Phyre2

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Description	P45577
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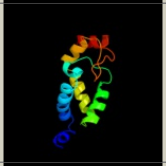
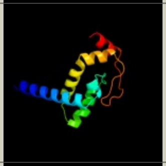
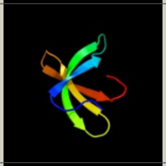
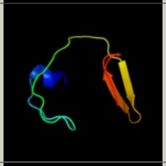
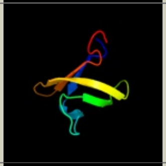
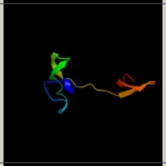
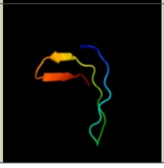
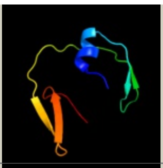
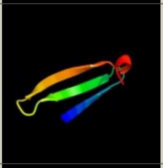
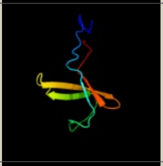
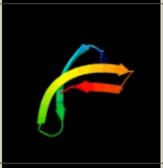
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dvoa_	Alignment		100.0	26	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
2	d2hxja1	Alignment		100.0	21	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
3	c2hxjF_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein of unknown function nmb1681 from2 neisseria meningitidis mc58, possible nucleic acid binding protein
4	c2e70A_	Alignment		91.3	26	**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
5	c3qiiA_	Alignment		88.1	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
6	c3p8dB_	Alignment		82.0	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**medulloblastoma antigen mu-mb-50.72; **PDBTitle:** crystal structure of the second tudor domain of human phf20 (homodimer2 form)
7	c2in0A_	Alignment		74.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease pi-mtui; **PDBTitle:** crystal structure of mtu reca intein splicing domain
8	c2k8iA_	Alignment		72.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
9	c2equA_	Alignment		70.9	20	**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
10	c2qqsB_	Alignment		67.8	13	**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
11	d1nxza1	Alignment		66.8	31	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like

12	c1zd7B_	Alignment		61.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803
13	c3dlmA_	Alignment		61.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setdb1; **PDBTitle:** crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
14	d2ix0a3	Alignment		60.8	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
15	d1kk1a2	Alignment		59.6	19	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
16	c2kfwA_	Alignment		58.9	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
17	c3d0fA_	Alignment		57.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
18	d1s0ua2	Alignment		56.4	20	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
19	d2qn6a2	Alignment		55.8	21	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
20	d3bzka4	Alignment		55.0	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	d1sroa_	Alignment	not modelled	54.9	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	c2xdpA_	Alignment	not modelled	51.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c; **PDBTitle:** crystal structure of the tudor domain of human jmjd2c
23	d1at0a_	Alignment	not modelled	48.5	18	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Hedgehog C-terminal (Hog) autoprocessing domain
24	c2k52A_	Alignment	not modelled	47.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1198; **PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
25	d1kl9a2	Alignment	not modelled	44.0	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	d2do3a1	Alignment	not modelled	43.2	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
27	d1ib8a1	Alignment	not modelled	40.9	24	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
28	d1biaa2	Alignment	not modelled	38.6	15	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
						PDB header:transcription

29	c2kvqG_	Alignment	not modelled	36.9	18	**Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
30	c2jvvA_	Alignment	not modelled	36.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
31	d1vqoq1	Alignment	not modelled	36.7	29	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
32	d1kk8a1	Alignment	not modelled	35.7	13	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
33	d1whma_	Alignment	not modelled	33.5	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
34	c2khiA_	Alignment	not modelled	32.8	20	**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	c2keqA_	Alignment	not modelled	31.8	9	**PDB header:**splicing **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit, nucleic acid **PDBTitle:** solution structure of dnae intein from nostoc punctiforme
36	c2khjA_	Alignment	not modelled	31.8	24	**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
37	c3p8bB_	Alignment	not modelled	30.0	25	**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
38	d1nppa2	Alignment	not modelled	29.5	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
39	c2ix1A_	Alignment	not modelled	28.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
40	c2hbpA_	Alignment	not modelled	28.3	24	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
41	c3q9qB_	Alignment	not modelled	26.6	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
42	d1wgka_	Alignment	not modelled	26.6	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
43	c1ssfA_	Alignment	not modelled	26.4	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**transformation related protein 53 binding **PDBTitle:** solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
44	c1zeqX_	Alignment	not modelled	25.9	17	**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
45	c2egwB_	Alignment	not modelled	25.5	9	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
46	c2ckkA_	Alignment	not modelled	25.1	16	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**kin17; **PDBTitle:** high resolution crystal structure of the human kin172 c-terminal domain containing a kow motif3 kin17.
47	c2cghB_	Alignment	not modelled	24.9	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin ligase; **PDBTitle:** crystal structure of biotin ligase from mycobacterium2 tuberculosis
48	c1vhkA_	Alignment	not modelled	24.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
49	c2imzA_	Alignment	not modelled	23.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease pi-mtui; **PDBTitle:** crystal structure of mtu reca intein splicing domain
50	d1nz9a_	Alignment	not modelled	23.4	29	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
51	c2eayB_	Alignment	not modelled	23.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin [acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from aquifex2 aeolicus
52	d1mi8a_	Alignment	not modelled	23.0	16	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
53	c1kl9A_	Alignment	not modelled	21.3	26	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 subunit 1; **PDBTitle:** crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
54	d2ba0a1	Alignment	not modelled	20.9	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						PDB header:transferase

55	c3kw2A_	Alignment	not modelled	20.8	18	**Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
56	c1ywuA_	Alignment	not modelled	20.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa4608; **PDBTitle:** solution nmr structure of pseudomonas aeruginosa protein pa4608.2 northeast structural genomics target pat7
57	d1ywua1	Alignment	not modelled	20.3	9	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
58	d2rdea1	Alignment	not modelled	20.1	17	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
59	d2z0sa1	Alignment	not modelled	20.0	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
60	c2wj7D_	Alignment	not modelled	19.8	14	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** human alphab crystallin
61	d2i5ua1	Alignment	not modelled	19.8	10	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain
62	c2kr7A_	Alignment	not modelled	19.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
63	d1vhka1	Alignment	not modelled	19.6	13	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
64	d1q46a2	Alignment	not modelled	18.9	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
65	d1alla_	Alignment	not modelled	18.8	26	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
66	d2je6i1	Alignment	not modelled	18.3	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
67	c2d7gD_	Alignment	not modelled	18.1	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**primosomal protein n; **PDBTitle:** crystal structure of the aa complex of the n-terminal2 domain of pria
68	c2l1tA_	Alignment	not modelled	17.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the n-terminal domain of np_954075.1
69	c2ej9A_	Alignment	not modelled	17.6	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative biotin ligase; **PDBTitle:** crystal structure of biotin protein ligase from2 methanococcus jannaschii
70	c2ewnA_	Alignment	not modelled	17.5	14	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
71	c2kq6A_	Alignment	not modelled	17.2	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**polycystin-2; **PDBTitle:** the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
72	d2nn6h1	Alignment	not modelled	16.2	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	d1go3e1	Alignment	not modelled	16.1	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
74	c1xniI_	Alignment	not modelled	15.8	13	**PDB header:**cell cycle **Chain:** I: **PDB Molecule:**tumor suppressor p53-binding protein 1; **PDBTitle:** tandem tudor domain of 53bp1
75	c2zrrA_	Alignment	not modelled	15.3	25	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**mundticin ks immunity protein; **PDBTitle:** crystal structure of an immunity protein that contributes2 to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
76	d1ixda_	Alignment	not modelled	15.0	21	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
77	c1i84V_	Alignment	not modelled	14.9	23	**PDB header:**contractile protein **Chain:** V: **PDB Molecule:**smooth muscle myosin heavy chain; **PDBTitle:** cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
78	d1b33a_	Alignment	not modelled	14.8	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
79	c2jkuA_	Alignment	not modelled	14.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain; **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
80	c3a8jF_	Alignment	not modelled	14.6	0	**PDB header:**transferase/transport protein **Chain:** F: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of et-ehred complex

81	c3mxuA_	Alignment	not modelled	14.5	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
82	c3iftA_	Alignment	not modelled	14.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
83	d1cpcb_	Alignment	not modelled	13.8	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
84	c3cgnA_	Alignment	not modelled	13.6	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
85	d1br2a1	Alignment	not modelled	13.3	25	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
86	d2ghra1	Alignment	not modelled	13.2	42	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
87	c1v1hB_	Alignment	not modelled	13.0	19	**PDB header:**adenovirus **Chain:** B: **PDB Molecule:**fibritin, fiber protein; **PDBTitle:** adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibritin foldon trimerisation motif with3 a short linker
88	d1gmea_	Alignment	not modelled	12.8	32	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
89	d1kn1a_	Alignment	not modelled	12.4	26	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
90	c2qjlA_	Alignment	not modelled	12.2	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
91	c2zkrq_	Alignment	not modelled	12.0	21	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **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
92	c3aabA_	Alignment	not modelled	11.9	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1653; **PDBTitle:** small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
93	c1br4E_	Alignment	not modelled	11.8	23	**PDB header:**muscle protein **Chain:** E: **PDB Molecule:**myosin; **PDBTitle:** smooth muscle myosin motor domain-essential light chain2 complex with mgadp.bef3 bound at the active site
94	d1hpca_	Alignment	not modelled	11.7	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
95	d1xo3a_	Alignment	not modelled	11.6	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
96	c1vdeA_	Alignment	not modelled	11.3	20	**PDB header:**endonuclease **Chain:** A: **PDB Molecule:**pi-scei; **PDBTitle:** pi-scei, a homing endonuclease with protein splicing2 activity
97	c1vftA_	Alignment	not modelled	11.1	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
98	d1dq3a1	Alignment	not modelled	11.0	11	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
99	d2h50a1	Alignment	not modelled	10.8	32	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20