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Author Correction: Structural basis of cell wall peptidoglycan amidation by the GatD/MurT complex of *Staphylococcus aureus*

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In Fig. 1A, a carbonyl group is missing in the schematic drawing of the reaction product. The correct Fig. 1 appears below.

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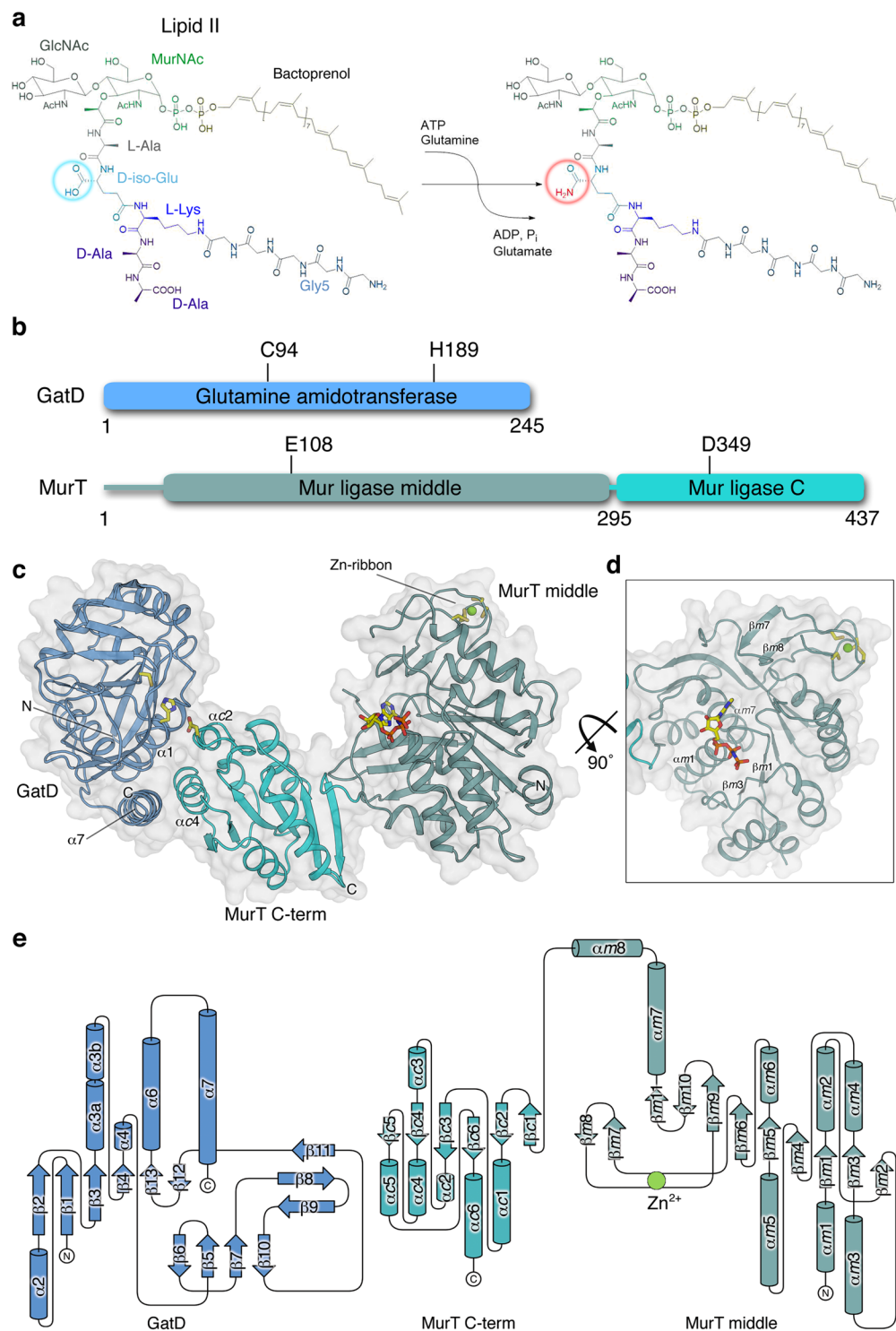


Figure 1. Overall structure and organization of the GatD/MurT complex. **(a)** Reaction catalyzed by GatD/MurT. The free α -carboxyl of D-iso-glutamate in the peptide stem is amidated in a glutamine- and ATP-dependent reaction. **(b)** Schematic overview of GatD and MurT proteins. GatD consists of a single glutamine amidotransferase (GATase) domain with a cysteine at position 94 as the active residue and a histidine at position 189 as a component of the catalytic triad¹⁹. MurT is composed of two domains: a Mur ligase middle domain (MurT middle) containing the canonical ATP binding site and, surprisingly, a ribbon-type Zinc finger, and a C-terminal Mur ligase domain (MurT C-term). MurT residue glutamate 108 participates in ATP hydrolysis, and aspartate 349 forms the third residue in the putative catalytic triad. **(c)** Overview of the GatD/MurT structure. GatD and MurT form a boomerang-shaped complex, with GatD contacting the MurT C-term domain through contacts that are in part mediated by helix α 7 of GatD. Catalytic triad residues GatD-C94, GatD-H189, MurT-D349 and the bound nucleotide AMPNP are shown in stick representation. The zinc ion in the Cys₄ zinc ribbon of MurT is shown as a green sphere, and the four cysteine residues ligating it are shown

as sticks. **(d)** Tilted view of the MurT middle domain to show the central β -sheet and the bound AMPNP and its surrounding secondary structure elements, as well as the zinc ribbon. **(e)** Topological representation of the GatD/MurT architecture. Secondary structure nomenclature of GatD was done according to Leisico *et al.*²⁴. As the short helices $\alpha 1$ and $\alpha 5$ in the isolated GatD structure do not conform to helical geometry in our complex, they were not assigned. The MurT domains were assigned separately with the prefixes *m* and *c* indicating the middle and C-terminal domains, respectively. The drawing was generated with TopDraw⁵⁴.



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