

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5cdiB_	Alignment		100.0	51	PDB header: chaperone Chain: B: PDB Molecule: chaperonin 60b1; PDBTitle: chloroplast chaperonin 60b1 of chlamydomonas
2	c1kp8B_	Alignment		100.0	60	PDB header: chaperone Chain: B: PDB Molecule: groel protein; PDBTitle: structural basis for groel-assisted protein folding from the crystal2 structure of (groel-kmgatp)14 at 2.0 a resolution
3	c1we3D_	Alignment		100.0	66	PDB header: chaperone Chain: D: PDB Molecule: cpn60(groel); PDBTitle: crystal structure of the chaperonin complex cpn60/cpn10/(adp)7 from2 thermus thermophilus
4	c4pj1E_	Alignment		100.0	47	PDB header: chaperone Chain: E: PDB Molecule: 60 kda heat shock protein, mitochondrial; PDBTitle: crystal structure of the human mitochondrial chaperonin symmetrical2 'football' complex
5	c5da8N_	Alignment		100.0	56	PDB header: chaperone Chain: N: PDB Molecule: 60 kda chaperonin; PDBTitle: crystal structure of chaperonin groel from
6	c1iokE_	Alignment		100.0	59	PDB header: chaperone Chain: E: PDB Molecule: chaperonin 60; PDBTitle: crystal structure of chaperonin-60 from paracoccus2 denitrificans
7	c3p9ei_	Alignment		100.0	19	PDB header: chaperone Chain: I: PDB Molecule: PDBTitle: the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
8	c3iygG_	Alignment		100.0	19	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 angstrom cryo-em map
9	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 angstrom cryo-em map
10	c3iygA_	Alignment		100.0	19	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 angstrom cryo-em map
11	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

12	c3iygD_	Alignment		100.0	23	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 angstrom cryo-em map
13	c4b2tE_	Alignment		100.0	21	PDB header: chaperone Chain: E: PDB Molecule: t-complex protein 1 subunit epsilon; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
14	c4b2tQ_	Alignment		100.0	21	PDB header: chaperone Chain: Q: PDB Molecule: t-complex protein 1 subunit theta; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
15	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
16	c4b2tD_	Alignment		100.0	25	PDB header: chaperone Chain: D: PDB Molecule: t-complex protein 1 subunit delta; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
17	c1q2vA_	Alignment		100.0	26	PDB header: chaperone Chain: A: PDB Molecule: thermosome alpha subunit; PDBTitle: crystal structure of the chaperonin from thermococcus strain ks-12 (nucleotide-free form)
18	c3losC_	Alignment		100.0	27	PDB header: chaperone Chain: C: PDB Molecule: chaperonin; PDBTitle: atomic model of mm-cpn in the closed state
19	c3iygZ_	Alignment		100.0	21	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 angstrom cryo-em map
20	c3p9eo_	Alignment		100.0	20	PDB header: chaperone Chain: O: PDB Molecule: PDBTitle: the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
21	c3j1bA_	Alignment	not modelled	100.0	23	PDB header: chaperone Chain: A: PDB Molecule: chaperonin alpha subunit; PDBTitle: cryo-em structure of 8-fold symmetric ratcpn-alpha in apo state
22	c3rtkA_	Alignment	not modelled	100.0	99	PDB header: chaperone Chain: A: PDB Molecule: 60 kda chaperonin 2; PDBTitle: crystal structure of cpn60.2 from mycobacterium tuberculosis at 2.8a
23	c3iygQ_	Alignment	not modelled	100.0	21	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 angstrom cryo-em map
24	c3p9ee_	Alignment	not modelled	100.0	18	PDB header: chaperone Chain: E: PDB Molecule: PDBTitle: the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
25	c1a6eA_	Alignment	not modelled	100.0	24	PDB header: chaperonin Chain: A: PDB Molecule: thermosome (alpha subunit); PDBTitle: thermosome-mg-adp-alf3 complex
26	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
27	c3izkF_	Alignment	not modelled	100.0	26	PDB header: chaperone Chain: F: PDB Molecule: chaperonin; PDBTitle: mm-cpn rls deltalid with atp
28	c3ko1H_	Alignment	not modelled	100.0	24	PDB header: chaperone Chain: H: PDB Molecule: chaperonin; PDBTitle: cystal structure of thermosome from acidianus tengchongensis strain s5
						PDB header: chaperone

29	c3kttB	Alignment	not modelled	100.0	23	Chain: B; PDB Molecule: t-complex protein 1 subunit beta; PDBTitle: atomic model of bovine tric cct2(beta) subunit derived from a 4.02 angstrom cryo-em map
30	c4b2tA	Alignment	not modelled	100.0	19	PDB header: chaperone Chain: A; PDB Molecule: t-complex protein 1 subunit alpha; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
31	c1a6eB	Alignment	not modelled	100.0	24	PDB header: chaperonin Chain: B; PDB Molecule: thermosome (beta subunit); PDBTitle: thermosome-mg-adp-alf3 complex
32	c4b2tH	Alignment	not modelled	100.0	21	PDB header: chaperone Chain: H; PDB Molecule: t-complex protein 1 subunit eta; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
33	c4b2tG	Alignment	not modelled	100.0	19	PDB header: chaperone Chain: G; PDB Molecule: t-complex protein 1 subunit gamma; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
34	c3iygH	Alignment	not modelled	100.0	19	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 angstrom cryo-em map
35	c3p9ec	Alignment	not modelled	100.0	19	PDB header: chaperone Chain: C; PDB Molecule: PDBTitle: the crystal structure of yeast cct reveals intrinsic asymmetry of 2 eukaryotic cytosolic chaperonins
36	c5x9vA	Alignment	not modelled	100.0	23	PDB header: chaperone Chain: A; PDB Molecule: thermosome, alpha subunit; PDBTitle: crystal structure of group iii chaperonin in the closed state
37	c4xcgB	Alignment	not modelled	100.0	25	PDB header: chaperone Chain: B; PDB Molecule: thermosome subunit beta; PDBTitle: crystal structure of a hexadecameric tf55 complex from s.2 solfataricus, crystal form i
38	c1sjpA	Alignment	not modelled	100.0	97	PDB header: chaperone Chain: A; PDB Molecule: 60 kda chaperonin 2; PDBTitle: mycobacterium tuberculosis chaperonin60.2
39	c3p9dP	Alignment	not modelled	100.0	17	PDB header: chaperone Chain: P; PDB Molecule: t-complex protein 1 subunit theta; PDBTitle: the crystal structure of yeast cct reveals intrinsic asymmetry of 2 eukaryotic cytosolic chaperonins
40	c4xciB	Alignment	not modelled	100.0	25	PDB header: chaperone Chain: B; PDB Molecule: thermosome subunit beta; PDBTitle: crystal structure of a hexadecameric tf55 complex from s.2 solfataricus, crystal form ii
41	c4b2tg	Alignment	not modelled	100.0	24	PDB header: chaperone Chain: G; PDB Molecule: t-complex protein 1 subunit gamma; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
42	c4b2th	Alignment	not modelled	100.0	26	PDB header: chaperone Chain: H; PDB Molecule: t-complex protein 1 subunit eta; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
43	c4b2tq	Alignment	not modelled	100.0	21	PDB header: chaperone Chain: Q; PDB Molecule: t-complex protein 1 subunit theta; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
44	c4b2ta	Alignment	not modelled	100.0	24	PDB header: chaperone Chain: A; PDB Molecule: t-complex protein 1 subunit alpha; PDBTitle: the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
45	c4xciA	Alignment	not modelled	100.0	32	PDB header: chaperone Chain: A; PDB Molecule: thermosome subunit alpha; PDBTitle: crystal structure of a hexadecameric tf55 complex from s.2 solfataricus, crystal form ii
46	c3aq1B	Alignment	not modelled	100.0	22	PDB header: chaperone Chain: B; PDB Molecule: thermosome subunit; PDBTitle: open state monomer of a group ii chaperonin from methanococcoides2 burtonii
47	d1q3qa1	Alignment	not modelled	100.0	41	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: Group II chaperonin (CCT, TRIC), ATPase domain
48	d1a6db1	Alignment	not modelled	100.0	38	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: Group II chaperonin (CCT, TRIC), ATPase domain
49	d1a6da1	Alignment	not modelled	100.0	39	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: Group II chaperonin (CCT, TRIC), ATPase domain
50	d1we3a1	Alignment	not modelled	100.0	76	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: GroEL chaperone, ATPase domain
51	d1ioka1	Alignment	not modelled	100.0	64	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: GroEL chaperone, ATPase domain
52	d1kp8a1	Alignment	not modelled	100.0	68	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: GroEL chaperone, ATPase domain
53	d1sjpa1	Alignment	not modelled	100.0	86	Fold: GroEL equatorial domain-like Superfamily: GroEL equatorial domain-like Family: GroEL chaperone, ATPase domain
54	c3m6cA	Alignment	not modelled	99.9	64	PDB header: chaperone Chain: A; PDB Molecule: 60 kda chaperonin 1; PDBTitle: crystal structure of mycobacterium tuberculosis groel1 apical domain
55	d1we3a2	Alignment	not modelled	99.9	68	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like

						Family: GroEL-like chaperone, apical domain
56	d1sjpa2	Alignment	not modelled	99.9	100	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
57	d1kida	Alignment	not modelled	99.9	67	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
58	c5cdjA	Alignment	not modelled	99.9	49	PDB header: chaperone Chain: A: PDB Molecule: rubisco large subunit-binding protein subunit alpha, PDBTitle: apical domain of chloroplast chaperonin 60a
59	d1oela2	Alignment	not modelled	99.9	65	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
60	d1dk7a	Alignment	not modelled	99.7	64	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
61	d1srva	Alignment	not modelled	99.7	70	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
62	d1gmla	Alignment	not modelled	99.5	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
63	d1assa	Alignment	not modelled	99.4	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
64	d1ioka2	Alignment	not modelled	99.4	68	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
65	d1q3qa2	Alignment	not modelled	99.3	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
66	d1a6db2	Alignment	not modelled	99.3	18	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
67	d1sjpa3	Alignment	not modelled	98.1	63	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: GroEL-like chaperone, intermediate domain
68	d1a6db3	Alignment	not modelled	98.0	13	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: Group II chaperonin (CCT, TRIC), intermediate domain
69	d1kp8a3	Alignment	not modelled	97.9	35	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: GroEL-like chaperone, intermediate domain
70	d1a6da3	Alignment	not modelled	97.8	12	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: Group II chaperonin (CCT, TRIC), intermediate domain
71	d1q3qa3	Alignment	not modelled	97.3	15	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: Group II chaperonin (CCT, TRIC), intermediate domain
72	d1ioka3	Alignment	not modelled	96.8	49	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: GroEL-like chaperone, intermediate domain
73	d1we3a3	Alignment	not modelled	94.8	38	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: GroEL-like chaperone, intermediate domain
74	d1d7ya2	Alignment	not modelled	25.2	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
75	c3hazA	Alignment	not modelled	21.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of bifunctional proline utilization a2 (puta) protein
76	d1q1ra2	Alignment	not modelled	19.3	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
77	d1m6ia2	Alignment	not modelled	17.1	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
78	c2ogxA	Alignment	not modelled	16.2	18	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein from <i>Zotobacter vinelandii</i> loaded with polyoxotungstates (wsto)
79	d1tj1a1	Alignment	not modelled	12.9	17	Fold: N-terminal domain of bifunctional PutA protein Superfamily: N-terminal domain of bifunctional PutA protein Family: N-terminal domain of bifunctional PutA protein
80	c4zn6B	Alignment	not modelled	12.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray crystal structure of 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase (ispc) from <i>Acinetobacter baumannii</i>
81	d1ovma1	Alignment	not modelled	12.3	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
82	d1xhca2	Alignment	not modelled	11.7	36	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

						Family: FAD/NAD-linked reductases, N-terminal and central domains
83	d1vl2a2	Alignment	not modelled	11.4	15	Fold: Argininosuccinate synthetase, C-terminal domain Superfamily: Argininosuccinate synthetase, C-terminal domain Family: Argininosuccinate synthetase, C-terminal domain
84	c5kf6B	Alignment	not modelled	11.4	24	PDB header: oxidoreductase Chain: B; PDB Molecule: bifunctional protein puta; PDBTitle: structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
85	d1j20a2	Alignment	not modelled	10.5	17	Fold: Argininosuccinate synthetase, C-terminal domain Superfamily: Argininosuccinate synthetase, C-terminal domain Family: Argininosuccinate synthetase, C-terminal domain
86	c2xdqA	Alignment	not modelled	10.2	17	PDB header: oxidoreductase Chain: A; PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
87	d1gv4a2	Alignment	not modelled	9.8	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
88	c3tekA	Alignment	not modelled	9.7	36	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
89	c6iczX	Alignment	not modelled	9.3	27	PDB header: splicing Chain: X; PDB Molecule: prkr-interacting protein 1; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
90	c2ynmC	Alignment	not modelled	9.1	14	PDB header: oxidoreductase Chain: C; PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
91	c3nrdB	Alignment	not modelled	9.1	19	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
92	c4gmjE	Alignment	not modelled	9.1	7	PDB header: rna binding protein Chain: E; PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: structure of human not1 mif4g domain co-crystallized with caf1
93	c4ct4C	Alignment	not modelled	9.0	7	PDB header: rna binding protein Chain: C; PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: cnot1 mif4g domain - ddx6 complex
94	c2d9sA	Alignment	not modelled	8.5	17	PDB header: ligase Chain: A; PDB Molecule: cbl e3 ubiquitin protein ligase; PDBTitle: solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
95	c2jnhA	Alignment	not modelled	8.0	26	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of the uba domain from cbl-b
96	c3i24B	Alignment	not modelled	8.0	18	PDB header: hydrolase Chain: B; PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
97	c1k87A	Alignment	not modelled	7.8	14	PDB header: oxidoreductase Chain: A; PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of e.coli puta (residues 1-669)
98	c2do6A	Alignment	not modelled	7.7	22	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of rsgi ruh-065, a uba domain from human2 cdna
99	c6jqsA	Alignment	not modelled	7.6	17	PDB header: dna binding protein Chain: A; PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere