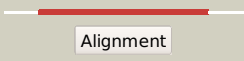

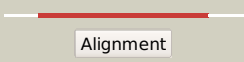

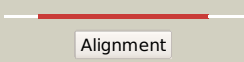

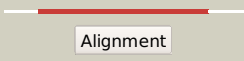

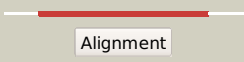

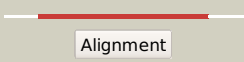
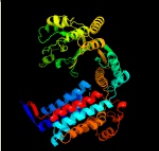
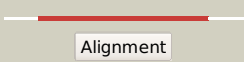

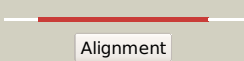

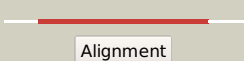

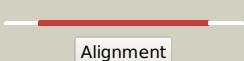

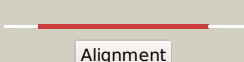



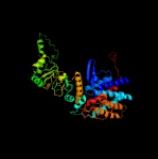





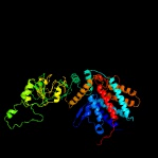


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3417c_groEL_3835452_3837071
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	d38a88a5fa9ea1e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1kp8B_</a>	 Alignment		100.0	52	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> groel protein; <b>PDBTitle:</b> structural basis for groel-assisted protein folding from the crystal2 structure of (groel-kmgatp)14 at 2.0 a resolution
2	<a href="#">c1we3D_</a>	 Alignment		100.0	54	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> cpn60(groel); <b>PDBTitle:</b> crystal structure of the chaperonin complex cpn60/cpn10/(adp)7 from2 thermus thermophilus
3	<a href="#">c4pj1E_</a>	 Alignment		100.0	42	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> 60 kda heat shock protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the human mitochondrial chaperonin symmetrical2 'football' complex
4	<a href="#">c1iokE_</a>	 Alignment		100.0	52	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> chaperonin 60; <b>PDBTitle:</b> crystal structure of chaperonin-60 from paracoccus2 denitrificans
5	<a href="#">c5cdiB_</a>	 Alignment		100.0	46	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> chaperonin 60b1; <b>PDBTitle:</b> chloroplast chaperonin 60b1 of chlamydomonas
6	<a href="#">c5da8N_</a>	 Alignment		100.0	50	<b>PDB header:</b> chaperone <b>Chain:</b> N; <b>PDB Molecule:</b> 60 kda chaperonin; <b>PDBTitle:</b> crystal structure of chaperonin groel from
7	<a href="#">c3p9ei_</a>	 Alignment		100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> I; <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
8	<a href="#">c3iygE_</a>	 Alignment		100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> t-complex protein 1 subunit; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
9	<a href="#">c4b2tQ_</a>	 Alignment		100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> Q; <b>PDB Molecule:</b> t-complex protein 1 subunit theta; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
10	<a href="#">c1q2vA_</a>	 Alignment		100.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> thermosome alpha subunit; <b>PDBTitle:</b> crystal structure of the chaperonin from thermococcus strain ks-12 (nucleotide-free form)
11	<a href="#">c3izkF_</a>	 Alignment		100.0	29	<b>PDB header:</b> chaperone <b>Chain:</b> F; <b>PDB Molecule:</b> chaperonin; <b>PDBTitle:</b> mm-cpn rls deltalid with atp

12	<a href="#">c3iygD_</a>	Alignment		100.0	24	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> t-complex protein 1 subunit delta; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
13	<a href="#">c3ko1H_</a>	Alignment		100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> H: <b>PDB Molecule:</b> chaperonin; <b>PDBTitle:</b> crystal structure of thermosome from acidianus tengchongensis strain s5
14	<a href="#">c3p9en_</a>	Alignment		100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> N: <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
15	<a href="#">c3iygA_</a>	Alignment		100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> t-complex protein 1 subunit alpha; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
16	<a href="#">c4b2tE_</a>	Alignment		100.0	23	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> t-complex protein 1 subunit epsilon; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
17	<a href="#">c3iygZ_</a>	Alignment		100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> Z: <b>PDB Molecule:</b> t-complex protein 1 subunit zeta; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
18	<a href="#">c4b2tD_</a>	Alignment		100.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> t-complex protein 1 subunit delta; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
19	<a href="#">c3p9eo_</a>	Alignment		100.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> O: <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
20	<a href="#">c3iygG_</a>	Alignment		100.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> G: <b>PDB Molecule:</b> t-complex protein 1 subunit gamma; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
21	<a href="#">c3losC_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> chaperonin; <b>PDBTitle:</b> atomic model of mm-cpn in the closed state
22	<a href="#">c3p9dL_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> L: <b>PDB Molecule:</b> t-complex protein 1 subunit delta; <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
23	<a href="#">c3p9ee_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
24	<a href="#">c4b2tA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> t-complex protein 1 subunit alpha; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
25	<a href="#">c1a6eA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> chaperonin <b>Chain:</b> A: <b>PDB Molecule:</b> thermosome (alpha subunit); <b>PDBTitle:</b> thermosome-mg-adp-alf3 complex
26	<a href="#">c3j1bA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperonin alpha subunit; <b>PDBTitle:</b> cryo-em structure of 8-fold symmetric ratcpn-alpha in apo state
27	<a href="#">c3iygQ_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> Q: <b>PDB Molecule:</b> t-complex protein 1 subunit theta; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
28	<a href="#">c4b2tH_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> H: <b>PDB Molecule:</b> t-complex protein 1 subunit eta; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
						<b>PDB header:</b> chaperone

29	<a href="#">c4xcgB_</a>	Alignment	not modelled	100.0	27	<b>Chain:</b> B; <b>PDB Molecule:</b> thermosome subunit beta; <b>PDBTitle:</b> crystal structure of a hexadecameric tf55 complex from s.2 solfataricus, crystal form i
30	<a href="#">c3kttB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> t-complex protein 1 subunit beta; <b>PDBTitle:</b> atomic model of bovine tric cct2(beta) subunit derived from a 4.02 angstrom cryo-em map
31	<a href="#">c4b2tG_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> G; <b>PDB Molecule:</b> t-complex protein 1 subunit gamma; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
32	<a href="#">c3iygH_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> H; <b>PDB Molecule:</b> t-complex protein 1 subunit eta; <b>PDBTitle:</b> ca model of bovine tric/cct derived from a 4.0 angstrom cryo-em map
33	<a href="#">c1sjpA_</a>	Alignment	not modelled	100.0	59	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> 60 kda chaperonin 2; <b>PDBTitle:</b> mycobacterium tuberculosis chaperonin60.2
34	<a href="#">c3p9eb_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of 2 eukaryotic cytosolic chaperonins
35	<a href="#">c3p9ec_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> C; <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of 2 eukaryotic cytosolic chaperonins
36	<a href="#">c1a6eB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> chaperonin <b>Chain:</b> B; <b>PDB Molecule:</b> thermosome (beta subunit); <b>PDBTitle:</b> thermosome-mg-adp-alf3 complex
37	<a href="#">c4xciB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> thermosome subunit beta; <b>PDBTitle:</b> crystal structure of a hexadecameric tf55 complex from s.2 solfataricus, crystal form ii
38	<a href="#">c5x9vA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> thermosome, alpha subunit; <b>PDBTitle:</b> crystal structure of group iii chaperonin in the closed state
39	<a href="#">c3p9dP_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> P; <b>PDB Molecule:</b> t-complex protein 1 subunit theta; <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of 2 eukaryotic cytosolic chaperonins
40	<a href="#">c3rtkA_</a>	Alignment	not modelled	100.0	61	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> 60 kda chaperonin 2; <b>PDBTitle:</b> crystal structure of cpn60.2 from mycobacterium tuberculosis at 2.8a
41	<a href="#">c4b2tq_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> Q; <b>PDB Molecule:</b> t-complex protein 1 subunit theta; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
42	<a href="#">c4b2th_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> H; <b>PDB Molecule:</b> t-complex protein 1 subunit eta; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
43	<a href="#">c4b2tg_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> G; <b>PDB Molecule:</b> t-complex protein 1 subunit gamma; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
44	<a href="#">c4b2ta_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> t-complex protein 1 subunit alpha; <b>PDBTitle:</b> the crystal structures of the eukaryotic chaperonin cct2 reveal its functional partitioning
45	<a href="#">c4xciA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> thermosome subunit alpha; <b>PDBTitle:</b> crystal structure of a hexadecameric tf55 complex from s.2 solfataricus, crystal form ii
46	<a href="#">c3aq1B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> thermosome subunit; <b>PDBTitle:</b> open state monomer of a group ii chaperonin from methanococcus burtonii
47	<a href="#">d1q3qa1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), ATPase domain
48	<a href="#">d1a6db1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), ATPase domain
49	<a href="#">d1a6da1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), ATPase domain
50	<a href="#">d1we3a1</a>	Alignment	not modelled	100.0	59	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> GroEL chaperone, ATPase domain
51	<a href="#">d1kp8a1</a>	Alignment	not modelled	100.0	62	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> GroEL chaperone, ATPase domain
52	<a href="#">d1ioka1</a>	Alignment	not modelled	100.0	55	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> GroEL chaperone, ATPase domain
53	<a href="#">d1sjpa1</a>	Alignment	not modelled	100.0	45	<b>Fold:</b> GroEL equatorial domain-like <b>Superfamily:</b> GroEL equatorial domain-like <b>Family:</b> GroEL chaperone, ATPase domain
54	<a href="#">c3m6cA_</a>	Alignment	not modelled	99.9	100	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> 60 kda chaperonin 1; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis groel1 apical domain
55	<a href="#">d1kida_</a>	Alignment	not modelled	99.9	53	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like

