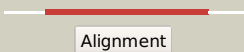

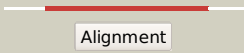



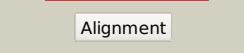



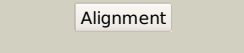

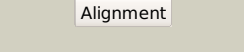




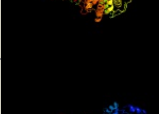

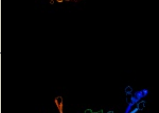
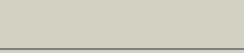

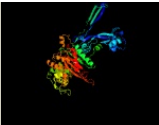










Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2163c_(pbpB)_2425056_2427095 |
| Date | Mon Aug 5 13:25:28 BST 2019 |
| Unique Job ID | 75887f96c05e9d89 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5u47A_ |  Alignment |  | 100.0 | 25 | PDB header: lipid-binding protein Chain: A; PDB Molecule: penicillin binding protein 2x; PDBTitle: 1.95 angstrom resolution crystal structure of penicillin binding2 protein 2x from streptococcus thermophilus |
| 2 | c3oc2A_ |  Alignment |  | 100.0 | 35 | PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa |
| 3 | c4ye5A_ |  Alignment |  | 100.0 | 32 | PDB header: penicillin binding protein Chain: A; PDB Molecule: peptidoglycan synthetase penicillin-binding protein 3; PDBTitle: the crystal structure of a peptidoglycan synthetase from2 bifidobacterium adolescentis atcc 15703 |
| 4 | c3pbqA_ |  Alignment |  | 100.0 | 34 | PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem |
| 5 | c6g9fA_ |  Alignment |  | 100.0 | 24 | PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: peptidoglycan d,d-transpeptidase mrda; PDBTitle: structural basis for the inhibition of e. coli pbp2 |
| 6 | c1pmdA_ |  Alignment |  | 100.0 | 27 | PDB header: peptidoglycan synthesis Chain: A; PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x) |
| 7 | c3ue3A_ |  Alignment |  | 100.0 | 34 | PDB header: transferase Chain: A; PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3 |
| 8 | c5lp4A_ |  Alignment |  | 100.0 | 21 | PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: penicillin-binding protein 2 (pbp2); PDBTitle: penicillin-binding protein (pbp2) from helicobacter pylori |
| 9 | c3vslB_ |  Alignment |  | 100.0 | 22 | PDB header: penicillin-binding protein Chain: B; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 (pbp3) from2 methicilin-resistant staphylococcus aureus in the cefotaxime bound3 form. |
| 10 | c5troA_ |  Alignment |  | 100.0 | 27 | PDB header: hydrolase Chain: A; PDB Molecule: penicillin-binding protein 1; PDBTitle: 1.8 angstrom resolution crystal structure of dimerization and2 transpeptidase domains (residues 39-608) of penicillin-binding3 protein 1 from staphylococcus aureus. |
| 11 | c3pbnA_ |  Alignment |  | 100.0 | 36 | PDB header: hydrolase/antibiotic Chain: A; PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo pbp3 from pseudomonas aeruginosa |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c1mwuA | Alignment |  | 100.0 | 20 | PDB header: biosynthetic protein Chain: A; PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a from 2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution. |
| 13 | c1qmfA | Alignment |  | 100.0 | 31 | PDB header: cell cycle Chain: A; PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex |
| 14 | c3equB | Alignment |  | 100.0 | 36 | PDB header: biosynthetic protein Chain: B; PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae |
| 15 | c4ovdA | Alignment |  | 100.0 | 32 | PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a putative peptidoglycan glycosyltransferase from 2 atopobium parvulum dsm 20469 |
| 16 | c4bjpA | Alignment |  | 100.0 | 33 | PDB header: transferase Chain: A; PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3 |
| 17 | c5dvyA | Alignment |  | 100.0 | 24 | PDB header: penicillin-binding protein Chain: A; PDB Molecule: penicillin binding protein 2 prime; PDBTitle: 2.95 angstrom crystal structure of the dimeric form of penicillin2 binding protein 2 prime from enterococcus faecium |
| 18 | c2wadB | Alignment |  | 100.0 | 23 | PDB header: peptide binding protein Chain: B; PDB Molecule: penicillin-binding protein 2b; PDBTitle: penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204) |
| 19 | c4jbfB | Alignment |  | 100.0 | 30 | PDB header: transferase Chain: B; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469. |
| 20 | c3lo7A | Alignment |  | 100.0 | 27 | PDB header: transferase Chain: A; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis |
| 21 | c4mnrA | Alignment | not modelled | 100.0 | 30 | PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of d,d-transpeptidase domain of peptidoglycan2 glycosyltransferase from eggerthella lenta |
| 22 | c6bsrA | Alignment | not modelled | 100.0 | 28 | PDB header: hydrolase Chain: A; PDB Molecule: pbp4 protein; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4) from 2 enterococcus faecalis in the benzylpenicillin bound form. |
| 23 | c3lo7B | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: B; PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis |
| 24 | d1pyya4 | Alignment | not modelled | 100.0 | 28 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 25 | d1rp5a4 | Alignment | not modelled | 100.0 | 28 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 26 | c5uy7A | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: A; PDB Molecule: peptidoglycan glycosyltransferase; PDBTitle: crystal structure of a peptidoglycan glycosyltransferase from 2 burkholderia ambifaria |
| 27 | d2c5wb1 | Alignment | not modelled | 100.0 | 21 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 28 | d1k25a4 | Alignment | not modelled | 100.0 | 28 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 29 | d1vqqa3 | Alignment | not modelled | 100.0 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 30 | c5u2gA | Alignment | not modelled | 100.0 | 24 | PDB header: lipid-binding protein Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: 2.6 angstrom resolution crystal structure of penicillin-binding2 protein 1a from haemophilus influenzae |
| 31 | c5crfA | Alignment | not modelled | 100.0 | 17 | PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: structure of the penicillin-binding protein pon1 from mycobacterium2 tuberculosis |
| 32 | c3zg8B | Alignment | not modelled | 100.0 | 23 | PDB header: penicillin-binding protein Chain: B: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 from2 listeria monocytogenes in the ampicillin bound form |
| 33 | c4oonA | Alignment | not modelled | 100.0 | 27 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of pbp1a in complex with compound 17 ((4z,8s,11e,2 14s)-5-(2-amino-1,3-thiazol-4-yl)-14-(5,6-dihydroxy-1,3-dioxo-1,3-3 dihydro-2h-isoindol-2-yl)-8-formyl-2-methyl-6-oxo-3,10-dioxa-4,7,11-4 triazatetradeca-4,11-diene-2,12,14-tricarboxylic acid) |
| 34 | c2bg1A | Alignment | not modelled | 100.0 | 24 | PDB header: peptidoglycan Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps) |
| 35 | c3udiA | Alignment | not modelled | 100.0 | 26 | PDB header: penicillin-binding protein/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g |
| 36 | c3dwcC | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer |
| 37 | c2jciA | Alignment | not modelled | 100.0 | 23 | PDB header: drug-binding protein Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b |
| 38 | c3fw1A | Alignment | not modelled | 100.0 | 22 | PDB header: transferase, hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b from2 escherichia coli |
| 39 | d2bg1a1 | Alignment | not modelled | 100.0 | 24 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 40 | c2olvA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein 2; PDBTitle: structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex |
| 41 | d2olua2 | Alignment | not modelled | 100.0 | 21 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 42 | c4ztkA | Alignment | not modelled | 100.0 | 31 | PDB header: transferase, cell cycle Chain: A: PDB Molecule: cell division protein ftsi/penicillin binding protein 2; PDBTitle: transpeptidase domain of ftsi4 d,d-transpeptidase from legionella2 pneumophila. |
| 43 | c6ni0A | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from burkholderia2 thailandensis |
| 44 | c6nhuD | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: D: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum |
| 45 | c2iwdA | Alignment | not modelled | 100.0 | 15 | PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mec1 protein; PDBTitle: oxacilloyl-acylated mec1 extracellular antibiotic-sensor domain. |
| 46 | c6n1nA | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from sebaldella termitidis2 atcc 33386 |
| 47 | d1m6ka | Alignment | not modelled | 100.0 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 48 | c5e2fB | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ybxi; PDBTitle: crystal structure of beta-lactamase class d from bacillus subtilis |
| 49 | c4gn2A | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: oxacillinase; PDBTitle: crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity |
| 50 | d1k38a | Alignment | not modelled | 100.0 | 14 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 51 | c4iedB | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: class d beta-lactamase; PDBTitle: crystal structure of fus-1 (oxa-85), a class d beta-lactamase from2 fusobacterium nucleatum subsp. polymorphum |
| 52 | c6nhsA | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc |
| 53 | d1nrfA | Alignment | not modelled | 100.0 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 54 | d1k55a | Alignment | not modelled | 100.0 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| | | | | | | PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 55 | c3hbrD_ | Alignment | not modelled | 100.0 | 17 | Chain: D; PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase |
| 56 | c3if6C_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: C; PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa |
| 57 | c4k0xA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from acinetobacter baumannii |
| 58 | c4zdxA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase |
| 59 | d1xa1a_ | Alignment | not modelled | 100.0 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 60 | c4oh0A_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase oxa-58; PDBTitle: crystal structure of oxa-58 carbapenemase |
| 61 | c2jc7A_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase oxa-24; PDBTitle: the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis |
| 62 | c5ctmB_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase |
| 63 | d1vqqa2 | Alignment | not modelled | 100.0 | 25 | Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain |
| 64 | c2wuqB_ | Alignment | not modelled | 100.0 | 19 | PDB header: transcription Chain: B; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi |
| 65 | c5vpqA_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum |
| 66 | c6bn3A_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: ctx-m-151 class a extended-spectrum beta-lactamase apo crystal2 structure at 1.3 angstrom resolution. |
| 67 | c5gs8A_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tla-3 extended-spectrum beta-lactamase |
| 68 | c2xftA_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway |
| 69 | d1g6aa_ | Alignment | not modelled | 100.0 | 19 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 70 | c2qpnA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase |
| 71 | c3w4pA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at ph7.5 |
| 72 | c4b88A_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a |
| 73 | d1iysa_ | Alignment | not modelled | 99.9 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 74 | c6mk6C_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: C; PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106 |
| 75 | d1e25a_ | Alignment | not modelled | 99.9 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 76 | c3w4qC_ | Alignment | not modelled | 99.9 | 18 | PDB header: hydrolase Chain: C; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2 |
| 77 | c2wuqA_ | Alignment | not modelled | 99.9 | 18 | PDB header: transcription Chain: A; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi |
| 78 | d1dy6a_ | Alignment | not modelled | 99.9 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 79 | d2cc1a1 | Alignment | not modelled | 99.9 | 22 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 80 | d1o7ea_ | Alignment | not modelled | 99.9 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 81 | c6niqB_ | Alignment | not modelled | 99.9 | 19 | PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 82 | c2ov5A | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase |
| 83 | d1m40a | Alignment | not modelled | 99.9 | 19 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 84 | c3dw0B | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: class a carbapenemase kpc-2; PDBTitle: crystal structure of the class a carbapenemase kpc-2 at 1.62 angstrom resolution |
| 85 | c5hw3A | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis |
| 86 | d1bsga | Alignment | not modelled | 99.9 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 87 | d1buea | Alignment | not modelled | 99.9 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 88 | c5hx9A | Alignment | not modelled | 99.9 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis |
| 89 | c4eqiA | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1 |
| 90 | d1k25a3 | Alignment | not modelled | 99.9 | 35 | Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain |
| 91 | d1djaa | Alignment | not modelled | 99.9 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 92 | d1n9ba | Alignment | not modelled | 99.9 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 93 | c3lezA | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase |
| 94 | c2j7vA | Alignment | not modelled | 99.9 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: tll2115 protein; PDBTitle: structure of pbp-a |
| 95 | c5e43A | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum |
| 96 | c4mxbB | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase/antibiotic Chain: B: PDB Molecule: bel-1; PDBTitle: crystal structure of extended-spectrum beta-lactamase bel-1 in complex2 with imipenem |
| 97 | c1w7fB | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate |
| 98 | c2v20A | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase tem; PDBTitle: structure of a tem-1 beta-lactamase insertant allosterically regulated2 by kanamycin and anions. complex with sulfate. |
| 99 | c6nj1A | Alignment | not modelled | 99.9 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluyveri2 dsm 555 |
| 100 | d1pyya3 | Alignment | not modelled | 99.9 | 28 | Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain |
| 101 | d1hzoa | Alignment | not modelled | 99.9 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 102 | c3qhyA | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structural, thermodynamic and kinetic analysis of the picomolar2 binding affinity interaction of the beta-lactamase inhibitor protein-3 ii (blip-ii) with class a beta-lactamases |
| 103 | c4ewfA | Alignment | not modelled | 99.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745 |
| 104 | c4yfmA | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus |
| 105 | c3cg5A | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate |
| 106 | d1i2sa | Alignment | not modelled | 99.8 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 107 | c1i2sA | Alignment | not modelled | 99.8 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3 |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 108 | c3p09B_ | Alignment | not modelled | 99.8 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis |
| 109 | c5e2eB_ | Alignment | not modelled | 99.8 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor bla _a from yersinia2 enterocolitica |
| 110 | d1alqa_ | Alignment | not modelled | 99.8 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 111 | c3p09A_ | Alignment | not modelled | 99.7 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis |
| 112 | c5tfqA_ | Alignment | not modelled | 99.7 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a representative of class a beta-lactamase from2 bacteroides cellulosilyticus dsm 14838 |
| 113 | c4hesA_ | Alignment | not modelled | 99.6 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase class a-like protein; PDBTitle: structure of a beta-lactamase class a-like protein from veillonella2 parvula. |
| 114 | d1xp4a2 | Alignment | not modelled | 99.4 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 115 | c3cjmA_ | Alignment | not modelled | 99.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: putative beta-lactamase; PDBTitle: crystal structure of putative beta-lactamase (np_815223.1) from2 enterococcus faecalis v583 at 1.50 a resolution |
| 116 | c4dxbB_ | Alignment | not modelled | 99.3 | 19 | PDB header: sugar binding protein, hydrolase Chain: B: PDB Molecule: maltose-binding periplasmic protein, beta-lactamase tem PDBTitle: 2.29a structure of the engineered mbp tem-1 fusion protein rg13 in2 complex with zinc, p1 space group |
| 117 | d1es5a_ | Alignment | not modelled | 99.3 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 118 | c5tr7A_ | Alignment | not modelled | 99.3 | 16 | PDB header: penicillin-binding protein Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of a putative d-alanyl-d-alanine carboxypeptidase2 from vibrio cholerae o1 biovar eltor str. n16961 |
| 119 | c5aq7B_ | Alignment | not modelled | 99.2 | 17 | PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography |
| 120 | d3beca2 | Alignment | not modelled | 99.2 | 19 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |