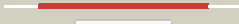



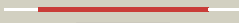

























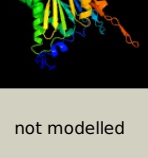


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2110c_(prcB)_2369734_2370609
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	3d49271b5a2002b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mka2_	 Alignment		100.0	100	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
2	d1q5rh_	 Alignment		100.0	67	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
3	c2h6jl_	 Alignment		100.0	68	PDB header: hydrolase Chain: I; PDB Molecule: proteasome beta-type subunit 1; PDBTitle: crystal structure of the beta f145a rhodococcus proteasome
4	c2fhgC_	 Alignment		100.0	100	PDB header: hydrolase Chain: C; PDB Molecule: proteasome, beta subunit; PDBTitle: crystal structure of mycobacterial tuberculosis proteasome
5	c6qm7C_	 Alignment		100.0	16	PDB header: hydrolase Chain: C; PDB Molecule: proteasome alpha3 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
6	d1q5qh_	 Alignment		100.0	67	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
7	c5ln3C_	 Alignment		100.0	18	PDB header: hydrolase Chain: C; PDB Molecule: proteasome subunit alpha type-4; PDBTitle: the human 26s proteasome at 6.8 ang.
8	d1liruc_	 Alignment		100.0	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
9	d1rypc_	 Alignment		100.0	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
10	c6qm7V_	 Alignment		100.0	30	PDB header: hydrolase Chain: V; PDB Molecule: proteasome beta1 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
11	c6qm7A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: proteasome alpha1 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245

12	c2jayA_	Alignment		100.0	99	PDB header: hydrolase Chain: A: PDB Molecule: proteasome; PDBTitle: proteasome beta subunit prcb from mycobacterium2 tuberculosis
13	d1rypb_	Alignment		100.0	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
14	d1rype_	Alignment		100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
15	c3nzxK_	Alignment		100.0	25	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
16	c6qm7Z_	Alignment		100.0	27	PDB header: hydrolase Chain: Z: PDB Molecule: proteasome beta5 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
17	d1lirul_	Alignment		100.0	31	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
18	c6qm8D_	Alignment		100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: proteasome alpha4 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
19	d1rypa_	Alignment		100.0	15	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
20	d1lirug_	Alignment		100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
21	d1lirub_	Alignment	not modelled	100.0	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
22	d1lirua_	Alignment	not modelled	100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
23	c6qm8Y_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: Y: PDB Molecule: proteasome beta4 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
24	d1yara1	Alignment	not modelled	100.0	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
25	d1rypl_	Alignment	not modelled	100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
26	c6avoC_	Alignment	not modelled	100.0	27	PDB header: hydrolase/hydrolase inhibitor 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
27	d1rypg_	Alignment	not modelled	100.0	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
28	c3bdmF_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: F: PDB Molecule: proteasome component c1; PDBTitle: yeast 20s proteasome:glidobactin a-complex

29	d1j2pa_	Alignment	not modelled	100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
30	c6qm7T_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: T: PDB Molecule: proteasome alpha6 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
31	c6qm8B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: proteasome alpha2 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
32	c1iruF_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: F: PDB Molecule: 20s proteasome; PDBTitle: crystal structure of the mammalian 20s proteasome at 2.75 a2 resolution
33	d1iruf_	Alignment	not modelled	100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
34	c6qm7E_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: E: PDB Molecule: proteasome alpha5 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit complexed with gsk3494245
35	d1rypi_	Alignment	not modelled	100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
36	c2zcyM_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: M: PDB Molecule: proteasome component pre4; PDBTitle: yeast 20s proteasome:syringolin a-complex
37	d1rypd_	Alignment	not modelled	100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
38	c3nzwH_	Alignment	not modelled	100.0	24	PDB header: hydrolase/hydrolase inhibitor Chain: H: PDB Molecule: proteasome component pup1; PDBTitle: crystal structure of the yeast 20s proteasome in complex with 2b
39	d1ryp2_	Alignment	not modelled	100.0	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
40	d1irud_	Alignment	not modelled	100.0	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
41	d1yarh1	Alignment	not modelled	100.0	32	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
42	d1irui_	Alignment	not modelled	100.0	22	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
43	d1iruh_	Alignment	not modelled	100.0	27	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
44	d1rypf_	Alignment	not modelled	100.0	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
45	c6qm8U_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: U: PDB Molecule: proteasome alpha7 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
46	d1ryph_	Alignment	not modelled	100.0	25	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
47	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
48	c3h4pB_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: proteasome subunit alpha; PDBTitle: proteasome 20s core particle from methanocaldococcus jannaschii
49	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
50	c3unhV_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: V: PDB Molecule: proteasome subunit beta type-10; PDBTitle: mouse 20s immunoproteasome
51	d1j2qh_	Alignment	not modelled	100.0	30	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
52	c6qm8W_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: W: PDB Molecule: proteasome beta2 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
53	c3unhb_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: proteasome subunit alpha type-4; PDBTitle: mouse 20s immunoproteasome
54	d1iruj_	Alignment	not modelled	100.0	23	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits

55	c1q5rD	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: D: PDB Molecule: proteasome alpha-type subunit 1; PDBTitle: the rhodococcus 20s proteasome with unprocessed pro-peptides
56	d1q5qa	Alignment	not modelled	100.0	14	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
57	d1iruk	Alignment	not modelled	100.0	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
58	d1iru2	Alignment	not modelled	100.0	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
59	d1irue	Alignment	not modelled	100.0	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
60	d1ryp1	Alignment	not modelled	100.0	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
61	c5fmga	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: proteasome subunit alpha, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
62	d1rypk	Alignment	not modelled	100.0	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
63	c5fmgs	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: S: PDB Molecule: proteasome subunit alpha type; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
64	d1iru1	Alignment	not modelled	100.0	23	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
65	c3h4pj	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: J: PDB Molecule: proteasome subunit alpha; PDBTitle: proteasome 20s core particle from methanocaldococcus jannaschii
66	c5fmqQ	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: Q: PDB Molecule: proteasome subunit alpha type; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
67	c5fmgl	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: I: PDB Molecule: proteasome subunit beta type; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
68	c5fmqV	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: V: PDB Molecule: proteasome, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
69	c5fmqT	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: T: PDB Molecule: proteasome subunit alpha type 1, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
70	c6qm8X	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: X: PDB Molecule: proteasome beta3 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
71	c5nygf	Alignment	not modelled	100.0	18	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)
72	c5fmgl	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: L: PDB Molecule: proteasome subunit beta type; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
73	d1rypj	Alignment	not modelled	100.0	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
74	c5fmgb	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: proteasome subunit alpha type 2, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
75	c5fmqK	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: K: PDB Molecule: proteasome subunit beta type; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
76	c6qm8a	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: proteasome alpha1 chain; PDBTitle: leishmania tarentolae proteasome 20s subunit apo structure
77	c5fmqU	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: U: PDB Molecule: proteasome component c8, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
78	c5loyD	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: designed anbu protein; PDBTitle: helical assembly of a designed anbu protein
79	c5fmqA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: proteasome subunit alpha, putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
						PDB header: hydrolase Chain: B: PDB Molecule: proteasome subunit alpha type 2,

80	c5fmgB_	Alignment	not modelled	100.0	16	putative; PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors
81	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
82	d2z3ba1	Alignment	not modelled	100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
83	c5loxH_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: H: PDB Molecule: peptidase; PDBTitle: helical assembly of the anbu complex from pseudomonas aeruginosa
84	c5nywT_	Alignment	not modelled	100.0	20	PDB header: unknown function Chain: T: PDB Molecule: proteasome subunit; PDBTitle: anbu (ancestral beta-subunit) from yersinia bercovieri
85	c5ovuB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-proteobacteria proteasome homologue; PDBTitle: cupriavidus metallidurans bph
86	c5ovsG_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: G: PDB Molecule: bph; PDBTitle: thiobacillus denitrificans bph
87	c4hnzG_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: G: PDB Molecule: hslvu complex proteolytic subunit, putative; PDBTitle: crystal structure of eukaryotic hslv from trypanosoma brucei
88	d1e94a_	Alignment	not modelled	100.0	28	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
89	d1g3ka_	Alignment	not modelled	100.0	27	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
90	d1m4ya_	Alignment	not modelled	100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
91	c5k12F_	Alignment	not modelled	78.1	19	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate dehydrogenase 1, mitochondrial; PDBTitle: cryo-em structure of glutamate dehydrogenase at 1.8 a resolution
92	d1bgva2	Alignment	not modelled	75.8	13	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
93	d1euza2	Alignment	not modelled	75.1	24	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
94	d1bvua2	Alignment	not modelled	75.0	21	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
95	d1hwxa2	Alignment	not modelled	72.6	19	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
96	d1l1fa2	Alignment	not modelled	72.0	19	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
97	d1gtma2	Alignment	not modelled	71.6	21	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
98	d1b26a2	Alignment	not modelled	65.5	21	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
99	d1v9la2	Alignment	not modelled	55.5	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
100	c2tmgD_	Alignment	not modelled	54.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
101	c4s1bA_	Alignment	not modelled	50.5	12	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: pyridoxal kinase of entamoeba histolytica with adp
102	c3fpvC_	Alignment	not modelled	46.2	15	PDB header: heme binding protein Chain: C: PDB Molecule: extracellular haem-binding protein; PDBTitle: crystal structure of hbps
103	d1cuka1	Alignment	not modelled	40.0	21	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
104	c4nkpD_	Alignment	not modelled	39.4	17	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
105	c3sirD_	Alignment	not modelled	37.9	13	PDB header: hydrolase Chain: D: PDB Molecule: caspase; PDBTitle: crystal structure of drice

106	c3ibqA_	Alignment	not modelled	36.3	21	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from lactobacillus plantarum in2 complex with atp
107	c1bvuf_	Alignment	not modelled	35.4	19	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
108	c2ddmA_	Alignment	not modelled	35.2	13	PDB header: transferase Chain: A: PDB Molecule: pyridoxine kinase; PDBTitle: crystal structure of pyridoxal kinase from the escherichia coli pdxk2 gene at 2.1 a resolution
109	c5xviA_	Alignment	not modelled	35.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of aspergillus niger apo- glutamate dehydrogenase
110	c1v9lA_	Alignment	not modelled	34.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
111	d1jgtA1	Alignment	not modelled	33.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
112	c3aoeC_	Alignment	not modelled	32.8	24	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
113	c6bwsA_	Alignment	not modelled	30.6	15	PDB header: unknown function Chain: A: PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
114	d2ahra1	Alignment	not modelled	30.0	14	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
115	d2a2la1	Alignment	not modelled	29.4	14	Fold: Profilin-like Superfamily: GlcG-like Family: GlcG-like
116	c2m4hA_	Alignment	not modelled	28.8	17	PDB header: viral protein Chain: A: PDB Molecule: feline calicivirus vpg protein; PDBTitle: solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
117	c5ncaA_	Alignment	not modelled	28.7	7	PDB header: structural protein Chain: A: PDB Molecule: competence protein comgc; PDBTitle: solution structure of comgc from streptococcus pneumoniae
118	c4xgiA_	Alignment	not modelled	26.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
119	c5afda_	Alignment	not modelled	24.8	15	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: native structure of n-acetylneuraminase lyase (sialic acid aldolase)2 from aliivibrio salmonicida
120	c1nr1A_	Alignment	not modelled	24.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate dehydrogenase