Phyre^2

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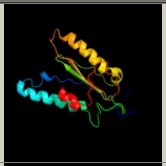
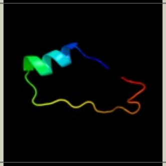
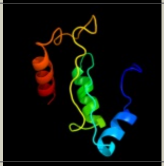
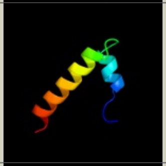
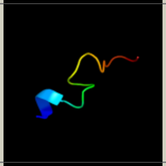
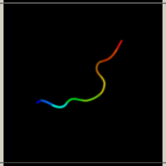
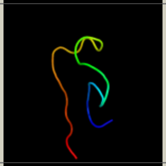
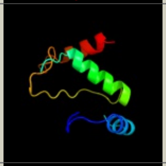
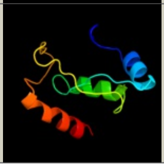
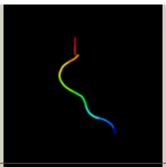
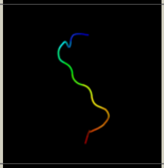
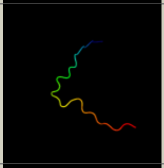
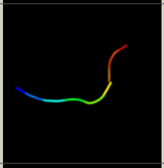
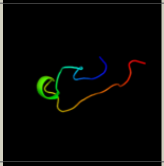
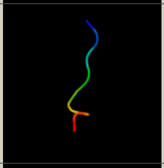
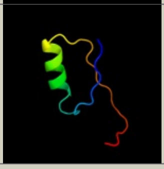
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ps0C_	Alignment		58.6	17	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**crispr-associated protein, csa2; **PDBTitle:** the structure of the crispr-associated protein, csa2, from sulfolobus2 solfataricus
2	c3myfB_	Alignment		51.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
3	c3iqtA_	Alignment		51.2	11	**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.
4	c3itcA_	Alignment		46.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
5	d2ooca1	Alignment		45.5	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**SphA-like
6	c1byvA_	Alignment		35.0	33	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**protein (calcitonin); **PDBTitle:** glycosylated eel calcitonin
7	d1i4pa1	Alignment		28.8	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
8	d2aq2b1	Alignment		27.0	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
9	c2q25C_	Alignment		25.9	8	**PDB header:**virus,hydrolase/rna **Chain:** C: **PDB Molecule:**protein alpha; **PDBTitle:** flock house virus coat protein d75n mutant
10	c2i5gB_	Alignment		23.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
11	c2ragB_	Alignment		23.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus

12	d1bxta1	Alignment		22.6	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
13	d1fnua1	Alignment		20.7	21	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
14	d2brja1	Alignment		20.5	17	**Fold:**AOC barrel-like **Superfamily:**Allene oxide cyclase-like **Family:**Allene oxide cyclase-like
15	d1esfa1	Alignment		19.3	22	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
16	d2bbvc_	Alignment		18.6	8	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Nodaviridae-like VP
17	d2bmta_	Alignment		17.9	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
18	d1enfa1	Alignment		17.9	22	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
19	c3b40A_	Alignment		16.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidase; **PDBTitle:** crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
20	d1nh8a2	Alignment		16.0	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
21	d1itua_	Alignment	not modelled	15.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
22	d1h3da2	Alignment	not modelled	15.5	22	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
23	d1klud1	Alignment	not modelled	14.8	25	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
24	c3fajA_	Alignment	not modelled	14.8	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of the structural protein p131 of the archaeal virus2 acidianus two-tailed virus (atv)
25	d1hywa_	Alignment	not modelled	14.6	17	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
26	c3fdgA_	Alignment	not modelled	14.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
27	d1r46a1	Alignment	not modelled	14.0	10	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
28	d2bbva_	Alignment	not modelled	13.7	8	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Nodaviridae-like VP

29	d1g0da1	Alignment	not modelled	13.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
30	c3oo2B_	Alignment	not modelled	12.9	37	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
31	c2ov7C_	Alignment	not modelled	12.4	13	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** the first domain of the ribosomal protein l1 from thermus2 thermophilus
32	c2jxzA_	Alignment	not modelled	12.0	8	**PDB header:**hormone **Chain:** A: **PDB Molecule:**calcitonin; **PDBTitle:** solution conformation of a non-amyloidogenic analogue of human2 calcitonin in sodium dodecyl sulfate micelles
33	d1vjja1	Alignment	not modelled	12.0	4	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
34	d2ywqa1	Alignment	not modelled	11.8	14	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
35	d1chka_	Alignment	not modelled	11.3	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Chitosanase
36	c3oo2A_	Alignment	not modelled	10.8	37	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
37	d1wd3a1	Alignment	not modelled	10.3	16	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Alpha-L-arabinofuranosidase B, N-terminal domain
38	d1ex0a1	Alignment	not modelled	10.3	4	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
39	c2rqlA_	Alignment	not modelled	10.3	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable sigma-54 modulation protein; **PDBTitle:** solution structure of the e. coli ribosome hibernation2 promoting factor hpf
40	c3iefA_	Alignment	not modelled	10.1	33	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
41	c1p4qA_	Alignment	not modelled	10.0	25	**PDB header:**transcription/transferase **Chain:** A: **PDB Molecule:**cbp/p300-interacting transactivator 2; **PDBTitle:** solution structure of the cited2 transactivation domain in2 complex with the p300 ch1 domain
42	c3lu2B_	Alignment	not modelled	9.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
43	d1oqja_	Alignment	not modelled	9.3	23	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SAND domain
44	d1t56a1	Alignment	not modelled	9.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
45	d2g9hd1	Alignment	not modelled	8.8	22	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
46	c2d44A_	Alignment	not modelled	8.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-l-arabinofuranosidase b; **PDBTitle:** crystal structure of arabinofuranosidase complexed with2 arabinofuranosyl-alpha-1,2-xylobiose
47	d1imua_	Alignment	not modelled	8.5	11	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
48	d2q3za1	Alignment	not modelled	8.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
49	d1h5pa_	Alignment	not modelled	8.1	30	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SAND domain
50	c3tqmD_	Alignment	not modelled	8.0	25	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** structure of an ribosomal subunit interface protein from coxiella2 burnetii
51	d1yfna1	Alignment	not modelled	7.6	23	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
52	c1y8qD_	Alignment	not modelled	7.4	31	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
53	d1ad2a_	Alignment	not modelled	7.3	13	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
54	d1m06f_	Alignment	not modelled	7.2	75	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
55	c2dzlA_	Alignment	not modelled	7.1	24	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**protein fam100b; **PDBTitle:** solution structure of the uba domain in human protein2 fam100b

56	d2id6a1	Alignment	not modelled	7.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
57	c3vh1A_	Alignment	not modelled	7.0	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
58	c1r8uA_	Alignment	not modelled	6.9	25	**PDB header:**transcription/transcription activator **Chain:** A: **PDB Molecule:**cbp/p300-interacting transactivator 2; **PDBTitle:** nmr structure of cbp taz1/cited2 complex
59	d1ufna_	Alignment	not modelled	6.8	23	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SAND domain
60	d1t07a_	Alignment	not modelled	6.7	14	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
61	d2fd5a1	Alignment	not modelled	6.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
62	c2w9jB_	Alignment	not modelled	6.6	43	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle subunit srp14; **PDBTitle:** the crystal structure of srp14 from the schizosaccharomyces2 pombe signal recognition particle
63	d1xs8a_	Alignment	not modelled	6.6	29	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
64	d1scoa_	Alignment	not modelled	6.4	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
65	d1kq1a_	Alignment	not modelled	6.4	80	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
66	d1r5sa_	Alignment	not modelled	6.3	42	**Fold:**Connexin43 **Superfamily:**Connexin43 **Family:**Connexin43
67	d2g7la1	Alignment	not modelled	6.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
68	d2hyja1	Alignment	not modelled	6.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
69	d1nova_	Alignment	not modelled	6.0	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Nodaviridae-like VP
70	c3ixrA_	Alignment	not modelled	5.9	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
71	d1qusa_	Alignment	not modelled	5.8	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
72	c3hsbB_	Alignment	not modelled	5.7	80	**PDB header:**rna binding protein/rna **Chain:** B: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
73	c2b7fD_	Alignment	not modelled	5.7	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**htlv protease; **PDBTitle:** crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design
74	d1u1sa1	Alignment	not modelled	5.7	80	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
75	d1novc_	Alignment	not modelled	5.6	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Nodaviridae-like VP
76	d1hk9a_	Alignment	not modelled	5.5	80	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
77	d1ou9a_	Alignment	not modelled	5.5	26	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
78	c1kq1W_	Alignment	not modelled	5.2	80	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
79	d2oi8a1	Alignment	not modelled	5.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain