Phyre2

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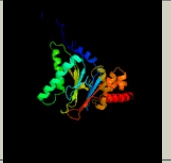
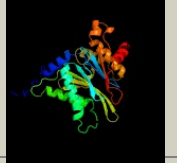
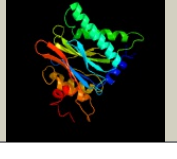
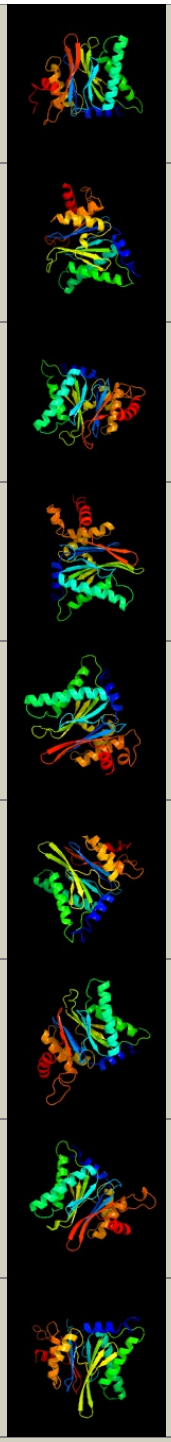
Description	RVBD2109c_(prcA)_2368991_2369737
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	c40a8dd9426e45b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q5qa_	Alignment		100.0	72	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
2	c1q5rD_	Alignment		100.0	72	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**proteasome alpha-type subunit 1; **PDBTitle:** the rhodococcus 20s proteasome with unprocessed pro-peptides
3	c6qm7C_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome alpha3 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
4	c5ln3C_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome subunit alpha type-4; **PDBTitle:** the human 26s proteasome at 6.8 ang.
5	d1rypb_	Alignment		100.0	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
6	d1iruc_	Alignment		100.0	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
7	d1irug_	Alignment		100.0	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
8	c3bdmF_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome component c1; **PDBTitle:** yeast 20s proteasome:glidobactin a-complex
9	d1rypg_	Alignment		100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
10	c6qm7A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteasome alpha1 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
11	c1iruF_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**20s proteasome; **PDBTitle:** crystal structure of the mammalian 20s proteasome at 2.75 a2 resolution

12	d1iruf_	Alignment		100.0	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
13	d1irua_	Alignment		100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
14	d1j2pa_	Alignment		100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
15	d1irud_	Alignment		100.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
16	d1rypc_	Alignment		100.0	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
17	c6qm7T_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**proteasome alpha6 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
18	c6qm8D_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**proteasome alpha4 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
19	c6qm8B_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome alpha2 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
20	d1irub_	Alignment		100.0	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
21	d1yara1	Alignment	not modelled	100.0	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
22	d1rype_	Alignment	not modelled	100.0	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
23	c6qm8U_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** U: **PDB Molecule:**proteasome alpha7 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
24	c5fmgQ_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** Q: **PDB Molecule:**proteasome subunit alpha type; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
25	d1rypa_	Alignment	not modelled	100.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
26	c5fmgD_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**proteasome subunit alpha type; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
27	d1rypf_	Alignment	not modelled	100.0	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
28	c6qm7E_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome alpha5 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245

29	d1rypd_	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
30	d1q5rh_	Alignment	not modelled	100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
31	d1irue_	Alignment	not modelled	100.0	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
32	c3h4pB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome subunit alpha; **PDBTitle:** proteasome 20s core particle from methanocaldococcus jannaschii
33	c5fmgT_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**proteosome subunit alpha type 1, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
34	c5fmgB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome subunit alpha type 2, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
35	c5fmgA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteasome subunit alpha, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
36	c5fmgS_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** S: **PDB Molecule:**proteasome subunit alpha type; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
37	c5fmgU_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** U: **PDB Molecule:**proteasome component c8, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
38	c3mka2_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** 2: **PDB Molecule:**proteasome subunit beta; **PDB Fragment:**20s proteasome beta-subunit; **PDBTitle:** crystal structure of mycobacterium tuberculosis proteasome with2 propetide and an t1a mutation at beta-subunit
39	c2jayA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteasome; **PDBTitle:** proteasome beta subunit prcb from mycobacterium2 tuberculosis
40	c2h6jI_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**proteasome beta-type subunit 1; **PDBTitle:** crystal structure of the beta f145a rhodococcus proteasome
41	d1j2qh_	Alignment	not modelled	100.0	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
42	c6qm8Y_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** Y: **PDB Molecule:**proteasome beta4 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
43	d1yarh1	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
44	c3nzxK_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** K: **PDB Molecule:**proteasome component pre2; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with ligand2 2c
45	c3h4pj_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**proteasome subunit alpha; **PDBTitle:** proteasome 20s core particle from methanocaldococcus jannaschii
46	c6qm7Z_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** Z: **PDB Molecule:**proteasome beta5 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
47	c2fhgC_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome, beta subunit; **PDBTitle:** crystal structure of mycobacterial tuberculosis proteasome
48	d1ryph_	Alignment	not modelled	100.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
49	d1q5qh_	Alignment	not modelled	100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
50	d1irul_	Alignment	not modelled	100.0	12	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
51	d1rypl_	Alignment	not modelled	100.0	12	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
52	d1iruj_	Alignment	not modelled	100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
53	d1rypi_	Alignment	not modelled	100.0	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
						PDB header:hydrolase/hydrolase inhibitor

54	c6avoC_	Alignment	not modelled	100.0	12	**Chain:** C: **PDB Molecule:**proteasome subunit beta type-8; **PDBTitle:** cryo-em structure of human immunoproteasome with a novel2 noncompetitive inhibitor that selectively inhibits activated3 lymphocytes
55	d1iru2_	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
56	c6qm7V_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** V: **PDB Molecule:**proteasome beta1 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
57	d1iruh_	Alignment	not modelled	100.0	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
58	c3nzwH_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** H: **PDB Molecule:**proteasome component pup1; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with 2b
59	d1ryp1_	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
60	c2zcyM_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**proteasome component pre4; **PDBTitle:** yeast 20s proteasome:syringolin a-complex
61	d1ryp2_	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
62	d1rypk_	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
63	c3unhb_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome subunit alpha type-4; **PDBTitle:** mouse 20s immunoproteasome
64	c6qm7N_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**proteasome beta7 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
65	c6qm8a_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteasome alpha1 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
66	d1iruk_	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
67	c3unhV_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** V: **PDB Molecule:**proteasome subunit beta type-10; **PDBTitle:** mouse 20s immunoproteasome
68	c5fmgV_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** V: **PDB Molecule:**proteasome, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
69	d1irui_	Alignment	not modelled	100.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
70	c5fmga_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteasome subunit alpha, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
71	d1iru1_	Alignment	not modelled	100.0	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
72	c6qm8W_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** W: **PDB Molecule:**proteasome beta2 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
73	d1rypj_	Alignment	not modelled	100.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
74	c5fmgK_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**proteasome subunit beta type; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
75	c6qm8X_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**proteasome beta3 chain; **PDBTitle:** leishmania tarentolae proteasome 20s subunit apo structure
76	c5nygF_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**anbu; **PDBTitle:** anbu (gly-1) mutant from hyphomicrobium sp. strain mc1 - sg p2(1)2(1)2 2(1)
77	c5fmgL_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**proteasome subunit beta type; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
78	c5fmgI_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**proteasome subunit beta type; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
79	c5fmgb_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome subunit alpha type 2, putative; **PDBTitle:** structure and function based design of plasmodium-

						selective proteasome2 inhibitors
80	c5loyD_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**designed anbu protein; **PDBTitle:** helical assembly of a designed anbu protein
81	c5nywT_	Alignment	not modelled	100.0	11	**PDB header:**unknown function **Chain:** T: **PDB Molecule:**proteasome subunit; **PDBTitle:** anbu (ancestral beta-subunit) from yersinia bercovieri
82	c5fmgJ_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**beta3 proteasome subunit, putative; **PDBTitle:** structure and function based design of plasmodium-selective proteasome2 inhibitors
83	c5loxH_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**peptidase; **PDBTitle:** helical assembly of the anbu complex from pseudomonas aeruginosa
84	c4hnzG_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**hslvu complex proteolytic subunit, putative; **PDBTitle:** crystal structure of eukaryotic hslv from trypanosoma brucei
85	d2z3ba1	Alignment	not modelled	100.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
86	c5ovuB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-proteobacteria proteasome homologue; **PDBTitle:** cupriavidus metallidurans bph
87	c5ovsG_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**bph; **PDBTitle:** thiobacillus denitrificans bph
88	d1e94a_	Alignment	not modelled	99.9	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
89	d1g3ka_	Alignment	not modelled	99.9	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
90	d1m4ya_	Alignment	not modelled	99.9	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
91	d1cuka1	Alignment	not modelled	61.7	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
92	c4nkpD_	Alignment	not modelled	59.4	20	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**putative extracellular heme-binding protein; **PDBTitle:** crystal structure of a putative extracellular heme-binding protein2 (despig_02683) from desulfovibrio piger atcc 29098 at 1.24 a3 resolution
93	c3fpvC_	Alignment	not modelled	57.0	38	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
94	d2a2la1	Alignment	not modelled	56.0	16	**Fold:**Profilin-like **Superfamily:**GlcG-like **Family:**GlcG-like
95	c6bwsA_	Alignment	not modelled	51.3	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycolate utilization protein; **PDBTitle:** crystal structure of efga from methylobacterium extorquens
96	c4eo3A_	Alignment	not modelled	47.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein/nadh dehydrogenase; **PDBTitle:** peroxiredoxin nitroreductase fusion enzyme
97	c2yztA_	Alignment	not modelled	40.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1756; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
98	d1u94a2	Alignment	not modelled	39.4	14	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
99	d1xp8a2	Alignment	not modelled	31.0	17	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
100	d1ubea2	Alignment	not modelled	28.6	23	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
101	d1mo6a2	Alignment	not modelled	27.3	23	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
102	c2rbgB_	Alignment	not modelled	26.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein st0493; **PDBTitle:** crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
103	d2odgc1	Alignment	not modelled	25.6	17	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
104	d2g84a1	Alignment	not modelled	24.5	30	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
						PDB header:transcription

105	c1wnmA_	Alignment	not modelled	24.3	59	**Chain:** A: **PDB Molecule:**fibroin-modulator binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 2 in 30%(v/v) tfe2 solution
106	c1hjpA_	Alignment	not modelled	22.3	19	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli