Phyre²

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Description	P36680
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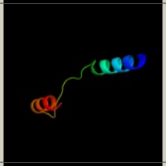
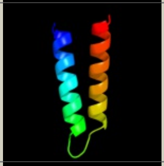
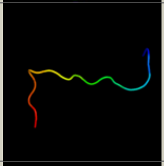
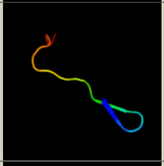
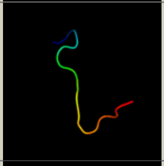
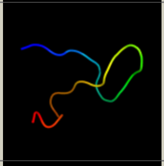
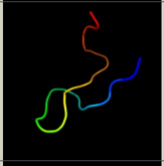
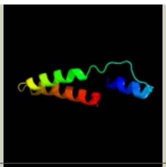
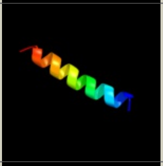
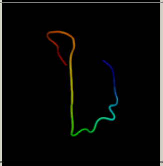
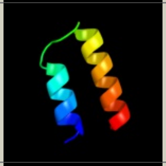
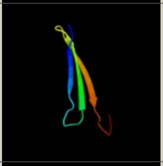
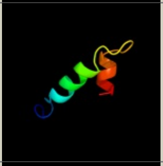
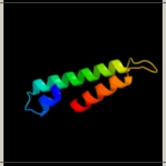
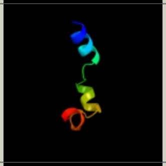
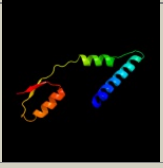
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2oeza1	Alignment		100.0	39	**Fold:**YacF-like **Superfamily:**YacF-like **Family:**YacF-like
2	d1eg3a2	Alignment		51.4	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
3	d1wmib1	Alignment		35.2	29	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**RelB-like **Family:**RelB-like
4	d2f5tx2	Alignment		24.3	42	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**TrmB middle domain-like
5	c3layF_	Alignment		23.1	16	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
6	c2r5iL_	Alignment		22.6	24	**PDB header:**viral protein **Chain:** L: **PDB Molecule:**l1 protein; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 18
7	c3iyjE_	Alignment		21.4	22	**PDB header:**virus **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** bovine papillomavirus type 1 outer capsid
8	c2r5kE_	Alignment		20.9	24	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 11
9	c1dzlA_	Alignment		20.4	30	**PDB header:**virus **Chain:** A: **PDB Molecule:**late major capsid protein l1; **PDBTitle:** l1 protein of human papillomavirus 16
10	d1dzla_	Alignment		20.4	30	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
11	c2f5tX_	Alignment		20.0	42	**PDB header:**transcription **Chain:** X: **PDB Molecule:**archaeal transcriptional regulator trmb; **PDBTitle:** crystal structure of the sugar binding domain of the archaeal2 transcriptional regulator trmb

12	d1x79a_	Alignment		16.1	19	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
13	c1hf9B_	Alignment		13.0	23	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
14	c1w8xN_	Alignment		12.2	17	**PDB header:**virus **Chain:** N: **PDB Molecule:**protein p31; **PDBTitle:** structural analysis of prd1
15	d1j8yf1	Alignment		12.2	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
16	d2it9a1	Alignment		12.1	14	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
17	d1p3qq_	Alignment		11.4	28	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
18	d1wr6a1	Alignment		11.3	22	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
19	c3m8jA_	Alignment		10.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**focb protein; **PDBTitle:** crystal structure of e.coli focb at 1.4 a resolution
20	c3ktdC_	Alignment		10.4	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
21	c1yisA_	Alignment	not modelled	10.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** structural genomics of caenorhabditis elegans: adenylosuccinate lyase
22	c1o7dD_	Alignment	not modelled	10.0	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
23	c3bqsB_	Alignment	not modelled	7.7	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
24	d1qzxa1	Alignment	not modelled	7.6	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
25	c2zxjB_	Alignment	not modelled	7.4	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus
26	c2gqcA_	Alignment	not modelled	7.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rhomboid intramembrane protease; **PDBTitle:** solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
27	d1p30a1	Alignment	not modelled	7.4	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Adenovirus hexon
28	c2w9pC_	Alignment	not modelled	7.3	4	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**multicystatin; **PDBTitle:** crystal structure of potato multicystatin
						PDB header:unknown function

29	c3cjlA_	Alignment	not modelled	7.2	13	**Chain:** A: **PDB Molecule:**domain of unknown function; **PDBTitle:** crystal structure of a protein of unknown function (eca1910) from2 pectobacterium atrosepticum scri1043 at 2.20 a resolution
30	d1txna_	Alignment	not modelled	7.1	26	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
31	c2inyA_	Alignment	not modelled	7.1	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hexon protein; **PDBTitle:** nanoporous crystals of chicken embryo lethal orphan (celo) adenovirus2 major coat protein, hexon
32	c2pjwH_	Alignment	not modelled	7.0	16	**PDB header:**endocytosis/exocytosis **Chain:** H: **PDB Molecule:**uncharacterized protein yhl002w; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
33	d2fug51	Alignment	not modelled	7.0	11	**Fold:**Nqo5-like **Superfamily:**Nqo5-like **Family:**Nqo5-like
34	c2js5B_	Alignment	not modelled	6.8	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
35	c1ot0A_	Alignment	not modelled	6.7	21	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy
36	c1p0jA_	Alignment	not modelled	6.7	21	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution asp to trp modification in sds-d252 micelles
37	c1p0gA_	Alignment	not modelled	6.6	21	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy
38	c2yy0D_	Alignment	not modelled	6.5	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
39	c3epuB_	Alignment	not modelled	6.4	36	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**stm2138 virulence chaperone; **PDBTitle:** crystal structure of stm2138, a novel virulence chaperone in2 salmonella
40	d1wgwa_	Alignment	not modelled	6.4	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
41	c2e21A_	Alignment	not modelled	6.3	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
42	d1p2za1	Alignment	not modelled	6.3	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Adenovirus hexon
43	c2qbxB_	Alignment	not modelled	6.3	43	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-b receptor 2; **PDBTitle:** ephb2/snew antagonistic peptide complex
44	d1shwb_	Alignment	not modelled	6.3	48	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Ephrin receptor ligand binding domain
45	c3iqtA_	Alignment	not modelled	6.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**signal transduction histidine-protein kinase bara; **PDBTitle:** structure of the hpt domain of sensor protein bara from escherichia2 coli cft073.
46	d2bm8a1	Alignment	not modelled	6.0	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CmcI-like
47	d1rwsa_	Alignment	not modelled	6.0	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
48	d2bbaa1	Alignment	not modelled	5.9	52	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Ephrin receptor ligand binding domain
49	d1p65a_	Alignment	not modelled	5.7	30	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Arterivirus nucleocapsid protein
50	c1p65A_	Alignment	not modelled	5.7	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** crystal structure of the nucleocapsid protein of porcine reproductive2 and respiratory syndrome virus (prrsv)
51	c2qmlA_	Alignment	not modelled	5.5	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bh2621 protein; **PDBTitle:** crystal structure of an uncharacterized protein (bh2621) from bacillus2 halodurans at 1.55 a resolution
52	c2pqrD_	Alignment	not modelled	5.5	41	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**wd repeat protein ykr036c; **PDBTitle:** crystal structure of yeast fis1 complexed with a fragment of yeast2 caf4
53	c1p5lA_	Alignment	not modelled	5.5	30	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution phe5 to ser modification in sds-d252 micelles

54	c3ic8D_	Alignment	not modelled	5.4	37	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
55	c1p0oA_	Alignment	not modelled	5.3	23	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
56	c3c8xA_	Alignment	not modelled	5.2	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** crystal structure of the ligand binding domain of human ephrin a22 (epha2) receptor protein kinase
57	c1p0lA_	Alignment	not modelled	5.2	23	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution gln to trp modification in sds-d252 micelles
58	d1ls1a1	Alignment	not modelled	5.1	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins