Phyre^2

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Description	P77169
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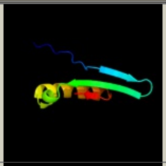
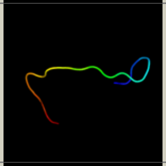
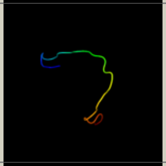
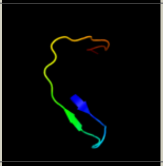
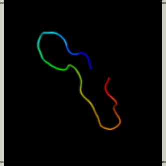
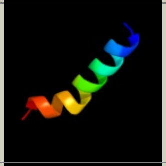
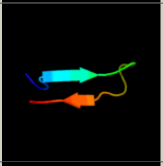
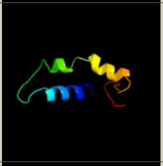
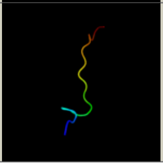
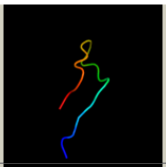
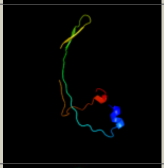
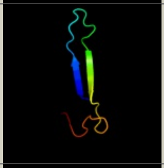
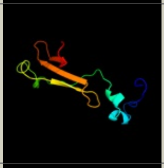
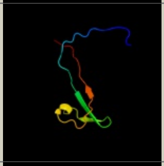
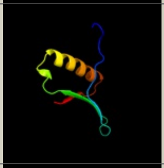
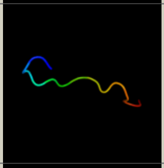
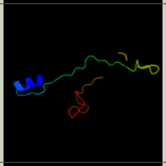
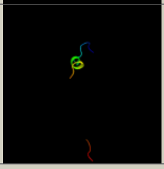
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t0fa2	Alignment		63.7	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**TnsA endonuclease, N-terminal domain
2	d1pk8a1	Alignment		43.2	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Synapsin domain
3	d1i7na1	Alignment		41.3	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Synapsin domain
4	c1i7nA_	Alignment		38.8	15	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
5	c2fqzC_	Alignment		27.8	16	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**r.ecl18ki; **PDBTitle:** metal-depleted ecl18ki in complex with uncleaved dna
6	d2vo1a1	Alignment		21.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
7	c3ctwB_	Alignment		20.2	41	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**rcda; **PDBTitle:** crystal structure of rcda from caulobacter crescentus cb15
8	d1az3a_	Alignment		20.1	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
9	d1sx5a_	Alignment		18.5	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
10	d1cf7b_	Alignment		18.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
11	c2ougC_	Alignment		17.9	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional activator rfah; **PDBTitle:** crystal structure of the rfah transcription factor at 2.1a2 resolution

12	c3bm3A_	Alignment		16.2	42	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**pspgi restriction endonuclease; **PDBTitle:** restriction endonuclease pspgi-substrate dna complex
13	d1c8da_	Alignment		15.8	14	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
14	c2hkeB_	Alignment		14.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diphosphomevalonate decarboxylase, putative; **PDBTitle:** mevalonate diphosphate decarboxylase from trypanosoma brucei
15	d1o7na1	Alignment		14.1	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
16	d1qhda2	Alignment		14.0	19	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
17	c1f1zB_	Alignment		13.9	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tnsa endonuclease; **PDBTitle:** tnsa, a catalytic component of the tn7 transposition system
18	d1x82a_	Alignment		13.8	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
19	d1s58a_	Alignment		13.1	14	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
20	d1m0da_	Alignment		12.2	45	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
21	d2i8da1	Alignment	not modelled	12.0	9	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
22	d2vv5a2	Alignment	not modelled	11.4	28	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
23	d1a21a2	Alignment	not modelled	11.2	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
24	d2raqa1	Alignment	not modelled	10.8	25	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
25	c1k3vA_	Alignment	not modelled	10.7	11	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein vp2; **PDBTitle:** porcine parvovirus capsid
26	d1k3va_	Alignment	not modelled	10.7	11	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
27	c1mtpB_	Alignment	not modelled	10.1	22	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**serine proteinase inhibitor (serpin), chain b; **PDBTitle:** the x-ray crystal structure of a serpin from a thermophilic2 prokaryote
28	d1tf5a2	Alignment	not modelled	10.0	13	**Fold:**Helical scaffold and wing domains of SecA **Superfamily:**Helical scaffold and wing domains of SecA **Family:**Helical scaffold and wing domains of SecA

29	d1uw4a_	Alignment	not modelled	9.9	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Smg-4/UPF3
30	d1g8fa3	Alignment	not modelled	9.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
31	d1gd8a_	Alignment	not modelled	9.8	29	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
32	c3f59A_	Alignment	not modelled	9.2	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin
33	d1na6a2	Alignment	not modelled	9.2	38	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Type II restriction endonuclease catalytic domain
34	d1dfca2	Alignment	not modelled	8.9	10	**Fold:**beta-Trefoil **Superfamily:**Actin-crosslinking proteins **Family:**Fascin
35	d2c1wa1	Alignment	not modelled	8.8	19	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Eukaryotic EndoU ribonuclease
36	d3bpda1	Alignment	not modelled	8.4	25	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
37	c3no0B_	Alignment	not modelled	8.3	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** aquifex aeolicus type iia topoisomerase c-terminal domain
38	d1gxua_	Alignment	not modelled	8.2	9	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
39	c3entB_	Alignment	not modelled	8.2	26	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of nitrollin, a betagamma-crystallin from2 nitrosospira multiformis-in alternate space group (p65)
40	c3a0oB_	Alignment	not modelled	8.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oligo alginate lyase; **PDBTitle:** crystal structure of alginate lyase from agrobacterium tumefaciens c58
41	d1igwa_	Alignment	not modelled	7.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
42	d1e1oa1	Alignment	not modelled	7.7	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
43	d2zjrk1	Alignment	not modelled	7.6	29	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
44	d1k9ca_	Alignment	not modelled	7.6	36	**Fold:**P-domain of calnexin/calreticulin **Superfamily:**P-domain of calnexin/calreticulin **Family:**P-domain of calnexin/calreticulin
45	c2bjeA_	Alignment	not modelled	7.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylphosphatase; **PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
46	c2q1fA_	Alignment	not modelled	7.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase; **PDBTitle:** crystal structure of chondroitin sulfate lyase abc from bacteroides2 thetaiotaomicron wal2926
47	c2eceA_	Alignment	not modelled	7.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**462aa long hypothetical selenium-binding protein; **PDBTitle:** x-ray structure of hypothetical selenium-binding protein2 from sulfolobus tokodaii, st0059
48	d2cqma1	Alignment	not modelled	7.4	21	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
49	d2qamn1	Alignment	not modelled	7.2	36	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
50	c1qhdA_	Alignment	not modelled	7.2	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**viral capsid vp6; **PDBTitle:** crystal structure of vp6, the major capsid protein of group a2 rotavirus
51	c3pisA_	Alignment	not modelled	7.2	32	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kazal-type serine protease inhibitor spi-1; **PDBTitle:** crystal structure of carcinoscorpius rotundicauda serine protease2 inhibitor domain 1
52	d1nz8a_	Alignment	not modelled	7.0	29	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
53	d1sa3a_	Alignment	not modelled	6.7	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease MspI
54	d1r3ha2	Alignment	not modelled	6.5	24	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
						Fold:OB-fold

55	d1krta_	Alignment	not modelled	6.5	21	**Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
56	d1m1ha2	Alignment	not modelled	6.5	6	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
57	d1v97a3	Alignment	not modelled	6.5	15	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
58	d1c4ea_	Alignment	not modelled	6.4	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Gurmarin-like **Family:**Gurmarin, a sweet taste-suppressing polypeptide
59	c2k06A_	Alignment	not modelled	6.3	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of the aminoterminal domain of e. coli2 nusg
60	c3bboP_	Alignment	not modelled	6.3	7	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**ribosomal protein l17; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
61	c3e5bB_	Alignment	not modelled	6.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
62	d1lp3a_	Alignment	not modelled	6.0	11	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Parvoviridae-like VP
63	d2coaa1	Alignment	not modelled	6.0	6	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
64	c2z84A_	Alignment	not modelled	5.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ufm1-specific protease 1; **PDBTitle:** insights from crystal and solution structures of mouse ufsp1
65	d1f61a_	Alignment	not modelled	5.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
66	c2r8rB_	Alignment	not modelled	5.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
67	d2oc6a1	Alignment	not modelled	5.8	17	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
68	d3elna1	Alignment	not modelled	5.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
69	c3hzpA_	Alignment	not modelled	5.8	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
70	c2raxY_	Alignment	not modelled	5.7	19	**PDB header:**cell cycle **Chain:** Y: **PDB Molecule:**borealin; **PDBTitle:** crystal structure of borealin (20-78) bound to survivin (1-120)
71	c3eubL_	Alignment	not modelled	5.7	17	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
72	c3c4mA_	Alignment	not modelled	5.6	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fusion protein of maltose-binding periplasmic protein and **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
73	d1bbua1	Alignment	not modelled	5.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
74	d1w2ia_	Alignment	not modelled	5.5	26	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
75	d1mn3a_	Alignment	not modelled	5.4	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
76	d1apsa_	Alignment	not modelled	5.3	20	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
77	d1urra_	Alignment	not modelled	5.3	33	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
78	c2x3dC_	Alignment	not modelled	5.3	25	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
79	d1ei1a1	Alignment	not modelled	5.3	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
80	d1jhna3	Alignment	not modelled	5.0	36	**Fold:**P-domain of calnexin/calreticulin **Superfamily:**P-domain of calnexin/calreticulin **Family:**P-domain of calnexin/calreticulin

81	d3b9jc1	Alignment	not modelled	5.0	17	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
82	d1z1ba1	Alignment	not modelled	5.0	30	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain