Phyre^2

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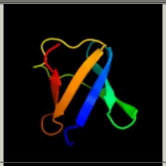
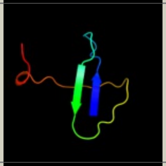
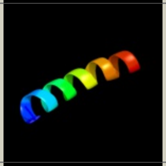
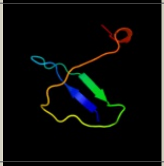
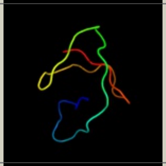
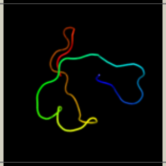
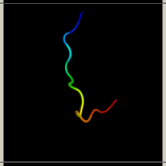
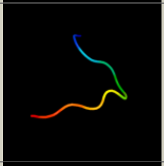
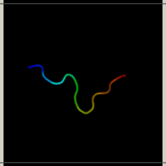
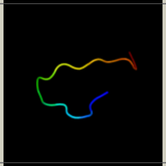
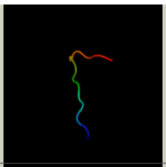
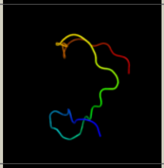
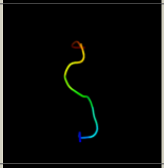
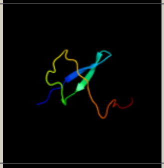
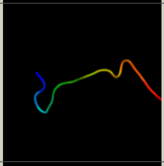
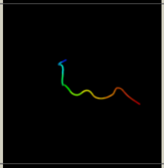
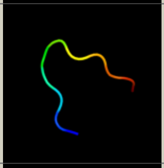
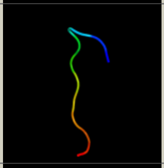
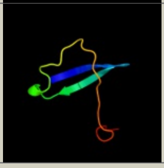
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rcnA_	Alignment		59.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
2	d2awna1	Alignment		50.2	7	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
3	c2lbgA_	Alignment		47.8	55	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles
4	d1oxxk1	Alignment		46.4	13	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
5	c2k14A_	Alignment		44.3	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**yuaf protein; **PDBTitle:** solution structure of the soluble domain of the nfed2 protein yuaf from bacillus subtilis
6	d2gnra1	Alignment		43.1	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
7	c3qz9D_	Alignment		40.9	29	**PDB header:**lyase **Chain:** D: **PDB Molecule:**co-type nitrile hydratase beta subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
8	c2dxcG_	Alignment		40.8	36	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
9	d1ugpb_	Alignment		39.9	21	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
10	c2jvvA_	Alignment		38.8	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
11	c2kvqG_	Alignment		38.8	29	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex

12	d1v29b_	Alignment		38.7	29	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
13	d1q1ca1	Alignment		38.6	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	c2e6zA_	Alignment		36.6	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
15	c1h9mB_	Alignment		33.5	20	**PDB header:**binding protein **Chain:** B: **PDB Molecule:**molybdenum-binding-protein; **PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
16	d1nppa2	Alignment		31.6	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
17	d1nz9a_	Alignment		30.1	31	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
18	d2qdyb1	Alignment		25.6	55	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
19	d2do3a1	Alignment		25.4	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
20	c1h9sA_	Alignment		24.0	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**molybdenum transport protein mode; **PDBTitle:** molybdate bound complex of dimop domain of mode from e.coli
21	d1h9ma1	Alignment	not modelled	23.8	19	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
22	d2zgwa1	Alignment	not modelled	20.4	43	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
23	d2zjrm1	Alignment	not modelled	19.9	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
24	d2vv5a1	Alignment	not modelled	18.8	25	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
25	c3cp0A_	Alignment	not modelled	18.8	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
26	d1guta_	Alignment	not modelled	18.6	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
27	c2yv5A_	Alignment	not modelled	18.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
28	d1u0la1	Alignment	not modelled	17.9	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

29	d1h9ra1	Alignment	not modelled	17.4	12	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
30	d2jnaa1	Alignment	not modelled	16.5	20	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
31	c3zvkG_	Alignment	not modelled	15.8	21	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
32	c3gd7C_	Alignment	not modelled	15.6	7	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fusion complex of cystic fibrosis transmembrane **PDBTitle:** crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
33	d1fr3a_	Alignment	not modelled	15.4	10	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
34	c1rouA_	Alignment	not modelled	15.3	24	**PDB header:**rotamase (isomerase) **Chain:** A: **PDB Molecule:**fkbp59-i; **PDBTitle:** structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
35	d1h9ma2	Alignment	not modelled	15.3	20	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
36	c2k8iA_	Alignment	not modelled	14.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
37	c2fhdA_	Alignment	not modelled	14.5	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
38	d1ah9a_	Alignment	not modelled	14.2	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c3hfwA_	Alignment	not modelled	13.6	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
40	d1h9ra2	Alignment	not modelled	13.5	24	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
41	c2kfwA_	Alignment	not modelled	12.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
42	c3i4oA_	Alignment	not modelled	12.6	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
43	c4a2iV_	Alignment	not modelled	11.5	16	**PDB header:**ribosome/hydrolase **Chain:** V: **PDB Molecule:**putative ribosome biogenesis gtpase rsga; **PDBTitle:** cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
44	d1pkla3	Alignment	not modelled	11.3	15	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
45	d1fdra1	Alignment	not modelled	11.2	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
46	d1hh2p1	Alignment	not modelled	11.0	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	d2cowa1	Alignment	not modelled	11.0	13	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
48	d1v6ga2	Alignment	not modelled	9.8	42	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
49	c3zv0D_	Alignment	not modelled	9.2	11	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1p-cbf5p complex
50	c3jt0B_	Alignment	not modelled	8.8	29	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
51	d2asba1	Alignment	not modelled	8.7	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
52	c2qtyB_	Alignment	not modelled	8.6	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
53	d1v43a2	Alignment	not modelled	8.4	21	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
54	d1t5ja_	Alignment	not modelled	8.3	50	**Fold:**ADP-ribosylglycohydrolase **Superfamily:**ADP-ribosylglycohydrolase **Family:**ADP-ribosylglycohydrolase
						Fold: GroES-like

55	d1uufa1	Alignment	not modelled	8.1	26	**Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
56	d1whha_	Alignment	not modelled	7.7	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
57	c2e12B_	Alignment	not modelled	7.2	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**hypothetical protein xcc3642; **PDBTitle:** the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
58	d1e2wa2	Alignment	not modelled	7.1	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
59	d3d31a1	Alignment	not modelled	6.9	24	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
60	c1zeqX_	Alignment	not modelled	6.8	14	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
61	c2wocA_	Alignment	not modelled	6.7	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosyl-[dinitrogen reductase] glycohydrolase; **PDBTitle:** crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
62	c2yzwA_	Alignment	not modelled	6.6	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
63	c1m1gB_	Alignment	not modelled	6.6	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
64	c3k6oA_	Alignment	not modelled	6.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf1344; **PDBTitle:** crystal structure of protein of unknown function duf13442 (yp_001299214.1) from bacteroides vulgatus atcc 8482 at 2.00 a3 resolution
65	d2gycn1	Alignment	not modelled	6.6	27	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
66	d2q07a1	Alignment	not modelled	6.5	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
67	c1u0lB_	Alignment	not modelled	6.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
68	d2qqsa2	Alignment	not modelled	6.4	23	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
69	d1whka_	Alignment	not modelled	6.1	27	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
70	c1vciA_	Alignment	not modelled	6.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar-binding transport atp-binding protein; **PDBTitle:** crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
71	d2coya1	Alignment	not modelled	5.9	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
72	c2vv5D_	Alignment	not modelled	5.9	25	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
73	d1iq8a3	Alignment	not modelled	5.8	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
74	c3g9dB_	Alignment	not modelled	5.7	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
75	d1i4ma_	Alignment	not modelled	5.6	33	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
76	c2kr7A_	Alignment	not modelled	5.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
77	d2ccwa1	Alignment	not modelled	5.4	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
78	c2k5hA_	Alignment	not modelled	5.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
79	d1r9ha_	Alignment	not modelled	5.3	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
80	d1tova_	Alignment	not modelled	5.3	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain

81	d1g2914	Alignment	not modelled	5.3	24	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
82	c3k8rA_	Alignment	not modelled	5.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
83	d1ex4a1	Alignment	not modelled	5.2	33	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase