Phyre²

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Description	P0AEV4
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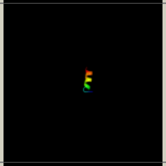
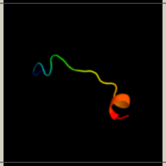
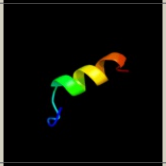
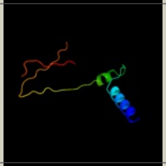
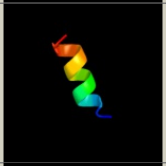
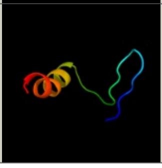
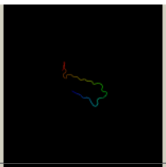
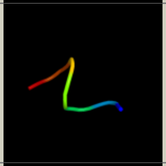
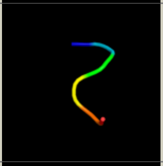
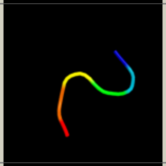
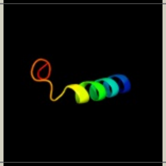
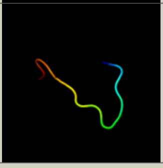
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wpvG_	Alignment		42.2	29	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**upf0363 protein yor164c; **PDBTitle:** crystal structure of s. cerevisiae get4-get5 complex
2	c3lpzA_	Alignment		21.7	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
3	c2qgoA_	Alignment		20.3	35	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative fe-s biosynthesis protein; **PDBTitle:** crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus
4	c3kcpA_	Alignment		17.2	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal-scaffolding protein a; **PDBTitle:** crystal structure of interacting clostridium thermocellum2 multimodular components
5	c3iz5F_	Alignment		16.8	16	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**60s ribosomal protein l9 (l6p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
6	d2idba2	Alignment		15.7	18	**Fold:**UbiD C-terminal domain-like **Superfamily:**UbiD C-terminal domain-like **Family:**UbiD C-terminal domain-like
7	d1or7c_	Alignment		14.6	23	**Fold:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Superfamily:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Family:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
8	c1or7C_	Alignment		14.6	23	**PDB header:**transcription **Chain:** C: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
9	d3besl1	Alignment		13.6	16	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
10	c3udiA_	Alignment		13.1	39	**PDB header:**penicillin-binding protein/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 1a; **PDBTitle:** crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
11	c2e9hA_	Alignment		12.1	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5

12	c2e32A_	Alignment		11.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**f-box only protein 2; **PDBTitle:** structural basis for selection of glycosylated substrate by2 scffbs1 ubiquitin ligase
13	c2dciA_	Alignment		10.6	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of influenza ha fusion peptide mutant w14a in2 dpc in ph5
14	c2olvA_	Alignment		9.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
15	c3dwkC_	Alignment		8.9	31	**PDB header:**transferase **Chain:** C: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
16	c1xooA_	Alignment		8.7	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1s mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
17	c1xopA_	Alignment		8.7	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
18	c3hlkB_	Alignment		8.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
19	c1ekuA_	Alignment		8.1	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**interferon gamma; **PDBTitle:** crystal structure of a biologically active single chain2 mutant of human ifn-gamma
20	d2oq0a1	Alignment		8.1	24	**Fold:**OB-fold **Superfamily:**HIN-2000 domain-like **Family:**HIN-200/IF120x domain
21	c2l4gA_	Alignment	not modelled	8.0	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**haemagglutinin; **PDBTitle:** influenza haemagglutinin fusion peptide mutant g13a
22	d1iyjb3	Alignment	not modelled	8.0	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
23	c2jrdA_	Alignment	not modelled	7.9	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** influenza hemagglutinin fusion domain mutant f9a
24	d1wi9a_	Alignment	not modelled	7.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
25	c2x49A_	Alignment	not modelled	7.4	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**invasion protein inva; **PDBTitle:** crystal structure of the c-terminal domain of inva
26	c2kk1A_	Alignment	not modelled	7.1	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase abl2; **PDBTitle:** solution structure of c-terminal domain of tyrosine-protein2 kinase abl2 from homo sapiens, northeast structural3 genomics consortium (nesg) target hr5537a
27	d2yrba1	Alignment	not modelled	6.9	23	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**PLC-like (P variant)
28	d2doda1	Alignment	not modelled	6.8	32	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
						Fold:beta-clip

29	d1e9ya1	Alignment	not modelled	6.8	11	**Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
30	c1iboA_	Alignment	not modelled	6.6	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha2 chain peptide; **PDBTitle:** nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 7.4
31	c1ibnA_	Alignment	not modelled	6.6	63	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha2 chain peptide; **PDBTitle:** nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 5
32	d1j5ya2	Alignment	not modelled	6.6	50	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
33	c3a5iB_	Alignment	not modelled	6.2	41	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha
34	c2oznB_	Alignment	not modelled	6.1	26	**PDB header:**toxin **Chain:** B: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** the cohesin-dockerin complex of nagj and nagh from clostridium2 perfringens
35	c2bgcA_	Alignment	not modelled	6.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
36	c3kz5E_	Alignment	not modelled	5.9	33	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**protein sopb; **PDBTitle:** structure of cdomain
37	c3mixA_	Alignment	not modelled	5.8	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** crystal structure of the cytosolic domain of b. subtilis flha
38	c3mydA_	Alignment	not modelled	5.7	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha from helicobacter pylori
39	d2oqoa1	Alignment	not modelled	5.4	38	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
40	d2f9yb1	Alignment	not modelled	5.3	30	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
41	c2f9yB_	Alignment	not modelled	5.3	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
42	c3p0dD_	Alignment	not modelled	5.3	37	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycoside hydrolase family 9; **PDBTitle:** crystal structure of a multimodular ternary protein complex from2 clostridium thermocellum
43	c2zibA_	Alignment	not modelled	5.3	29	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**type ii antifreeze protein; **PDBTitle:** crystal structure analysis of calcium-independent type ii2 antifreeze protein
44	d2olua1	Alignment	not modelled	5.3	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
45	d2cqna1	Alignment	not modelled	5.2	4	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain