Phyre^2

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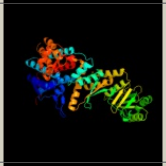
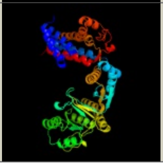
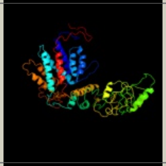
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kp8B_	Alignment		100.0	99	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**groel protein; **PDBTitle:** structural basis for groel-assisted protein folding from2 the crystal structure of (groel-kmgatp)14 at 2.0 a3 resolution
2	c1we3D_	Alignment		100.0	63	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**cpn60(groel); **PDBTitle:** crystal structure of the chaperonin complex2 cpn60/cpn10/(adp)7 from thermus thermophilus
3	c1iokE_	Alignment		100.0	69	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**chaperonin 60; **PDBTitle:** crystal structure of chaperonin-60 from paracoccus2 denitrificans
4	c3iygE_	Alignment		100.0	20	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**t-complex protein 1 subunit; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
5	c1q2vA_	Alignment		100.0	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thermosome alpha subunit; **PDBTitle:** crystal structure of the chaperonin from thermococcus strain ks-12 (nucleotide-free form)
6	c3p9ei_	Alignment		100.0	20	**PDB header:**chaperone **Chain:** I: **PDB Molecule:** **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
7	c3izkF_	Alignment		100.0	23	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**chaperonin; **PDBTitle:** mm-cpn rls deltalid with atp
8	c3iygD_	Alignment		100.0	22	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**t-complex protein 1 subunit delta; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
9	c3ko1H_	Alignment		100.0	22	**PDB header:**chaperone **Chain:** H: **PDB Molecule:**chaperonin; **PDBTitle:** cystal structure of thermosome from acidianus tengchongensis strain s5
10	c3iygA_	Alignment		100.0	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**t-complex protein 1 subunit alpha; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
11	c1sjpA_	Alignment		100.0	57	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**60 kda chaperonin 2; **PDBTitle:** mycobacterium tuberculosis chaperonin60.2

12	c3p9ee_	Alignment		100.0	22	**PDB header:**chaperone **Chain:** E: **PDB Molecule:** **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
13	c3losC_	Alignment		100.0	23	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**chaperonin; **PDBTitle:** atomic model of mm-cpn in the closed state
14	c1a6eA_	Alignment		100.0	24	**PDB header:**chaperonin **Chain:** A: **PDB Molecule:**thermosome (alpha subunit); **PDBTitle:** thermosome-mg-adp-alf3 complex
15	c3iygG_	Alignment		100.0	21	**PDB header:**chaperone **Chain:** G: **PDB Molecule:**t-complex protein 1 subunit gamma; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
16	c3p9en_	Alignment		100.0	19	**PDB header:**chaperone **Chain:** N: **PDB Molecule:** **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
17	c3iygQ_	Alignment		100.0	20	**PDB header:**chaperone **Chain:** Q: **PDB Molecule:**t-complex protein 1 subunit theta; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
18	c3iygZ_	Alignment		100.0	17	**PDB header:**chaperone **Chain:** Z: **PDB Molecule:**t-complex protein 1 subunit zeta; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
19	c3p9dL_	Alignment		100.0	21	**PDB header:**chaperone **Chain:** L: **PDB Molecule:**t-complex protein 1 subunit delta; **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
20	c3p9eo_	Alignment		100.0	21	**PDB header:**chaperone **Chain:** O: **PDB Molecule:** **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
21	c3kttB_	Alignment	not modelled	100.0	25	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**t-complex protein 1 subunit beta; **PDBTitle:** atomic model of bovine tric cct2(beta) subunit derived from2 a 4.0 angstrom cryo-em map
22	c3p9dP_	Alignment	not modelled	100.0	20	**PDB header:**chaperone **Chain:** P: **PDB Molecule:**t-complex protein 1 subunit theta; **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
23	c1a6eB_	Alignment	not modelled	100.0	24	**PDB header:**chaperonin **Chain:** B: **PDB Molecule:**thermosome (beta subunit); **PDBTitle:** thermosome-mg-adp-alf3 complex
24	c3iygH_	Alignment	not modelled	100.0	23	**PDB header:**chaperone **Chain:** H: **PDB Molecule:**t-complex protein 1 subunit eta; **PDBTitle:** ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
25	c3p9eb_	Alignment	not modelled	100.0	22	**PDB header:**chaperone **Chain:** B: **PDB Molecule:** **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
26	c3p9ec_	Alignment	not modelled	100.0	22	**PDB header:**chaperone **Chain:** C: **PDB Molecule:** **PDBTitle:** the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
27	c3rtkA_	Alignment	not modelled	100.0	60	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**60 kda chaperonin 2; **PDBTitle:** crystal structure of cpn60.2 from mycobacterium tuberculosis at 2.8a
28	c3aq1B_	Alignment	not modelled	100.0	24	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**thermosome subunit; **PDBTitle:** open state monomer of a group ii chaperonin from methanococcoides2 burtonii

29	d1q3qa1	Alignment	not modelled	100.0	33	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**Group II chaperonin (CCT, TRIC), ATPase domain
30	d1a6db1	Alignment	not modelled	100.0	35	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**Group II chaperonin (CCT, TRIC), ATPase domain
31	d1a6da1	Alignment	not modelled	100.0	38	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**Group II chaperonin (CCT, TRIC), ATPase domain
32	d1we3a1	Alignment	not modelled	100.0	67	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**GroEL chaperone, ATPase domain
33	d1kp8a1	Alignment	not modelled	100.0	100	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**GroEL chaperone, ATPase domain
34	d1ioka1	Alignment	not modelled	100.0	73	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**GroEL chaperone, ATPase domain
35	c3m6cA_	Alignment	not modelled	100.0	55	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**60 kda chaperonin 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis groel1 apical domain
36	d1kida_	Alignment	not modelled	100.0	97	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
37	d1we3a2	Alignment	not modelled	100.0	65	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
38	d1sjpa2	Alignment	not modelled	100.0	66	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
39	d1oela2	Alignment	not modelled	100.0	99	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
40	d1sjpa1	Alignment	not modelled	100.0	40	**Fold:**GroEL equatorial domain-like **Superfamily:**GroEL equatorial domain-like **Family:**GroEL chaperone, ATPase domain
41	d1dk7a_	Alignment	not modelled	100.0	100	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
42	d1srva_	Alignment	not modelled	100.0	69	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
43	d1ioka2	Alignment	not modelled	99.9	74	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
44	d1gmla_	Alignment	not modelled	99.6	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
45	d1q3qa2	Alignment	not modelled	99.4	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
46	d1a6db2	Alignment	not modelled	99.4	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
47	d1assa_	Alignment	not modelled	99.4	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
48	d1sjpa3	Alignment	not modelled	99.0	31	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
49	d1kp8a3	Alignment	not modelled	99.0	66	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
50	d1a6db3	Alignment	not modelled	98.9	12	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**Group II chaperonin (CCT, TRIC), intermediate domain
51	d1q3qa3	Alignment	not modelled	98.8	20	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**Group II chaperonin (CCT, TRIC), intermediate domain
52	d1a6da3	Alignment	not modelled	98.7	10	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**Group II chaperonin (CCT, TRIC), intermediate domain
53	d1ioka3	Alignment	not modelled	98.5	80	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
54	d1we3a3	Alignment	not modelled	97.5	51	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
55	d1d7ya2	Alignment	not modelled	22.3	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
56	d1q1ra2	Alignment	not modelled	17.4	31	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central

						domains
57	d1m6ia2	Alignment	not modelled	12.0	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
58	c2ogxA_	Alignment	not modelled	11.8	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**molybdenum storage protein subunit alpha; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
59	c2ah6B_	Alignment	not modelled	11.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
60	d1ovma1	Alignment	not modelled	10.0	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
61	d3e5ua1	Alignment	not modelled	9.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
62	c3tekA_	Alignment	not modelled	9.3	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
63	d1xhca2	Alignment	not modelled	8.7	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
64	d2a29a1	Alignment	not modelled	8.2	13	**Fold:**Metal cation-transporting ATPase, ATP-binding domain N **Superfamily:**Metal cation-transporting ATPase, ATP-binding domain N **Family:**Metal cation-transporting ATPase, ATP-binding domain N
65	c3nrdB_	Alignment	not modelled	7.9	17	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
66	c2veqA_	Alignment	not modelled	7.8	8	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** insights into kinetochore-dna interactions from the2 structure of cep3p
67	c2f8mB_	Alignment	not modelled	7.8	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
68	c2b0tA_	Alignment	not modelled	7.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase
69	c2xdqA_	Alignment	not modelled	7.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
70	d1ijwc_	Alignment	not modelled	7.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
71	d1itwa_	Alignment	not modelled	7.3	13	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase
72	c3cwcB_	Alignment	not modelled	7.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
73	c2x48B_	Alignment	not modelled	7.0	6	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
74	c3i24B_	Alignment	not modelled	6.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
75	c2kztA_	Alignment	not modelled	6.8	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
76	c2jnhA_	Alignment	not modelled	6.8	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
77	d2nvma1	Alignment	not modelled	6.8	21	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
78	c1z8yP_	Alignment	not modelled	6.7	16	**PDB header:**virus **Chain:** P: **PDB Molecule:**spike glycoprotein e2; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
79	c1z8yJ_	Alignment	not modelled	6.7	16	**PDB header:**virus **Chain:** J: **PDB Molecule:**spike glycoprotein e2; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
80	c1z8yL_	Alignment	not modelled	6.7	16	**PDB header:**virus **Chain:** L: **PDB Molecule:**spike glycoprotein e2; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
81	c1z8yN_	Alignment	not modelled	6.7	16	**PDB header:**virus **Chain:** N: **PDB Molecule:**spike glycoprotein e2; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses

82	d1gv4a2	Alignment	not modelled	6.6	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
83	d1o5ha_	Alignment	not modelled	6.5	50	**Fold:**Methenyltetrahydrofolate cyclohydrolase-like **Superfamily:**Methenyltetrahydrofolate cyclohydrolase-like **Family:**Methenyltetrahydrofolate cyclohydrolase-like
84	c1rg9D_	Alignment	not modelled	6.3	42	**PDB header:**transferase **Chain:** D: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** s-adenosylmethionine synthetase complexed with sam and ppnp
85	d1fita_	Alignment	not modelled	6.3	6	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
86	c3so4C_	Alignment	not modelled	6.2	42	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
87	c3rv2B_	Alignment	not modelled	6.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
88	c3imlB_	Alignment	not modelled	5.9	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
89	d1m1na_	Alignment	not modelled	5.9	22	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
90	d2h6ca1	Alignment	not modelled	5.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
91	d2nlva1	Alignment	not modelled	5.8	21	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
92	c2obvA_	Alignment	not modelled	5.8	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine synthetase isoform type-1; **PDBTitle:** crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
93	c2p9wA_	Alignment	not modelled	5.7	11	**PDB header:**allergen **Chain:** A: **PDB Molecule:**mal s 1 allergenic protein; **PDBTitle:** crystal structure of the major malassezia sympodialis allergen mala s2 1
94	d3bula1	Alignment	not modelled	5.6	9	**Fold:**Methionine synthase domain-like **Superfamily:**Methionine synthase domain **Family:**Methionine synthase domain
95	d1hcra_	Alignment	not modelled	5.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
96	d1wv3a2	Alignment	not modelled	5.4	27	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**EssC N-terminal domain-like
97	c2koyA_	Alignment	not modelled	5.4	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
98	d1v97a6	Alignment	not modelled	5.3	19	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
99	c3kinB_	Alignment	not modelled	5.3	14	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**kinesin heavy chain; **PDBTitle:** kinesin (dimeric) from rattus norvegicus