Phyre^2

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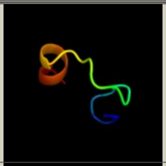
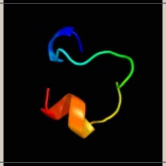
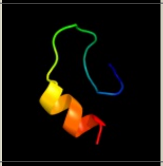
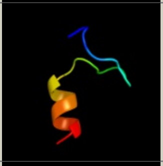
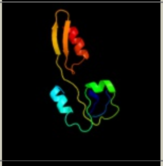
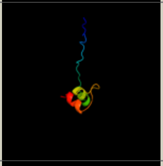
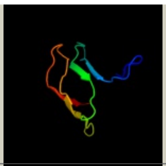
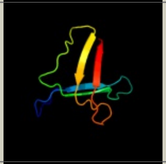
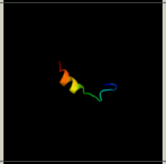
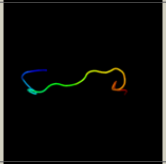
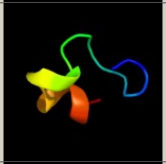
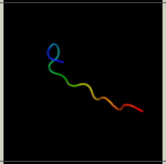
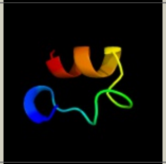
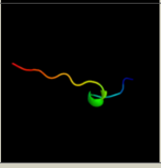
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fpoA_	Alignment		40.2	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hscb; **PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli
2	d1fafa_	Alignment		40.0	20	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
3	c3hhoA_	Alignment		37.0	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog; **PDBTitle:** chaperone hscb from vibrio cholerae
4	d1fpoa1	Alignment		36.1	14	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
5	d1gh6a_	Alignment		30.3	23	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
6	c2pf4E_	Alignment		26.5	23	**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
7	c2dn9A_	Alignment		25.6	25	**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
8	d1uxya1	Alignment		20.1	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
9	c2ctqA_	Alignment		19.6	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 member 12
10	d1xbla_	Alignment		19.0	33	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
11	c2ctwA_	Alignment		18.8	22	**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

12	c1k5gH_	Alignment		18.0	13	**PDB header:**signaling protein/signaling activator **Chain:** H: **PDB Molecule:**ran-specific gtpase-activating protein; **PDBTitle:** crystal structure of ran-gdp-alfx-ranbp1-rangap complex
13	d1k5db_	Alignment		18.0	13	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Ran-binding domain
14	c3bvoA_	Alignment		17.9	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
15	d1z67a1	Alignment		17.2	29	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
16	d1z84a1	Alignment		17.2	32	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
17	c2kqxA_	Alignment		16.1	22	**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
18	d1guqa1	Alignment		15.1	38	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
19	c2o37A_	Alignment		14.0	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
20	d1ta3a_	Alignment		13.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
21	c2ctpA_	Alignment	not modelled	13.4	30	**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
22	c2bvfA_	Alignment	not modelled	13.3	10	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase; **PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
23	c2lgwA_	Alignment	not modelled	12.4	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2; **PDBTitle:** solution structure of the j domain of hsj1a
24	c3mfbA_	Alignment	not modelled	12.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the s-type pyocin domain of eca16692 protein from erwinia carotovora, northeast structural3 genomics consortium target ewr82c
25	c2l6lA_	Alignment	not modelled	12.1	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
26	c1bq0A_	Alignment	not modelled	11.9	33	**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	d1r53a_	Alignment	not modelled	11.7	27	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
28	c2an7A_	Alignment	not modelled	11.4	42	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard

29	c2y3rC_	Alignment	not modelled	11.3	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
30	c2guzO_	Alignment	not modelled	10.9	0	**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
31	c2yuaA_	Alignment	not modelled	10.9	40	**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
32	d1u5tb1	Alignment	not modelled	10.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
33	d1vjha_	Alignment	not modelled	10.6	17	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
34	d3bz6a1	Alignment	not modelled	10.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PSPTO2686-like
35	d1gff1_	Alignment	not modelled	10.6	30	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
36	d1uyra1	Alignment	not modelled	10.5	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
37	c3js8A_	Alignment	not modelled	10.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** solvent-stable cholesterol oxidase
38	c2ntxB_	Alignment	not modelled	10.3	30	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
39	c2ys2A_	Alignment	not modelled	10.1	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** solution structure of the btk motif of human cytoplasmic2 tyrosine-protein kinase bmx
40	c2dmxA_	Alignment	not modelled	10.1	29	**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
41	c2yxyA_	Alignment	not modelled	10.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein, gk0453; **PDBTitle:** crystarl structure of hypothetical conserved protein, gk0453
42	c2dvkA_	Alignment	not modelled	9.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0130 protein ape0816; **PDBTitle:** crystal structure of hypothetical protein from aeropyrum pernix
43	d1w7pd2	Alignment	not modelled	9.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
44	d2i9fa1	Alignment	not modelled	9.6	18	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Arterivirus nucleocapsid protein
45	c2ctrA_	Alignment	not modelled	9.4	35	**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
46	c2ochA_	Alignment	not modelled	9.4	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
47	c2hjhB_	Alignment	not modelled	9.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
48	d1hdja_	Alignment	not modelled	9.1	33	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
49	d1ewsa_	Alignment	not modelled	9.1	63	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
50	d1uc6a_	Alignment	not modelled	9.0	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
51	c1gupC_	Alignment	not modelled	8.8	38	**PDB header:**nucleotidyltransferase **Chain:** C: **PDB Molecule:**galactose-1-phosphate uridylyltransferase; **PDBTitle:** structure of nucleotidyltransferase complexed with udp-2 galactose
52	c2cugA_	Alignment	not modelled	8.8	35	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mkiaa0962 protein; **PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
53	c1zwjA_	Alignment	not modelled	8.6	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative galactose-1-phosphate uridyl transferase; **PDBTitle:** x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
54	d1wjza_	Alignment	not modelled	8.5	15	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain

55	c1mbbA_	Alignment	not modelled	8.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
56	c1vexA_	Alignment	not modelled	7.9	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**f-spondin; **PDBTitle:** f-spondin tsr domain 4
57	d1sq1a_	Alignment	not modelled	7.9	24	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
58	d1sf9a_	Alignment	not modelled	7.9	26	**Fold:**SH3-like barrel **Superfamily:**Hypothetical protein YfhH **Family:**Hypothetical protein YfhH
59	c1fmhB_	Alignment	not modelled	7.8	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
60	c2o59B_	Alignment	not modelled	7.8	14	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0
61	c2dzlA_	Alignment	not modelled	7.8	75	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**protein fam100b; **PDBTitle:** solution structure of the uba domain in human protein2 fam100b
62	d1qb5d_	Alignment	not modelled	7.0	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
63	c2e6iA_	Alignment	not modelled	6.9	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase itk/tsk; **PDBTitle:** solution structure of the btk motif of tyrosine-protein2 kinase itk from human
64	c2qsaA_	Alignment	not modelled	6.5	10	**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.
65	c1xjvA_	Alignment	not modelled	6.5	8	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protection of telomeres 1; **PDBTitle:** crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
66	c2c55A_	Alignment	not modelled	6.5	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein p6; **PDBTitle:** solution structure of the human immunodeficiency virus type2 1 p6 protein
67	c3s88J_	Alignment	not modelled	6.5	17	**PDB header:**immune system/viral protein **Chain:** J: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
68	c3pkzK_	Alignment	not modelled	6.4	17	**PDB header:**recombination **Chain:** K: **PDB Molecule:**recombinase sin; **PDBTitle:** structural basis for catalytic activation of a serine recombinase
69	d1zsoa1	Alignment	not modelled	6.2	18	**Fold:**MAL13P1.257-like **Superfamily:**MAL13P1.257-like **Family:**MAL13P1.257-like
70	c3mlhA_	Alignment	not modelled	6.2	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
71	c3k7bA_	Alignment	not modelled	6.1	36	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein a33; **PDBTitle:** the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains.
72	d2i0ka2	Alignment	not modelled	5.9	7	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
73	d1vjza_	Alignment	not modelled	5.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
74	c2bjqA_	Alignment	not modelled	5.8	30	**PDB header:**motility **Chain:** A: **PDB Molecule:**mfp2a; **PDBTitle:** crystal structure of the nematode sperm cell motility2 protein mfp2
75	d1vyia_	Alignment	not modelled	5.8	36	**Fold:**Phosphoprotein M1, C-terminal domain **Superfamily:**Phosphoprotein M1, C-terminal domain **Family:**Phosphoprotein M1, C-terminal domain
76	d1ewqa3	Alignment	not modelled	5.7	45	**Fold:**Ribonuclease H-like motif **Superfamily:**DNA repair protein MutS, domain II **Family:**DNA repair protein MutS, domain II
77	c1junB_	Alignment	not modelled	5.6	67	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
78	d1cnva_	Alignment	not modelled	5.6	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
79	c3hrdH_	Alignment	not modelled	5.6	36	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
80	d1d0qa_	Alignment	not modelled	5.5	20	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
						Fold:CO dehydrogenase ISP C-domain like

81	d1ffva1	Alignment	not modelled	5.5	18	**Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
82	d2ix0a2	Alignment	not modelled	5.5	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
83	c2lcyA_	Alignment	not modelled	5.3	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**virion spike glycoprotein; **PDBTitle:** nmr structure of the complete internal fusion loop from ebolavirus gp22 at ph 5.5
84	c3siiA_	Alignment	not modelled	5.3	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
85	d1uc8a1	Alignment	not modelled	5.3	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
86	d1e6yb2	Alignment	not modelled	5.3	25	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
87	d1nu9c1	Alignment	not modelled	5.2	19	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Staphylocoagulase **Family:**Staphylocoagulase
88	c2vfvA_	Alignment	not modelled	5.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xylitol oxidase; **PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
89	c2exrA_	Alignment	not modelled	5.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7; **PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482
90	d1zxoa1	Alignment	not modelled	5.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like