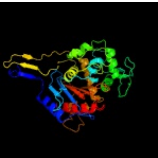



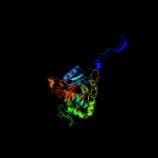



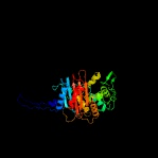


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3593_(lpqF)_4034531_4035889
 Date Fri Aug 9 18:20:27 BST 2019
 Unique Job ID 0b2711a1eaeaf41

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xftA_	Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
2	c3fwlA_	Alignment		100.0	12	PDB header: transferase, hydrolase Chain: A; PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b from2 escherichia coli
3	c3udiA_	Alignment		100.0	12	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
4	c3zg8B_	Alignment		100.0	12	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
5	c5u2gA_	Alignment		100.0	13	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	c3dwcC_	Alignment		100.0	12	PDB header: transferase Chain: C; PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
7	c2olvA_	Alignment		100.0	11	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
8	c4oonA_	Alignment		100.0	12	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-isindol-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	9	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	d2c5wb1	Alignment		100.0	11	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
11	c2bg1A_	Alignment		100.0	7	PDB header: peptidoglycan Chain: A; PDB Molecule: penicillin-binding protein 1b; PDBTitle: active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)

12	d2bg1a1	Alignment		100.0	7	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
13	c6g9fA_	Alignment		100.0	16	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2
14	c4jbfB_	Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469.
15	c5crfA_	Alignment		100.0	12	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: structure of the penicillin-binding protein pon1 from mycobacterium2 tuberculosis
16	c5dvyA_	Alignment		100.0	12	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
17	c2wadB_	Alignment		100.0	12	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)
18	c5u47A_	Alignment		100.0	10	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
19	c3pbnA_	Alignment		100.0	13	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa
20	c3equB_	Alignment		100.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
21	c3vslB_	Alignment	not modelled	100.0	12	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.
22	c5lp4A_	Alignment	not modelled	100.0	9	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori
23	c3pbqA_	Alignment	not modelled	100.0	12	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
24	c1qmfA_	Alignment	not modelled	100.0	10	PDB header: cell cycle Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
25	c3lo7A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
26	c3oc2A_	Alignment	not modelled	100.0	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
27	c1mwuA_	Alignment	not modelled	100.0	13	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.
28	d2olua2	Alignment	not modelled	100.0	9	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

29	c4ye5A_	Alignment	not modelled	100.0	10	PDB header: penicillin binding protein Chain: A; PDB Molecule: peptidoglycan synthetase penicillin-binding protein 3; PDBTitle: the crystal structure of a peptidoglycan synthetase from <i>Bifidobacterium adolescentis</i> atcc 15703
30	c5troA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A; PDB Molecule: penicillin-binding protein 1; PDBTitle: 1.8 angstrom resolution crystal structure of dimerization and 2 transpeptidase domains (residues 39-608) of penicillin-binding protein 3 from <i>Staphylococcus aureus</i> .
31	c4mnrA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan 2 glycosyltransferase from <i>Eggerthella lenta</i>
32	c3ue3A_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A; PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of <i>Acinetobacter baumannii</i> pbp3
33	c1pmdA_	Alignment	not modelled	100.0	10	PDB header: peptidoglycan synthesis Chain: A; PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
34	c3lo7B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from <i>Mycobacterium tuberculosis</i>
35	c4ovdA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from <i>Atopobium parvulum</i> dsm 20469
36	c4bjpA_	Alignment	not modelled	100.0	10	PDB header: transferase Chain: A; PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of <i>E. coli</i> penicillin binding protein 3
37	c5uy7A_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from <i>Burkholderia ambifaria</i>
38	d1vqqa3	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
39	d1rp5a4	Alignment	not modelled	100.0	10	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
40	c2wuqB_	Alignment	not modelled	100.0	19	PDB header: transcription Chain: B; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from <i>Streptomyces cacaoi</i>
41	c5hx9A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from <i>Burkholderia vietnamiensis</i>
42	c5e2eB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor blaa from <i>Yersinia enterocolitica</i>
43	c2v20A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase tem; PDBTitle: structure of a tem-1 beta-lactamase insertant allosterically regulated by kanamycin and anions. complex with sulfate.
44	d1pyya4	Alignment	not modelled	100.0	11	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
45	d1n9ba_	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
46	c2wuqA_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: A; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from <i>Streptomyces cacaoi</i>
47	d1g6aa_	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
48	d1m40a_	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
49	c2ov5A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
50	c6bsrA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: pbp4 protein; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4) from <i>Enterococcus faecalis</i> in the benzylpenicillin bound form.
51	d1hzoa_	Alignment	not modelled	100.0	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
52	c2j7vA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: tl12115 protein; PDBTitle: structure of pbp-a
53	c3dw0B_	Alignment	not modelled	100.0	16	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
54	c1hpcA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase class a-like protein;

54	c4tesA	Alignment	not modelled	100.0	14	PDBTitle: structure of a beta-lactamase class a-like protein from veillonella2 parvula.
55	c4yfmA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
56	c3qhyA	Alignment	not modelled	100.0	17	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
57	c5hw3A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
58	c6niqB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris
59	c4mxbB	Alignment	not modelled	100.0	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
60	d1buea	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
61	d1o7ea	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
62	c4ewfA	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
63	d1iysa	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
64	c5vpqA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum
65	c4b88A	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a
66	c4eqiA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1
67	d1dy6a	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
68	d2cc1a1	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
69	c3w4pA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at ph7.5
70	c6bn3A	Alignment	not modelled	100.0	18	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.
71	c3w4qC	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2
72	d1bsga	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
73	c6mk6C	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C; PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106
74	c5e43A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum
75	c6nj1A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluveri2 dsm 555
76	c4ztkA	Alignment	not modelled	100.0	14	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.
77	c2qpnA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
78	c4dxBB	Alignment	not modelled	100.0	17	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
79	d1i2sa	Alignment	not modelled	100.0	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

80	c1i2sA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
81	c3lezA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
82	d1djaa	Alignment	not modelled	100.0	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
83	c3cg5A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
84	c5tfqA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a representative of class a beta-lactamase from2 bacteroides cellulosityticus dsm 14838
85	c1w7fB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
86	c3p09A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
87	c3p09B	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
88	c3cjmA	Alignment	not modelled	100.0	19	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
89	d1xp4a2	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
90	d1tvfa2	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
91	d1alqa	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
92	d1k25a4	Alignment	not modelled	100.0	10	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
93	d1e25a	Alignment	not modelled	100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	c5gs8A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tla-3 extended-spectrum beta-lactamase
95	c5tr7A	Alignment	not modelled	100.0	18	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
96	d3beca2	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
97	c2iwdA	Alignment	not modelled	100.0	11	PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mecR1 protein; PDBTitle: oxacilloyl-acylated mecR1 extracellular antibiotic-sensor domain.
98	c5zqeC	Alignment	not modelled	100.0	18	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
99	c1xp4C	Alignment	not modelled	100.0	12	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
100	c5aq7B	Alignment	not modelled	100.0	17	PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography
101	c3humB	Alignment	not modelled	100.0	13	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
102	c1tvfA	Alignment	not modelled	100.0	14	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
103	c6ni0A	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
104	d1xa1a	Alignment	not modelled	100.0	8	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
105	d1nrfa	Alignment	not modelled	100.0	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
106	c6nbaA	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase;

106	c0m1sA_	Alignment	not modelled	100.0	11	PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc PDB header: hydrolase
107	c5e2fB_	Alignment	not modelled	100.0	13	Chain: B; PDB Molecule: beta-lactamase ybxi; PDBTitle: crystal structure of beta-lactamase class d from bacillus subtilis
108	c4zdxA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase
109	c4k91A_	Alignment	not modelled	99.9	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
110	c6n1nA_	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from sebalidella termitidis2 atcc 33386
111	c2bcfA_	Alignment	not modelled	99.9	19	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.
112	c6osuA_	Alignment	not modelled	99.9	21	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
113	c1z6fA_	Alignment	not modelled	99.9	15	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
114	c4oh0A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase
115	c5fsrB_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B; PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacd; PDBTitle: crystal structure of penicillin binding protein 6b from2 escherichia coli
116	c3it9B_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B; PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacc; PDBTitle: crystal structure of penicillin-binding protein 6 (pbp6) from e. coli2 in apo state
117	c2jc7A_	Alignment	not modelled	99.9	13	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
118	c3if6C_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: C; PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa
119	c3a3jA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A; PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from haemophilus2 influenzae
120	d1es5a_	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase