



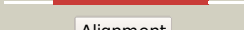

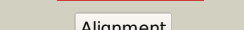

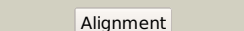





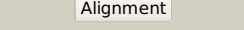

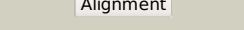

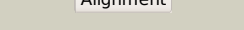

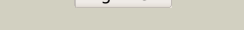












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3330_(dacB1)_3715948_3717165
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	1ba20748602f9ad7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4pprA_</a>	 Alignment		100.0	98	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein dacb1; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis d,d-peptidase rv33302 in complex with meropenem
2	<a href="#">c6osuA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase (penicillin binding) <b>PDBTitle:</b> crystal structure of the d-alanyl-d-alanine carboxypeptidase dacd from2 francisella tularensis
3	<a href="#">c4k91A_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> d-ala-d-ala-carboxypeptidase; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 5 (pbp5) from2 pseudomonas aeruginosa in apo state
4	<a href="#">c3mfdB_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dacb; <b>PDBTitle:</b> the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
5	<a href="#">c1z6fA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein 5; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 5 from e. coli in2 complex with a boronic acid inhibitor
6	<a href="#">c3it9B_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dacc; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 6 (pbp6) from e. coli2 in apo state
7	<a href="#">c5fsrB_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dacc; <b>PDBTitle:</b> crystal structure of penicillin binding protein 6b from2 escherichia coli
8	<a href="#">c3a3jA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> pbp5; <b>PDBTitle:</b> crystal structures of penicillin binding protein 5 from haemophilus2 influenzae
9	<a href="#">c1xp4C_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase; <b>PDBTitle:</b> crystal structure of a peptidoglycan synthesis regulatory2 factor (pbp3) from streptococcus pneumoniae
10	<a href="#">c1tvfA_</a>	 Alignment		100.0	19	<b>PDB header:</b> penicillin binding <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus
11	<a href="#">c3humB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase/antibiotics <b>Chain:</b> B; <b>PDB Molecule:</b> penicillin-binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin binding protein 4 from staphylococcus2 aureus col in complex with cefotaxime

12	<a href="#">c2bcfA_</a>	Alignment		100.0	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable d-alanyl-d-alanine carboxypeptidase dacb2; <b>PDBTitle:</b> crystal structure of a evolved putative penicillin-binding protein2 homolog, rv2911, from mycobacterium tuberculosis.
13	<a href="#">c6aziA_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl-d-alanine endopeptidase; <b>PDBTitle:</b> 1.75 angstrom resolution crystal structure of d-alanyl-d-alanine2 endopeptidase from enterobacter cloacae in complex with covalently3 bound boronic acid
14	<a href="#">d1tvfa2</a>	Alignment		100.0	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
15	<a href="#">d3beca2</a>	Alignment		100.0	29	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
16	<a href="#">d1es5a_</a>	Alignment		100.0	27	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
17	<a href="#">d1xp4a2</a>	Alignment		100.0	27	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
18	<a href="#">c5tr7A_</a>	Alignment		100.0	28	<b>PDB header:</b> penicillin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase; <b>PDBTitle:</b> crystal structure of a putative d-alanyl-d-alanine carboxypeptidase2 from vibrio cholerae o1 biovar eltor str. n16961
19	<a href="#">c5zqeC_</a>	Alignment		100.0	28	<b>PDB header:</b> antibiotic <b>Chain:</b> C: <b>PDB Molecule:</b> lmo2812 protein; <b>PDBTitle:</b> crystal structure of penicillin-binding protein d2 from listeria2 monocytogenes in the cefuroxime bound form
20	<a href="#">c3cg5A_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
21	<a href="#">c2v20A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase tem; <b>PDBTitle:</b> structure of a tem-1 beta-lactamase insertant allosterically regulated2 by kanamycin and anions. complex with sulfate.
22	<a href="#">c5e2eB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase precursor blaA from yersinia2 enterocolitica
23	<a href="#">d1m40a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
24	<a href="#">c3qhyA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> 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
25	<a href="#">d1n9ba_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
26	<a href="#">c1i2sa_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> beta-lactamase from bacillus licheniformis bs3
27	<a href="#">d1i2sa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
28	<a href="#">c3dw0B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> class a carbapenemase kpc-2; <b>PDBTitle:</b> crystal structure of the class a carbapenemase kpc-2 at 1.62 angstrom resolution
						<b>Fold:</b> beta-lactamase/transpeptidase-like

29	<a href="#">d1o7ea_</a>	Alignment	not modelled	100.0	15	<b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
30	<a href="#">c4hesA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase class a-like protein; <b>PDBTitle:</b> structure of a beta-lactamase class a-like protein from veillonella2 parvula.
31	<a href="#">d1dy6a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
32	<a href="#">c2j7vA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tll2115 protein; <b>PDBTitle:</b> structure of pbp-a
33	<a href="#">c4b88A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> ancestral (gnca) beta-lactamase class a
34	<a href="#">d2cc1a1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
35	<a href="#">d1hzoa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
36	<a href="#">c4eqiA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbapenem-hydrolyzing beta-lactamase sfc-1; <b>PDBTitle:</b> crystal structure of serratia fonticola carbapenemase sfc-1
37	<a href="#">c5tfqA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of a representative of class a beta-lactamase from2 bacteroides cellulosilyticus dsm 14838
38	<a href="#">c6niqB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris
39	<a href="#">c5e43A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum
40	<a href="#">d1iysa_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
41	<a href="#">c4ewfA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745
42	<a href="#">c5hw3A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of a beta lactamase from burkholderia vietnamiensis
43	<a href="#">c6mk6C_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> carbapenemase vcc-1 from vibrio cholerae n14-02106
44	<a href="#">c6nj1A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of class a beta-lactamase from clostridium kluverii2 dsm 555
45	<a href="#">c4yfmA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> class a beta-lactamase from mycobacterium abscessus
46	<a href="#">c2ov5A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbapenemase; <b>PDBTitle:</b> crystal structure of the kpc-2 carbapenemase
47	<a href="#">c4mxbB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> bel-1; <b>PDBTitle:</b> crystal structure of extended-spectrum beta-lactamase bel-1 in complex2 with imipenem
48	<a href="#">c5hx9A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from burkholderia vietnamiensis
49	<a href="#">c3lezA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of a halotolerant bacterial beta-lactamase
50	<a href="#">c1w7fB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
51	<a href="#">c5vpgA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from burkholderia phymatum
52	<a href="#">c3w4qC_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2
53	<a href="#">d1bsga_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
54	<a href="#">d1buea_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
55	<a href="#">d1g6aa_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like

						<b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
56	<a href="#">c3p09B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from francisella tularensis
57	<a href="#">c3w4pA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at pH7.5
58	<a href="#">c2wuqA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase regulatory protein blab; <b>PDBTitle:</b> crystal structure of blab protein from streptomyces cacaoi
59	<a href="#">d1dja_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
60	<a href="#">c6bn3A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> ctx-m-151 class a extended-spectrum beta-lactamase apo crystal2 structure at 1.3 angstrom resolution.
61	<a href="#">c2qpnA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase ges-1; <b>PDBTitle:</b> ges-1 beta-lactamase
62	<a href="#">d1alqa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
63	<a href="#">c3cjmA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-lactamase; <b>PDBTitle:</b> crystal structure of putative beta-lactamase (np_815223.1) from2 enterococcus faecalis v583 at 1.50 a resolution
64	<a href="#">c2wuqB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase regulatory protein blab; <b>PDBTitle:</b> crystal structure of blab protein from streptomyces cacaoi
65	<a href="#">c3p09A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from francisella tularensis
66	<a href="#">d1e25a_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
67	<a href="#">c5aq7B_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> d12_db04v3; <b>PDBTitle:</b> darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography
68	<a href="#">c4dxbB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> sugar binding protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose-binding periplasmic protein, beta-lactamase tem <b>PDBTitle:</b> 2.29a structure of the engineered mbp tem-1 fusion protein rg13 in2 complex with zinc, p1 space group
69	<a href="#">c2xftA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> orf12; <b>PDBTitle:</b> structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
70	<a href="#">c5gs8A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of tla-3 extended-spectrum beta-lactamase
71	<a href="#">c3a3eB_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin binding protein 4 (dacb) from2 haemophilus influenzae, complexed with novel beta-lactam (cmv)
72	<a href="#">d1w79a1</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
73	<a href="#">d1w5da1</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
74	<a href="#">d2ex2a1</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
75	<a href="#">c4gn2A_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxacillinase; <b>PDBTitle:</b> crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
76	<a href="#">c5cer1_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> immune system <b>Chain:</b> I: <b>PDB Molecule:</b> bd0816; <b>PDBTitle:</b> bd0816 predatory endopeptidase from bdellovibrio bacteriovorus in2 complex with immunity protein bd3460
77	<a href="#">c3v39A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase; <b>PDBTitle:</b> bd3459, a predatory peptidoglycan endopeptidase from bdellovibrio2 bacteriovorus
78	<a href="#">c6nhsA_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from nostoc
79	<a href="#">c6nhuD_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum
80	<a href="#">d1nrfa_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
						<b>PDB header:</b> hydrolase

81	<a href="#">c5ctmB_</a>	Alignment	not modelled	99.5	15	<b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of bpu1 beta-lactamase
82	<a href="#">d1xa1a_</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
83	<a href="#">c2iwdA_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> methicillin resistance mecr1 protein; <b>PDBTitle:</b> oxacilloyl-acylated mecr1 extracellular antibiotic-sensor domain.
84	<a href="#">c6ni0A_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis
85	<a href="#">c3i7jB_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase mb2281c; <b>PDBTitle:</b> crystal structure of a beta-lactamase (mb2281c) from mycobacterium2 bovis, northeast structural genomics consortium target mbr246
86	<a href="#">c2jc7A_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase oxa-24; <b>PDBTitle:</b> the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
87	<a href="#">c5uy7A_</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan glycosyltransferase; <b>PDBTitle:</b> crystal structure of a peptidoglycan glycosyltransferase from2 burkholderia ambifaria
88	<a href="#">c6n1nA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of class d beta-lactamase from sebaldella termitidis2 atcc 33386
89	<a href="#">c5e2fB_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase ybxi; <b>PDBTitle:</b> crystal structure of beta-lactamase class d from bacillus subtilis
90	<a href="#">c3if6C_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> oxa-46 oxacillinase; <b>PDBTitle:</b> crystal structure of oxa-46 beta-lactamase from p. aeruginosa
91	<a href="#">c3pbnA_</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of apo pbp3 from pseudomonas aeruginosa
92	<a href="#">c3hbrD_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> oxa-48; <b>PDBTitle:</b> crystal structure of oxa-48 beta-lactamase
93	<a href="#">c2wadB_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 2b; <b>PDBTitle:</b> penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
94	<a href="#">d1k38a_</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
95	<a href="#">c5lp4A_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2 (pbp2); <b>PDBTitle:</b> penicillin-binding protein (pbp2) from helicobacter pylori
96	<a href="#">c3oc2A_</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> penicillin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
97	<a href="#">c3pbqA_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of pbp3 complexed with imipenem
98	<a href="#">c4oh0A_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase oxa-58; <b>PDBTitle:</b> crystal structure of oxa-58 carbapenemase
99	<a href="#">d1k55a_</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
100	<a href="#">c3fwlA_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> crystal structure of the full-length transglycosylase pbp1b from2 escherichia coli
101	<a href="#">c5gmxA_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of a family viii carboxylesterase
102	<a href="#">c3lo7A_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein a; <b>PDBTitle:</b> crystal structure of pbpa from mycobacterium tuberculosis
103	<a href="#">c4bjpA_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin binding protein transpeptidase domain protein; <b>PDBTitle:</b> crystal structure of e. coli penicillin binding protein 3
104	<a href="#">d1vqqa3</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
105	<a href="#">c5troA_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of dimerization and2 transpeptidase domains (residues 39-608) of penicillin-binding3 protein 1 from staphylococcus aureus.
106	<a href="#">c4jfbB_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidoglycan glycosyltransferase; <b>PDBTitle:</b> crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469. <b>PDB header:</b> lipid-binding protein

107	<a href="#">c5u47A_</a>	Alignment	not modelled	99.0	17	<b>Chain:</b> A: <b>PDB Molecule:</b> penicillin binding protein 2x; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of penicillin binding2 protein 2x from streptococcus thermophilus
108	<a href="#">c1qmfA_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2x; <b>PDBTitle:</b> penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
109	<a href="#">d1pyya4</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
110	<a href="#">c3vslB_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> penicillin-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 3 (pbp3) from2 methicilin-resistant staphylococcus aureus in the cefotaxime bound3 form.
111	<a href="#">c4iedB_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> class d beta-lactamase; <b>PDBTitle:</b> crystal structure of fus-1 (oxa-85), a class d beta-lactamase from2 fusobacterium nucleatum subsp. polymorphum
112	<a href="#">c4k0xA_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> x-ray crystal structure of oxa-23 from acinetobacter baumannii
113	<a href="#">c3equB_</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
114	<a href="#">d1rp5a4</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
115	<a href="#">c3lo7B_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein a; <b>PDBTitle:</b> crystal structure of pbpa from mycobacterium tuberculosis
116	<a href="#">d1m6ka_</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
117	<a href="#">c6g9fA_</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan d,d-transpeptidase mrda; <b>PDBTitle:</b> structural basis for the inhibition of e. coli pbp2
118	<a href="#">c3ue3A_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> septum formation, penicillin binding protein 3, <b>PDBTitle:</b> crystal structure of acinetobacter baumannii pbp3
119	<a href="#">c4zdxA_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of oxa-51 beta-lactamase
120	<a href="#">c4ye5A_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> penicillin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan synthetase penicillin-binding protein 3; <b>PDBTitle:</b> the crystal structure of a peptidoglycan synthetase from2 bifidobacterium adolescentis atcc 15703