



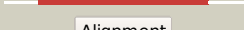

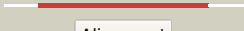









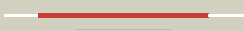












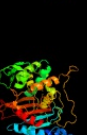
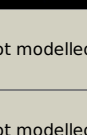


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0016c_(pbpA)_18759_20234
Date	Tue Jul 23 14:50:04 BST 2019
Unique Job ID	df044111ba43cecc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lo7A_	 Alignment		100.0	99	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
2	c5u47A_	 Alignment		100.0	21	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
3	c6g9fA_	 Alignment		100.0	25	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2
4	c1qmfA_	 Alignment		100.0	21	PDB header: cell cycle Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
5	c3lo7B_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
6	c1pmdA_	 Alignment		100.0	21	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
7	c4ye5A_	 Alignment		100.0	23	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
8	c3pbqA_	 Alignment		100.0	26	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
9	c3ue3A_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
10	c3oc2A_	 Alignment		100.0	26	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
11	c3vslB_	 Alignment		100.0	21	PDB header: penicillin-binding protein Chain: B: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 (pbp3) from2 methicilin-resistant staphylococcus aureus in the cefotaxime bound3 form.

12	c4jbfB	Alignment		100.0	33	PDB header: transferase Chain: B: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469.
13	c4mnrA	Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan2 glycosyltransferase from eggerthella lenta
14	c5lp4A	Alignment		100.0	23	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori
15	c4ovdA	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from2 atopobium parvulum dsm 20469
16	c3equB	Alignment		100.0	26	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
17	c1mwuA	Alignment		100.0	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.
18	c5troA	Alignment		100.0	26	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.
19	c4bjpA	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3
20	c3pbnA	Alignment		100.0	26	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa
21	c5dvyA	Alignment	not modelled	100.0	25	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
22	c2wadB	Alignment	not modelled	100.0	26	PDB header: peptide binding protein Chain: B: PDB Molecule: penicillin-binding protein 2b; PDBTitle: penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
23	c6bsrA	Alignment	not modelled	100.0	26	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.
24	d1pyya4	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
25	d1rp5a4	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
26	c3zg8B	Alignment	not modelled	100.0	19	PDB header: penicillin-binding protein Chain: B: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 from2 listeria monocytogenes in the ampicillin bound form
27	c3udiA	Alignment	not modelled	100.0	24	PDB header: penicillin-binding protein/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
28	c3fwlA	Alignment	not modelled	100.0	20	PDB header: transferase, hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b from2 escherichia coli PDB header: lipid-binding protein

29	c5u2gA	Alignment	not modelled	100.0	23	Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: 2.6 angstrom resolution crystal structure of penicillin-binding2 protein 1a from haemophilus influenzae
30	d2c5wb1	Alignment	not modelled	100.0	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
31	c3dwkC	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C; PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
32	d1vqqa3	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
33	c5crfA	Alignment	not modelled	100.0	23	PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: structure of the penicillin-binding protein pon1 from mycobacterium2 tuberculosis
34	c2olvA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: penicillin-binding protein 2; PDBTitle: structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
35	c4oonA	Alignment	not modelled	100.0	29	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of pbb1a in complex with compound 17 ((4z,8s,11e,2 14s)-5-(2-amino-1,3-thiazol-4-yl)-14-(5,6-dihydroxy-1,3-dioxo-1,3-3 dihydro-2h-isoindol-2-yl)-8-formyl-2-methyl-6-oxo-3,10-dioxo-4,7,11-4 triazatetradeca-4,11-diene-2,12,14-tricarboxylic acid)
36	c5uy7A	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from2 burkholderia ambifaria
37	c2bg1A	Alignment	not modelled	100.0	19	PDB header: peptidoglycan Chain: A; PDB Molecule: penicillin-binding protein 1b; PDBTitle: active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
38	d1k25a4	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
39	c2jcia	Alignment	not modelled	100.0	19	PDB header: drug-binding protein Chain: A; PDB Molecule: penicillin-binding protein 1b; PDBTitle: structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbb1b
40	d2bg1a1	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
41	d2olua2	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
42	c4ztkA	Alignment	not modelled	100.0	30	PDB header: transferase, cell cycle Chain: A; PDB Molecule: cell division protein ftsi/penicillin binding protein 2; PDBTitle: transpeptidase domain of ftsi4 d,d-transpeptidase from legionella2 pneumophila.
43	c2iwdA	Alignment	not modelled	100.0	13	PDB header: antibiotic resistance Chain: A; PDB Molecule: methicillin resistance mecrl protein; PDBTitle: oxacilloyl-acylated mecrl extracellular antibiotic-sensor domain.
44	c6ni0A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
45	c6nhsA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc
46	c6n1nA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from sebalidella termitidis2 atcc 33386
47	c5e2fB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase ybxi; PDBTitle: crystal structure of beta-lactamase class d from bacillus subtilis
48	d1m6ka	Alignment	not modelled	100.0	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
49	c4gn2A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: oxacillinase; PDBTitle: crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
50	c6nhuD	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum
51	d1k38a	Alignment	not modelled	100.0	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
52	c4iedB	Alignment	not modelled	100.0	17	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
53	d1k55a	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
54	d1nrfa	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

55	c3if6C_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa
56	d1xa1a_	Alignment	not modelled	100.0	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
57	c3hbrD_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
58	c4k0xA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from acinetobacter baumannii
59	c4oh0A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase
60	c5ctmB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase
61	c4zdxA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase
62	c2jc7A_	Alignment	not modelled	100.0	21	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
63	c5gs8A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tla-3 extended-spectrum beta-lactamase
64	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
65	c6bn3A_	Alignment	not modelled	100.0	21	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.
66	c2qpnA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
67	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
68	c5vpqA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum
69	d1g6aa_	Alignment	not modelled	100.0	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
70	d1iysa_	Alignment	not modelled	100.0	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
71	c3w4pA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at pH7.5
72	c6mk6C_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106
73	d1e25a_	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
74	c4b88A_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a
75	c2wuqA_	Alignment	not modelled	99.9	22	PDB header: transcription Chain: A: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
76	d1dy6a_	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
77	d2cc1a1	Alignment	not modelled	99.9	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
78	c2ov5A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
79	d1o7ea_	Alignment	not modelled	99.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
80	c6niqB_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodospseudomonas palustris
81	c3dw0B_	Alignment	not modelled	99.9	20	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

82	c3w4qC_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2
83	d1djaa_	Alignment	not modelled	99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
84	c5hw3A_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
85	d1m40a_	Alignment	not modelled	99.9	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
86	d1bsga_	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
87	c3lezA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
88	c5hx9A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis
89	d1buea_	Alignment	not modelled	99.9	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
90	c2j7vA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: tl12115 protein; PDBTitle: structure of pbb-a
91	c5e43A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum
92	c1w7fB_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
93	d1n9ba_	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	c2v20A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase tem; PDBTitle: structure of a tem-1 beta-lactamase insertant2 allosterically regulated by kanamycin and anions. complex3 with sulfate.
95	c4mxbB_	Alignment	not modelled	99.9	22	PDB header: hydrolase/antibiotic Chain: B: PDB Molecule: bel-1; PDBTitle: crystal structure of extended-spectrum beta-lactamase bel-1 in complex2 with imipenem
96	c4eqiA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1
97	c4ewfA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
98	d1hzoa_	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
99	c3qhyA_	Alignment	not modelled	99.8	21	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
100	c6nj1A_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluyveri2 dsm 555
101	d1k25a3	Alignment	not modelled	99.8	20	Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain
102	d1vqqa2	Alignment	not modelled	99.8	20	Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain
103	c4yfmA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
104	d1i2sa_	Alignment	not modelled	99.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
105	c1i2sA_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
106	c3cg5A_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
107	d1alqa_	Alignment	not modelled	99.8	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

108	c3p09B	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
109	c5e2eB	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor bla _a from yersinia2 enterocolitica
110	c3p09A	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
111	c4hesA	Alignment	not modelled	99.7	16	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.
112	c5tfqA	Alignment	not modelled	99.7	20	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
113	d1pyya3	Alignment	not modelled	99.6	27	Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain
114	d1es5a	Alignment	not modelled	99.4	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
115	d1xp4a2	Alignment	not modelled	99.4	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
116	c4dxbB	Alignment	not modelled	99.4	23	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
117	c3cjmA	Alignment	not modelled	99.4	16	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
118	d3beca2	Alignment	not modelled	99.4	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
119	c5tr7A	Alignment	not modelled	99.4	17	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
120	c2bcfA	Alignment	not modelled	99.3	20	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.