Phyre^{2}

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Description	P75829
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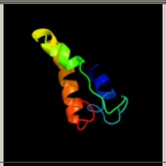
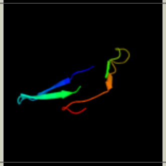
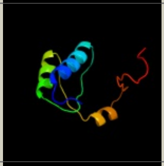
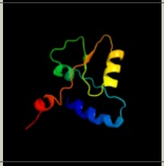
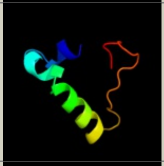
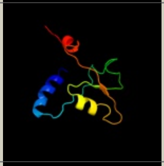
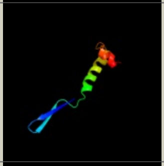
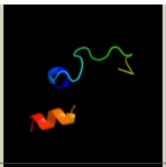
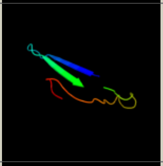
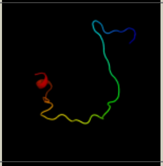
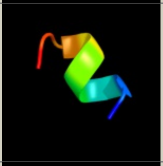
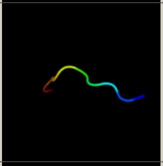
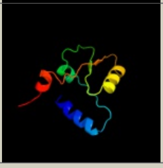
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cx6a1	Alignment		32.0	19	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
2	d3saka_	Alignment		26.9	24	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
3	c3bvhE_	Alignment		25.2	15	**PDB header:**blood clotting **Chain:** E: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
4	d2o3aa1	Alignment		24.3	17	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
5	c3peiA_	Alignment		22.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
6	c3nw0B_	Alignment		22.0	14	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**melanoma-associated antigen g1; **PDBTitle:** crystal structure of mageg1 and nse1 complex
7	c3zy1A_	Alignment		20.4	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of the human p63 tetramerization domain
8	c4a9zD_	Alignment		20.0	43	**PDB header:**transcription **Chain:** D: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
9	d1gyta2	Alignment		19.9	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
10	d1zc6a2	Alignment		19.8	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
11	c2hpcH_	Alignment		19.5	15	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.

12	c3qu3A_	Alignment		18.8	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**interferon regulatory factor 7; **PDBTitle:** crystal structure of irf-7 dbd apo form
13	c1lwuH_	Alignment		18.0	10	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of fragment d from lamprey fibrinogen complexed with2 the peptide gly-his-arg-pro-amide
14	c3d35A_	Alignment		17.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** crystal structure of rtt109-ac-coa complex
15	c3h8gC_	Alignment		17.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
16	d2fh1a2	Alignment		16.3	56	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
17	c2c4rL_	Alignment		15.9	50	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
18	c3rayA_	Alignment		15.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pr domain-containing protein 11; **PDBTitle:** crystal structure of methyltransferase domain of human pr domain-2 containing protein 11
19	c3jruB_	Alignment		15.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
20	c3kr5E_	Alignment		14.5	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m17 leucyl aminopeptidase; **PDBTitle:** structure of a protease 4
21	d1v8ca2	Alignment	not modelled	14.1	35	**Fold:**TBP-like **Superfamily:**MoaD-related protein, C-terminal domain **Family:**MoaD-related protein, C-terminal domain
22	c2gutA_	Alignment	not modelled	13.4	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arc/mediator, positive cofactor 2 glutamine/q- **PDBTitle:** solution structure of the trans-activation domain of the2 human co-activator arc105
23	d1lama1	Alignment	not modelled	13.3	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
24	c2vcpE_	Alignment	not modelled	13.1	27	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**neural wiskott-aldrich syndrome protein; **PDBTitle:** crystal structure of n-wasp vc domain in complex with2 skeletal actin
25	d1d0na5	Alignment	not modelled	13.0	45	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
26	d1e7ua2	Alignment	not modelled	12.9	8	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**PLC-like (P variant)
27	c3ghgK_	Alignment	not modelled	12.6	15	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
28	c1gytG_	Alignment	not modelled	12.4	20	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
						Fold: Gelsolin-like

29	d1npha2	Alignment	not modelled	12.2	56	**Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
30	d2a90a2	Alignment	not modelled	11.1	43	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
31	c3k13A_	Alignment	not modelled	11.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
32	d1lwub1	Alignment	not modelled	11.0	10	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
33	c3nztA_	Alignment	not modelled	10.9	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ftom francisella tularensis in complex with amp
34	d2tsra_	Alignment	not modelled	10.8	20	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
35	c1ei3E_	Alignment	not modelled	10.8	15	**PDB header:** **PDB COMPND:**
36	c2dymE_	Alignment	not modelled	10.6	17	**PDB header:**protein turnover/protein turnover **Chain:** E: **PDB Molecule:**autophagy protein 5; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
37	c3fpjA_	Alignment	not modelled	10.5	19	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
38	d2czla1	Alignment	not modelled	10.5	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
39	c3cz7A_	Alignment	not modelled	10.3	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** molecular basis for the autoregulation of the protein acetyl2 transferase rtt109
40	c2zfnA_	Alignment	not modelled	9.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
41	c3mwbA_	Alignment	not modelled	9.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
42	d1kzfa_	Alignment	not modelled	9.6	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
43	c3luyA_	Alignment	not modelled	9.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
44	d1wh6a_	Alignment	not modelled	9.4	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
45	d2it9a1	Alignment	not modelled	9.3	21	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
46	c3ix6B_	Alignment	not modelled	9.1	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of thymidylate synthase thya from brucella2 melitensis
47	c2hc9A_	Alignment	not modelled	8.7	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
48	c2a3zC_	Alignment	not modelled	8.6	31	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** ternary complex of the wh2 domain of wasp with actin-dnase i
49	c2kerA_	Alignment	not modelled	8.6	38	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**alpha-amylase inhibitor z-2685; **PDBTitle:** alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus
50	d1tf5a1	Alignment	not modelled	8.4	17	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
51	d2o0ma1	Alignment	not modelled	8.3	9	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
52	c2o0mA_	Alignment	not modelled	8.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
53	d1nkta1	Alignment	not modelled	8.2	18	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
54	d1ok0a_	Alignment	not modelled	8.2	50	**Fold:**alpha-Amylase inhibitor tendamistat **Superfamily:**alpha-Amylase inhibitor tendamistat **Family:**alpha-Amylase inhibitor tendamistat

55	d1fzda_	Alignment	not modelled	8.0	10	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
56	d1uw4a_	Alignment	not modelled	8.0	4	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Smg-4/UPF3
57	d1v66a_	Alignment	not modelled	7.7	36	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
58	d1m1jb1	Alignment	not modelled	7.5	15	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
59	c2e1nA_	Alignment	not modelled	7.5	23	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**pex; **PDBTitle:** crystal structure of the cyanobacterium circadian clock modifier pex
60	d2a90a1	Alignment	not modelled	7.5	7	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
61	d2oz4a2	Alignment	not modelled	7.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
62	d1yvoa1	Alignment	not modelled	7.1	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
63	d1o6la_	Alignment	not modelled	7.0	15	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
64	d1oe4a_	Alignment	not modelled	6.8	30	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
65	c3dwdB_	Alignment	not modelled	6.8	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1; **PDBTitle:** crystal structure of the arfgap domain of human arfgap1
66	d1t62a_	Alignment	not modelled	6.7	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein EF3133
67	d2qqsa2	Alignment	not modelled	6.7	24	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
68	c3jqxA_	Alignment	not modelled	6.7	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**colh protein; **PDBTitle:** crystal structure of clostridium histolyticum colh collagenase2 collagen binding domain 3 at 2.2 angstrom resolution in the presence3 of calcium and cadmium
69	c3a9lB_	Alignment	not modelled	6.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
70	c3km3B_	Alignment	not modelled	6.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** crystal structure of eoxycytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
71	d1n6za_	Alignment	not modelled	6.5	40	**Fold:**Hypothetical protein Yml108w **Superfamily:**Hypothetical protein Yml108w **Family:**Hypothetical protein Yml108w
72	d1ufwa_	Alignment	not modelled	6.5	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
73	c1vbiA_	Alignment	not modelled	6.4	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
74	d1tqza1	Alignment	not modelled	6.4	29	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Necap1 N-terminal domain-like
75	c1jjoE_	Alignment	not modelled	6.3	9	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**neuroserpin; **PDBTitle:** crystal structure of mouse neuroserpin (cleaved form)
76	c2yy8B_	Alignment	not modelled	6.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
77	c3m3nW_	Alignment	not modelled	6.1	31	**PDB header:**structural protein **Chain:** W: **PDB Molecule:**neural wiskott-aldrich syndrome protein; **PDBTitle:** structure of a longitudinal actin dimer assembled by tandem w domains
78	c3f02C_	Alignment	not modelled	6.0	14	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**neuroserpin; **PDBTitle:** cleaved human neuroserpin
79	d1v8ha1	Alignment	not modelled	6.0	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
80	d1x4fa1	Alignment	not modelled	6.0	8	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
81	d1ua4a_	Alignment	not modelled	5.9	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like

						Family:ADP-specific Phosphofructokinase/Glucokinase
82	c3lyrA_	Alignment	not modelled	5.9	25	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**transcription factor coe1; **PDBTitle:** human early b-cell factor 1 (ebf1) dna-binding domain
83	c3kgbA_	Alignment	not modelled	5.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase 1/2; **PDBTitle:** crystal structure of thymidylate synthase 1/2 from encephalitozoon2 cuniculi at 2.2 a resolution
84	c2jx2A_	Alignment	not modelled	5.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**negative elongation factor e; **PDBTitle:** solution conformation of rna-bound nelf-e rrm
85	d1l2la_	Alignment	not modelled	5.8	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
86	c1deqO_	Alignment	not modelled	5.8	15	**PDB header:** **PDB COMPND:**
87	c3s9xA_	Alignment	not modelled	5.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asch domain; **PDBTitle:** high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
88	c2qsrA_	Alignment	not modelled	5.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of c-terminal domain of transcription-repair2 coupling factor
89	d1umya_	Alignment	not modelled	5.6	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
90	d2irfg_	Alignment	not modelled	5.5	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Interferon regulatory factor
91	c1hleB_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase inhibitor(serine proteinase) **Chain:** B: **PDB Molecule:**horse leukocyte elastase inhibitor; **PDBTitle:** crystal structure of cleaved equine leucocyte elastase2 inhibitor determined at 1.95 angstroms resolution
92	c2bn5A_	Alignment	not modelled	5.5	50	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**psi; **PDBTitle:** p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
93	d1duvg1	Alignment	not modelled	5.5	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
94	d2o4aa1	Alignment	not modelled	5.4	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
95	d1px5a1	Alignment	not modelled	5.4	18	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**2'-5'-oligoadenylate synthetase 1, OAS1, second domain
96	d1tswa_	Alignment	not modelled	5.4	23	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
97	d2b4jc1	Alignment	not modelled	5.3	9	**Fold:**N-cbl like **Superfamily:**HIV integrase-binding domain **Family:**HIV integrase-binding domain
98	c1wtjB_	Alignment	not modelled	5.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
99	c2h4qB_	Alignment	not modelled	5.3	20	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**heterochromatin-associated protein ment; **PDBTitle:** crystal structure of a m-loop deletion variant of ment in2 the cleaved conformation