argos
19	c2bsjB_	Alignment		14.3	31	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein syct; **PDBTitle:** native crystal structure of the type iii secretion2 chaperone syct from yersinia enterocolitica
20	c2jo1A_	Alignment		12.8	32	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
21	d2pi2a1	Alignment	not modelled	12.2	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
22	c1y6zA_	Alignment	not modelled	12.2	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
23	c2pi2A_	Alignment	not modelled	12.1	9	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
24	d1iknc_	Alignment	not modelled	11.8	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
25	c3isyA_	Alignment	not modelled	11.7	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
26	d1eiga_	Alignment	not modelled	10.9	33	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
27	c3ulcA_	Alignment	not modelled	10.6	60	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**target of rapamycin complex 2 subunit avo1; **PDBTitle:** crystal structure of the pleckstrin homology domain of saccharomyces2 cerevisiae avo1, a torc2 subunit, in the p3121 crystal form
28	d1ft8a2	Alignment	not modelled	10.5	38	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Non-canonical RBD domain

29	c1svcP_	Alignment	not modelled	9.8	19	**PDB header:**transcription/dna **Chain:** P: **PDB Molecule:**protein (nuclear factor kappa-b (nf-kb)); **PDBTitle:** nfkb p50 homodimer bound to dna
30	c3u5gh_	Alignment	not modelled	9.7	35	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**40s ribosomal protein s7-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
31	d1ytla1	Alignment	not modelled	9.4	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**ACDE2-like
32	c3mxtA_	Alignment	not modelled	9.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
33	c3hyjD_	Alignment	not modelled	9.0	20	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**protein duf199/whia; **PDBTitle:** crystal structure of the n-terminal laglidadg domain of duf199/whia
34	d1ylea1	Alignment	not modelled	8.8	38	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
35	d1ifva_	Alignment	not modelled	8.7	26	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
36	d1mi2a_	Alignment	not modelled	8.4	29	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
37	d1esra_	Alignment	not modelled	7.9	25	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
38	d1mgsa_	Alignment	not modelled	7.7	24	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
39	c2xueB_	Alignment	not modelled	7.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of jmjd3
40	c2xzbB_	Alignment	not modelled	7.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h,k-atpase with bound bef and sch28080
41	c1nfkA_	Alignment	not modelled	7.4	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (nuclear factor kappa-b (nf-kb)); **PDBTitle:** structure of the nuclear factor kappa-b (nf-kb) p502 homodimer
42	c3ag5A_	Alignment	not modelled	7.2	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus
43	c2ejcA_	Alignment	not modelled	7.1	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
44	d1z0jb1	Alignment	not modelled	7.1	23	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
45	c3uk2B_	Alignment	not modelled	7.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis
46	d1pvma3	Alignment	not modelled	6.7	31	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
47	d2auwa2	Alignment	not modelled	6.6	22	**Fold:**NE0471 N-terminal domain-like **Superfamily:**NE0471 N-terminal domain-like **Family:**NE0471 N-terminal domain-like
48	d1kshb_	Alignment	not modelled	6.6	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
49	c3rh0A_	Alignment	not modelled	6.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
50	d1qnka_	Alignment	not modelled	6.3	29	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
51	c2fd4A_	Alignment	not modelled	6.3	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**avirulence protein avrptob; **PDBTitle:** crystal structure of avrptob (436-553)
52	d1icwa_	Alignment	not modelled	6.1	17	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
53	c1ixtA_	Alignment	not modelled	5.9	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**spasmodic protein tx9a-like protein; **PDBTitle:** structure of a novel p-superfamily spasmodic conotoxin2 reveals an inhibitory cystine knot motif
54	d1ixta_	Alignment	not modelled	5.9	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
55	d1e6vc_	Alignment	not modelled	5.9	29	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain

56	d1hn6a_	Alignment	not modelled	5.8	30	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
57	c2cwoD_	Alignment	not modelled	5.8	44	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**rna silencing suppressor; **PDBTitle:** crystal structure of rna silencing suppressor p21 from beet yellows2 virus
58	d1itxa2	Alignment	not modelled	5.7	20	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
59	c1lj2C_	Alignment	not modelled	5.7	57	**PDB header:**viral protein/ translation **Chain:** C: **PDB Molecule:**eukaryotic protein synthesis initiation factor; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
60	d1xwea_	Alignment	not modelled	5.6	14	**Fold:**OB-fold **Superfamily:**TIMP-like **Family:**Netrin-like domain (NTR/C345C module)
61	d1v8fa_	Alignment	not modelled	5.5	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
62	d1f9ra_	Alignment	not modelled	5.5	26	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
63	d1koha2	Alignment	not modelled	5.5	42	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Non-canonical RBD domain
64	d1k6za_	Alignment	not modelled	5.4	14	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
65	c4f02F_	Alignment	not modelled	5.3	57	**PDB header:**translation/rna **Chain:** F: **PDB Molecule:**eukaryotic translation initiation factor 4 gamma 1; **PDBTitle:** crystal structure of the pabp-binding site of eif4g in complex with2 rrm1-2 of pabp and poly(a)
66	c4f02C_	Alignment	not modelled	5.3	57	**PDB header:**translation/rna **Chain:** C: **PDB Molecule:**eukaryotic translation initiation factor 4 gamma 1; **PDBTitle:** crystal structure of the pabp-binding site of eif4g in complex with2 rrm1-2 of pabp and poly(a)
67	d1fs1b1	Alignment	not modelled	5.3	31	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
68	d2eota_	Alignment	not modelled	5.1	31	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
69	c3rpjA_	Alignment	not modelled	5.0	36	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**curlin genes transcriptional regulator; **PDBTitle:** structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
70	c3ve5D_	Alignment	not modelled	5.0	36	**PDB header:**recombination **Chain:** D: **PDB Molecule:**recombination protein recr; **PDBTitle:** structure of recombination mediator protein recr16-196 deletion mutant