Phyre^2

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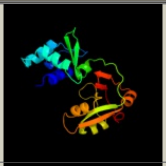
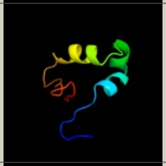
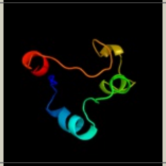
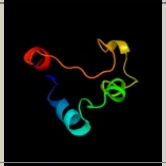
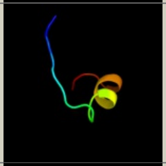
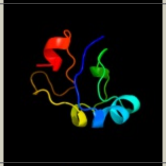
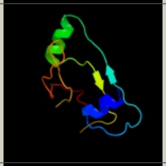
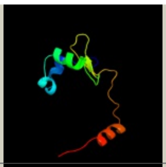
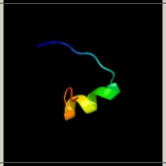
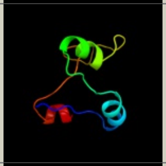
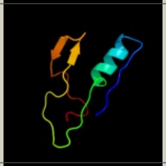
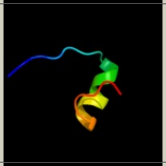
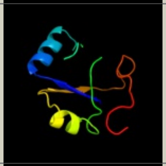
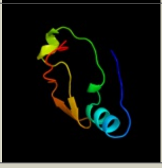
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wfxa_	Alignment		100.0	33	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Tpt1/KptA
2	d2cqka1	Alignment		96.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
3	d1s29a_	Alignment		96.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
4	d1zh5a1	Alignment		95.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
5	c2paxA_	Alignment		89.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase; **PDBTitle:** the catalytic fragment of poly(adp-ribose) polymerase2 complexed with 4-amino-1,8-naphthalimide
6	c1gs0B_	Alignment		87.5	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly (adp-ribose) polymerase-2; **PDBTitle:** crystal structure of the catalytic fragment of murine poly2 (adp-ribose) polymerase-2
7	d1gs0a2	Alignment		86.5	23	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Poly(ADP-ribose) polymerase, C-terminal domain
8	c3c4hA_	Alignment		84.6	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase 3; **PDBTitle:** human poly(adp-ribose) polymerase 3, catalytic fragment in complex2 with an inhibitor dr2313
9	c2x5yA_	Alignment		81.4	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**zinc finger ccch-type antiviral protein 1; **PDBTitle:** human zc3hav1 (artd13), c-terminal domain
10	c3q6nF_	Alignment		80.4	15	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein hsp 90-alpha; **PDBTitle:** crystal structure of human mc-hsp90 in p21 space group
11	d1efya2	Alignment		78.8	23	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Poly(ADP-ribose) polymerase, C-terminal domain

12	c2vopA_	Alignment		78.7	15	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**lupus la protein; **PDBTitle:** crystal structure of n-terminal domains of human la protein2 complexed with rna oligomer auuuu
13	c3goyD_	Alignment		74.6	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** crystal structure of human poly(adp-ribose) polymerase 14,2 catalytic fragment in complex with an inhibitor 3-3 aminobenzamide
14	d2rd6a2	Alignment		74.4	23	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Poly(ADP-ribose) polymerase, C-terminal domain
15	c3bljA_	Alignment		73.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase 15; **PDBTitle:** crystal structure of human poly(adp-ribose) polymerase 15, catalytic2 fragment
16	c2pqfF_	Alignment		71.3	36	**PDB header:**transferase **Chain:** F: **PDB Molecule:**poly [adp-ribose] polymerase 12; **PDBTitle:** human poly(adp-ribose) polymerase 12, catalytic fragment in complex2 with an inhibitor 3-aminobenzoic acid
17	c3pryA_	Alignment		66.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-beta; **PDBTitle:** crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution
18	c3hkvA_	Alignment		63.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 10; **PDBTitle:** human poly(adp-ribose) polymerase 10, catalytic fragment in2 complex with an inhibitor 3-aminobenzamide
19	d2o0qa1	Alignment		62.9	27	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**CC0527-like
20	c1y6zA_	Alignment		53.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
21	c3mhkA_	Alignment	not modelled	48.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tankyrase-2; **PDBTitle:** human tankyrase 2 - catalytic parp domain in complex with 2-(2-2 pyridyl)-7,8-dihydro-5h-thiino[4,3-d]pyrimidin-4-ol
22	c2d58A_	Alignment	not modelled	47.1	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** human microglia-specific protein iba1
23	d1n0yb_	Alignment	not modelled	44.5	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
24	c2amiA_	Alignment	not modelled	42.9	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
25	c2vtgA_	Alignment	not modelled	40.4	18	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**ionized calcium-binding adapter molecule 2; **PDBTitle:** crystal structure of human iba2, trigonal crystal form
26	d1wrka1	Alignment	not modelled	40.3	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
27	c2gq0B_	Alignment	not modelled	38.8	19	**PDB header:**chaperone, hydrolase **Chain:** B: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of the middle domain of htpg, the e. coli2 hsp90
28	d1sw8a_	Alignment	not modelled	38.6	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
						PDB header:structural genomics, unknown function

29	c2kzvA_	Alignment	not modelled	38.0	20	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
30	c2aucC_	Alignment	not modelled	37.2	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**myosin a tail interacting protein; **PDBTitle:** structure of the plasmodium mtip-myoa complex, a key component of the2 parasite invasion motor
31	c3hjcA_	Alignment	not modelled	36.3	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 83-1; **PDBTitle:** crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
32	c1hk7A_	Alignment	not modelled	35.7	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp82; **PDBTitle:** middle domain of hsp90
33	c2o1uA_	Alignment	not modelled	35.2	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
34	d2fcea1	Alignment	not modelled	35.2	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
35	d1tiza_	Alignment	not modelled	34.4	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
36	c2g2bA_	Alignment	not modelled	34.4	21	**PDB header:**immune system **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** nmr structure of the human allograft inflammatory factor 1
37	c2cgeD_	Alignment	not modelled	34.2	20	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
38	d1m39a_	Alignment	not modelled	32.8	24	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
39	c2cg9A_	Alignment	not modelled	32.8	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
40	c2fcdA_	Alignment	not modelled	32.7	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
41	d1s6ja_	Alignment	not modelled	29.7	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
42	d1avsa_	Alignment	not modelled	29.3	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
43	c2o1tB_	Alignment	not modelled	28.9	24	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of middle plus c-terminal domains (m+c) of grp94
44	d1usua_	Alignment	not modelled	28.8	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Hsp90 middle domain
45	d1fw4a_	Alignment	not modelled	28.5	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
46	c2o1wB_	Alignment	not modelled	27.8	28	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
47	d1ap4a_	Alignment	not modelled	27.8	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
48	d1jc2a_	Alignment	not modelled	27.4	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
49	c1jc2A_	Alignment	not modelled	27.4	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, skeletal muscle; **PDBTitle:** complex of the c-domain of troponin c with residues 1-40 of2 troponin i
50	d2pq3a1	Alignment	not modelled	26.6	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
51	c2l98A_	Alignment	not modelled	26.4	24	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** structure of trans-resveratrol in complex with the cardiac regulatory2 protein troponin c
52	c2kdhA_	Alignment	not modelled	26.4	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate
53	c2k2aA_	Alignment	not modelled	26.1	16	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c; **PDBTitle:** solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1
						Fold:EF Hand-like

54	d1r2ua_	Alignment	not modelled	25.2	18	**Superfamily:**EF-hand **Family:**Calmodulin-like
55	d1oqpa_	Alignment	not modelled	25.2	29	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
56	c2jojA_	Alignment	not modelled	24.6	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centrin protein; **PDBTitle:** nmr solution structure of n-terminal domain of euplotes2 octocarinatus centrin
57	c2kn2A_	Alignment	not modelled	24.0	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin; **PDBTitle:** solution structure of the c-terminal domain of soybean calmodulin2 isoform 4 fused with the calmodulin-binding domain of ntmkp1
58	d1ikpa2	Alignment	not modelled	23.2	32	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
59	c1ih0A_	Alignment	not modelled	22.6	22	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** structure of the c-domain of human cardiac troponin c in2 complex with ca2+ sensitizer emd 57033
60	d1ih0a_	Alignment	not modelled	22.6	22	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
61	c2k7bA_	Alignment	not modelled	21.7	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain
62	c2a4jA_	Alignment	not modelled	20.8	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centrin 2; **PDBTitle:** solution structure of the c-terminal domain (t94-y172) of2 the human centrin 2 in complex with a 17 residues peptide3 (p1-xpc) from xeroderma pigmentosum group c protein
63	d1f54a_	Alignment	not modelled	20.4	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
64	c3li6A_	Alignment	not modelled	19.9	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein; **PDBTitle:** crystal structure and trimer-monomer transition of n-terminal domain2 of ehcabp1 from entamoeba histolytica
65	c3li6G_	Alignment	not modelled	19.9	13	**PDB header:**metal binding protein **Chain:** G: **PDB Molecule:**calcium-binding protein; **PDBTitle:** crystal structure and trimer-monomer transition of n-terminal domain2 of ehcabp1 from entamoeba histolytica
66	c3li6J_	Alignment	not modelled	19.9	13	**PDB header:**metal binding protein **Chain:** J: **PDB Molecule:**calcium-binding protein; **PDBTitle:** crystal structure and trimer-monomer transition of n-terminal domain2 of ehcabp1 from entamoeba histolytica
67	d2cxaa1	Alignment	not modelled	18.8	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
68	c2cxaA_	Alignment	not modelled	18.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
69	c2rf5A_	Alignment	not modelled	18.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tankyrase-1; **PDBTitle:** crystal structure of human tankyrase 1- catalytic parp domain
70	c1scvA_	Alignment	not modelled	18.4	21	**PDB header:**contractile protein, structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i
71	d1fi5a_	Alignment	not modelled	18.4	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
72	c1sbjA_	Alignment	not modelled	18.4	21	**PDB header:**contractile protein, structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** nmr structure of the mg2+-loaded c terminal domain of2 cardiac troponin c bound to the n terminal domain of3 cardiac troponin i
73	c1fi5A_	Alignment	not modelled	18.4	21	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**protein (troponin c); **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i.
74	c3rhgA_	Alignment	not modelled	18.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
75	c2kz2A_	Alignment	not modelled	17.1	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin; **PDBTitle:** calmodulin, c-terminal domain, f92e mutant
76	d1np8a_	Alignment	not modelled	15.1	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Penta-EF-hand proteins
77	c1ozsA_	Alignment	not modelled	15.0	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i
78	c2k9lA_	Alignment	not modelled	14.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54

79	c2ktgA_	Alignment	not modelled	14.7	18	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**calmodulin, putative; **PDBTitle:** calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein
80	c2iopD_	Alignment	not modelled	14.2	17	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
81	d1n0ya_	Alignment	not modelled	14.1	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
82	d1ctda_	Alignment	not modelled	13.9	26	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
83	c2b1uA_	Alignment	not modelled	13.3	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin-like protein 5; **PDBTitle:** solution structure of calmodulin-like skin protein c2 terminal domain
84	d1zaca_	Alignment	not modelled	13.3	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
85	d1cmga_	Alignment	not modelled	12.7	22	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
86	c3sibA_	Alignment	not modelled	12.4	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ure3-bp sequence specific dna binding protein; **PDBTitle:** crystal structure of ure3-binding protein, wild-type
87	c1y4sA_	Alignment	not modelled	12.2	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
88	c3li6D_	Alignment	not modelled	11.9	13	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**calcium-binding protein; **PDBTitle:** crystal structure and trimer-monomer transition of n-terminal domain2 of ehcabp1 from entamoeba histolytica
89	c2k7cA_	Alignment	not modelled	11.8	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 c-domain
90	d2fsua1	Alignment	not modelled	11.2	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PhnH-like **Family:**PhnH-like
91	c2fsuA_	Alignment	not modelled	11.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein phnh; **PDBTitle:** crystal structure of the phnh protein from escherichia coli
92	c1npqA_	Alignment	not modelled	11.0	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c; **PDBTitle:** structure of a rhodamine-labeled n-domain troponin c mutant2 (ca2+ saturated) in complex with skeletal troponin i 115-3 131
93	c3ctnA_	Alignment	not modelled	11.0	21	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**troponin c; **PDBTitle:** structure of calcium-saturated cardiac troponin c, nmr, 302 structures
94	d1q46a1	Alignment	not modelled	11.0	37	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
95	c1novE_	Alignment	not modelled	10.4	33	**PDB header:**virus **Chain:** E: **PDB Molecule:**nodamura virus coat proteins; **PDBTitle:** nodamura virus
96	c3uatA_	Alignment	not modelled	10.3	13	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**disks large homolog 1; **PDBTitle:** guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules
97	d2qtva4	Alignment	not modelled	9.8	33	**Fold:**Gelsolin-like **Superfamily:**C-terminal, gelsolin-like domain of Sec23/24 **Family:**C-terminal, gelsolin-like domain of Sec23/24
98	d1biaa1	Alignment	not modelled	9.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
99	c1ikqA_	Alignment	not modelled	9.5	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**exotoxin a; **PDBTitle:** pseudomonas aeruginosa exotoxin a, wild type