Phyre^2

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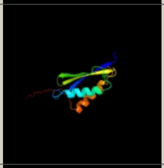
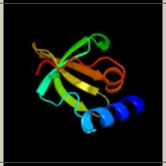
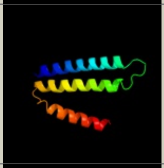
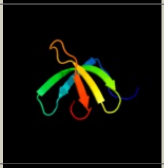
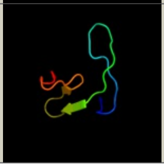
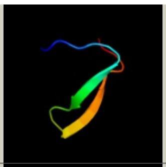
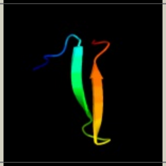
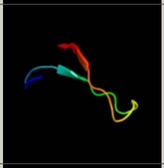
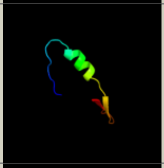
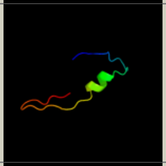
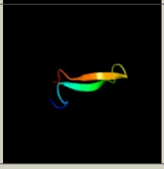
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vv5D_	Alignment		100.0	22	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
2	d2vv5a2	Alignment		99.7	20	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
3	d2vv5a1	Alignment		99.7	27	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
4	d2vv5a3	Alignment		98.9	21	**Fold:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Superfamily:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Family:**Mechanosensitive channel protein MscS (YggB), transmembrane region
5	d2hqha1	Alignment		77.2	30	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
6	d1nppa2	Alignment		74.7	39	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
7	d1nz9a_	Alignment		74.5	31	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
8	c2e6zA_	Alignment		73.3	17	**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
9	c2kvqG_	Alignment		71.4	26	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
10	c2jvvA_	Alignment		71.4	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
11	c2zkrt_	Alignment		61.5	15	**PDB header:**ribosomal protein/rna **Chain:** T: **PDB Molecule:**rna expansion segment es39 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map

12	d2coya1	Alignment		57.1	32	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
13	c3p8bB_	Alignment		52.7	17	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
14	c3cnrA_	Alignment		52.3	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**type iv fimbriae assembly protein; **PDBTitle:** crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
15	d1whka_	Alignment		50.7	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
16	d2cqaa1	Alignment		50.4	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
17	d2eyqa1	Alignment		48.1	22	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
18	d2gvha1	Alignment		47.4	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
19	d1y7ua1	Alignment		45.1	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
20	d1whma_	Alignment		44.7	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
21	c2gvhC_	Alignment	not modelled	44.5	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**agr_l_2016p; **PDBTitle:** crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
22	c4a1cS_	Alignment	not modelled	43.7	18	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
23	c1dvpA_	Alignment	not modelled	39.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
24	d1vqot1	Alignment	not modelled	38.8	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
25	d1u0la1	Alignment	not modelled	38.5	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	d1vpma_	Alignment	not modelled	37.5	23	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
27	c1m1gB_	Alignment	not modelled	36.7	39	**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)
						Fold:SH3-like barrel

28	d2cp6a1	Alignment	not modelled	36.3	29	**Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
29	d2g50a1	Alignment	not modelled	35.6	14	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
30	c3b7kA_	Alignment	not modelled	35.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
31	d2e3ia1	Alignment	not modelled	35.3	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
32	c1mv3A_	Alignment	not modelled	34.7	20	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**myc box dependent interacting protein 1; **PDBTitle:** nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc
33	c2rcnA_	Alignment	not modelled	34.5	23	**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.
34	d1t9ha1	Alignment	not modelled	34.4	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	c3iz5Y_	Alignment	not modelled	33.3	23	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
36	d2cp5a1	Alignment	not modelled	33.2	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
37	c2qq2C_	Alignment	not modelled	32.9	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosolic acyl coenzyme a thioester hydrolase; **PDBTitle:** crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
38	d1e0ta1	Alignment	not modelled	32.5	19	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
39	d2cp0a1	Alignment	not modelled	32.5	19	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
40	d1ylia1	Alignment	not modelled	31.4	30	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
41	d2coza1	Alignment	not modelled	28.3	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
42	d2do3a1	Alignment	not modelled	28.3	16	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
43	d2cp2a1	Alignment	not modelled	28.1	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
44	d1whja_	Alignment	not modelled	27.9	23	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
45	c2yv5A_	Alignment	not modelled	27.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
46	c2e4hA_	Alignment	not modelled	27.0	30	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
47	d1pkma1	Alignment	not modelled	27.0	16	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
48	c2eisA_	Alignment	not modelled	26.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein tthb207; **PDBTitle:** x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
49	d1pkla1	Alignment	not modelled	26.2	19	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
50	c2z0wA_	Alignment	not modelled	25.5	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cap-gly domain-containing linker protein 4; **PDBTitle:** crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
51	d1vqoq1	Alignment	not modelled	25.3	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
52	d2cp3a1	Alignment	not modelled	24.9	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
53	d2gvha2	Alignment	not modelled	24.9	23	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
54	d2e3ha1	Alignment	not modelled	24.7	29	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain

55	d2bi0a1	Alignment	not modelled	24.3	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
56	c3d6lA_	Alignment	not modelled	24.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
57	c2v1oF_	Alignment	not modelled	23.9	7	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cytosolic acyl coenzyme a thioester hydrolase; **PDBTitle:** crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
58	c2dxcG_	Alignment	not modelled	23.6	41	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
59	c1oy8A_	Alignment	not modelled	22.8	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
60	d2cowa1	Alignment	not modelled	22.7	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
61	d1whha_	Alignment	not modelled	22.6	21	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
62	c2qqsB_	Alignment	not modelled	22.1	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
63	c3mlcC_	Alignment	not modelled	21.8	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
64	d1yeza1	Alignment	not modelled	21.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
65	c3h0mE_	Alignment	not modelled	21.3	10	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
66	c3qz9D_	Alignment	not modelled	20.7	45	**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.
67	d1v6ga2	Alignment	not modelled	20.2	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
68	c2k4kA_	Alignment	not modelled	19.2	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
69	d1yvca1	Alignment	not modelled	19.0	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
70	d1ppje2	Alignment	not modelled	18.8	24	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
71	d1s04a_	Alignment	not modelled	18.6	26	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
72	c2khjA_	Alignment	not modelled	18.1	15	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
73	c2kcuA_	Alignment	not modelled	18.1	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ctr107; **PDBTitle:** nmr solution structure of an uncharacterized protein from2 chlorobium tepidum. northeast structural genomics target3 ctr107
74	d1a3xa1	Alignment	not modelled	17.7	19	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
75	c3pifD_	Alignment	not modelled	17.5	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**5'->3' exoribonuclease (xrn1); **PDBTitle:** crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
76	d1liua1	Alignment	not modelled	17.4	32	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
77	c1u0lB_	Alignment	not modelled	16.2	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
78	d2z0sa1	Alignment	not modelled	16.2	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
79	d1v29b_	Alignment	not modelled	15.8	36	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
80	c2xdpA_	Alignment	not modelled	14.7	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c; **PDBTitle:** crystal structure of the tudor domain of human jmjd2c

81	d2j01t1	Alignment	not modelled	14.6	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
82	c1s1iU_	Alignment	not modelled	14.1	18	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l26-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
83	c2xhcA_	Alignment	not modelled	14.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
84	d1i9ga_	Alignment	not modelled	13.5	42	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
85	d1bcce2	Alignment	not modelled	13.0	24	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
86	d3bzka4	Alignment	not modelled	12.6	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
87	d1sroa_	Alignment	not modelled	12.6	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
88	d1oqka_	Alignment	not modelled	12.5	30	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
89	d2je6i1	Alignment	not modelled	12.4	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
90	d1xnea_	Alignment	not modelled	12.4	30	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
91	c3a35B_	Alignment	not modelled	12.3	10	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**lumazine protein; **PDBTitle:** crystal structure of lump complexed with riboflavin
92	c1t9hA_	Alignment	not modelled	12.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
93	c3iz5U_	Alignment	not modelled	12.2	17	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
94	d1ugpb_	Alignment	not modelled	12.1	52	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
95	d2qdya1	Alignment	not modelled	12.1	11	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
96	c1t0jA_	Alignment	not modelled	12.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**voltage-gated calcium channel subunit beta2a; **PDBTitle:** crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
97	d2zjrm1	Alignment	not modelled	11.7	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
98	c2z0sA_	Alignment	not modelled	11.6	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable exosome complex rna-binding protein 1; **PDBTitle:** crystal structure of putative exosome complex rna-binding2 protein
99	d2p13a1	Alignment	not modelled	11.5	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like