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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **NAMLA amidase family** | **Organism** | **Gram status** | **Name of the structure in PDB** | **PDB ID** | **PDB**  **chain** | **Year in PDB** | **Ligand** | **Identified in** | **% identity to *E. coli* AmiC (4BIN)** |
| Amidase 3 | *Escherichia coli* | - | E. coli N-acetylmuramoyl-L-alanine amidase AmiC | [4BIN](https://www.rcsb.org/structure/4BIN) | A | 2013 | Zn2+ ,Na+ | PDB search for AmiC | 100% (100% coverage) |
| Amidase 3 | *Thermus parvatiensis* | - | AmiP amidase-3 from Thermus parvatiensis | [7B3N](https://www.rcsb.org/structure/7B3N) | A | 2020 | Zn2+, Na+, Cl-, Glycerol, SO42-, Ethanesulfonic Acid | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 43.53% (21% coverage) |
| Amidase 3 | *Neisseria meningitidis* | - | putative N-acetylmuramoyl-L-alanine amidase from *Neisseria meningitidis* | [3CZX](https://www.rcsb.org/structure/3CZX) | A | 2008 | Zn2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Clostridium difficile* | + | Cwp6 from Clostridium difficile | [5J72](https://www.rcsb.org/structure/5J72) | A | 2016 | Citric Acid, Zn2+, Ca2+, Cl-, Na+ | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 27.73% (57% coverage) |
| Amidase 3 | *Staphylococcus aureus* | + | Structure of the S. aureus amidase LytH and activator ActH extracellular domains | [7TJ4](https://www.rcsb.org/structure/7TJ4) | B | 2022 | Zn2+ | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 30.18% (54% coverage) |
| Amidase 3 | *Clostridium difficile* | + | The crystal structure of N-acetylmuramoyl-L-alanine amidase from Clostridium difficile 630 | [4RN7](https://www.rcsb.org/structure/4RN7) | A | 2014 | Zn2+, Formic Acid, Glycerol, EPE (Ethanesulfonic Acid) | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 27.48% (54% coverage) |
| Amidase 3 | *Nostoc punctiforme* | + | N-acetylmuramoyl-L-alanine amidase AmiC2 of Nostoc punctiforme | [5EMI](https://www.rcsb.org/structure/5EMI) | A | 2015/  2016 | MES, MRD, Zn2+ | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 27.6% (54% coverage) |
| Amidase 3 | *Bartonella henselae* | - | NAMLA amidase of *Bartonella henselae* str. Houston-1 | [3NE8](https://www.rcsb.org/structure/3NE8) | A | 2010 | ACETATE ION, FORMIC ACID, GLYCEROL, Zn2+ | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 40.18% (53% coverage) |
| Amidase 3 | *Mycobacterium tuberculosis* | NA | *Mycobacterium tuberculosis* peptidoglycan amidase Rv3717 in complex with L-Alanine-iso-D-Glutamine reaction product | [4M6G](https://www.rcsb.org/structure/4M6G) | A | 2013 | Zn2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Bacillus(* *Paenibacillus polymyxa)* | + | Catalytic domain of CwlV, N-acetylmuramoyl-L-alanine amidase from *Bacillus(Paenibacillus) polymyxa var.colistinus* | [1JWQ](https://www.rcsb.org/structure/1JWQ#entity-1) | A | 2001 | Zn2+ | BLASTp search 1 (restricted to PDB, FASTA seq. search of 4BIN) | 27.95% (54% coverage) |
| Amidase 3 | *Mycobacterium tuberculosis* | NA | Crystal structure of Rv3717 reveals a novel amidase from M. tuberculosis | [4LQ6](https://www.rcsb.org/structure/4LQ6) | A | 2013 | SO4-, Zn2+, Cl-, Pt2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Mycobacterium tuberculosis H37Rv* | NA | Structure of the reduced, metal-free form of Mycobacterium tuberculosis peptidoglycan amidase Rv3717 | [4M6H](https://www.rcsb.org/structure/4M6H) | A | 2013 | None reported | PDB search of N-acetylmuramoyl-L-alanine activity (GO annotation) |  |
| Amidase 3 | *Mycobacterium tuberculosis* | NA | Structure of the reduced, Zn-bound form of Mycobacterium tuberculosis peptidoglycan amidase Rv3717 (metal-free structure: [4M6H](https://www.rcsb.org/structure/4M6H)) | [4M6I](https://www.rcsb.org/structure/4M6I) | A | 2013 | Zn2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Mycobacteroides abscessus* | + | crystal structure of the N-acetylmuramyl-L-alanine amidase, Ami1, from Mycobacterium abscessus bound to L-Alanine-D-isoglutamine | [7AGO](https://www.rcsb.org/structure/7AGO) | A | 2020 | Zn2+, D-alpha-glutamine, Alanine | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Mycolicibacterium smegmatis* | + | Crystal structure of the N-acetylmuramyl-L-alanine amidase, Ami1, from Mycobacterium smegmatis | [7AGM](https://www.rcsb.org/structure/7AGM) | A | 2020 | Zn2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Mycobacteroides abscessus* | + | crystal structure of the apo form of the N-acetylmuramyl-L-alanine amidase, Ami1, from Mycobacterium abscessus. | [7AGL](https://www.rcsb.org/structure/7AGL) | A | 2020 | Zn2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Clostridium difficile* | + | Structure of the CwlD amidase from Clostridioides difficile in complex with the GerS lipoprotein | [7RAG](https://www.rcsb.org/structure/7RAG) | B | 2021 | Zn2+, 1,2-Ethanediol | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Listeria monocytogenes* | NA | *Listeria monocytogenes* bacteriophage PSA endolysin PlyPSA | [1XOV](https://www.rcsb.org/structure/1XOV) | A | 2004 | Cl- ,GLUTAMIC ACID, LYSINE, 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL, SO4-, Zn2+ | PDB search of Amidase\_3 protein family annotation |  |
| Amidase 3 | *Clostridium difficile* | + | Catalytic domain of CD27L endolysin targeting *Clostridium difficile* | [3QAY](https://www.rcsb.org/structure/3QAY) | A | 2011 | SO4-, Zn2+ | PDB search of Amidase\_3 protein family annotation |  |