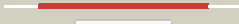



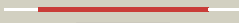














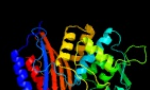













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3627c_(-)_4066079_4067464
Date	Fri Aug 9 18:20:31 BST 2019
Unique Job ID	58b8444521374b35

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w5da1	 Alignment		100.0	28	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
2	d2ex2a1	 Alignment		100.0	30	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
3	d1w79a1	 Alignment		100.0	31	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
4	c3a3eB	 Alignment		100.0	27	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)
5	c3v39A	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: bd3459, a predatory peptidoglycan endopeptidase from bdellovibrio2 bacteriovorus
6	c5cerI	 Alignment		100.0	17	PDB header: immune system Chain: I; PDB Molecule: bd0816; PDBTitle: bd0816 predatory endopeptidase from bdellovibrio bacteriovorus in2 complex with immunity protein bd3460
7	c3qhyA	 Alignment		99.9	16	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
8	c2v20A	 Alignment		99.9	16	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.
9	c5hw3A	 Alignment		99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis
10	c2j7vA	 Alignment		99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: tl12115 protein; PDBTitle: structure of pbb-a
11	c5hx9A	 Alignment		99.9	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis

12	c5e2eB_	Alignment		99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor blaA from Yersinia enterocolitica
13	c6nj1A_	Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class A beta-lactamase from Clostridium kluyveri DSM 555
14	d1hzoa_	Alignment		99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
15	c3cg5A_	Alignment		99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between beta-lactamase and clavulanate
16	c4mxbB_	Alignment		99.9	20	PDB header: hydrolase/antibiotic Chain: B: PDB Molecule: bel-1; PDBTitle: crystal structure of extended-spectrum beta-lactamase bel-1 in complex with imipenem
17	c2ov5A_	Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
18	c6niqB_	Alignment		99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class A beta-lactamase penP from Rhodospirillum rubrum
19	d1n9ba_	Alignment		99.9	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
20	c4eqiA_	Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of Serratia fonticola carbapenemase sfc-1
21	d1bsga_	Alignment	not modelled	99.9	26	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
22	c5e43A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from Streptosporangium roseum
23	c2wuqB_	Alignment	not modelled	99.9	24	PDB header: transcription Chain: B: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from Streptomyces cacaoi
24	c2wuqA_	Alignment	not modelled	99.9	24	PDB header: transcription Chain: A: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from Streptomyces cacaoi
25	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
26	d1m40a_	Alignment	not modelled	99.9	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
27	d1o7ea_	Alignment	not modelled	99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
28	c3dw0B_	Alignment	not modelled	99.9	18	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 Å resolution
						PDB header: hydrolase

29	c4yfmA	Alignment	not modelled	99.9	16	Chain: A: PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
30	c5vvpqA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum
31	d1iysa	Alignment	not modelled	99.9	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
32	d1g6aa	Alignment	not modelled	99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
33	c3w4qC	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2
34	d2cc1a1	Alignment	not modelled	99.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
35	d1dy6a	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
36	c1i2sa	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
37	d1i2sa	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
38	c5tr7A	Alignment	not modelled	99.9	20	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
39	d1xp4a2	Alignment	not modelled	99.9	27	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
40	c5tfqA	Alignment	not modelled	99.9	19	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
41	c4b88A	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a
42	d1djaa	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
43	d1buea	Alignment	not modelled	99.9	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
44	c4ewfA	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
45	d3beca2	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
46	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
47	c3lezA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
48	d1e25a	Alignment	not modelled	99.8	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
49	c2qpna	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
50	c3a3jA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from haemophilus2 influenzae
51	c6bn3A	Alignment	not modelled	99.8	20	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.
52	c3cjmA	Alignment	not modelled	99.8	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
53	c4pprA	Alignment	not modelled	99.8	22	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
54	c4hesA	Alignment	not modelled	99.8	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.
55	d1tvfa2	Alignment	not modelled	99.8	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						PDB header: hydrolase

56	c1z6fA_	Alignment	not modelled	99.8	21	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
57	c5fsrB_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacd; PDBTitle: crystal structure of penicillin binding protein 6b from2 escherichia coli
58	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
59	d1es5a_	Alignment	not modelled	99.8	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
60	c6mk6C_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106
61	d1alqa_	Alignment	not modelled	99.8	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
62	c5zqeC_	Alignment	not modelled	99.8	16	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
63	c3it9B_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacd; PDBTitle: crystal structure of penicillin-binding protein 6 (pbp6) from e. coli2 in apo state
64	c2bcfA_	Alignment	not modelled	99.8	29	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.
65	c4k91A_	Alignment	not modelled	99.8	23	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
66	c6aziA_	Alignment	not modelled	99.8	20	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
67	c3p09A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
68	c6osuA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase (penicillin binding PDBTitle: crystal structure of the d-alanyl-d-alanine carboxypeptidase dacd from2 francisella tularensis
69	c3humB_	Alignment	not modelled	99.8	19	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
70	c1xp4C_	Alignment	not modelled	99.8	27	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
71	c3mfdB_	Alignment	not modelled	99.8	23	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
72	c5gs8A_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tia-3 extended-spectrum beta-lactamase
73	c1tvfA_	Alignment	not modelled	99.8	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
74	c4dxbB_	Alignment	not modelled	99.7	16	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
75	c2xftA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
76	c2jc7A_	Alignment	not modelled	99.5	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
77	c5aq7B_	Alignment	not modelled	99.5	11	PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography
78	d1nrfA_	Alignment	not modelled	99.4	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
79	c5ctmB_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase
80	c6ni0A_	Alignment	not modelled	99.3	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
						PDB header: hydrolase

81	c4gn2A	Alignment	not modelled	99.3	23	Chain: A; PDB Molecule: oxacillinase; PDBTitle: crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
82	c2iwdA	Alignment	not modelled	99.2	15	PDB header: antibiotic resistance Chain: A; PDB Molecule: methicillin resistance mecrl protein; PDBTitle: oxacilloyl-acylated mecrl extracellular antibiotic-sensor domain.
83	c6nhuD	Alignment	not modelled	99.2	26	PDB header: hydrolase Chain: D; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum
84	c6nhsA	Alignment	not modelled	99.1	21	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc
85	d1xa1a	Alignment	not modelled	99.1	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
86	c5uy7A	Alignment	not modelled	99.0	24	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from2 burkholderia ambifaria
87	c4bjpA	Alignment	not modelled	98.9	25	PDB header: transferase Chain: A; PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3
88	d1vqqa3	Alignment	not modelled	98.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
89	d1rp5a4	Alignment	not modelled	98.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
90	c4oh0A	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase
91	c6g9fA	Alignment	not modelled	98.8	19	PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2
92	c4zdxA	Alignment	not modelled	98.8	15	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase
93	d1pyya4	Alignment	not modelled	98.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	c5lp4A	Alignment	not modelled	98.8	22	PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori
95	c3ue3A	Alignment	not modelled	98.8	24	PDB header: transferase Chain: A; PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
96	c3hbrD	Alignment	not modelled	98.8	20	PDB header: hydrolase Chain: D; PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
97	d1k38a	Alignment	not modelled	98.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
98	c3if6C	Alignment	not modelled	98.8	18	PDB header: hydrolase Chain: C; PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa
99	c4k0xA	Alignment	not modelled	98.8	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from acinetobacter baumannii
100	c1qmfA	Alignment	not modelled	98.8	22	PDB header: cell cycle Chain: A; PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
101	c3pbnA	Alignment	not modelled	98.7	20	PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa
102	c3lo7B	Alignment	not modelled	98.7	26	PDB header: transferase Chain: B; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
103	c3equB	Alignment	not modelled	98.7	24	PDB header: biosynthetic protein Chain: B; PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
104	c2wadB	Alignment	not modelled	98.7	19	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)
105	c6n1nA	Alignment	not modelled	98.7	13	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from seabaldella termitidis2 atcc 33386
106	c3oc2A	Alignment	not modelled	98.6	22	PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
107	c5e2fB	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase ybxi; PDBTitle: crystal structure of beta-lactamase class d from bacillus

						subtilis
108	c3lo7A_	Alignment	not modelled	98.6	27	PDB header: transferase Chain: A; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
109	c4ztkA_	Alignment	not modelled	98.6	34	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.
110	d1k55a_	Alignment	not modelled	98.6	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
111	c5troA_	Alignment	not modelled	98.5	25	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.
112	c5u47A_	Alignment	not modelled	98.5	20	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
113	d1m6ka_	Alignment	not modelled	98.5	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
114	c4iedB_	Alignment	not modelled	98.5	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
115	c4ovdA_	Alignment	not modelled	98.5	17	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from2 atopobium parvulum dsm 20469
116	c4mnrA_	Alignment	not modelled	98.4	25	PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan2 glycosyltransferase from eggertella lenta
117	c3vslB_	Alignment	not modelled	98.3	19	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.
118	c4ye5A_	Alignment	not modelled	98.3	19	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
119	d1k25a4	Alignment	not modelled	98.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
120	c5u2gA_	Alignment	not modelled	98.0	23	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