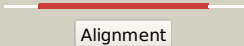

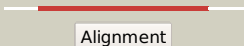

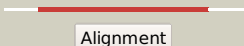







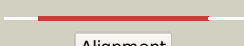











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1922 (- )_2174074_2175189
Date	Fri Aug 2 13:30:54 BST 2019
Unique Job ID	b6c0e3c2009d8ad3

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qmiH_</a>	 Alignment		100.0	25	<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	25	<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="#">c4y7pA_</a>	 Alignment		100.0	26	<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
4	<a href="#">d2drwa1</a>	 Alignment		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
5	<a href="#">d1ei5a3</a>	 Alignment		100.0	25	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
6	<a href="#">d1onha_</a>	 Alignment		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
7	<a href="#">c4gdnB_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> protein f1p; <b>PDBTitle:</b> structure of fmta-like protein
8	<a href="#">c3tg9A_</a>	 Alignment		100.0	24	<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
9	<a href="#">c2wzzA_</a>	 Alignment		100.0	24	<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
10	<a href="#">c5zh8B_</a>	 Alignment		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
11	<a href="#">d1yqsa1</a>	 Alignment		100.0	25	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase

12	<a href="#">d1rgya_</a>	Alignment		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
13	<a href="#">c4ivkA_</a>	Alignment		100.0	24	<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.
14	<a href="#">d2hdsa1</a>	Alignment		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
15	<a href="#">c3o3vB_</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 clbp peptidase domain
16	<a href="#">c2qz6A_</a>	Alignment		100.0	26	<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
17	<a href="#">c5e2hB_</a>	Alignment		100.0	25	<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="#">c3wwwxA_</a>	Alignment		100.0	24	<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
19	<a href="#">c3ozhA_</a>	Alignment		100.0	22	<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
20	<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
21	<a href="#">c1zjkA_</a>	Alignment	not modelled	100.0	24	<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 cmv-2 10, a plasmid-encoded class c beta-lactamase
22	<a href="#">c3ws1A_</a>	Alignment	not modelled	100.0	23	<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)
23	<a href="#">c5gkvA_</a>	Alignment	not modelled	100.0	23	<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
24	<a href="#">c4netA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampc; <b>PDBTitle:</b> crystal structure of adc-1 beta-lactamase
25	<a href="#">d1ci9a_</a>	Alignment	not modelled	100.0	28	<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="#">c5e2gA_</a>	Alignment	not modelled	100.0	22	<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
27	<a href="#">c3hleA_</a>	Alignment	not modelled	100.0	17	<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
28	<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 <b>PDB header:</b> hydrolase

29	<a href="#">c6njka_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from sulfitolbacter sp. ee-36
30	<a href="#">c5gmxA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of a family viii carboxylesterase
31	<a href="#">c5eviC_</a>	Alignment	not modelled	100.0	22	<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
32	<a href="#">c5evIA_</a>	Alignment	not modelled	100.0	23	<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	21	<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	20	<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	19	<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	29	<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="#">c2j7vA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tl12115 protein; <b>PDBTitle:</b> structure of pbp-a
38	<a href="#">d1m40a_</a>	Alignment	not modelled	99.5	17	<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="#">d1tvfa2</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
40	<a href="#">c4hesA_</a>	Alignment	not modelled	99.5	15	<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.
41	<a href="#">c4ewfA_</a>	Alignment	not modelled	99.4	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
42	<a href="#">c5tr7A_</a>	Alignment	not modelled	99.4	17	<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
43	<a href="#">c2qpnA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase ges-1; <b>PDBTitle:</b> ges-1 beta-lactamase
44	<a href="#">d1hzoa_</a>	Alignment	not modelled	99.4	16	<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="#">c1xp4C_</a>	Alignment	not modelled	99.4	23	<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
46	<a href="#">d1n9ba_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
47	<a href="#">c1tvfA_</a>	Alignment	not modelled	99.4	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
48	<a href="#">c3humB_</a>	Alignment	not modelled	99.4	17	<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
49	<a href="#">d1xp4a2</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
50	<a href="#">c2v20A_</a>	Alignment	not modelled	99.4	17	<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.
51	<a href="#">c1z6fA_</a>	Alignment	not modelled	99.4	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
52	<a href="#">c5vpqA_</a>	Alignment	not modelled	99.3	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
53	<a href="#">c5tfqA_</a>	Alignment	not modelled	99.3	15	<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 cellulolyticus dsm 14838
54	<a href="#">c4b88A_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> ancestral (gnca) beta-lactamase class a

55	<a href="#">c4mxB_B</a>	Alignment	not modelled	99.3	19	<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
56	<a href="#">d1g6aa</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
57	<a href="#">d1buea</a>	Alignment	not modelled	99.3	14	<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="#">c2wuqA</a>	Alignment	not modelled	99.3	18	<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="#">c5fsrB</a>	Alignment	not modelled	99.3	15	<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
60	<a href="#">d1o7ea</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
61	<a href="#">d1iysa</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
62	<a href="#">c4k91A</a>	Alignment	not modelled	99.3	18	<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
63	<a href="#">c3p09B</a>	Alignment	not modelled	99.3	17	<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
64	<a href="#">d3beca2</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
65	<a href="#">c5hw3A</a>	Alignment	not modelled	99.3	19	<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
66	<a href="#">d2cc1a1</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
67	<a href="#">c3a3jA</a>	Alignment	not modelled	99.3	15	<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
68	<a href="#">c6bn3A</a>	Alignment	not modelled	99.3	17	<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.
69	<a href="#">c3it9B</a>	Alignment	not modelled	99.3	17	<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 6 (pbp6) from e. coli2 in apo state
70	<a href="#">c2wuqB</a>	Alignment	not modelled	99.3	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
71	<a href="#">c6niqB</a>	Alignment	not modelled	99.3	17	<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 rhodospseudomonas palustris
72	<a href="#">c2ov5A</a>	Alignment	not modelled	99.3	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
73	<a href="#">c5zqeC</a>	Alignment	not modelled	99.2	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
74	<a href="#">c3p09A</a>	Alignment	not modelled	99.2	18	<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
75	<a href="#">c6mk6C</a>	Alignment	not modelled	99.2	17	<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
76	<a href="#">d1i2sa</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
77	<a href="#">c1i2sA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> beta-lactamase from bacillus licheniformis bs3
78	<a href="#">d1bsga</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
79	<a href="#">d1dy6a</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
80	<a href="#">c6osuA</a>	Alignment	not modelled	99.2	22	<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
						<b>Fold:</b> beta-lactamase/transpeptidase-like

81	<a href="#">d1es5a_</a>	Alignment	not modelled	99.2	20	<b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
82	<a href="#">c3w4pA_</a>	Alignment	not modelled	99.2	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
83	<a href="#">c4eqiA_</a>	Alignment	not modelled	99.2	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
84	<a href="#">c5hx9A_</a>	Alignment	not modelled	99.1	14	<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
85	<a href="#">c5e2eB_</a>	Alignment	not modelled	99.1	16	<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
86	<a href="#">d1e25a_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
87	<a href="#">c4dxbB_</a>	Alignment	not modelled	99.1	24	<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
88	<a href="#">c5e43A_</a>	Alignment	not modelled	99.1	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
89	<a href="#">c3cjmA_</a>	Alignment	not modelled	99.0	15	<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
90	<a href="#">c4yfmA_</a>	Alignment	not modelled	99.0	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
91	<a href="#">c3w4qC_</a>	Alignment	not modelled	99.0	18	<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
92	<a href="#">c3cg5A_</a>	Alignment	not modelled	99.0	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="#">c6aziA_</a>	Alignment	not modelled	99.0	18	<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
94	<a href="#">c3dw0B_</a>	Alignment	not modelled	99.0	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
95	<a href="#">c5gs8A_</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 tla-3 extended-spectrum beta-lactamase
96	<a href="#">c4pprA_</a>	Alignment	not modelled	98.9	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
97	<a href="#">c1w7fB_</a>	Alignment	not modelled	98.9	17	<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
98	<a href="#">c3qhyA_</a>	Alignment	not modelled	98.9	14	<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
99	<a href="#">c3lezA_</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> crystal structure of a halotolerant bacterial beta-lactamase
100	<a href="#">d1alqa_</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
101	<a href="#">c6nj1A_</a>	Alignment	not modelled	98.8	18	<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
102	<a href="#">c2xftA_</a>	Alignment	not modelled	98.8	13	<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
103	<a href="#">d1djaa_</a>	Alignment	not modelled	98.8	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="#">c2bcfA_</a>	Alignment	not modelled	98.6	17	<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.
105	<a href="#">c5aq7B_</a>	Alignment	not modelled	98.6	21	<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 <b>PDB header:</b> hydrolase

106	<a href="#">c3mfdB_</a>	Alignment	not modelled	98.4	17	<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
107	<a href="#">c6nhuD_</a>	Alignment	not modelled	97.5	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
108	<a href="#">c2jc7A_</a>	Alignment	not modelled	97.5	16	<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
109	<a href="#">c3oc2A_</a>	Alignment	not modelled	97.3	14	<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
110	<a href="#">c4gn2A_</a>	Alignment	not modelled	97.2	16	<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
111	<a href="#">c6ni0A_</a>	Alignment	not modelled	97.0	16	<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
112	<a href="#">d1nrfa_</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
113	<a href="#">c6nhsA_</a>	Alignment	not modelled	96.9	17	<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="#">d1xa1a_</a>	Alignment	not modelled	96.9	11	<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="#">c5ctmB_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of bpu1 beta-lactamase
116	<a href="#">c4zdxA_</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of oxa-51 beta-lactamase
117	<a href="#">c3pbqA_</a>	Alignment	not modelled	96.5	13	<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
118	<a href="#">c3lo7B_</a>	Alignment	not modelled	96.5	16	<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
119	<a href="#">c4bjpA_</a>	Alignment	not modelled	96.0	17	<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
120	<a href="#">d1rp5a4</a>	Alignment	not modelled	95.9	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase