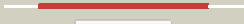



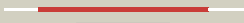























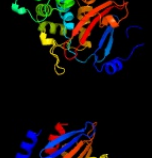
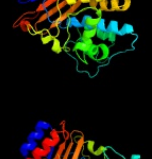
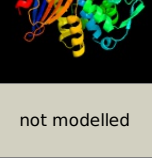


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2068c_blaC_2325894_2326817
Date	Mon Aug 5 13:25:18 BST 2019
Unique Job ID	604c8e4c6a0b660a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cg5A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
2	c5e2eB_	 Alignment		100.0	47	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor blaA from yersinia2 enterocolitica
3	c3qhyA_	 Alignment		100.0	49	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structural, thermodynamic and kinetic analysis of the picomolar2 binding affinity interaction of the beta-lactamase inhibitor protein-3 ii (blip-ii) with class a beta-lactamases
4	c5hx9A_	 Alignment		100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis
5	c1i2sA_	 Alignment		100.0	49	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
6	d1i2sa_	 Alignment		100.0	49	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
7	c6niqB_	 Alignment		100.0	48	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris
8	c6nj1A_	 Alignment		100.0	47	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluverii2 dsm 555
9	d1hzoa_	 Alignment		100.0	44	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
10	c2v20A_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase tem; PDBTitle: structure of a tem-1 beta-lactamase insertant allosterically regulated2 by kanamycin and anions. complex with sulfate.
11	c1w7fB_	 Alignment		100.0	49	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate

12	c5e43A_	Alignment		100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum
13	d1o7ea_	Alignment		100.0	45	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
14	c5vpgA_	Alignment		100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum
15	c3lezA_	Alignment		100.0	46	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
16	c3dw0B_	Alignment		100.0	47	PDB header: hydrolase Chain: B: PDB Molecule: class a carbapenemase kpc-2; PDBTitle: crystal structure of the class a carbapenemase kpc-2 at 1.62 angstrom resolution
17	c3w4qC_	Alignment		100.0	52	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of penicillin G beta-lactamase from burkholderia multivorans2 at pH4.2
18	d1alqa_	Alignment		100.0	36	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
19	c4eqiA_	Alignment		100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1
20	d1g6aa_	Alignment		100.0	33	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
21	d2cc1a1	Alignment	not modelled	100.0	42	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
22	d1n9ba_	Alignment	not modelled	100.0	35	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
23	c2ov5A_	Alignment	not modelled	100.0	48	PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
24	c4dxbB_	Alignment	not modelled	100.0	35	PDB header: sugar binding protein, hydrolase Chain: B: PDB Molecule: maltose-binding periplasmic protein, beta-lactamase tem PDBTitle: 2.29a structure of the engineered mbp tem-1 fusion protein rg13 in2 complex with zinc, p1 space group
25	c5hw3A_	Alignment	not modelled	100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
26	d1bsga_	Alignment	not modelled	100.0	47	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
27	c4yfmA_	Alignment	not modelled	100.0	45	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
28	d1m40a_	Alignment	not modelled	100.0	36	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						Fold: beta-lactamase/transpeptidase-like

29	d1buea_	Alignment	not modelled	100.0	41	Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
30	c3w4pA_	Alignment	not modelled	100.0	50	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at ph7.5
31	c4mxbB_	Alignment	not modelled	100.0	39	PDB header: hydrolase/antibiotic Chain: B: PDB Molecule: bel-1; PDBTitle: crystal structure of extended-spectrum beta-lactamase bel-1 in complex2 with imipenem
32	c4b88A_	Alignment	not modelled	100.0	55	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a
33	d1dy6a_	Alignment	not modelled	100.0	41	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
34	d1iysa_	Alignment	not modelled	100.0	46	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
35	c3p09B_	Alignment	not modelled	100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
36	c3p09A_	Alignment	not modelled	100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
37	c6bn3A_	Alignment	not modelled	100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: ctx-m-151 class a extended-spectrum beta-lactamase apo crystal2 structure at 1.3 angstrom resolution.
38	c6mk6C_	Alignment	not modelled	100.0	39	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106
39	d1djaa_	Alignment	not modelled	100.0	33	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
40	c2qpnA_	Alignment	not modelled	100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
41	c2j7vA_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: tlI2115 protein; PDBTitle: structure of pbp-a
42	c5tfqA_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a representative of class a beta-lactamase from2 bacteroides cellulolyticus dsm 14838
43	c2wuqA_	Alignment	not modelled	100.0	22	PDB header: transcription Chain: A: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
44	c4hesA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase class a-like protein; PDBTitle: structure of a beta-lactamase class a-like protein from veillonella2 parvula.
45	c2wuqB_	Alignment	not modelled	100.0	23	PDB header: transcription Chain: B: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
46	d1e25a_	Alignment	not modelled	100.0	27	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
47	c4ewfA_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
48	c5gs8A_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tia-3 extended-spectrum beta-lactamase
49	c3cjmA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-lactamase; PDBTitle: crystal structure of putative beta-lactamase (np_815223.1) from2 enterococcus faecalis v583 at 1.50 a resolution
50	c5aq7B_	Alignment	not modelled	100.0	36	PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography
51	c2bcfA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: probable d-alanyl-d-alanine carboxypeptidase dacb2; PDBTitle: crystal structure of a evolved putative penicillin-binding protein2 homolog, rv2911, from mycobacterium tuberculosis.
52	c4pprA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: penicillin-binding protein dacb1; PDBTitle: crystal structure of mycobacterium tuberculosis d,d-peptidase rv33302 in complex with meropenem
53	c5tr7A_	Alignment	not modelled	100.0	16	PDB header: penicillin-binding protein Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of a putative d-alanyl-d-alanine carboxypeptidase2 from vibrio cholerae o1 biovar eltor str. n16961
54	d1xp4a2	Alignment	not modelled	100.0	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
55	d3beca2	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like

						Family: beta-Lactamase/D-ala carboxypeptidase
56	d1es5a_	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
57	d1tvfa2	Alignment	not modelled	100.0	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
58	c5zqeC_	Alignment	not modelled	100.0	14	PDB header: antibiotic Chain: C: PDB Molecule: lmo2812 protein; PDBTitle: crystal structure of penicillin-binding protein d2 from listeria2 monocytogenes in the cefuroxime bound form
59	c4k91A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: d-ala-d-ala-carboxypeptidase; PDBTitle: crystal structure of penicillin-binding protein 5 (pbp5) from2 pseudomonas aeruginosa in apo state
60	c6osuA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase (penicillin binding PDBTitle: crystal structure of the d-alanyl-d-alanine carboxypeptidase dacd from2 francisella tularensis
61	c1z6fA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: penicillin-binding protein 5; PDBTitle: crystal structure of penicillin-binding protein 5 from e. coli in2 complex with a boronic acid inhibitor
62	c1tvfA_	Alignment	not modelled	100.0	15	PDB header: penicillin binding Chain: A: PDB Molecule: penicillin binding protein 4; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus
63	c3a3jA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from haemophilus2 influenzae
64	c3humB_	Alignment	not modelled	100.0	15	PDB header: hydrolase/antibiotics Chain: B: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 from staphylococcus2 aureus col in complex with cefotaxime
65	c3it9B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacd; PDBTitle: crystal structure of penicillin-binding protein 6 (pbp6) from e. coli2 in apo state
66	c5fsrB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacd; PDBTitle: crystal structure of penicillin binding protein 6b from2 escherichia coli
67	c3mfdB_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacb; PDBTitle: the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
68	c1xp4C_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of a peptidoglycan synthesis regulatory2 factor (pbp3) from streptococcus pneumoniae
69	c6aziA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine endopeptidase; PDBTitle: 1.75 angstrom resolution crystal structure of d-alanyl-d-alanine2 endopeptidase from enterobacter cloacae in complex with covalently3 bound boronic acid
70	c2xftA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
71	c3a3eB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 (dacb) from2 haemophilus influenzae, complexed with novel beta-lactam (cmv)
72	d1w5da1	Alignment	not modelled	100.0	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
73	d1w79a1	Alignment	not modelled	100.0	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
74	c2jc7A_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase oxa-24; PDBTitle: the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
75	d2ex2a1	Alignment	not modelled	100.0	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
76	c4oh0A_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase
77	d1nrfa_	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
78	c4zdxA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase
79	c3hbrD_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
80	d1xa1a_	Alignment	not modelled	99.9	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						PDB header: hydrolase

81	c5ctmB	Alignment	not modelled	99.9	15	Chain: B: PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase
82	c4k0xA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from acinetobacter baumannii
83	d1k38a	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
84	c6n1nA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from sealdella termitidis2 atcc 33386
85	d1k55a	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
86	c2iwdA	Alignment	not modelled	99.9	14	PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mecR1 protein; PDBTitle: oxacilloyl-acylated mecR1 extracellular antibiotic-sensor domain.
87	c5uy7A	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from2 burkholderia ambifaria
88	c3if6C	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa
89	c4iedB	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: class d beta-lactamase; PDBTitle: crystal structure of fus-1 (oxa-85), a class d beta-lactamase from2 fusobacterium nucleatum subsp. polymorphum
90	c6nhsA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc
91	c6ni0A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
92	c3oc2A	Alignment	not modelled	99.9	13	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
93	c3pbnA	Alignment	not modelled	99.9	13	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa
94	c6g9fA	Alignment	not modelled	99.9	18	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2
95	c3pbqA	Alignment	not modelled	99.9	13	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
96	c5lp4A	Alignment	not modelled	99.9	15	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori
97	d1vqqa3	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
98	c6nhuD	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: D: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum
99	c3ue3A	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
100	c4jbfB	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469.
101	c5cerI	Alignment	not modelled	99.9	12	PDB header: immune system Chain: I: PDB Molecule: bd0816; PDBTitle: bd0816 predatory endopeptidase from bdellovibrio bacteriovorus in2 complex with immunity protein bd3460
102	d1m6ka	Alignment	not modelled	99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
103	c3lo7A	Alignment	not modelled	99.9	24	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
104	c5e2fB	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ybxi; PDBTitle: crystal structure of beta-lactamase class d from bacillus subtilis
105	c4gn2A	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: oxacillinase; PDBTitle: crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
106	c4bjpA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3
107	c3equB	Alignment	not modelled	99.8	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from

						neisseria2 gonorrhoeae
108	c5dvyA_	Alignment	not modelled	99.8	17	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin binding protein 2 prime; PDBTitle: 2.95 angstrom crystal structure of the dimeric form of penicillin2 binding protein 2 prime from enterococcus faecium
109	d1pyya4	Alignment	not modelled	99.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
110	d1rp5a4	Alignment	not modelled	99.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
111	c3v39A_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: bd3459, a predatory peptidoglycan endopeptidase from belloviobrio2 bacteriovirus
112	c1mwuA_	Alignment	not modelled	99.8	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a from2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
113	c4mnrA_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan2 glycosyltransferase from eggertella lenta
114	c1qmfA_	Alignment	not modelled	99.8	18	PDB header: cell cycle Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
115	c5troA_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1; PDBTitle: 1.8 angstrom resolution crystal structure of dimerization and2 transpeptidase domains (residues 39-608) of penicillin-binding3 protein 1 from staphylococcus aureus.
116	c5u47A_	Alignment	not modelled	99.8	17	PDB header: lipid-binding protein Chain: A: PDB Molecule: penicillin binding protein 2x; PDBTitle: 1.95 angstrom resolution crystal structure of penicillin binding2 protein 2x from streptococcus thermophilus
117	c6bsrA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: pbp4 protein; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4) from2 enterococcus faecalis in the benzylpenicillin bound form.
118	c3lo7B_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
119	d2c5wb1	Alignment	not modelled	99.8	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
120	c4ye5A_	Alignment	not modelled	99.8	12	PDB header: penicillin binding protein Chain: A: PDB Molecule: peptidoglycan synthetase penicillin-binding protein 3; PDBTitle: the crystal structure of a peptidoglycan synthetase from2 bifidobacterium adolescentis atcc 15703