Phyre^2

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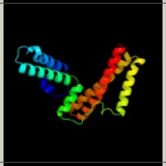
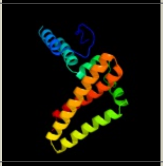
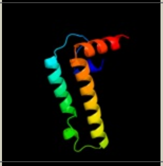
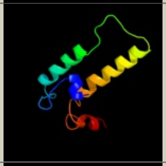
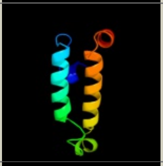
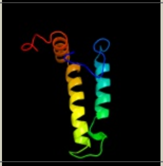
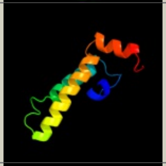
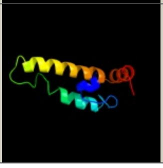
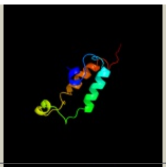
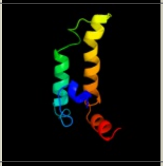
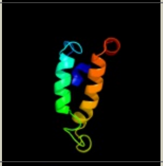
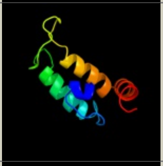
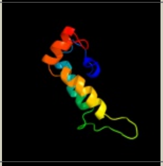
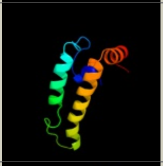
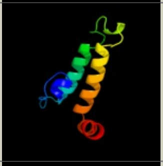
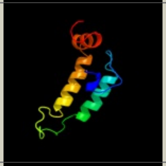
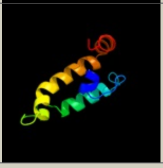
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fpoA_	Alignment		100.0	99	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hscb; **PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli
2	c3bvoA_	Alignment		100.0	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
3	c3hhoA_	Alignment		100.0	48	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog; **PDBTitle:** chaperone hscb from vibrio cholerae
4	c3uo2A_	Alignment		99.9	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**j-type co-chaperone jac1, mitochondrial; **PDBTitle:** jac1 co-chaperone from saccharomyces cerevisiae
5	d1fpoa1	Alignment		99.9	100	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
6	c3apqB_	Alignment		99.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
7	c2l6lA_	Alignment		99.8	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
8	c2ctqA_	Alignment		99.8	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 menber 12
9	c2qsaA_	Alignment		99.8	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog dnj-2; **PDBTitle:** crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 c.elegans.
10	c2cugA_	Alignment		99.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mkiaa0962 protein; **PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
11	d1wjza_	Alignment		99.7	27	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain

12	d1gh6a_	Alignment		99.7	16	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
13	c2yuaA_	Alignment		99.7	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**williams-beuren syndrome chromosome region 18 **PDBTitle:** solution structure of the dnaj domain from human williams-2 beuren syndrome chromosome region 18 protein
14	c2ctwA_	Alignment		99.7	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 5; **PDBTitle:** solution structure of j-domain from mouse dnaj subfamily c2 member 5
15	c2kqxA_	Alignment		99.7	27	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
16	d1hdja_	Alignment		99.7	22	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
17	c2dmxA_	Alignment		99.7	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8; **PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8
18	c2lgwA_	Alignment		99.7	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2; **PDBTitle:** solution structure of the j domain of hsj1a
19	d1xbla_	Alignment		99.7	25	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
20	c2dn9A_	Alignment		99.7	21	**PDB header:**apoptosis, chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein
21	c2ctrA_	Alignment	not modelled	99.7	30	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 9; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 member 9
22	c2ctpA_	Alignment	not modelled	99.7	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 menber 12
23	c2o37A_	Alignment	not modelled	99.7	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
24	c2ochA_	Alignment	not modelled	99.7	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
25	d1fafa_	Alignment	not modelled	99.7	22	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
26	c1bq0A_	Alignment	not modelled	99.6	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj; **PDBTitle:** j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
27	c2ys8A_	Alignment	not modelled	99.6	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**rab-related gtp-binding protein rabj; **PDBTitle:** solution structure of the dnaj-like domain from human ras-2 associated protein rap1
28	c2pf4E_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase regulator/viral protein **Chain:** E: **PDB Molecule:**small t antigen; **PDBTitle:** crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha

						subunit
29	d1iura_	Alignment	not modelled	99.6	13	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
30	d1nz6a_	Alignment	not modelled	99.4	16	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
31	d1n4ca_	Alignment	not modelled	99.4	17	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
32	d1fpoa2	Alignment	not modelled	99.4	99	**Fold:**Open three-helical up-and-down bundle **Superfamily:**HSC20 (HSCB), C-terminal oligomerisation domain **Family:**HSC20 (HSCB), C-terminal oligomerisation domain
33	c2guzO_	Alignment	not modelled	99.3	21	**PDB header:**chaperone, protein transport **Chain:** O: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
34	c3ag7A_	Alignment	not modelled	99.2	18	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5; **PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain
35	c2y4tA_	Alignment	not modelled	99.1	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
36	c2guzD_	Alignment	not modelled	99.1	17	**PDB header:**chaperone, protein transport **Chain:** D: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
37	c3apoA_	Alignment	not modelled	98.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
38	d1ug2a_	Alignment	not modelled	63.3	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
39	d1fc2c_	Alignment	not modelled	30.8	16	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
40	d1deeg_	Alignment	not modelled	24.2	13	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
41	d1lp1b_	Alignment	not modelled	23.7	18	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
42	d2jwda1	Alignment	not modelled	20.7	18	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
43	d1ni7a_	Alignment	not modelled	20.4	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
44	d2d00a1	Alignment	not modelled	14.6	19	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
45	c3epvB_	Alignment	not modelled	14.1	19	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
46	c2zfdB_	Alignment	not modelled	12.2	18	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
47	c2ehbD_	Alignment	not modelled	11.4	24	**PDB header:**signalling protein/transferase **Chain:** D: **PDB Molecule:**cbl-interacting serine/threonine-protein kinase 24; **PDBTitle:** the structure of the c-terminal domain of the protein kinase atsos22 bound to the calcium sensor atsos3
48	d2etva1	Alignment	not modelled	10.9	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
49	c2vrgA_	Alignment	not modelled	10.1	16	**PDB header:**transport **Chain:** A: **PDB Molecule:**multiple coagulation factor deficiency protein 2; **PDBTitle:** structure of human mcfd2
50	d1pmia_	Alignment	not modelled	9.8	44	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
51	c3pshA_	Alignment	not modelled	9.7	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein hi_1472; **PDBTitle:** classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
52	c3h1yA_	Alignment	not modelled	8.8	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
53	c2l53B_	Alignment	not modelled	8.7	14	**PDB header:**ca-binding protein/proton transport **Chain:** B: **PDB Molecule:**voltage-gated sodium channel type v alpha isoform b **PDBTitle:** solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5

54	d2py6a1	Alignment	not modelled	8.6	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**FkbM-like
55	c2j8kA_	Alignment	not modelled	8.5	19	**PDB header:**toxin **Chain:** A: **PDB Molecule:**np275-np276; **PDBTitle:** structure of the fusion of np275 and np276, pentapeptide2 repeat proteins from nostoc punctiforme
56	d2gtad1	Alignment	not modelled	8.3	15	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
57	d1uf2a_	Alignment	not modelled	8.2	33	**Fold:**Reovirus inner layer core protein p3 **Superfamily:**Reovirus inner layer core protein p3 **Family:**Phytoreovirus core
58	c1uf2A_	Alignment	not modelled	8.2	33	**PDB header:**virus **Chain:** A: **PDB Molecule:**core protein p3; **PDBTitle:** the atomic structure of rice dwarf virus (rdv)
59	c2kxwB_	Alignment	not modelled	8.1	0	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
60	d1edla_	Alignment	not modelled	8.0	14	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
61	d1c20a_	Alignment	not modelled	7.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
62	c2rq5A_	Alignment	not modelled	7.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein jumonji; **PDBTitle:** solution structure of the at-rich interaction domain (arid)2 of jumonji/jarid2
63	d1mxaa1	Alignment	not modelled	7.1	100	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
64	d2p02a1	Alignment	not modelled	6.7	100	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
65	c2eqyA_	Alignment	not modelled	6.6	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji, at rich interactive domain 1b; **PDBTitle:** solution structure of the arid domain of jarid1b protein
66	d2dara2	Alignment	not modelled	6.5	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
67	d3saka_	Alignment	not modelled	6.4	17	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
68	c2ov6A_	Alignment	not modelled	6.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit f; **PDBTitle:** the nmr structure of subunit f of the methanogenic a1ao atp synthase2 and its interaction with the nucleotide-binding subunit b
69	c3fn2A_	Alignment	not modelled	6.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sensor histidine kinase domain; **PDBTitle:** crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
70	d1boda_	Alignment	not modelled	6.2	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calbindin D9K
71	c1b0nB_	Alignment	not modelled	6.0	0	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**protein (sini protein); **PDBTitle:** sinr protein/sini protein complex
72	d1b0nb_	Alignment	not modelled	6.0	0	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
73	d3fapb_	Alignment	not modelled	6.0	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) **Family:**FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
74	d1bh9b_	Alignment	not modelled	5.8	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
75	d1p77a2	Alignment	not modelled	5.7	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
76	d1ig6a_	Alignment	not modelled	5.4	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
77	d1qwra_	Alignment	not modelled	5.3	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
78	d1cf7a_	Alignment	not modelled	5.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
79	d2oeea1	Alignment	not modelled	5.2	11	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YheA-like
80	c2jrzA	Alignment	not modelled	5.2	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1c;

80	c2jrzA_	Alignment	not modelled	5.2	9	**PDBTitle:** solution structure of the bright/arid domain from the human2 jarid1c protein.