						<b>Family:</b> GroEL-like chaperone, apical domain
56	<a href="#">d1we3a2</a>	Alignment	not modelled	99.9	56	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
57	<a href="#">d1sjpa2</a>	Alignment	not modelled	99.9	64	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
58	<a href="#">c5cdjA</a>	Alignment	not modelled	99.9	41	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco large subunit-binding protein subunit alpha, <b>PDBTitle:</b> apical domain of chloroplast chaperonin 60a
59	<a href="#">d1oela2</a>	Alignment	not modelled	99.9	53	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
60	<a href="#">d1dk7a</a>	Alignment	not modelled	99.8	56	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
61	<a href="#">d1srva</a>	Alignment	not modelled	99.8	58	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
62	<a href="#">d1ioka2</a>	Alignment	not modelled	99.5	59	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
63	<a href="#">d1gmla</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
64	<a href="#">d1assa</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
65	<a href="#">d1q3qa2</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
66	<a href="#">d1a6db2</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
67	<a href="#">d1sjpa3</a>	Alignment	not modelled	98.4	36	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
68	<a href="#">d1a6db3</a>	Alignment	not modelled	98.2	12	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> Group II chaperonin (CCT, TRIC), intermediate domain
69	<a href="#">d1kp8a3</a>	Alignment	not modelled	98.1	35	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
70	<a href="#">d1a6da3</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> Group II chaperonin (CCT, TRIC), intermediate domain
71	<a href="#">d1q3qa3</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> Group II chaperonin (CCT, TRIC), intermediate domain
72	<a href="#">d1ioka3</a>	Alignment	not modelled	96.9	49	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
73	<a href="#">d1we3a3</a>	Alignment	not modelled	96.3	36	<b>Fold:</b> GroEL-intermediate domain like <b>Superfamily:</b> GroEL-intermediate domain like <b>Family:</b> GroEL-like chaperone, intermediate domain
74	<a href="#">d1vl2a2</a>	Alignment	not modelled	17.4	17	<b>Fold:</b> Argininosuccinate synthetase, C-terminal domain <b>Superfamily:</b> Argininosuccinate synthetase, C-terminal domain <b>Family:</b> Argininosuccinate synthetase, C-terminal domain
75	<a href="#">c3nrdB</a>	Alignment	not modelled	13.4	8	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> histidine triad (hit) protein; <b>PDBTitle:</b> crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
76	<a href="#">d1a6qa1</a>	Alignment	not modelled	12.5	14	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> Protein serine/threonine phosphatase 2C, C-terminal domain <b>Family:</b> Protein serine/threonine phosphatase 2C, C-terminal domain
77	<a href="#">c3tekA</a>	Alignment	not modelled	11.8	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> thermodbp-single stranded dna binding protein; <b>PDBTitle:</b> thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
78	<a href="#">c4zn6B</a>	Alignment	not modelled	11.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> x-ray crystal structure of 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase (ispc) from acinetobacter baumannii
79	<a href="#">c5ujmB</a>	Alignment	not modelled	10.6	9	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2; <b>PDBTitle:</b> structure of the active form of human origin recognition complex and2 its atpase motor module
80	<a href="#">c4c53A</a>	Alignment	not modelled	9.9	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> pre-glycoprotein polyprotein gp complex; <b>PDBTitle:</b> crystal structure of guararito virus gp2 in the post-fusion2 conformation
81	<a href="#">c3mkoA</a>	Alignment	not modelled	9.8	21	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycoprotein c; <b>PDBTitle:</b> crystal structure of the lymphocytic choriomeningitis virus membrane2 fusion glycoprotein gp2 in its postfusion conformation <b>Fold:</b> PH1570-like

82	<a href="#">d2hq4a1</a>	Alignment	not modelled	9.6	24	<b>Superfamily:</b> PH1570-like <b>Family:</b> PH1570-like
83	<a href="#">d1j20a2</a>	Alignment	not modelled	9.3	17	<b>Fold:</b> Argininosuccinate synthetase, C-terminal domain <b>Superfamily:</b> Argininosuccinate synthetase, C-terminal domain <b>Family:</b> Argininosuccinate synthetase, C-terminal domain
84	<a href="#">c5kqoA_</a>	Alignment	not modelled	9.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus
85	<a href="#">c6jqsA_</a>	Alignment	not modelled	8.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> structure of transcription factor, gere
86	<a href="#">c3kinB_</a>	Alignment	not modelled	8.7	19	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin heavy chain; <b>PDBTitle:</b> kinesin (dimeric) from rattus norvegicus
87	<a href="#">d1fita_</a>	Alignment	not modelled	8.5	3	<b>Fold:</b> HIT-like <b>Superfamily:</b> HIT-like <b>Family:</b> HIT (HINT, histidine triad) family of protein kinase-interacting proteins
88	<a href="#">d1n1ea1</a>	Alignment	not modelled	8.2	12	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Glycerol-3-phosphate dehydrogenase
89	<a href="#">c3au9A_</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> crystal structure of the quaternary complex-1 of an isomerase
90	<a href="#">c2k37A_</a>	Alignment	not modelled	7.6	11	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> chlorosome protein a; <b>PDBTitle:</b> csma
91	<a href="#">c4mjsQ_</a>	Alignment	not modelled	7.5	15	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> Q: <b>PDB Molecule:</b> protein kinase c zeta type; <b>PDBTitle:</b> crystal structure of a pb1 complex
92	<a href="#">c3i24B_</a>	Alignment	not modelled	7.5	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hit family hydrolase; <b>PDBTitle:</b> crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
93	<a href="#">c1ddiA_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [nadph] flavoprotein alpha-component; <b>PDBTitle:</b> crystal structure of sir-fp60
94	<a href="#">d1q0qa3</a>	Alignment	not modelled	7.0	24	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
95	<a href="#">d1cf7b_</a>	Alignment	not modelled	6.9	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Cell cycle transcription factor e2f-dp
96	<a href="#">c4wgiA_</a>	Alignment	not modelled	6.8	11	<b>PDB header:</b> apoptosis/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,induced myeloid <b>PDBTitle:</b> a single diastereomer of a macrolactam core binds specifically to2 myeloid cell leukemia 1 (mcl1)
97	<a href="#">c2kinB_</a>	Alignment	not modelled	6.8	12	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin; <b>PDBTitle:</b> kinesin (monomeric) from rattus norvegicus
98	<a href="#">d2caza1</a>	Alignment	not modelled	6.8	14	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
99	<a href="#">c2cazD_</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> suppressor protein stp22 of temperature-sensitive alpha- <b>PDBTitle:</b> esct-i core