Phyre^2

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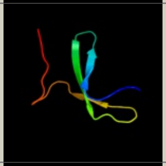
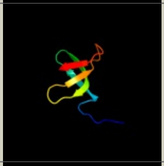
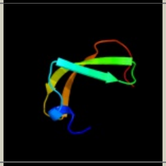
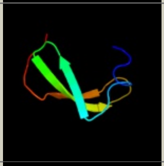
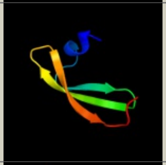
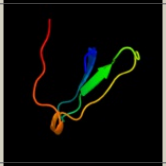
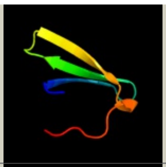
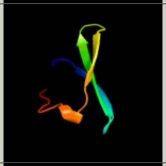
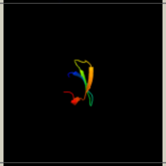
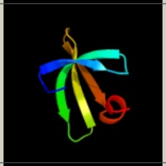
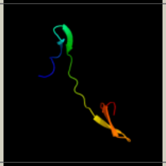
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rddB_	Alignment		99.1	100	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
2	c2j5uB_	Alignment		88.7	27	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
3	c2qf4A_	Alignment		88.1	35	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cell shape determining protein mrec; **PDBTitle:** high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
4	d2do3a1	Alignment		83.5	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
5	d1pkma1	Alignment		77.4	12	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
6	d2g50a1	Alignment		76.9	12	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
7	d1a3xa1	Alignment		73.8	14	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
8	d1pkla1	Alignment		72.7	9	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
9	d1liua1	Alignment		72.6	12	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
10	c1kq1W_	Alignment		70.4	6	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
11	c3qhsD_	Alignment		68.5	18	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of full-length hfq from escherichia coli

12	d1hk9a_	Alignment		67.5	18	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
13	c2vv5D_	Alignment		64.6	26	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
14	d1u1sa1	Alignment		63.3	18	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
15	d2oara1	Alignment		60.6	16	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
16	c2e70A_	Alignment		56.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the fifth kow motif of human2 transcription elongation factor spt5
17	d2vv5a1	Alignment		56.2	26	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
18	d2cp6a1	Alignment		55.4	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
19	c2qqsB_	Alignment		54.5	24	**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
20	c2e6zA_	Alignment		52.5	26	**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
21	c3hsbB_	Alignment	not modelled	51.1	18	**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
22	c2l8kA_	Alignment	not modelled	51.0	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
23	c2equA_	Alignment	not modelled	49.8	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
24	c3qiiA_	Alignment	not modelled	49.5	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
25	c3m9bK_	Alignment	not modelled	49.4	7	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
26	d3bzka4	Alignment	not modelled	47.7	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
27	c2oarA_	Alignment	not modelled	47.5	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
28	d1e0ta1	Alignment	not modelled	43.7	17	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain

29	c1rl2A_	Alignment	not modelled	43.5	20	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**protein (ribosomal protein l2); **PDBTitle:** ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
30	c3nx6A_	Alignment	not modelled	41.4	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**10kda chaperonin; **PDBTitle:** crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
31	c2xdpA_	Alignment	not modelled	38.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c; **PDBTitle:** crystal structure of the tudor domain of human jmjd2c
32	d2j01d1	Alignment	not modelled	38.0	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
33	c4a1cA_	Alignment	not modelled	36.6	17	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**rpl8; **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.
34	c2khiA_	Alignment	not modelled	36.3	16	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
35	d1pw4a_	Alignment	not modelled	36.1	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
36	c2jwaA_	Alignment	not modelled	35.5	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
37	c3d5bD_	Alignment	not modelled	34.7	13	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
38	c2ivwA_	Alignment	not modelled	33.9	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**pilp pilot protein; **PDBTitle:** the solution structure of a domain from the neisseria2 meningitidis pilp pilot protein.
39	c2dzcA_	Alignment	not modelled	33.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin--[acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from pyrococcus2 horikoshii, mutation r48a
40	d2qamc1	Alignment	not modelled	32.4	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
41	d1aono_	Alignment	not modelled	31.1	21	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
42	d1p3ha_	Alignment	not modelled	30.3	25	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
43	d2isba1	Alignment	not modelled	30.2	25	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
44	d2ar1a1	Alignment	not modelled	28.7	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
45	c1aqfB_	Alignment	not modelled	28.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
46	c1kqsA_	Alignment	not modelled	27.8	11	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**ribosomal protein l2; **PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
47	d1vqot1	Alignment	not modelled	27.3	31	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
48	d1we3o_	Alignment	not modelled	27.0	19	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
49	d2zjrr1	Alignment	not modelled	26.7	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
50	d1rl2a1	Alignment	not modelled	26.6	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
51	c2pqaB_	Alignment	not modelled	26.5	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
52	c2khjA_	Alignment	not modelled	26.2	34	**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
53	c3iz5Y_	Alignment	not modelled	25.9	34	**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
54	c3pifD_	Alignment	not modelled	25.8	26	**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

55	c3qnqD_	Alignment	not modelled	25.6	8	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
56	d1ib8a1	Alignment	not modelled	25.5	21	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
57	d2pi2e1	Alignment	not modelled	25.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
58	c3bdlA_	Alignment	not modelled	25.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing **PDBTitle:** crystal structure of a truncated human tudor-sn
59	c3p8bB_	Alignment	not modelled	24.4	30	**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
60	d1tova_	Alignment	not modelled	23.9	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
61	c1dbgA_	Alignment	not modelled	23.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
62	c4a1cS_	Alignment	not modelled	23.6	41	**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.
63	d2evea1	Alignment	not modelled	23.4	26	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
64	d1a8pa1	Alignment	not modelled	22.9	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
65	c3hfoC_	Alignment	not modelled	22.8	14	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**ssr3341 protein; **PDBTitle:** crystal structure of an hfq protein from synechocystis sp.
66	d1sroa_	Alignment	not modelled	22.8	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
67	c2y35A_	Alignment	not modelled	20.3	23	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ld22664p; **PDBTitle:** crystal structure of xrn1-substrate complex
68	c1vpzB_	Alignment	not modelled	20.3	21	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**carbon storage regulator homolog; **PDBTitle:** crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
69	c3pr9A_	Alignment	not modelled	19.0	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
70	c2jvvA_	Alignment	not modelled	18.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
71	c2kvqG_	Alignment	not modelled	18.7	23	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
72	c2jppB_	Alignment	not modelled	18.6	13	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**translational repressor; **PDBTitle:** structural basis of rsma/csra rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
73	c3qglD_	Alignment	not modelled	18.5	31	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
74	d1vpza_	Alignment	not modelled	18.3	21	**Fold:**CsrA-like **Superfamily:**CsrA-like **Family:**CsrA-like
75	c2dluA_	Alignment	not modelled	17.9	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the second pdz domain of human inad-2 like protein
76	c3ma8A_	Alignment	not modelled	17.8	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
77	d1g31a_	Alignment	not modelled	17.7	36	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
78	c2lc4A_	Alignment	not modelled	17.6	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**pilp protein; **PDBTitle:** solution structure of pilp from pseudomonas aeruginosa
79	d1wfva_	Alignment	not modelled	17.6	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like

						Family:PDZ domain
80	d1nxza1	Alignment	not modelled	17.4	3	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
81	d1x5qa1	Alignment	not modelled	17.4	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	d1fdra1	Alignment	not modelled	17.4	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
83	d2g2xa1	Alignment	not modelled	17.3	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
84	c3e0vB_	Alignment	not modelled	17.3	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
85	d1fnda1	Alignment	not modelled	17.1	30	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
86	c2e4hA_	Alignment	not modelled	17.0	32	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
87	c2he4A_	Alignment	not modelled	16.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf2; **PDBTitle:** the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
88	d2eyqa1	Alignment	not modelled	16.8	15	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
89	d2cp2a1	Alignment	not modelled	16.6	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
90	d2bmwa1	Alignment	not modelled	16.4	35	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
91	d1nz9a_	Alignment	not modelled	16.3	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
92	c2q9vA_	Alignment	not modelled	16.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the c890s mutant of the 4th pdz domain of human2 membrane associated guanylate kinase
93	d1xnea_	Alignment	not modelled	16.0	26	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
94	d2cp0a1	Alignment	not modelled	15.8	27	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
95	d1h9ra2	Alignment	not modelled	15.6	20	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
96	c1t5aB_	Alignment	not modelled	15.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
97	d2piaa1	Alignment	not modelled	15.1	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
98	c2p5dA_	Alignment	not modelled	15.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0310 protein mjecl36; **PDBTitle:** crystal structure of mjecl36 from methanocaldococcus2 jannaschii dsm 2661
99	c3iz5G_	Alignment	not modelled	14.9	23	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein l6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome