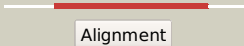

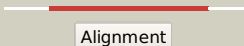

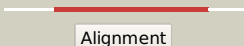







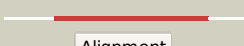









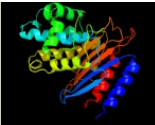
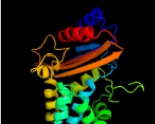

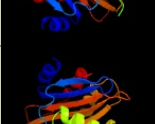

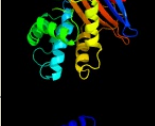





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2905_(lppW)_3214638_3215582
Date	Thu Aug 8 16:20:06 BST 2019
Unique Job ID	879feae9568fc9e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5e2eB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor bla _a from yersinia2 enterocolitica
2	c2j7vA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: tl12115 protein; PDBTitle: structure of pbp-a
3	c3cjmA_	 Alignment		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
4	c5e43A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum
5	c6niqB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris
6	c4dxbB_	 Alignment		100.0	19	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
7	c4mxbB_	 Alignment		100.0	19	PDB header: hydrolase/antibiotic Chain: B: PDB Molecule: bel-1; PDBTitle: crystal structure of extended-spectrum beta-lactamase bel-1 in complex2 with imipenem
8	c5hw3A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
9	c2v20A_	 Alignment		100.0	17	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.
10	d1hzoa_	 Alignment		100.0	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
11	d1alqa_	 Alignment		100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

12	c4eqiA	Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1
13	c4hesA	Alignment		100.0	17	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.
14	c1i2sA	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
15	d1i2sa	Alignment		100.0	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
16	c5hx9A	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis
17	c4ewfA	Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
18	c4yfmA	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
19	c5vpqA	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum
20	c5tfqA	Alignment		100.0	18	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
21	d1bsga	Alignment	not modelled	100.0	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
22	d1o7ea	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
23	c2ov5A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
24	d1buea	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
25	c3qhyA	Alignment	not modelled	100.0	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
26	c6nj1A	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluveri2 dsm 555
27	d1m40a	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
28	d1n9ba	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
29	d1g6aa	Alignment	not modelled	100.0	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like

					Family: beta-Lactamase/D-ala carboxypeptidase
30	c2qpnA	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
31	c4b88A	Alignment	not modelled	100.0	24 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a
32	d1dy6a	Alignment	not modelled	100.0	22 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
33	d2cc1a1	Alignment	not modelled	100.0	21 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
34	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
35	c1w7fB	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
36	c3dw0B	Alignment	not modelled	100.0	22 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
37	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
38	c3w4qC	Alignment	not modelled	100.0	23 PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2
39	c3lezA	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
40	c3p09A	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
41	d1lysa	Alignment	not modelled	100.0	22 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
42	c3cg5A	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
43	d1e25a	Alignment	not modelled	100.0	21 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
44	c6mk6C	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106
45	c2wuqB	Alignment	not modelled	100.0	22 PDB header: transcription Chain: B: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
46	c3w4pA	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at ph7.5
47	d1djaa	Alignment	not modelled	100.0	19 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
48	c6bn3A	Alignment	not modelled	100.0	23 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.
49	c5gs8A	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tla-3 extended-spectrum beta-lactamase
50	c5tr7A	Alignment	not modelled	100.0	15 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
51	c5aq7B	Alignment	not modelled	100.0	18 PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography
52	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
53	d1xp4a2	Alignment	not modelled	100.0	17 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
54	d3beca2	Alignment	not modelled	100.0	14 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
55	d1tvfa2	Alignment	not modelled	99.9	21 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
					Fold: beta-lactamase/transpeptidase-like

56	d1es5a_	Alignment	not modelled	99.9	19	Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
57	c2bcfA_	Alignment	not modelled	99.9	22	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.
58	c4pprA_	Alignment	not modelled	99.9	21	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
59	d1w5da1	Alignment	not modelled	99.9	25	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
60	c3a3jA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from haemophilus2 influenzae
61	c2xftA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
62	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
63	c5fsrB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacd; PDBTitle: crystal structure of penicillin binding protein 6b from2 escherichia coli
64	c3it9B_	Alignment	not modelled	99.9	17	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
65	c6aziA_	Alignment	not modelled	99.9	19	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
66	d1w79a1	Alignment	not modelled	99.9	27	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
67	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
68	c3a3eB_	Alignment	not modelled	99.9	21	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)
69	c6osuA_	Alignment	not modelled	99.9	17	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
70	c1tvfA_	Alignment	not modelled	99.9	19	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
71	c3humB_	Alignment	not modelled	99.9	18	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
72	c1xp4C_	Alignment	not modelled	99.9	17	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
73	c2jc7A_	Alignment	not modelled	99.9	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
74	c3mfdB_	Alignment	not modelled	99.9	20	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
75	d1nrfa_	Alignment	not modelled	99.8	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
76	c4oh0A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase
77	d2ex2a1	Alignment	not modelled	99.8	25	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
78	c3hbrD_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: D: PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
79	c5ctmB_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase
80	d1k55a_	Alignment	not modelled	99.7	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
81	c4zdxA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase

82	d1xa1a	Alignment	not modelled	99.7	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
83	c4iedB	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: B: PDB Molecule: class d beta-lactamase; PDBTitle: crystal structure of fus-1 (oxa-85), a class d beta-lactamase from <i>2 fusbacterium nucleatum subsp. polymorphum</i>
84	c6n1nA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from <i>sebaldella termitidis2 atcc 33386</i>
85	c4k0xA	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from <i>acinetobacter baumannii</i>
86	c2iwdA	Alignment	not modelled	99.6	11	PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mecR1 protein; PDBTitle: oxacilloyl-acylated mecR1 extracellular antibiotic-sensor domain.
87	c6nhuD	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: D: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from <i>2 agrobacterium fabrum</i>
88	c3if6C	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from <i>p. aeruginosa</i>
89	c4gn2A	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: oxacillinase; PDBTitle: crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
90	d1k38a	Alignment	not modelled	99.6	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
91	c6ni0A	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from <i>burkholderia2 thailandensis</i>
92	c6nhsA	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from <i>nostoc</i>
93	c5uy7A	Alignment	not modelled	99.5	16	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from <i>2 burkholderia ambifaria</i>
94	c3oc2A	Alignment	not modelled	99.5	19	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from <i>pseudomonas2 aeruginosa</i>
95	d1m6ka	Alignment	not modelled	99.4	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
96	c5e2fB	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ybxi; PDBTitle: crystal structure of beta-lactamase class d from <i>bacillus subtilis</i>
97	c4ztkA	Alignment	not modelled	99.4	21	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 <i>legionella2 pneumophila</i> .
98	c5jp4A	Alignment	not modelled	99.4	19	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from <i>helicobacter pylori</i>
99	c5cer1	Alignment	not modelled	99.4	16	PDB header: immune system Chain: I: PDB Molecule: bd0816; PDBTitle: bd0816 predatory endopeptidase from <i>bdellovibrio bacteriovorus in2</i> complex with immunity protein bd3460
100	c6g9fA	Alignment	not modelled	99.3	19	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of <i>e. coli</i> pbp2
101	c3pbnA	Alignment	not modelled	99.3	20	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from <i>pseudomonas aeruginosa</i>
102	c3lo7B	Alignment	not modelled	99.3	15	PDB header: transferase Chain: B: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from <i>mycobacterium tuberculosis</i>
103	d1vqqa3	Alignment	not modelled	99.3	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
104	c4jbfB	Alignment	not modelled	99.3	15	PDB header: transferase Chain: B: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from <i>atopobium2 parvulum dsm 20469</i> .
105	c3v39A	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: bd3459, a predatory peptidoglycan endopeptidase from <i>bdellovibrio2 bacteriovorus</i>
106	d1rp5a4	Alignment	not modelled	99.3	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
107	c4bjpA	Alignment	not modelled	99.3	23	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

108	d1pyya4	Alignment	not modelled	99.3	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
109	c3pbqA	Alignment	not modelled	99.2	20	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
110	c3ue3A	Alignment	not modelled	99.2	20	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
111	c3lo7A	Alignment	not modelled	99.2	20	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
112	c5troA	Alignment	not modelled	99.2	14	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 1 from staphylococcus aureus.
113	c4mnrA	Alignment	not modelled	99.1	21	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan 2 glycosyltransferase from eggerthella lenta
114	c1qmfA	Alignment	not modelled	99.1	14	PDB header: cell cycle Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
115	d1yqsa1	Alignment	not modelled	99.1	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
116	c4ovdA	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from 2 atopobium parvulum dsm 20469
117	c4ye5A	Alignment	not modelled	99.1	15	PDB header: penicillin binding protein Chain: A: PDB Molecule: peptidoglycan synthetase penicillin-binding protein 3; PDBTitle: the crystal structure of a peptidoglycan synthetase from 2 bifidobacterium adolescentis atcc 15703
118	c5u47A	Alignment	not modelled	99.1	16	PDB header: lipid-binding protein Chain: A: PDB Molecule: penicillin binding protein 2x; PDBTitle: 1.95 angstrom resolution crystal structure of penicillin binding 2 protein 2x from streptococcus thermophilus
119	c1mwuA	Alignment	not modelled	99.1	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a from 2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
120	c3equB	Alignment	not modelled	99.1	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae