Phyre^2

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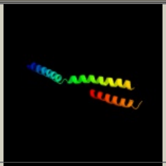
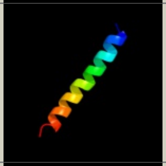
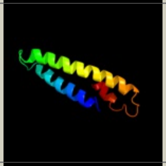
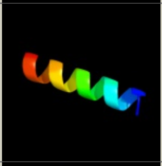
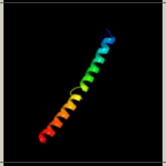
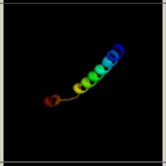
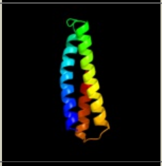
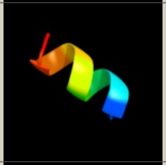
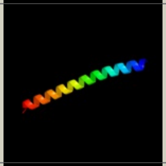
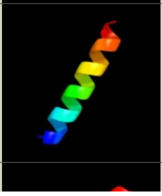
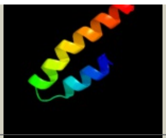
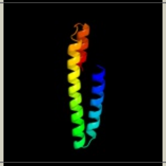
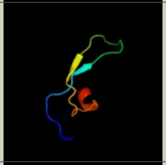
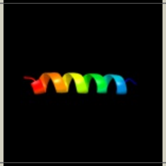
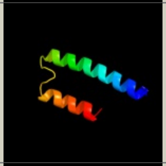
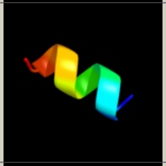
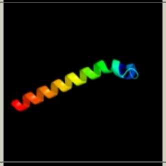
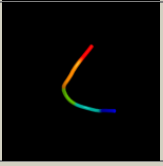
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nt2b_	Alignment		35.9	22	**Fold:**Nop domain **Superfamily:**Nop domain **Family:**Nop domain
2	c1junB_	Alignment		26.9	26	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
3	d1vcsa1	Alignment		25.4	14	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
4	d2gtsa1	Alignment		24.9	22	**Fold:**Ferritin-like **Superfamily:**HP0062-like **Family:**HP0062-like
5	c2xzml_	Alignment		24.5	12	**PDB header:**ribosome **Chain:** l: **PDB Molecule:**rps16e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
6	c3n4xB_	Alignment		23.7	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
7	c3swfA_	Alignment		22.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
8	d1lvfa_	Alignment		22.7	15	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
9	c2f3yB_	Alignment		18.1	40	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**voltage-dependent l-type calcium channel alpha- **PDBTitle:** calmodulin/iq domain complex
10	c1t3jA_	Alignment		17.1	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
11	d1wmib1	Alignment		13.9	35	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**RelB-like **Family:**RelB-like

12	c2rpaA_	Alignment		13.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a1; **PDBTitle:** the solution structure of n-terminal domain of microtubule severing2 enzyme
13	c3onjA_	Alignment		13.5	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t-snare vti1; **PDBTitle:** crystal structure of yeast vti1p_habc domain
14	d1wgda_	Alignment		12.7	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
15	d3saka_	Alignment		12.0	57	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
16	c3q9dB_	Alignment		11.9	30	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**protein cpn_0803/cp_1068/cpj0803/cpb0832; **PDBTitle:** crystal structure of cpn0803 from c. pneumoniae.
17	c3n1bA_	Alignment		11.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 54; **PDBTitle:** c-terminal domain of vps54 subunit of the garp complex
18	c2vayB_	Alignment		10.4	40	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**voltage-dependent l-type calcium channel subunit **PDBTitle:** calmodulin complexed with cav1.1 iq peptide
19	c3f42A_	Alignment		10.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hp0035; **PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
20	d1a9xb1	Alignment		9.8	80	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Carbamoyl phosphate synthetase, small subunit N-terminal domain **Family:**Carbamoyl phosphate synthetase, small subunit N-terminal domain
21	c2jroA_	Alignment	not modelled	9.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
22	d2elba1	Alignment	not modelled	9.1	12	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**BAR domain
23	c2j11D_	Alignment	not modelled	8.9	57	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant y327s t329g q331g
24	c1gngX_	Alignment	not modelled	8.8	35	**PDB header:**transferase **Chain:** X: **PDB Molecule:**frattide; **PDBTitle:** glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
25	c3r2cJ_	Alignment	not modelled	8.7	21	**PDB header:**transcription/rna **Chain:** J: **PDB Molecule:**30s ribosomal protein s10; **PDBTitle:** crystal structure of antitermination factors nusb and nuse in complex2 with boxa rna
26	c2ywfA_	Alignment	not modelled	8.4	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
27	d1aiea_	Alignment	not modelled	8.1	57	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
28	c1mpgB_	Alignment	not modelled	7.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
29	d1we3a2	Alignment	not modelled	7.9	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like

						Family: GroEL-like chaperone, apical domain
30	c2j10D_	Alignment	not modelled	7.7	57	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
31	c2j10B_	Alignment	not modelled	7.7	57	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
32	c2j10A_	Alignment	not modelled	7.7	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
33	d3bypa1	Alignment	not modelled	7.5	15	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
34	c2zkqi_	Alignment	not modelled	7.5	22	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
35	c4a4kI_	Alignment	not modelled	7.5	12	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae ski2 insertion domain
36	d1jjcb2	Alignment	not modelled	7.5	33	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
37	c3n6sA_	Alignment	not modelled	7.5	24	**PDB header:**transcription, replication/dna **Chain:** A: **PDB Molecule:**transcription termination factor, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial mterf in complex with a 15-2 mer dna encompassing the trnaleu(uur) binding sequence
38	c1keeH_	Alignment	not modelled	7.4	80	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
39	d1z1va1	Alignment	not modelled	7.4	50	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
40	d1g3nc2	Alignment	not modelled	7.2	50	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
41	c2it3B_	Alignment	not modelled	7.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0130 protein ph1069; **PDBTitle:** structure of ph1069 protein from pyrococcus horikoshii
42	c3eabK_	Alignment	not modelled	7.1	31	**PDB header:**cell cycle **Chain:** K: **PDB Molecule:**chmp1b; **PDBTitle:** crystal structure of spastin mit in complex with escrt iii
43	c1lj2C_	Alignment	not modelled	7.0	50	**PDB header:**viral protein/ translation **Chain:** C: **PDB Molecule:**eukaryotic protein synthesis initiation factor; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
44	c2kdbA_	Alignment	not modelled	6.9	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**homocysteine-responsive endoplasmic reticulum- **PDBTitle:** solution structure of human ubiquitin-like domain of2 herpud2_9_85, northeast structural genomics consortium3 (nesg) target ht53a
45	d1k1fa_	Alignment	not modelled	6.8	22	**Fold:**Bcr-Abl oncoprotein oligomerization domain **Superfamily:**Bcr-Abl oncoprotein oligomerization domain **Family:**Bcr-Abl oncoprotein oligomerization domain
46	c3n5aA_	Alignment	not modelled	6.8	31	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**synaptotagmin-7; **PDBTitle:** synaptotagmin-7, c2b-domain, calcium bound
47	c3kizA_	Alignment	not modelled	6.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of putative phosphoribosylformylglycinamidine cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
48	d1kida_	Alignment	not modelled	6.7	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
49	d1sjpa2	Alignment	not modelled	6.7	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
50	c3p8cD_	Alignment	not modelled	6.6	10	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**wiskott-aldrich syndrome protein family member 1; **PDBTitle:** structure and control of the actin regulatory wave complex
51	c1lj2D_	Alignment	not modelled	6.6	50	**PDB header:**viral protein/ translation **Chain:** D: **PDB Molecule:**eukaryotic protein synthesis initiation factor; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
52	c2elxA_	Alignment	not modelled	6.6	44	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 8th c2h2 zinc finger of mouse2 zinc finger protein 406
53	d2oufa1	Alignment	not modelled	6.4	18	**Fold:**HP0242-like **Superfamily:**HP0242-like

						Family:HP0242-like
54	c3ks7D_	Alignment	not modelled	6.4	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative putative pngase f; **PDBTitle:** crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
55	d1g73a_	Alignment	not modelled	6.4	14	**Fold:**Spectrin repeat-like **Superfamily:**Smac/diablo **Family:**Smac/diablo
56	d1igqa_	Alignment	not modelled	6.1	14	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
57	d3efza1	Alignment	not modelled	6.1	8	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
58	c3efzA_	Alignment	not modelled	6.1	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**14-3-3 protein; **PDBTitle:** crystal structure of a 14-3-3 protein from cryptosporidium parvum2 (cgd1_2980)
59	c3swyB_	Alignment	not modelled	6.0	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
60	c3c19A_	Alignment	not modelled	6.0	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mk0293; **PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19
61	c1gw4A_	Alignment	not modelled	6.0	31	**PDB header:**high density lipoproteins **Chain:** A: **PDB Molecule:**apoa-i; **PDBTitle:** the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
62	d1dula_	Alignment	not modelled	6.0	50	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
63	d1igub_	Alignment	not modelled	5.9	14	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
64	d1fewa_	Alignment	not modelled	5.8	14	**Fold:**Spectrin repeat-like **Superfamily:**Smac/diablo **Family:**Smac/diablo
65	c1zvaA_	Alignment	not modelled	5.8	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
66	c1jqmA_	Alignment	not modelled	5.8	5	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid
67	c1rrqA_	Alignment	not modelled	5.8	26	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
68	d1ip9a_	Alignment	not modelled	5.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
69	d1orja_	Alignment	not modelled	5.8	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
70	c3bboK_	Alignment	not modelled	5.7	13	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**ribosomal protein l11; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
71	c3degC_	Alignment	not modelled	5.7	17	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
72	c3cb4D_	Alignment	not modelled	5.6	17	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
73	d1a1ua_	Alignment	not modelled	5.3	57	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
74	d1dfca1	Alignment	not modelled	5.3	56	**Fold:**beta-Trefoil **Superfamily:**Actin-crosslinking proteins **Family:**Fascin
75	c2v8sV_	Alignment	not modelled	5.2	11	**PDB header:**protein transport **Chain:** V: **PDB Molecule:**vesicle transport through interaction with **PDBTitle:** vti1b habc domain - epsinr enth domain complex
76	c2be6F_	Alignment	not modelled	5.2	40	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
77	d1js8a2	Alignment	not modelled	5.2	5	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
78	c1bf5A_	Alignment	not modelled	5.2	16	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
79	c3okqA_	Alignment	not modelled	5.1	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin

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