

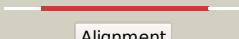

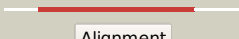




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0907_(-)_1010050_1011738
Date	Fri Jul 26 01:50:50 BST 2019
Unique Job ID	a4ed8172dc00cfd6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qmiH_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> pbp related beta-lactamase; <b>PDBTitle:</b> structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssii
2	<a href="#">c1ei5A_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-aminopeptidase; <b>PDBTitle:</b> crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
3	<a href="#">c4ivkA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterases; <b>PDBTitle:</b> crystal structure of a fammily viii carboxylesterase in a complex with2 cephalothin.
4	<a href="#">c3ozhA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase/d-alanine carboxypeptidase; <b>PDBTitle:</b> crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
5	<a href="#">c4p6bB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> est-y29; <b>PDBTitle:</b> crystal structure of est-y29,a novel penicillin-binding protein/beta-2 lactamase homolog from a metagenomic library
6	<a href="#">c5gkvA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase a; <b>PDBTitle:</b> crystal structure of a novel penicillin-binding protein (pbp) homolog2 from caulobacter crescentus
7	<a href="#">d1onha_</a>	 Alignment		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
8	<a href="#">d1rgya_</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
9	<a href="#">c3o3vB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of clbp peptidase domain
10	<a href="#">d2hdsa1</a>	 Alignment		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
11	<a href="#">c4y7pA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline d-peptidase; <b>PDBTitle:</b> structure of alkaline d-peptidase from bacillus cereus

12	<a href="#">c4gdnB</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein flp; <b>PDBTitle:</b> structure of fmta-like protein
13	<a href="#">d2drwa1</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
14	<a href="#">c2wzzA</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
15	<a href="#">d1yqsa1</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
16	<a href="#">c3ws1A</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> n288q-n321q mutant beta-lactamase derived from chromohalobacter sp.5602 (condition-1b)
17	<a href="#">c5e2hB</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of d-alanine carboxypeptidase ampC from2 mycobacterium smegmatis
18	<a href="#">c2qz6A</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> first crystal structure of a psychrophile class c beta-2 lactamase
19	<a href="#">c3wwxA</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s12 family peptidase; <b>PDBTitle:</b> crystal structure of d-stereospecific amidohydrolase from streptomyces2 sp. 82f2
20	<a href="#">c3tg9A</a>	Alignment		100.0	19	<b>PDB header:</b> penicillin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein; <b>PDBTitle:</b> the crystal structure of penicillin binding protein from bacillus2 halodurans
21	<a href="#">c3hleA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transesterase; <b>PDBTitle:</b> simvastatin synthase (lovD), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
22	<a href="#">d1ei5a3</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
23	<a href="#">c4netA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampc; <b>PDBTitle:</b> crystal structure of adc-1 beta-lactamase
24	<a href="#">c1zkjA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extended-spectrum beta-lactamase; <b>PDBTitle:</b> structural basis for the extended substrate spectrum of cmY-2 10, a plasmid-encoded class c beta-lactamase
25	<a href="#">c3zytA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase a; <b>PDBTitle:</b> structure determination of esta from arthrobacter nitroguajacolicus2 rue61a
26	<a href="#">c5gmxA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of a family viii carboxylesterase
27	<a href="#">c5eviC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-lactamase/d-alanine carboxypeptidase; <b>PDBTitle:</b> crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 pseudomonas syringae
28	<a href="#">c5e2gA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of d-alanine carboxypeptidase ampC from burkholderia2 cenocepacia

29	<a href="#">d1ci9a_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
30	<a href="#">c6njka_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from sulfitebacter sp. ee-36
31	<a href="#">c5zh8B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein fmta; <b>PDBTitle:</b> crystal structure of fmta from staphylococcus aureus at 2.58 a
32	<a href="#">c5evla_</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 beta-lactamase/d-alanine carboxypeptidase from2 chromobacterium violaceum
33	<a href="#">c5tgfb_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative beta-lactamase from bacteroides dorei2 dsm 17855
34	<a href="#">d2dcfa1</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
35	<a href="#">c4gb7A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-aminohexanoate-dimer hydrolase; <b>PDBTitle:</b> putative 6-aminohexanoate-dimer hydrolase from bacillus anthracis
36	<a href="#">c3i7jb_</a>	Alignment	not modelled	100.0	32	<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
37	<a href="#">c4whia_</a>	Alignment	not modelled	99.9	97	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of c-terminal domain of penicillin binding protein2 rv0907
38	<a href="#">d1tvfa2</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
39	<a href="#">c1tvfa_</a>	Alignment	not modelled	99.3	25	<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
40	<a href="#">d1hzoa_</a>	Alignment	not modelled	99.3	12	<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="#">c2v20A_</a>	Alignment	not modelled	99.3	16	<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.
42	<a href="#">c2j7va_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tlI2115 protein; <b>PDBTitle:</b> structure of pbp-a
43	<a href="#">c5tr7A_</a>	Alignment	not modelled	99.3	19	<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
44	<a href="#">d1n9ba_</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
45	<a href="#">d1m40a_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
46	<a href="#">c3p09A_</a>	Alignment	not modelled	99.2	11	<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
47	<a href="#">c2qpnA_</a>	Alignment	not modelled	99.2	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
48	<a href="#">c4hesA_</a>	Alignment	not modelled	99.2	14	<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.
49	<a href="#">c3humB_</a>	Alignment	not modelled	99.2	26	<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
50	<a href="#">c5fsrB_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dacd; <b>PDBTitle:</b> crystal structure of penicillin binding protein 6b from2 escherichia coli
51	<a href="#">d1iysa_</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
52	<a href="#">c4ewfa_</a>	Alignment	not modelled	99.2	19	<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
53	<a href="#">d1buea_</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
54	<a href="#">c4mxbB_</a>	Alignment	not modelled	99.2	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

55	<a href="#">c1z6fA_</a>	Alignment	not modelled	99.2	17	<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
56	<a href="#">c2wuqB_</a>	Alignment	not modelled	99.2	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
57	<a href="#">d2cc1a1</a>	Alignment	not modelled	99.1	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
58	<a href="#">c3it9B_</a>	Alignment	not modelled	99.1	21	<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
59	<a href="#">c6mk6C_</a>	Alignment	not modelled	99.1	14	<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
60	<a href="#">c4b88A_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> ancestral (gnca) beta-lactamase class a
61	<a href="#">c3a3jA_</a>	Alignment	not modelled	99.1	17	<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
62	<a href="#">c2wuqA_</a>	Alignment	not modelled	99.1	15	<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
63	<a href="#">d1g6aa_</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
64	<a href="#">c3p09B_</a>	Alignment	not modelled	99.0	12	<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
65	<a href="#">c2ov5A_</a>	Alignment	not modelled	99.0	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
66	<a href="#">d3beca2</a>	Alignment	not modelled	99.0	19	<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="#">c5hw3A_</a>	Alignment	not modelled	99.0	17	<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
68	<a href="#">c5tfqA_</a>	Alignment	not modelled	99.0	13	<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
69	<a href="#">d1bsga_</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
70	<a href="#">c6bn3A_</a>	Alignment	not modelled	99.0	15	<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.
71	<a href="#">d1xp4a2</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
72	<a href="#">c1i2sA_</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> beta-lactamase from bacillus licheniformis bs3
73	<a href="#">d1i2sa_</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
74	<a href="#">c6niqB_</a>	Alignment	not modelled	98.9	19	<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
75	<a href="#">d1e25a_</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
76	<a href="#">c3cjmA_</a>	Alignment	not modelled	98.9	17	<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
77	<a href="#">c1xp4C_</a>	Alignment	not modelled	98.9	27	<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
78	<a href="#">c4yfmA_</a>	Alignment	not modelled	98.9	19	<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
79	<a href="#">c3w4pA_</a>	Alignment	not modelled	98.9	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
80	<a href="#">d1o7ea_</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
81	<a href="#">c5vpqA_</a>	Alignment	not modelled	98.9	12	<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
82	<a href="#">c6osuA</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase <b>PDBTitle:</b> crystal structure of the d-alanyl-d-alanine carboxypeptidase dacd from2 francisella tularensis
83	<a href="#">c5hx9A</a>	Alignment	not modelled	98.9	17	<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
84	<a href="#">c4k91A</a>	Alignment	not modelled	98.9	22	<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
85	<a href="#">d1es5a</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
86	<a href="#">c5zqeC</a>	Alignment	not modelled	98.8	23	<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
87	<a href="#">c3w4qC</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of pema beta-lactamase from burkholderia multivorans2 at ph4.2
88	<a href="#">d1dy6a</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
89	<a href="#">c5e43A</a>	Alignment	not modelled	98.8	15	<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
90	<a href="#">c3dw0B</a>	Alignment	not modelled	98.8	18	<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
91	<a href="#">c5e2eB</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase precursor bla from yersinia2 enterocolitica
92	<a href="#">c3cg5A</a>	Alignment	not modelled	98.7	14	<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
93	<a href="#">c4dxbB</a>	Alignment	not modelled	98.7	14	<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
94	<a href="#">c5gs8A</a>	Alignment	not modelled	98.6	13	<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
95	<a href="#">c4eqiA</a>	Alignment	not modelled	98.6	16	<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
96	<a href="#">c2xftA</a>	Alignment	not modelled	98.4	14	<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
97	<a href="#">c4pprA</a>	Alignment	not modelled	98.4	21	<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
98	<a href="#">c6nj1A</a>	Alignment	not modelled	98.4	16	<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 kluyveri2 dsm 555
99	<a href="#">c3lezA</a>	Alignment	not modelled	98.4	15	<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
100	<a href="#">d1alqa</a>	Alignment	not modelled	98.4	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
101	<a href="#">c1w7fB</a>	Alignment	not modelled	98.3	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
102	<a href="#">c3qhyA</a>	Alignment	not modelled	98.3	15	<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
103	<a href="#">d1djaa</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
104	<a href="#">c3mfdB</a>	Alignment	not modelled	98.2	26	<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
105	<a href="#">c6aziA</a>	Alignment	not modelled	98.1	16	<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
106	<a href="#">c3nc2A</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> penicillin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 3;

106	<a href="#">c3uc2A</a>	Alignment	not modelled	97.4	10	<b>PDBTitle:</b> crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
107	<a href="#">c3pbqA</a>	Alignment	not modelled	97.4	19	<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
108	<a href="#">c4gn2A</a>	Alignment	not modelled	97.4	12	<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
109	<a href="#">c5aq7B</a>	Alignment	not modelled	97.4	15	<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
110	<a href="#">c4bjpA</a>	Alignment	not modelled	97.3	15	<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
111	<a href="#">c2jc7A</a>	Alignment	not modelled	97.3	12	<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
112	<a href="#">c4zdxA</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of oxa-51 beta-lactamase
113	<a href="#">c6nhsA</a>	Alignment	not modelled	97.1	19	<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
114	<a href="#">c5uy7A</a>	Alignment	not modelled	96.9	18	<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
115	<a href="#">c2bcfA</a>	Alignment	not modelled	96.9	21	<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.
116	<a href="#">c6nhuD</a>	Alignment	not modelled	96.9	14	<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
117	<a href="#">c3pbnA</a>	Alignment	not modelled	96.3	14	<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
118	<a href="#">d1w79a1</a>	Alignment	not modelled	96.0	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
119	<a href="#">c6g9fA</a>	Alignment	not modelled	95.8	18	<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
120	<a href="#">c3lo7A</a>	Alignment	not modelled	95.5	15	<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