

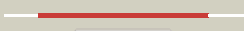


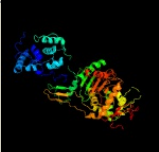



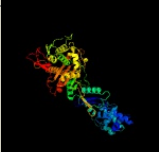

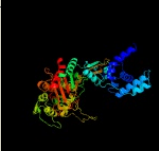

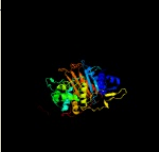

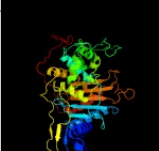







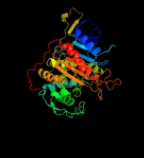

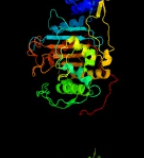


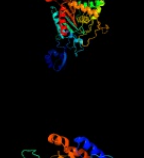

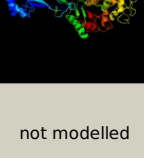


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0050_(ponA1)_53663_55696
Date	Tue Jul 23 14:50:08 BST 2019
Unique Job ID	2da4d1bcb92ddf66

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dwkC_	 Alignment		100.0	26	PDB header: transferase Chain: C; PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
2	c2olvA_	 Alignment		100.0	25	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
3	c3fwlA_	 Alignment		100.0	27	PDB header: transferase, hydrolase Chain: A; PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b from2 escherichia coli
4	c3udiA_	 Alignment		100.0	33	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
5	c5u2gA_	 Alignment		100.0	29	PDB header: lipid-binding protein Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: 2.6 angstrom resolution crystal structure of penicillin-binding2 protein 1a from haemophilus influenzae
6	c3zg8B_	 Alignment		100.0	28	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
7	c5crfA_	 Alignment		100.0	97	PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: structure of the penicillin-binding protein ponA1 from mycobacterium2 tuberculosis
8	c4oonA_	 Alignment		100.0	29	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of pbp1a 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)
9	c2jciA_	 Alignment		100.0	23	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 pbp1b
10	c3vslB_	 Alignment		100.0	16	PDB header: penicillin-binding protein Chain: B; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 (pbp3) from2 methicillin-resistant staphylococcus aureus in the cefotaxime bound3 form.
11	c5dvyA_	 Alignment		100.0	18	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

12	c2bg1A	Alignment		100.0	23	PDB header: peptidoglycan Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
13	d2c5wb1	Alignment		100.0	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
14	c2wadB	Alignment		100.0	15	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)
15	d2bg1a1	Alignment		100.0	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
16	c1pmdA	Alignment		100.0	17	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
17	d2olua2	Alignment		100.0	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
18	c3pbnA	Alignment		100.0	17	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa
19	c5u47A	Alignment		100.0	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
20	c6g9fA	Alignment		100.0	18	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2
21	c4ye5A	Alignment	not modelled	100.0	20	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
22	c4jbfB	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469.
23	c1qmfA	Alignment	not modelled	100.0	18	PDB header: cell cycle Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
24	c3lo7A	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
25	c5troA	Alignment	not modelled	100.0	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.
26	c4mnrA	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan2 glycosyltransferase from eggertella lenta
27	c3pbqA	Alignment	not modelled	100.0	21	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
28	c3ue3A	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3,

					PDBTitle: crystal structure of acinetobacter baumannii pbp3
29	c4ovdA_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from2 atopobium parvulum dsm 20469
30	c3oc2A_	Alignment	not modelled	100.0	21 PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
31	c4bjpA_	Alignment	not modelled	100.0	20 PDB header: transferase Chain: A: PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3
32	c3equB_	Alignment	not modelled	100.0	21 PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
33	d1pyya4	Alignment	not modelled	100.0	18 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
34	d1rp5a4	Alignment	not modelled	100.0	19 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
35	c3hzsA_	Alignment	not modelled	100.0	29 PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
36	d2olu1	Alignment	not modelled	100.0	31 Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
37	c5uy7A_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from2 burkholderia ambifaria
38	d1vqqa3	Alignment	not modelled	100.0	18 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
39	c3lo7B_	Alignment	not modelled	100.0	26 PDB header: transferase Chain: B: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
40	c5lp4A_	Alignment	not modelled	100.0	21 PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori
41	d2oqa1	Alignment	not modelled	100.0	40 Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
42	c3vmtA_	Alignment	not modelled	100.0	30 PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: crystal structure of staphylococcus aureus membrane-bound2 transglycosylase in complex with a lipid ii analog
43	c1mwuA_	Alignment	not modelled	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.
44	c6bsrA_	Alignment	not modelled	100.0	18 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.
45	d1k25a4	Alignment	not modelled	100.0	20 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
46	c4ztkA_	Alignment	not modelled	100.0	20 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.
47	c2iwdA_	Alignment	not modelled	100.0	16 PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mec1 protein; PDBTitle: oxacilloyl-acylated mec1 extracellular antibiotic-sensor domain.
48	c6nhsA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc
49	c6ni0A_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
50	c4iedB_	Alignment	not modelled	100.0	15 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
51	c3if6C_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa
52	c6n1nA_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from sebaldeella termitidis2 atcc 33386
53	d1k38a_	Alignment	not modelled	100.0	16 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
54	c5a2fB_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ybxi;

54	c6z1b_	Alignment	not modelled	100.0	20	PDBTitle: crystal structure of beta-lactamase class d from bacillus subtilis
55	d1k55a_	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
56	d1m6ka_	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
57	c6nhuD_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum
58	c2jc7A_	Alignment	not modelled	100.0	17	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
59	c4oh0A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase
60	d1nrfa_	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
61	c4k0xA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from acinetobacter baumannii
62	c4zdxA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase
63	d1xa1a_	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
64	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
65	c3hbrD_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: D; PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
66	c5ctmB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase
67	c2wuqB_	Alignment	not modelled	99.9	15	PDB header: transcription Chain: B; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
68	c6bn3A_	Alignment	not modelled	99.9	19	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.
69	c5vpgA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum
70	c5gs8A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tia-3 extended-spectrum beta-lactamase
71	c2qpnA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
72	d1g6aa_	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
73	d1lysa_	Alignment	not modelled	99.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
74	c3w4pA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at ph7.5
75	d1dy6a_	Alignment	not modelled	99.9	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
76	d2cc1a1	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
77	c2wuqA_	Alignment	not modelled	99.9	16	PDB header: transcription Chain: A; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
78	c4b88A_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a
79	d1e25a_	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
80	c2xftA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A; PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
						PDB header: hydrolase

81	c6mk6C_	Alignment	not modelled	99.9	17	Chain: C; PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106
82	c5hw3A_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
83	c2ov5A_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A; PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
84	c6niqB_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris
85	d1bsga_	Alignment	not modelled	99.8	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
86	c3w4qC_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: C; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2
87	c3lezA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
88	d1m40a_	Alignment	not modelled	99.8	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
89	c2j7vA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A; PDB Molecule: tlI2115 protein; PDBTitle: structure of pbp-a
90	c4mxB_	Alignment	not modelled	99.8	16	PDB header: hydrolase/antibiotic Chain: B; PDB Molecule: bel-1; PDBTitle: crystal structure of extended-spectrum beta-lactamase bel-1 in complex2 with imipenem
91	d1o7ea_	Alignment	not modelled	99.8	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
92	d1buea_	Alignment	not modelled	99.8	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
93	d1djaa_	Alignment	not modelled	99.8	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	c3dw0B_	Alignment	not modelled	99.8	17	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
95	c5e43A_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum
96	c5hx9A_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis
97	d1n9ba_	Alignment	not modelled	99.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
98	c4eqiA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A; PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1
99	c2v20A_	Alignment	not modelled	99.7	18	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.
100	c1w7fB_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
101	d1hzoa_	Alignment	not modelled	99.7	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
102	c3qhyA_	Alignment	not modelled	99.7	19	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
103	c6nj1A_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluverii2 dsm 555
104	d1alqa_	Alignment	not modelled	99.6	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
105	c4ewfA_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
106	c4yfmA_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
						PDB header: hydrolase

107	c3cg5A_	Alignment	not modelled	99.6	20	Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
108	d1i2sa_	Alignment	not modelled	99.6	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
109	c1i2sA_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
110	c3p09B_	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
111	c5e2eB_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor bla _a from yersinia2 enterocolitica
112	c5tfqA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a representative of class a beta-lactamase from 2 bacteroides cellulosilyticus dsm 14838
113	c4hesA_	Alignment	not modelled	99.4	13	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.
114	c3p09A_	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
115	c3cjmA_	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-lactamase; PDBTitle: crystal structure of putative beta-lactamase (np_815223.1) from 2 enterococcus faecalis v583 at 1.50 a resolution
116	c4dxbB_	Alignment	not modelled	99.3	21	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	c3zgaA_	Alignment	not modelled	99.0	20	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin-binding protein 4 from 2 listeria monocytogenes in the carbenicillin bound form
118	c5aq7B_	Alignment	not modelled	98.8	20	PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography
119	c2bcfA_	Alignment	not modelled	98.8	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.
120	d1xp4a2	Alignment	not modelled	98.7	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase