


























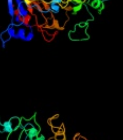


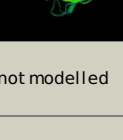



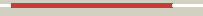







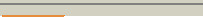





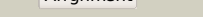

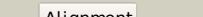


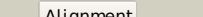
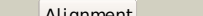

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2hdsa1</a>	 Alignment		100.0	100	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
2	<a href="#">dlrgya_</a>	 Alignment		100.0	77	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
3	<a href="#">d1onha_</a>	 Alignment		100.0	70	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
4	<a href="#">c2wzA_</a>	 Alignment		100.0	44	<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
5	<a href="#">c2qz6A_</a>	 Alignment		100.0	50	<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
6	<a href="#">c1zkjA_</a>	 Alignment		100.0	42	<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
7	<a href="#">c2qmiH_</a>	 Alignment		100.0	24	<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 abyssi
8	<a href="#">c3ozhA_</a>	 Alignment		100.0	23	<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 from yersinia pestis
9	<a href="#">c1ei5A_</a>	 Alignment		100.0	19	<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
10	<a href="#">c3o3vB_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of clbp peptidase domain
11	<a href="#">d2drwa1</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

12	<a href="#">dlyqsa1</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
13	<a href="#">c3tg9A_</a>	Alignment		100.0	21	<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
14	<a href="#">dlei5a3</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
15	<a href="#">d1ci9a_</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
16	<a href="#">c3hleA_</a>	Alignment		100.0	20	<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
17	<a href="#">d2dcfa1</a>	Alignment		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
18	<a href="#">c3i7jB_</a>	Alignment		100.0	26	<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) from2 mycobacterium bovis, northeast structural genomics3 consortium target mbr246
19	<a href="#">d1m40a_</a>	Alignment		99.5	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
20	<a href="#">c2j7vA_</a>	Alignment		99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tlf2115 protein; <b>PDBTitle:</b> structure of pbp-a
21	<a href="#">d1hzoa_</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
22	<a href="#">d1buea_</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
23	<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
24	<a href="#">d1tvfa2</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
25	<a href="#">c2wuqb_</a>	Alignment	not modelled	99.4	15	<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
26	<a href="#">c3p09A_</a>	Alignment	not modelled	99.4	15	<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
27	<a href="#">d1n9ba_</a>	Alignment	not modelled	99.4	18	<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="#">d1iysa_</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
29	<a href="#">c1hvfA</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> penicillin binding <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin binding protein 4;

29	<a href="#">c1w7A_</a>	Alignment	not modelled	99.4	10	<b>PDBTitle:</b> crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus <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
30	<a href="#">c2wuqA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbapenemase; <b>PDBTitle:</b> crystal structure of the kpc-2 carbapenemase
31	<a href="#">c2ov5A_</a>	Alignment	not modelled	99.4	15	<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="#">d2cc1a1</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
33	<a href="#">d1dy6a_</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
34	<a href="#">d1bsga_</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
35	<a href="#">d1g6aa_</a>	Alignment	not modelled	99.3	16	<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="#">c2v20A_</a>	Alignment	not modelled	99.3	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 insertant2 allosterically regulated by kanamycin and anions. complex3 with sulfate.
37	<a href="#">c3p09B_</a>	Alignment	not modelled	99.3	18	<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
38	<a href="#">d1o7ea_</a>	Alignment	not modelled	99.3	15	<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="#">d1e25a_</a>	Alignment	not modelled	99.2	14	<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="#">c3humB_</a>	Alignment	not modelled	99.2	19	<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 from2 staphylococcus aureus col in complex with cefotaxime
41	<a href="#">d1i2sa_</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
42	<a href="#">c1i2sa_</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> beta-lactamase from bacillus licheniformis bs3
43	<a href="#">c3a3jA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pbbp5; <b>PDBTitle:</b> crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
44	<a href="#">d3beca2</a>	Alignment	not modelled	99.2	23	<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="#">c1z6fA_</a>	Alignment	not modelled	99.2	27	<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
46	<a href="#">c3cjmA_</a>	Alignment	not modelled	99.1	18	<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
47	<a href="#">c1xp4C_</a>	Alignment	not modelled	99.1	15	<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 (pbbp3) from streptococcus pneumoniae
48	<a href="#">c3dw0B_</a>	Alignment	not modelled	99.1	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
49	<a href="#">c3cg5A_</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 the covalent adduct formed between tb2 b-lactamase and clavulanate
50	<a href="#">c3it9B_</a>	Alignment	not modelled	99.1	24	<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 (pbbp6)2 from e. coli in apo state
51	<a href="#">c3leza_</a>	Alignment	not modelled	99.1	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
52	<a href="#">c3qhyA_</a>	Alignment	not modelled	99.0	16	<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
53	<a href="#">d1xp4a2</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
54	<a href="#">c1w7fB_</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 class a beta-lactamase bs32 inhibited with isocitrate

55	<a href="#">dles5a_</a>	Alignment	not modelled	98.9	19	<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="#">d1dja_</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
57	<a href="#">c2xftA_</a>	Alignment	not modelled	98.8	12	<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
58	<a href="#">d1alqa_</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
59	<a href="#">c2jc7A_</a>	Alignment	not modelled	98.7	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
60	<a href="#">c2bcfA_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable d-alanyl-d-alanine carboxypeptidase <b>PDBTitle:</b> crystal structure of a evolved putative penicillin-binding2 protein homolog, rv2911, from mycobacterium tuberculosis.
61	<a href="#">c3mfdB_</a>	Alignment	not modelled	98.3	20	<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
62	<a href="#">c3oc2A_</a>	Alignment	not modelled	98.2	17	<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
63	<a href="#">d1nrfA_</a>	Alignment	not modelled	98.0	13	<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="#">c3if6C_</a>	Alignment	not modelled	97.9	16	<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.2 aeruginosa
65	<a href="#">c1pmdA_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> peptidoglycan synthesis <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan synthesis multifunctional enzyme; <b>PDBTitle:</b> penicillin-binding protein 2x (pbp-2x)
66	<a href="#">c3pbqA_</a>	Alignment	not modelled	97.8	15	<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
67	<a href="#">d1k38a_</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
68	<a href="#">d1rp5a4</a>	Alignment	not modelled	97.7	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
69	<a href="#">c2wadB_</a>	Alignment	not modelled	97.5	15	<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)
70	<a href="#">d1k55a_</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
71	<a href="#">d1pyya4</a>	Alignment	not modelled	97.5	15	<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="#">d1xa1a_</a>	Alignment	not modelled	97.4	11	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
73	<a href="#">c1qmFA_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> peptidoglycan synthesis <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2x; <b>PDBTitle:</b> penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
74	<a href="#">c3ue3A_</a>	Alignment	not modelled	97.1	16	<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
75	<a href="#">c3equB_</a>	Alignment	not modelled	96.9	14	<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
76	<a href="#">d1vqqa3</a>	Alignment	not modelled	96.8	15	<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="#">d1k25a4</a>	Alignment	not modelled	96.4	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
78	<a href="#">c3lo7A_</a>	Alignment	not modelled	96.4	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
79	<a href="#">c2iwdA_</a>	Alignment	not modelled	96.2	11	<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-sensor2 domain.
80	<a href="#">c3hbrD_</a>	Alignment	not modelled	96.2	13	<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

81	<a href="#">c3dwcC</a>	 Alignment	not modelled	95.9	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
82	<a href="#">d1m6ka</a>	 Alignment	not modelled	95.3	13	<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="#">c3fwlA</a>	 Alignment	not modelled	95.2	15	<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 pbp1b2 from escherichia coli
84	<a href="#">d1w79a1</a>	 Alignment	not modelled	94.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
85	<a href="#">d2olua2</a>	 Alignment	not modelled	94.5	11	<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="#">c1mwuA</a>	 Alignment	not modelled	94.3	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2a; <b>PDBTitle:</b> structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
87	<a href="#">d2c5wb1</a>	 Alignment	not modelled	93.7	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
88	<a href="#">c2olva</a>	 Alignment	not modelled	91.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
89	<a href="#">d1w5da1</a>	 Alignment	not modelled	91.9	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
90	<a href="#">c2bg1A</a>	 Alignment	not modelled	84.7	15	<b>PDB header:</b> peptidoglycan <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
91	<a href="#">d2ex2a1</a>	 Alignment	not modelled	83.9	22	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
92	<a href="#">c3udiA</a>	 Alignment	not modelled	82.6	23	<b>PDB header:</b> penicillin-binding protein/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1a; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
93	<a href="#">c3czdA</a>	 Alignment	not modelled	82.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminase kidney isoform; <b>PDBTitle:</b> crystal structure of human glutaminase in complex with l-glutamate
94	<a href="#">c3a3eB</a>	 Alignment	not modelled	82.3	24	<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)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
95	<a href="#">c2jciA</a>	 Alignment	not modelled	82.0	13	<b>PDB header:</b> drug-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b
96	<a href="#">c3uo9B</a>	 Alignment	not modelled	81.2	12	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> glutaminase kidney isoform, mitochondrial; <b>PDBTitle:</b> crystal structure of human gac in complex with glutamate and bptes
97	<a href="#">d1u60a</a>	 Alignment	not modelled	80.7	24	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Glutaminase
98	<a href="#">d2bg1a1</a>	 Alignment	not modelled	76.5	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
99	<a href="#">c2pbyB</a>	 Alignment	not modelled	74.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> probable glutaminase from geobacillus kaustophilus hta426
100	<a href="#">c2dfwA</a>	 Alignment	not modelled	65.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
101	<a href="#">c3ih9A</a>	 Alignment	not modelled	63.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure analysis of mglu in its tris form
102	<a href="#">c3ss4C</a>	 Alignment	not modelled	63.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glutaminase c; <b>PDBTitle:</b> crystal structure of mouse glutaminase c, phosphate-bound form
103	<a href="#">d1mkia</a>	 Alignment	not modelled	27.8	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Glutaminase