Phyre2

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Description	P39220
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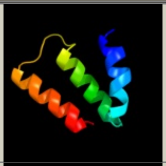
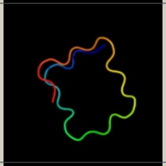
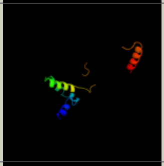
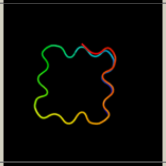
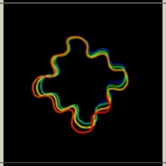
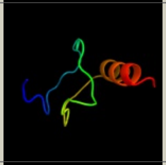
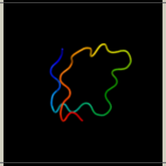
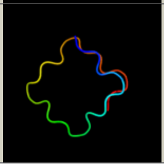
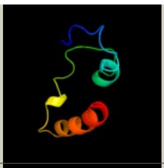
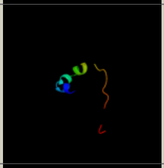
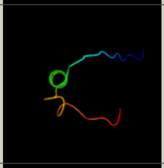
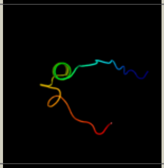
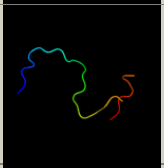
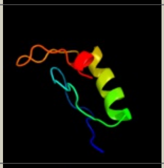
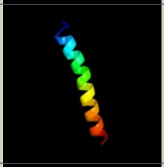
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cxbA_	Alignment		96.6	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein sifa; **PDBTitle:** crystal structure of sifa and skip
2	c3n90A_	Alignment		47.0	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thylakoid lumenal 15 kda protein 1, chloroplastic; **PDBTitle:** the 1.7 angstrom resolution crystal structure of at2g44920, a2 pentapeptide repeat protein from arabidopsis thaliana thylakoid3 lumen.
3	d2j8ia1	Alignment		43.0	20	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
4	c1v0dA_	Alignment		32.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna fragmentation factor 40 kda subunit; **PDBTitle:** crystal structure of caspase-activated dnase (cad)
5	d1v0da_	Alignment		32.0	22	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Caspase-activated DNase, CAD (DffB, DFF40)
6	d2fvka1	Alignment		27.0	14	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
7	d2j8ka1	Alignment		25.0	29	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
8	c2j8iB_	Alignment		18.1	20	**PDB header:**toxin **Chain:** B: **PDB Molecule:**np275; **PDBTitle:** structure of np275, a pentapeptide repeat protein from2 nostoc punctiforme
9	c2xtwB_	Alignment		15.9	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnrb1; **PDBTitle:** structure of qnrb1 (full length), a plasmid-mediated2 fluoroquinolone resistance protein
10	c2j8kA_	Alignment		15.0	29	**PDB header:**toxin **Chain:** A: **PDB Molecule:**np275-np276; **PDBTitle:** structure of the fusion of np275 and np276, pentapeptide2 repeat proteins from nostoc punctiforme
11	c3du1X_	Alignment		14.1	29	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**all3740 protein; **PDBTitle:** the 2.0 angstrom resolution crystal structure of hetl, a pentapeptide2 repeat protein involved in heterocyst differentiation regulation from3 the cyanobacterium nostoc sp. strain pcc 7120

12	c2jx3A_	Alignment		14.1	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein dek; **PDBTitle:** nmr solution structure of the n-terminal domain of dek
13	c1soxB_	Alignment		13.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite oxidase; **PDBTitle:** sulfite oxidase from chicken liver
14	d1zh5a1	Alignment		13.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
15	c1i8nA_	Alignment		13.1	48	**PDB header:**toxin **Chain:** A: **PDB Molecule:**anti-platelet protein; **PDBTitle:** crystal structure of leech anti-platelet protein
16	d1i8na_	Alignment		13.1	48	**Fold:**Hairpin loop containing domain-like **Superfamily:**Hairpin loop containing domain-like **Family:**Anti-platelet protein
17	c2o6wA_	Alignment		12.9	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**repeat five residue (rfr) protein or **PDBTitle:** crystal structure of a pentapeptide repeat protein (rfr23)2 from the cyanobacterium cyanothece 51142
18	d2f3la1	Alignment		11.8	24	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
19	d1tuaa2	Alignment		11.6	10	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
20	c1nh1A_	Alignment		11.4	27	**PDB header:**avirulence protein **Chain:** A: **PDB Molecule:**avirulence b protein; **PDBTitle:** crystal structure of the type iii effector avrb from2 pseudomonas syringae.
21	d1nh1a_	Alignment	not modelled	11.4	27	**Fold:**Antivirulence factor **Superfamily:**Antivirulence factor **Family:**Antivirulence factor
22	c3ia0c_	Alignment	not modelled	11.3	26	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
23	c2g0yA_	Alignment	not modelled	11.1	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pentapeptide repeat protein; **PDBTitle:** crystal structure of a lumenal pentapeptide repeat protein from2 cyanothece sp 51142 at 2.3 angstrom resolution. tetragonal crystal3 form
24	c3lo0A_	Alignment	not modelled	10.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
25	c2wknE_	Alignment	not modelled	10.7	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**formamidase; **PDBTitle:** gamma lactamase from delftia acidovorans
26	c2wvmA_	Alignment	not modelled	9.6	53	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
27	c2xt4B_	Alignment	not modelled	9.4	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.
28	c3ifuA_	Alignment	not modelled	9.1	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**non-structural protein; **PDBTitle:** the crystal structure of porcine reproductive and2

						respiratory syndrome virus (prrsv) leader protease nsp1
29	d1yj5a1	Alignment	not modelled	9.0	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
30	c2xt4A_	Alignment	not modelled	8.7	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.
31	c3mjjD_	Alignment	not modelled	8.5	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted acetamidase/formamidase; **PDBTitle:** crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
32	d1isia_	Alignment	not modelled	8.4	21	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
33	d1j2za_	Alignment	not modelled	8.4	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
34	c2w7zB_	Alignment	not modelled	8.3	21	**PDB header:**inhibitor **Chain:** B: **PDB Molecule:**pentapeptide repeat family protein; **PDBTitle:** structure of the pentapeptide repeat protein efsqnr, a dna2 gyrase inhibitor. free amines modified by cyclic3 pentylation with glutaraldehyde.
35	c3t2dA_	Alignment	not modelled	8.0	41	**PDB header:**lyase, hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphate aldolase/phosphatase; **PDBTitle:** fructose-1,6-bisphosphate aldolase/phosphatase from thermoproteus2 neutrophilus, fbp-bound form
36	c1jrjA_	Alignment	not modelled	8.0	26	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
37	c3b9eA_	Alignment	not modelled	7.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
38	c3b9tD_	Alignment	not modelled	7.9	40	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of predicted acetamidase/formamidase (yp_546212.1)2 from methylobacillus flagellatus kt at 1.58 a resolution
39	c2zu8A_	Alignment	not modelled	7.6	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
40	c3pssB_	Alignment	not modelled	7.6	17	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnr; **PDBTitle:** crystal structure of ahqnr, the qnr protein from aeromonas hydrophila2 (p21 crystal form)
41	c2eg9B_	Alignment	not modelled	7.1	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-ribosyl cyclase 1; **PDBTitle:** crystal structure of the truncated extracellular domain of2 mouse cd38
42	d2cqka1	Alignment	not modelled	7.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
43	d1xnta_	Alignment	not modelled	6.9	27	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**N-terminal domain of xrcc1
44	c1xnaA_	Alignment	not modelled	6.9	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein (dna-repair protein xrcc1); **PDBTitle:** nmr solution structure of the single-strand break repair2 protein xrcc1-n-terminal domain
45	d1sura_	Alignment	not modelled	6.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
46	c3n3fB_	Alignment	not modelled	6.7	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**collagen alpha-1(xv) chain; **PDBTitle:** crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
47	c2xz2A_	Alignment	not modelled	6.6	26	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**cstf-50, isoform b; **PDBTitle:** crystal structure of cstf-50 homodimerization domain
48	c2vbeA_	Alignment	not modelled	6.6	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike-protein; **PDBTitle:** tailspike protein of bacteriophage sf6
49	c3cgiD_	Alignment	not modelled	6.4	50	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
50	d1hs5a_	Alignment	not modelled	6.4	34	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
51	c2goyC_	Alignment	not modelled	6.4	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
52	c1d0rA_	Alignment	not modelled	6.3	26	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
53	c2bhlB_	Alignment	not modelled	6.3	43	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-

						phosphate
54	c1yj5B_	Alignment	not modelled	6.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase catalytic domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
55	d2a1ja1	Alignment	not modelled	6.2	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
56	c3nb2B_	Alignment	not modelled	6.1	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nleI
57	c2j9wB_	Alignment	not modelled	6.1	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vps28-prov protein; **PDBTitle:** structural insight into the escrt-i-ii link and its role in2 mvb trafficking
58	d1khia2	Alignment	not modelled	6.1	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
59	d1whra_	Alignment	not modelled	6.0	14	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
60	d1wvfa1	Alignment	not modelled	5.9	31	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
61	d2f4la1	Alignment	not modelled	5.8	24	**Fold:**CUB-like **Superfamily:**Acetamidase/Formamidase-like **Family:**Acetamidase/Formamidase-like
62	c3hugJ_	Alignment	not modelled	5.8	30	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
63	d1edqa2	Alignment	not modelled	5.8	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
64	d2bm5a1	Alignment	not modelled	5.7	4	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
65	d1mjea2	Alignment	not modelled	5.7	28	**Fold:**BRCA2 tower domain **Superfamily:**BRCA2 tower domain **Family:**BRCA2 tower domain
66	c2c1tA_	Alignment	not modelled	5.6	17	**PDB header:**protein transport/membrane protein **Chain:** A: **PDB Molecule:**importin alpha subunit; **PDBTitle:** structure of the kap60p:nup2 complex
67	c1qkiE_	Alignment	not modelled	5.6	43	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
68	d1r4pb_	Alignment	not modelled	5.5	39	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
69	d1l8na1	Alignment	not modelled	5.5	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
70	d2ef1a1	Alignment	not modelled	5.5	23	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
71	d1c4qa_	Alignment	not modelled	5.3	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
72	d1zs4a1	Alignment	not modelled	5.3	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Bacteriophage CII protein
73	c2o8vA_	Alignment	not modelled	5.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a