Phyre^2

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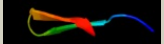
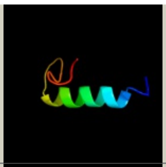
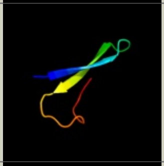
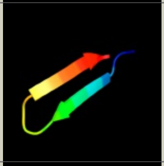
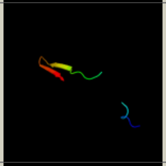
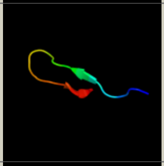
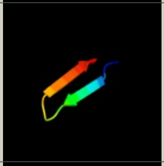
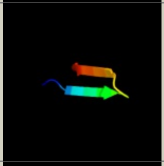
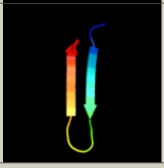
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kheA_	Alignment		88.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**toxin-like protein; **PDBTitle:** solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
2	c2otrA_	Alignment		81.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp0892; **PDBTitle:** solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
3	d1wmia1	Alignment		71.4	9	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
4	c3g5oC_	Alignment		45.9	16	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**uncharacterized protein rv2866; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
5	c3bpqD_	Alignment		44.0	16	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
6	d1z8ma1	Alignment		40.3	16	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
7	d3kvta_	Alignment		39.1	27	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
8	c3kixy_	Alignment		32.7	17	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:** **PDBTitle:** structure of rele nuclease bound to the 70s ribosome2 (postcleavage state; part 3 of 4)
9	d1qdva_	Alignment		31.8	21	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
10	d1t1da_	Alignment		31.6	29	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
11	d1s1ga_	Alignment		28.2	33	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels

12	d2g39a2	Alignment		27.4	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
13	c3q1jA_	Alignment		26.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
14	d1exbe_	Alignment		26.0	21	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
15	c2i2rK_	Alignment		24.9	21	**PDB header:**transport protein **Chain:** K: **PDB Molecule:**potassium voltage-gated channel subfamily d member 3; **PDBTitle:** crystal structure of the kchip1/kv4.3 t1 complex
16	c3dryA_	Alignment		24.1	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**btb/poz domain-containing protein kctd5; **PDBTitle:** x-ray crystal structure of human kctd5 protein crystallized in low-2 salt buffer
17	d1dsxa_	Alignment		23.9	29	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
18	d1a68a_	Alignment		20.1	29	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
19	d1bwva1	Alignment		17.9	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
20	d1u6za3	Alignment		17.8	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
21	c2r9rH_	Alignment	not modelled	16.5	20	**PDB header:**membrane protein, transport protein **Chain:** H: **PDB Molecule:**paddle chimera voltage gated potassium channel kv1.2-kv2.1; **PDBTitle:** shaker family voltage dependent potassium channel (kv1.2-kv2.1 paddle2 chimera channel) in association with beta subunit
22	d1q18a1	Alignment	not modelled	14.7	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
23	d1kyza2	Alignment	not modelled	13.8	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
24	d1t6ca2	Alignment	not modelled	13.6	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
25	c2daeA_	Alignment	not modelled	12.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa0733 protein; **PDBTitle:** solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting protein 2 (map3k7ip2)
26	c2eqmA_	Alignment	not modelled	12.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
27	d1u5ta1	Alignment	not modelled	12.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
28	d1u6za2	Alignment	not modelled	12.2	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family: Ppx/GppA phosphatase
29	c3bnwA_	Alignment	not modelled	11.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase, putative; **PDBTitle:** crystal structure of riboflavin kinase from trypanosoma brucei
30	c1bwvA_	Alignment	not modelled	11.9	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ribulose bisphosphate carboxylase); **PDBTitle:** activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
31	c3drzE_	Alignment	not modelled	11.8	36	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**btb/poz domain-containing protein kctd5; **PDBTitle:** x-ray crystal structure of the n-terminal btb domain of human kctd52 protein
32	d1czan3	Alignment	not modelled	11.7	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
33	d1t6ca1	Alignment	not modelled	11.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
34	c3n5bB_	Alignment	not modelled	11.2	29	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**asr0485 protein; **PDBTitle:** the complex of pii and pipx from anabaena
35	d1sz2a1	Alignment	not modelled	11.1	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
36	c2kd2A_	Alignment	not modelled	11.0	46	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** nmr structure of faim-ctd
37	d1fs1b1	Alignment	not modelled	10.6	36	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
38	d1wgla_	Alignment	not modelled	10.5	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
39	c2yumA_	Alignment	not modelled	10.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger zz-type-containing protein 3; **PDBTitle:** solution structure of the myb-like dna-binding domain of2 human zzz3 protein
40	c2dhyA_	Alignment	not modelled	10.2	33	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
41	d2ajta1	Alignment	not modelled	10.1	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**AraA C-terminal domain-like
42	c2qgzA_	Alignment	not modelled	10.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative primosome component; **PDBTitle:** crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
43	d8ruca1	Alignment	not modelled	9.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
44	d1t95a2	Alignment	not modelled	9.9	25	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein AF0491, N-terminal domain
45	d1rbla1	Alignment	not modelled	9.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
46	c2xg8D_	Alignment	not modelled	9.8	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**pipx; **PDBTitle:** structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942
47	d1czan1	Alignment	not modelled	9.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
48	d1gk8a1	Alignment	not modelled	9.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
49	d1v4sa1	Alignment	not modelled	9.2	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
50	d1bdga1	Alignment	not modelled	9.1	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
51	d1o57a1	Alignment	not modelled	9.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
52	d1fs2b1	Alignment	not modelled	8.9	36	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
53	c1u5tA_	Alignment	not modelled	8.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
54	d1nn7a_	Alignment	not modelled	8.6	33	**Fold:**POZ domain **Superfamily:**POZ domain

						Family: Tetramerization domain of potassium channels
55	c3a8uX_	Alignment	not modelled	8.5	3	**PDB header:**transferase **Chain:** X: **PDB Molecule:**omega-amino acid--pyruvate aminotransferase; **PDBTitle:** crystal structure of omega-amino acid:pyruvate aminotransferase
56	d1bg3a1	Alignment	not modelled	8.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
57	d2cqqa1	Alignment	not modelled	8.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
58	c3kj1B_	Alignment	not modelled	8.1	50	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** mcl-1 in complex with bim bh3 mutant i2da
59	c2h2wA_	Alignment	not modelled	7.7	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
60	d1nexa1	Alignment	not modelled	7.6	27	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
61	c1rcxH_	Alignment	not modelled	7.3	11	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
62	d1bg3a3	Alignment	not modelled	7.0	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
63	d1wdda1	Alignment	not modelled	6.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
64	d1d1la_	Alignment	not modelled	6.8	47	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
65	c3c0rC_	Alignment	not modelled	6.7	14	**PDB header:**cell cycle, hydrolase **Chain:** C: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** structure of ovarian tumor (otu) domain in complex with ubiquitin
66	c2ksnA_	Alignment	not modelled	6.7	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
67	c2q2rA_	Alignment	not modelled	6.6	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
68	d1gr0a2	Alignment	not modelled	6.5	54	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
69	d4croa_	Alignment	not modelled	6.4	47	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
70	d1iufa2	Alignment	not modelled	6.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
71	d1dqaa1	Alignment	not modelled	6.4	23	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
72	c2cseW_	Alignment	not modelled	6.3	11	**PDB header:**virus **Chain:** W: **PDB Molecule:**major core protein lambda 1; **PDBTitle:** features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
73	d2f9zc1	Alignment	not modelled	6.2	38	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**CheD-like
74	c2pijB_	Alignment	not modelled	6.2	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
75	c2zvkC_	Alignment	not modelled	6.1	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**proliferating cell nuclear antigen; **PDBTitle:** crystal structure of pcna in complex with dna polymerase eta fragment
76	c3md1B_	Alignment	not modelled	6.0	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**nuclear and cytoplasmic polyadenylated rna-binding protein **PDBTitle:** crystal structure of the second rrm domain of yeast poly(u)-binding2 protein (pub1)
77	d1xhja_	Alignment	not modelled	6.0	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
78	d1pmea_	Alignment	not modelled	6.0	20	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
79	d1o66a_	Alignment	not modelled	6.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
						PDB header:viral protein, membrane protein

80	c2jxfA_	Alignment	not modelled	5.9	20	**Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** the solution structure of hcv ns4b(40-69)
81	d2ovra1	Alignment	not modelled	5.8	36	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
82	c2k4vA_	Alignment	not modelled	5.8	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1076; **PDBTitle:** solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
83	d1p9qc2	Alignment	not modelled	5.7	25	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein AF0491, N-terminal domain
84	d1vjpa2	Alignment	not modelled	5.7	45	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
85	c2g39A_	Alignment	not modelled	5.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
86	c3cerD_	Alignment	not modelled	5.4	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein; **PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
87	d2p0ta1	Alignment	not modelled	5.2	23	**Fold:**PSPTO4464-like **Superfamily:**PSPTO4464-like **Family:**PSPTO4464-like
88	c2p0tA_	Alignment	not modelled	5.2	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0307 protein pspto_4464; **PDBTitle:** structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
89	d3orca_	Alignment	not modelled	5.2	47	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
90	c3hi0B_	Alignment	not modelled	5.1	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution