



STRUCTURAL BIOLOGY
COMMUNICATIONS

Volume 79 (2023)

Supporting information for article:

**Crystal structure of a GCN5-related *N*-acetyltransferase from
*Lactobacillus curiae***

Jennifer R. Fleming, Franziskus Hauth, Jörg S. Hartig and Olga Mayans

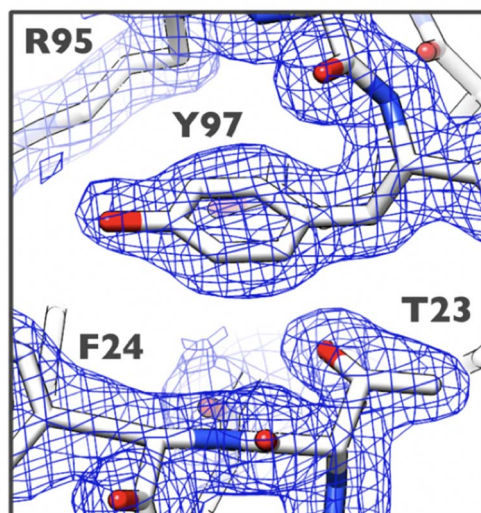
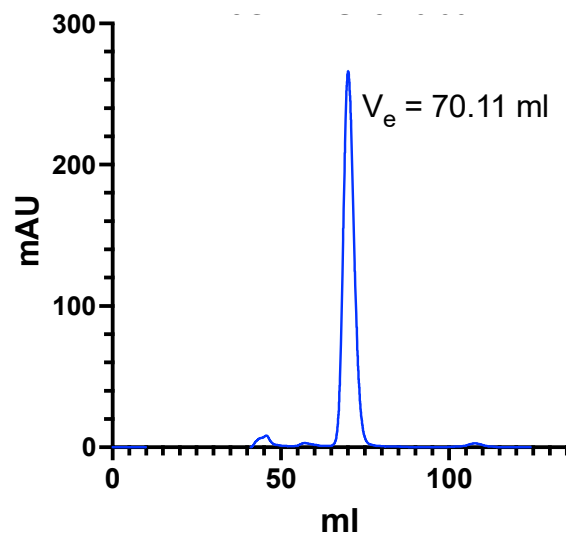


Figure S1 Representative electron density. $(2mF_{\text{obs}} - DF_{\text{calc}})\alpha_{\text{calc}}$ electron density map contoured at 1σ for the region local to the catalytically relevant residue Y97.

A



B

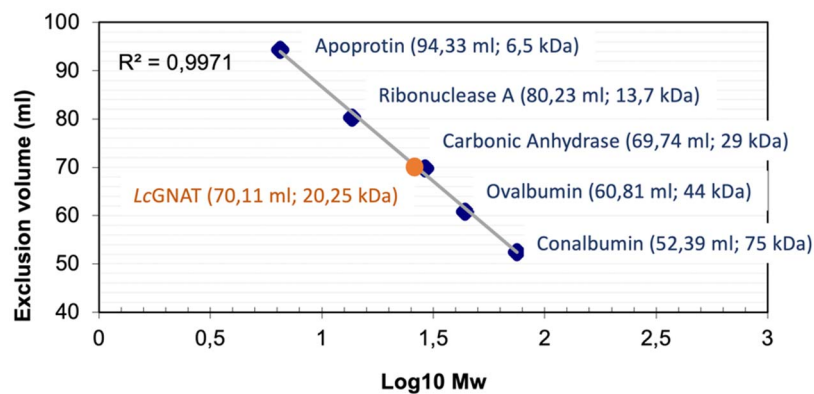


Figure S2 Size exclusion chromatogram of LcGNAT. Size exclusion was performed on a Superdex S75 16/60 column (GE Healthcare) pre-equilibrated in 50 mM Tris pH 8.0, 100 mM NaCl. The loaded sample (volume approx. 3ml) had been concentrated to 6 mg/ml; **B**. The exclusion volume (V_e) of LcGNAT (orange), interpreted in the light of column calibration standards (blue), suggests a monomeric form of the protein (MM= 20.25 kDa; calculated from sequence data). For each protein, exclusion volume and molecular mass are quoted in brackets.

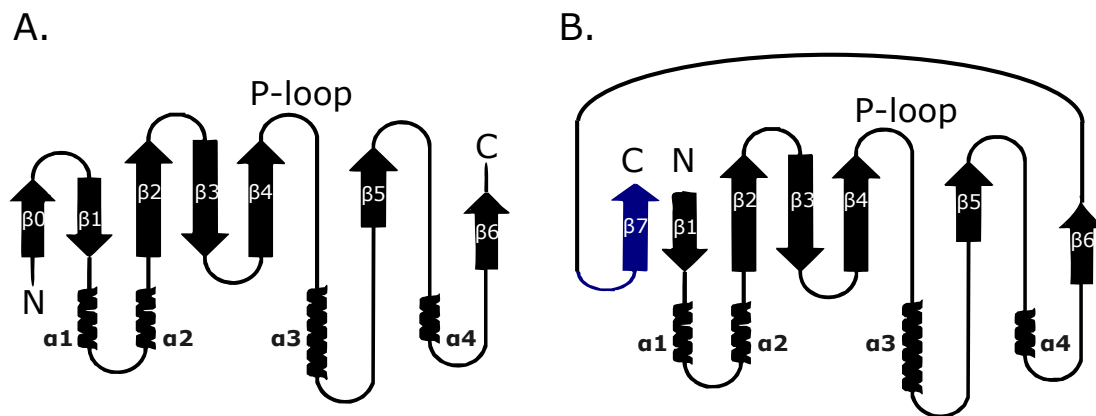


Figure S3 Topological differences in GNAT enzymes. **(A)** Canonical topology of the GNAT superfamily **(B)** and *LcGNAT* topology representative of the subfamily of polyamine acetyltransferases. In the latter, β-strand β₀ is not present. Instead, an extra C-terminal β-strand β₇ (dark blue) forms an antiparallel interaction with β-strand β₁.