Phyre^2

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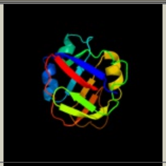
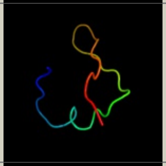
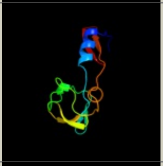
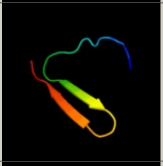
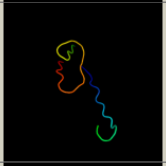
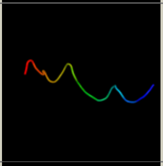
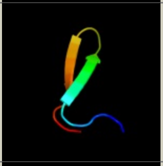
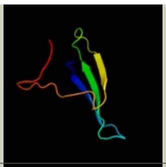
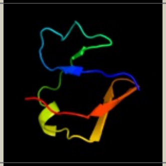
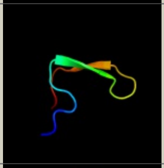
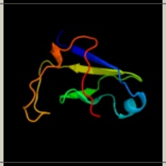
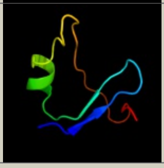
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f9ha1	Alignment		100.0	30	**Fold:**PTSIIA/GutA-like **Superfamily:**PTSIIA/GutA-like **Family:**PTSIIA/GutA-like
2	c2xdpA_	Alignment		74.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c; **PDBTitle:** crystal structure of the tudor domain of human jmjd2c
3	d1k0ha_	Alignment		37.8	16	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
4	d2gp4a1	Alignment		37.7	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
5	c2qqsB_	Alignment		30.4	15	**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
6	d1p9ka_	Alignment		27.8	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
7	c2jqlA_	Alignment		27.1	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
8	c3vg8F_	Alignment		26.1	41	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**hypothetical protein tthb210; **PDBTitle:** crystal structure of hypothetical protein tthb210 from thermus2 thermophilus hb8
9	c3a5zF_	Alignment		26.0	29	**PDB header:**ligase **Chain:** F: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p
10	d1ueba1	Alignment		23.9	14	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
11	c3cpfB_	Alignment		23.5	12	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-1; **PDBTitle:** crystal structure of human eukaryotic translation initiation factor2 eif5a

12	c2fhdA_	Alignment		22.9	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
13	d2g50a1	Alignment		22.2	12	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
14	d2vv5a1	Alignment		20.9	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
15	d1kzla2	Alignment		20.8	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
16	c1xtdA_	Alignment		20.5	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic initiation factor 5a; **PDBTitle:** structural analysis of leishmania mexicana eukaryotic initiation2 factor 5a
17	d2pp6a1	Alignment		20.5	25	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
18	d1k8ga2	Alignment		20.3	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
19	d1i8da2	Alignment		19.2	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
20	c2fphX_	Alignment		19.1	11	**PDB header:**dna binding protein **Chain:** X: **PDB Molecule:**ylmh; **PDBTitle:** cell division protein ylmh from streptococcus pneumoniae
21	c3hksB_	Alignment	not modelled	18.8	14	**PDB header:**translation, rna binding protein **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
22	c1bkbA_	Alignment	not modelled	18.3	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
23	d1liua1	Alignment	not modelled	17.3	10	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
24	c3treA_	Alignment	not modelled	17.2	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of a translation elongation factor p (efp) from coxiella2 burnetii
25	d1pkma1	Alignment	not modelled	16.8	12	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
26	c2v43A_	Alignment	not modelled	16.7	12	**PDB header:**regulator **Chain:** A: **PDB Molecule:**sigma-e factor regulatory protein rseb; **PDBTitle:** crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
27	d1jb7a2	Alignment	not modelled	16.7	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
28	c3degC_	Alignment	not modelled	16.5	19	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp

29	c3er0A_	Alignment	not modelled	16.4	7	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of the full length eif5a from2 saccharomyces cerevisiae
30	d2cqaa1	Alignment	not modelled	16.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
31	c2jkdB_	Alignment	not modelled	15.8	22	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex
32	d1a3xa1	Alignment	not modelled	14.5	7	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
33	d1mzka_	Alignment	not modelled	14.4	11	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
34	c2eifA_	Alignment	not modelled	13.7	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (eukaryotic translation initiation factor 5a); **PDBTitle:** eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
35	c3igzB_	Alignment	not modelled	13.5	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
36	c2kzbA_	Alignment	not modelled	13.5	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**autophagy-related protein 19; **PDBTitle:** solution structure of alpha-mannosidase binding domain of atg19
37	d1udxa3	Alignment	not modelled	13.1	11	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
38	d1bdoa_	Alignment	not modelled	12.8	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
39	c1r21A_	Alignment	not modelled	12.7	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
40	d2c78a1	Alignment	not modelled	12.3	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
41	c2z14A_	Alignment	not modelled	12.1	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ef-hand domain-containing family member c2; **PDBTitle:** crystal structure of the n-terminal duf1126 in human ef-2 hand domain containing 2 protein
42	d1e0ta1	Alignment	not modelled	11.9	18	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
43	d2dy1a1	Alignment	not modelled	11.8	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
44	d2affa1	Alignment	not modelled	11.4	11	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
45	c1uebB_	Alignment	not modelled	11.2	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of translation elongation factor p from2 thermus thermophilus hb8
46	c2vv5D_	Alignment	not modelled	11.1	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
47	d1njjb1	Alignment	not modelled	11.1	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
48	d1awwa_	Alignment	not modelled	11.1	9	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
49	c3gqsB_	Alignment	not modelled	11.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
50	d1kzla1	Alignment	not modelled	10.9	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
51	c2jpeA_	Alignment	not modelled	10.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear inhibitor of protein phosphatase 1; **PDBTitle:** fha domain of nipp1
52	d1s04a_	Alignment	not modelled	10.6	24	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
53	c3oyyA_	Alignment	not modelled	10.5	5	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of pseudomonas aeruginosa elongation factor p
54	d2phcb1	Alignment	not modelled	10.5	29	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like

55	d1gl4a1	Alignment	not modelled	10.3	18	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Domain G2 of nidogen-1
56	c2phcB_	Alignment	not modelled	10.3	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
57	d1f60a1	Alignment	not modelled	10.3	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
58	d1o8ba1	Alignment	not modelled	10.2	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
59	c1i8dB_	Alignment	not modelled	10.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of riboflavin synthase
60	c1a3wB_	Alignment	not modelled	9.7	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
61	d1mkfa_	Alignment	not modelled	9.6	21	**Fold:**Viral chemokine binding protein m3 **Superfamily:**Viral chemokine binding protein m3 **Family:**Viral chemokine binding protein m3
62	c3elsA_	Alignment	not modelled	9.6	22	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204
63	c1iz6B_	Alignment	not modelled	9.6	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**initiation factor 5a; **PDBTitle:** crystal structure of translation initiation factor 5a from pyrococcus2 horikoshii
64	c3poaA_	Alignment	not modelled	9.5	28	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
65	d1yjma1	Alignment	not modelled	9.0	35	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
66	d2g1la1	Alignment	not modelled	8.8	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
67	c2kzkA_	Alignment	not modelled	8.8	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein yol083w; **PDBTitle:** solution structure of alpha-mannosidase binding domain of atg34
68	c1ybyB_	Alignment	not modelled	8.6	24	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation elongation factor p; **PDBTitle:** conserved hypothetical protein cth-95 from clostridium2 thermocellum
69	c3fm8A_	Alignment	not modelled	8.3	29	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
70	d1pkla1	Alignment	not modelled	8.3	12	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
71	d1bkba1	Alignment	not modelled	8.3	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
72	d2qqra2	Alignment	not modelled	8.2	17	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
73	c2zpmA_	Alignment	not modelled	8.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
74	c3e20A_	Alignment	not modelled	8.1	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
75	d2g82a1	Alignment	not modelled	7.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	c1h4uA_	Alignment	not modelled	7.7	20	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
77	d1gtta1	Alignment	not modelled	7.5	12	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
78	d2zjrm1	Alignment	not modelled	7.4	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
79	d3etja1	Alignment	not modelled	7.4	44	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
80	d2p13a1	Alignment	not modelled	7.4	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
81	d1o8bb1	Alignment	not modelled	7.3	31	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
						PDB header:structural genomics, unknown function

82	c3gmgB_	Alignment	not modelled	7.3	15	**Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
83	d2eifa1	Alignment	not modelled	7.3	14	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
84	c2p5dA_	Alignment	not modelled	7.3	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0310 protein mjecl36; **PDBTitle:** crystal structure of mjecl36 from methanocaldococcus2 jannaschii dsm 2661
85	c3gqjA_	Alignment	not modelled	7.2	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cell inhibiting factor (cif); **PDBTitle:** crystal structure of cell inhibiting factor (cif) from photorhabdus2 luminescens
86	d2brfa1	Alignment	not modelled	7.1	29	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
87	d1iz6a1	Alignment	not modelled	7.0	14	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
88	c3llbA_	Alignment	not modelled	7.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
89	d3deda1	Alignment	not modelled	7.0	11	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
90	c1yj5C_	Alignment	not modelled	7.0	35	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
91	d2cowa1	Alignment	not modelled	6.9	29	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
92	d1f3ta1	Alignment	not modelled	6.7	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
93	c3hx1B_	Alignment	not modelled	6.6	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
94	d2plia1	Alignment	not modelled	6.5	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
95	d2o3ga1	Alignment	not modelled	6.5	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
96	c3cfuA_	Alignment	not modelled	6.5	28	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
97	d2toda1	Alignment	not modelled	6.5	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
98	d2o1ra1	Alignment	not modelled	6.4	11	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
99	d2ff4a3	Alignment	not modelled	6.4	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain