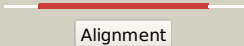

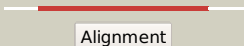

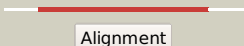







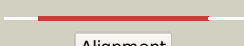











Phyre2

| | |
|---------------|--------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0399c_(lpqK)_477330_478559 |
| Date | Tue Jul 23 14:50:47 BST 2019 |
| Unique Job ID | 1b78251e7e9c6132 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c1ei5A_ |  Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: d-aminopeptidase; PDBTitle: crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi |
| 2 | c2qmiH_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: H: PDB Molecule: pbp related beta-lactamase; PDBTitle: structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi |
| 3 | c4ivkA_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterases; PDBTitle: crystal structure of a fammily viii carboxylesterase in a complex with2 cephalothin. |
| 4 | c2wzzA_ |  Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03 |
| 5 | d2drwa1 |  Alignment |  | 100.0 | 20 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 6 | d1onha_ |  Alignment |  | 100.0 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 7 | c3ws1A_ |  Alignment |  | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: n288q-n321q mutant beta-lactamase derived from chromhalobacter sp.5602 (condition-1b) |
| 8 | c4p6bB_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: est-y29; PDBTitle: crystal structure of est-y29,a novel penicillin-binding protein/beta-2 lactamase homolog from a metagenomic library |
| 9 | c3ozhA_ |  Alignment |  | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis |
| 10 | d1rgya_ |  Alignment |  | 100.0 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 11 | c5e2hB_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of d-alanine carboxypeptidase ampC from2 mycobacterium smegmatis |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c2qz6A_ | Alignment | | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: first crystal structure of a psychrophile class c beta-2 lactamase |
| 13 | c5gkvA_ | Alignment | | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: crystal structure of a novel penicillin-binding protein (pbp) homolog2 from caulobacter crescentus |
| 14 | d2hdsA1 | Alignment | | 100.0 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 15 | d1yqsA1 | Alignment | | 100.0 | 22 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 16 | c5eviC_ | Alignment | | 100.0 | 16 | PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 pseudomonas syringae |
| 17 | c4gdnB_ | Alignment | | 100.0 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: protein flp; PDBTitle: structure of fmta-like protein |
| 18 | c3o3vB_ | Alignment | | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of clbp peptidase domain |
| 19 | c4netA_ | Alignment | | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: ampc; PDBTitle: crystal structure of adc-1 beta-lactamase |
| 20 | c1zkiA_ | Alignment | | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: extended-spectrum beta-lactamase; PDBTitle: structural basis for the extended substrate spectrum of cmy-2 10, a plasmid-encoded class c beta-lactamase |
| 21 | c5zh8B_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: protein fmta; PDBTitle: crystal structure of fmta from staphylococcus aureus at 2.58 a |
| 22 | c3tg9A_ | Alignment | not modelled | 100.0 | 18 | PDB header: penicillin binding protein Chain: A: PDB Molecule: penicillin-binding protein; PDBTitle: the crystal structure of penicillin binding protein from bacillus2 halodurans |
| 23 | d1ei5a3 | Alignment | not modelled | 100.0 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 24 | c4y7pA_ | Alignment | not modelled | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: alkaline d-peptidase; PDBTitle: structure of alkaline d-peptidase from bacillus cereus |
| 25 | d1ci9a_ | Alignment | not modelled | 100.0 | 20 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 26 | c6njkA_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from sulfitobacter sp. ee-36 |
| 27 | c5e2gA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of d-alanine carboxypeptidase ampc from burkholderia2 cenocepacia |
| 28 | c3hleA_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: transesterase; PDBTitle: simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | c3zytA_ | Alignment | not modelled | 100.0 | 14 | Chain: A: PDB Molecule: esterase a; PDBTitle: structure determination of esta from arthrobacter nitroguajacolicus2 rue61a |
| 30 | c3wwxA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: s12 family peptidase; PDBTitle: crystal structure of d-stereospecific amidohydrolase from streptomyces2 sp. 82f2 |
| 31 | c5evlA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 chromobacterium violaceum |
| 32 | c5gmxA_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of a family viii carboxylesterase |
| 33 | c5tqfB_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative beta-lactamase from bacteroides dorei2 dsm 17855 |
| 34 | d2dcfa1 | Alignment | not modelled | 100.0 | 13 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 35 | c4gb7A_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: 6-aminohexanoate-dimer hydrolase; PDBTitle: putative 6-aminohexanoate-dimer hydrolase from bacillus anthracis |
| 36 | c3i7jB_ | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase mb2281c; PDBTitle: crystal structure of a beta-lactamase (mb2281c) from mycobacterium2 bovis, northeast structural genomics consortium target mbr246 |
| 37 | d1m40a_ | Alignment | not modelled | 99.6 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 38 | c4ewfA_ | Alignment | not modelled | 99.5 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: the crystal structure of beta-lactamase from sphaerobacter2 thermophilus dsm 20745 |
| 39 | d1tvfa2 | Alignment | not modelled | 99.5 | 14 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 40 | c4hesA_ | Alignment | not modelled | 99.5 | 11 | 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. |
| 41 | d1hzoa_ | Alignment | not modelled | 99.5 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 42 | c2j7vA_ | Alignment | not modelled | 99.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: tl12115 protein; PDBTitle: structure of pbp-a |
| 43 | c2qpnA_ | Alignment | not modelled | 99.5 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase |
| 44 | c1tvfA_ | Alignment | not modelled | 99.5 | 15 | PDB header: penicillin binding Chain: A: PDB Molecule: penicillin binding protein 4; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus |
| 45 | d1n9ba_ | Alignment | not modelled | 99.4 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 46 | c2wuqA_ | Alignment | not modelled | 99.4 | 10 | PDB header: transcription Chain: A: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi |
| 47 | c4b88A_ | Alignment | not modelled | 99.4 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: ancestral (gnca) beta-lactamase class a |
| 48 | c2wuqB_ | Alignment | not modelled | 99.4 | 12 | PDB header: transcription Chain: B: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi |
| 49 | d1lysa_ | Alignment | not modelled | 99.4 | 19 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 50 | d1bsga_ | Alignment | not modelled | 99.4 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 51 | c6bn3A_ | Alignment | not modelled | 99.4 | 14 | 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. |
| 52 | c6mk6C_ | Alignment | not modelled | 99.4 | 14 | PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: carbapenemase vcc-1 from vibrio cholerae n14-02106 |
| 53 | c5tfqA_ | Alignment | not modelled | 99.4 | 16 | 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 |
| 54 | d1buea_ | Alignment | not modelled | 99.4 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 55 | c2v20A_ | Alignment | not modelled | 99.4 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase tem; PDBTitle: structure of a tem-1 beta-lactamase insertant |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | allosterically regulated2 by kanamycin and anions. complex with sulfate. |
| 56 | c4mxbB_ | Alignment | not modelled | 99.4 | 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 |
| 57 | c3humB_ | Alignment | not modelled | 99.4 | 16 | PDB header: hydrolase/antibiotics Chain: B: PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 from staphylococcus2 aureus col in complex with cefotaxime |
| 58 | c3w4pA_ | Alignment | not modelled | 99.4 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of peni beta-lactamase from burkholderia2 pseudomallei at ph7.5 |
| 59 | d1g6aa_ | Alignment | not modelled | 99.3 | 13 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 60 | c3p09A_ | Alignment | not modelled | 99.3 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis |
| 61 | d2cc1a1 | Alignment | not modelled | 99.3 | 18 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 62 | c3p09B_ | Alignment | not modelled | 99.3 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis |
| 63 | c5e43A_ | Alignment | not modelled | 99.3 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase sros_5706 from streptosporangium2 roseum |
| 64 | c6niqB_ | Alignment | not modelled | 99.3 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the putative class a beta-lactamase penp from2 rhodopseudomonas palustris |
| 65 | c5hw3A_ | Alignment | not modelled | 99.3 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a beta lactamase from burkholderia vietnamiensis |
| 66 | d1xp4a2 | Alignment | not modelled | 99.3 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 67 | c5fsrB_ | Alignment | not modelled | 99.3 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacc; PDBTitle: crystal structure of penicillin binding protein 6b from2 escherichia coli |
| 68 | d1dy6a_ | Alignment | not modelled | 99.3 | 13 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 69 | c2ov5A_ | Alignment | not modelled | 99.3 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase |
| 70 | c5vpqA_ | Alignment | not modelled | 99.3 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia phymatum |
| 71 | d1o7ea_ | Alignment | not modelled | 99.3 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 72 | c5hx9A_ | Alignment | not modelled | 99.3 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from burkholderia vietnamiensis |
| 73 | c1xp4C_ | Alignment | not modelled | 99.3 | 13 | PDB header: hydrolase Chain: C: PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of a peptidoglycan synthesis regulatory2 factor (pbp3) from streptococcus pneumoniae |
| 74 | c1i2sa_ | Alignment | not modelled | 99.3 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3 |
| 75 | d1i2sa_ | Alignment | not modelled | 99.3 | 17 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 76 | c3w4qC_ | Alignment | not modelled | 99.3 | 14 | PDB header: hydrolase Chain: C: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of pena beta-lactamase from burkholderia multivorans2 at ph4.2 |
| 77 | c1z6fA_ | Alignment | not modelled | 99.2 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: penicillin-binding protein 5; PDBTitle: crystal structure of penicillin-binding protein 5 from e. coli in2 complex with a boronic acid inhibitor |
| 78 | c3a3jA_ | Alignment | not modelled | 99.2 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from haemophilus2 influenzae |
| 79 | d1e25a_ | Alignment | not modelled | 99.2 | 16 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 80 | c3it9B_ | Alignment | not modelled | 99.2 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacc; PDBTitle: crystal structure of penicillin-binding protein 6 (pbp6) from e. coli2 in apo state |
| 81 | c5tr7A_ | Alignment | not modelled | 99.2 | 13 | 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 |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 82 | c5e2eB | Alignment | not modelled | 99.2 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase precursor bla _a from yersinia2 enterocolitica |
| 83 | c3cg5A | Alignment | not modelled | 99.2 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate |
| 84 | c3dw0B | Alignment | not modelled | 99.2 | 15 | 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 | c4eqiA | Alignment | not modelled | 99.2 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: carbapenem-hydrolyzing beta-lactamase sfc-1; PDBTitle: crystal structure of serratia fonticola carbapenemase sfc-1 |
| 86 | c4dxbB | Alignment | not modelled | 99.2 | 14 | 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 |
| 87 | c4k91A | Alignment | not modelled | 99.2 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: d-ala-d-ala-carboxypeptidase; PDBTitle: crystal structure of penicillin-binding protein 5 (pbp5) from2 pseudomonas aeruginosa in apo state |
| 88 | d3beca2 | Alignment | not modelled | 99.1 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 89 | c4yfmA | Alignment | not modelled | 99.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus |
| 90 | c3qhyA | Alignment | not modelled | 99.1 | 16 | 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 |
| 91 | c5gs8A | Alignment | not modelled | 99.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of tla-3 extended-spectrum beta-lactamase |
| 92 | d1es5a | Alignment | not modelled | 99.1 | 19 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 93 | c3lezA | Alignment | not modelled | 99.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase |
| 94 | d1alqa | Alignment | not modelled | 99.0 | 21 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 95 | c3cjmA | Alignment | not modelled | 99.0 | 12 | 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 |
| 96 | c6nj1A | Alignment | not modelled | 99.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class a beta-lactamase from clostridium kluyveri2 dsm 555 |
| 97 | c5zqcC | Alignment | not modelled | 99.0 | 16 | PDB header: antibiotic Chain: C: PDB Molecule: lmo2812 protein; PDBTitle: crystal structure of penicillin-binding protein d2 from listeria2 monocytogenes in the cefuroxime bound form |
| 98 | c1w7fB | Alignment | not modelled | 98.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate |
| 99 | d1djaa | Alignment | not modelled | 98.9 | 15 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 100 | c6osuA | Alignment | not modelled | 98.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine carboxypeptidase (penicillin binding PDBTitle: crystal structure of the d-alanyl-d-alanine carboxypeptidase dacd from2 francisella tularensis |
| 101 | c4pprA | Alignment | not modelled | 98.9 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: penicillin-binding protein dacb1; PDBTitle: crystal structure of mycobacterium tuberculosis d,d-peptidase rv33302 in complex with meropenem |
| 102 | c2xftA | Alignment | not modelled | 98.8 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway |
| 103 | c6aziA | Alignment | not modelled | 98.8 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: d-alanyl-d-alanine endopeptidase; PDBTitle: 1.75 angstrom resolution crystal structure of d-alanyl-d-alanine2 endopeptidase from enterobacter cloacae in complex with covalently3 bound boronic acid |
| 104 | c2bcfA | Alignment | not modelled | 98.6 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: probable d-alanyl-d-alanine carboxypeptidase dacb2; PDBTitle: crystal structure of a evolved putative penicillin-binding protein2 homolog, rv2911, from mycobacterium tuberculosis. |
| 105 | c3mfdB | Alignment | not modelled | 98.4 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacb; PDBTitle: the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis |
| 106 | c5e2eB | Alignment | not modelled | 98.2 | 10 | PDB header: chaperone Chain: B: PDB Molecule: d12_db04v3; |

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|-----|------------------------|-----------|--------------|------|----|---|
| 106 | c2qy7D | Alignment | not modelled | 98.3 | 13 | PDBTitle: darpin-based crystallization chaperones exploit molecular geometry as2 a screening dimension in protein crystallography PDB header: hydrolase |
| 107 | c2jc7A | Alignment | not modelled | 98.2 | 13 | 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 |
| 108 | c4zdxA | Alignment | not modelled | 98.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structure of oxa-51 beta-lactamase |
| 109 | c6nhsA | Alignment | not modelled | 97.8 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from nostoc |
| 110 | c6n1nA | Alignment | not modelled | 97.6 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of class d beta-lactamase from sebalidella termitidis2 atcc 33386 |
| 111 | c6nhuD | Alignment | not modelled | 97.5 | 14 | PDB header: hydrolase Chain: D: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the beta lactamase class d ybxi from2 agrobacterium fabrum |
| 112 | c3if6C | Alignment | not modelled | 97.4 | 12 | PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p. aeruginosa |
| 113 | c4k0xA | Alignment | not modelled | 97.3 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: x-ray crystal structure of oxa-23 from acinetobacter baumannii |
| 114 | d1k38a | Alignment | not modelled | 97.3 | 12 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 115 | d1nrfa | Alignment | not modelled | 97.2 | 13 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase |
| 116 | c5ctmB | Alignment | not modelled | 97.1 | 10 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: structure of bpu1 beta-lactamase |
| 117 | c3pbnA | Alignment | not modelled | 97.0 | 14 | PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of apo bbp3 from pseudomonas aeruginosa |
| 118 | c4gn2A | Alignment | not modelled | 96.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: oxacillinase; PDBTitle: crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity |
| 119 | c3oc2A | Alignment | not modelled | 96.9 | 14 | PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa |
| 120 | c3hbrD | Alignment | not modelled | 96.9 | 13 | PDB header: hydrolase Chain: D: PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase |