Supplementary Data

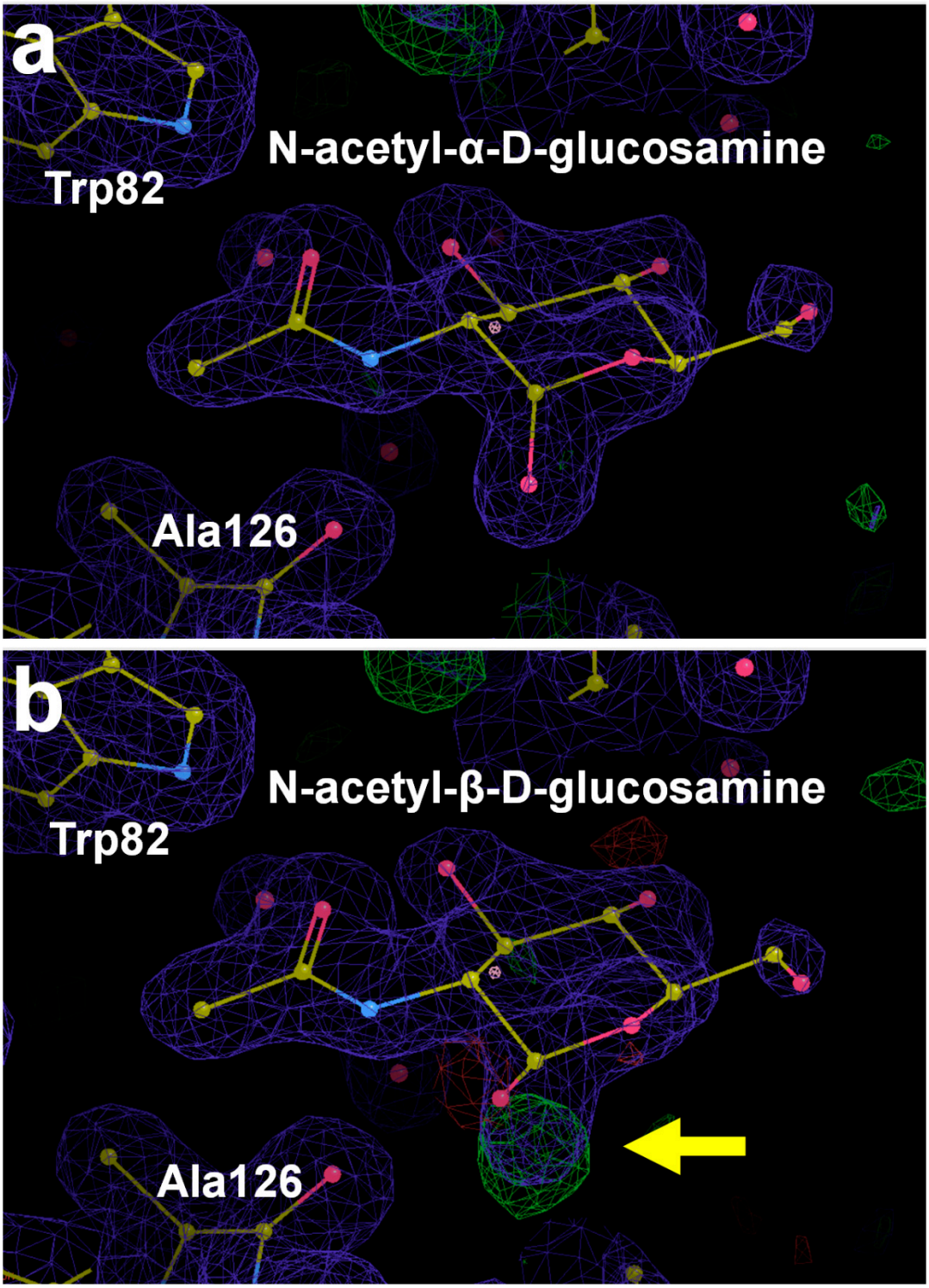
Crystal Structure of Human Lysozyme Complexed with *N*-Acetyl-α-D-Glucosamine

Ki Hyun Nam [1,2]*

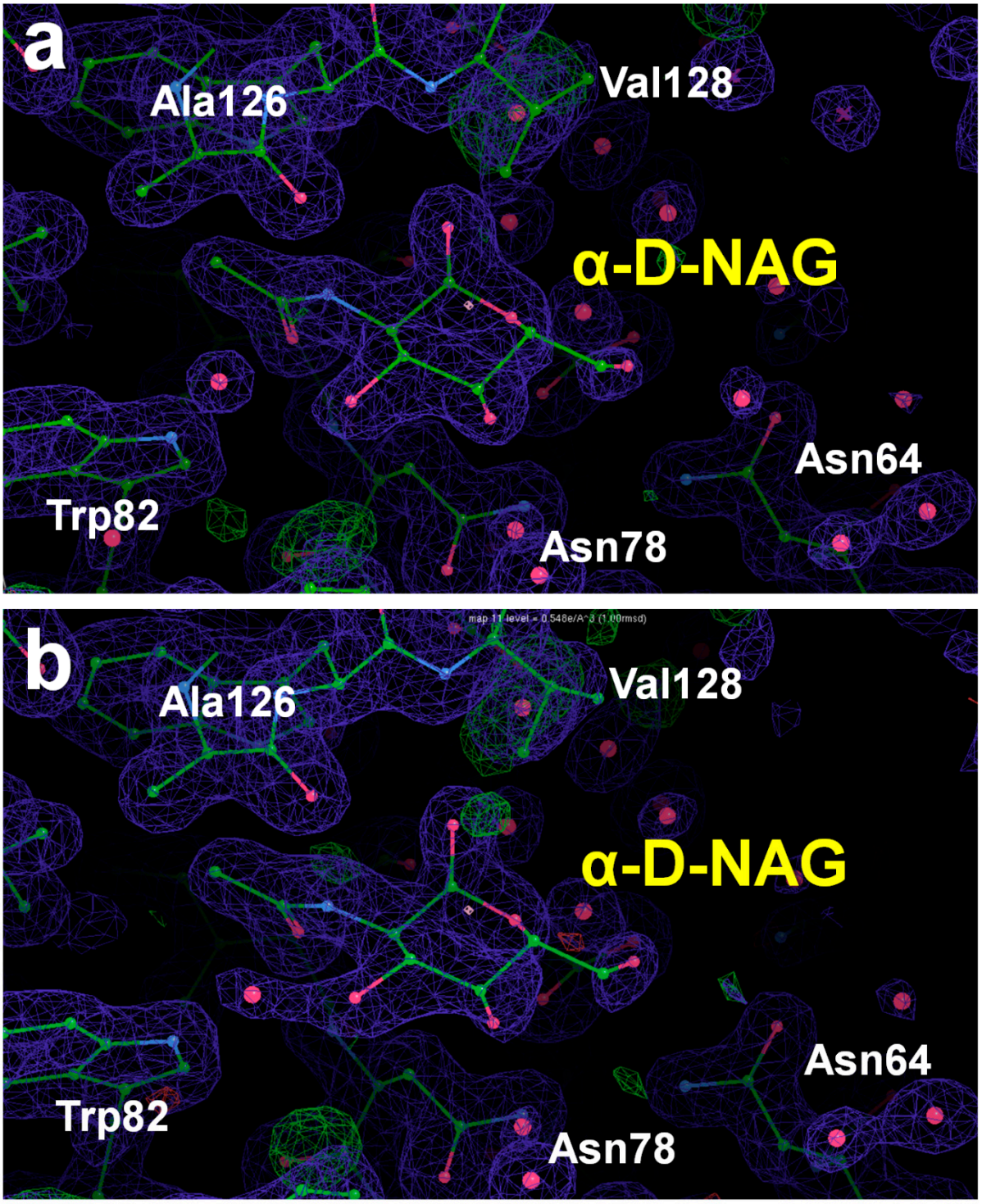
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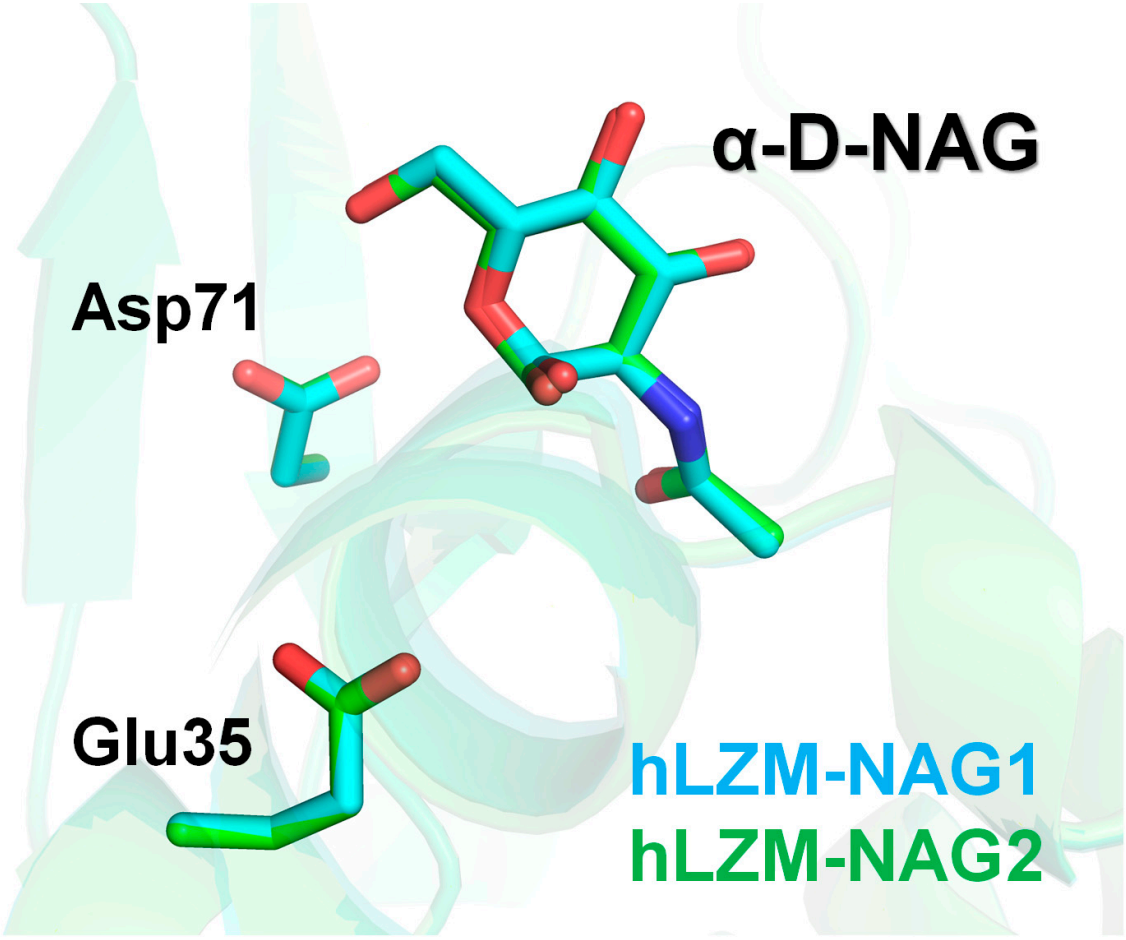
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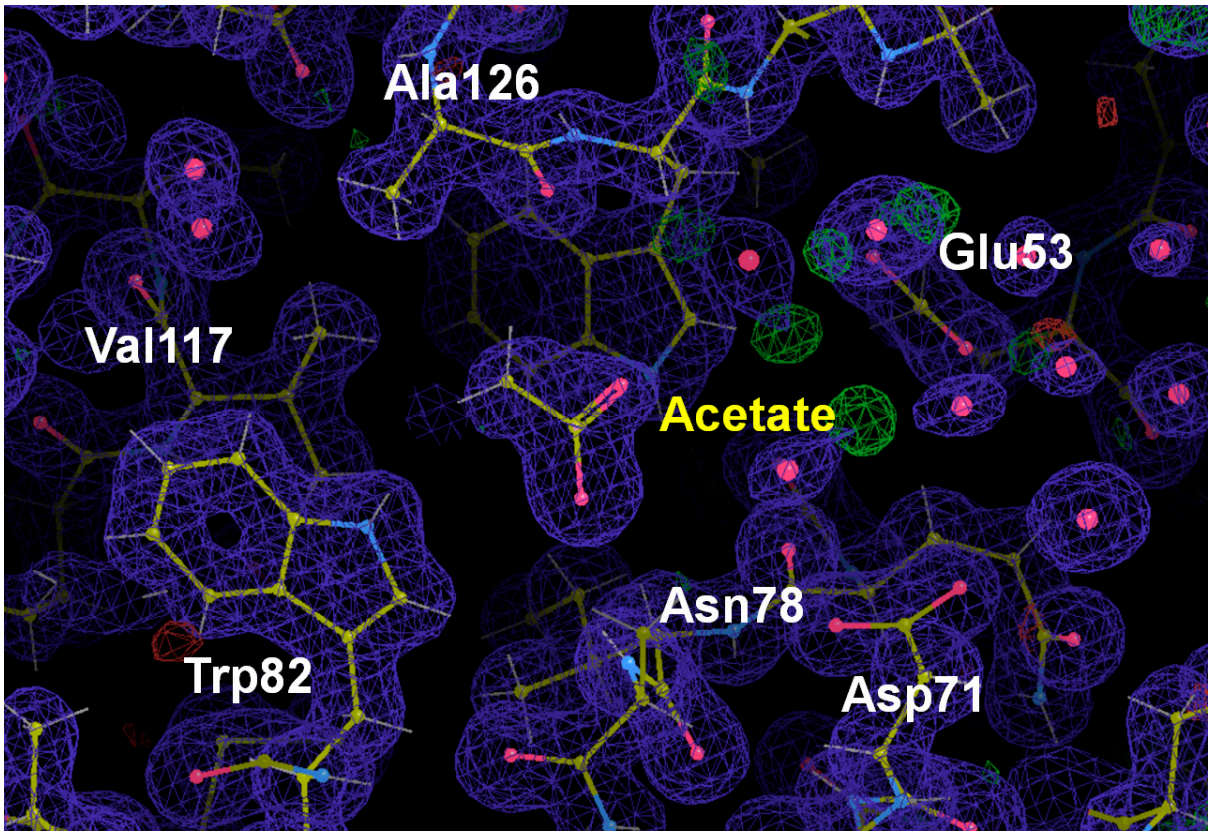
Supplementary Figure S1. 2mFo-DFc (1.0σ, grey mesh) and mFo-DFc (+3σ: green mesh, -3σ: red mesh) electron-density map of hLZM after refinement and the addition of (a) N-acetyl-α-D-glucosamine or (b) N-acetyl-β-D-glucosamine. No positive Fo-Fc electron-density map is observed for the N-acetyl-α-D-glucosamine model in hLZM, whereas a positive Fo-Fc electron-density map is observed for the N-acetyl-β-D-glucosamine model in hLZM, indicating that N-acetyl-α-D-glucosamine bound to hLZM.



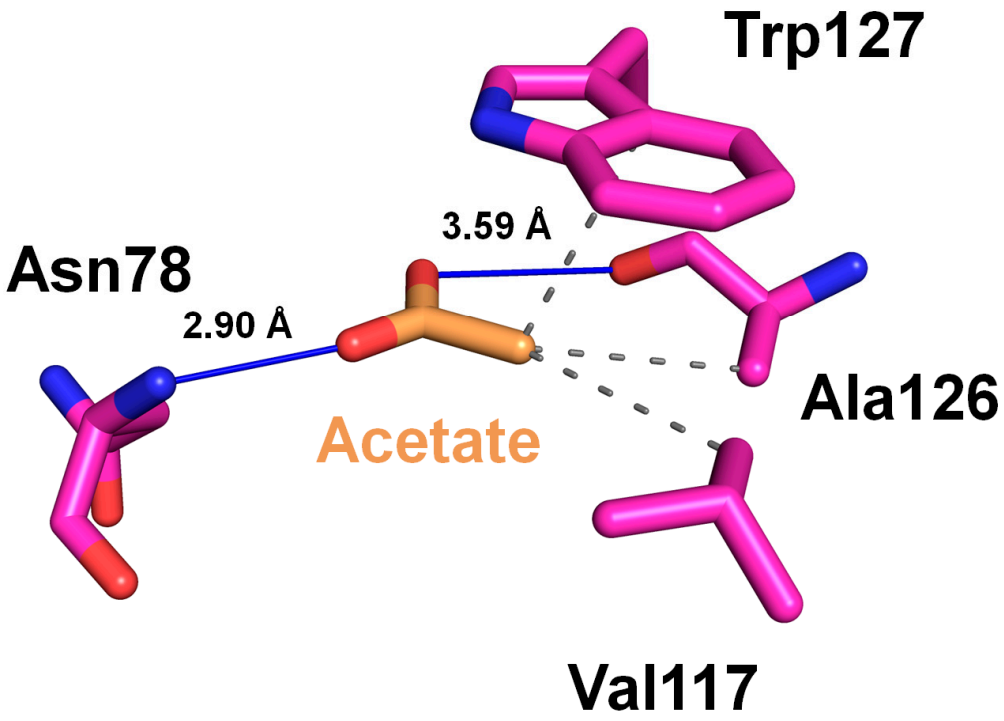
Supplementary Figure S2. 2mFo-DFc (1.0σ, grey mesh) and mFo-DFc (+3σ: green mesh, -3σ: red mesh) electron-density map of (a) hLZM-NAG1 and (b) hLZM-NAG2.



Supplementary Figure S3. Superimposition of the crystal structures of hLZM-NAG1 and hLZM-NAG2.



Supplementary Figure S4. 2mFo-DFc (1.2σ, grey mesh) and mFo-DFc (+3σ: green mesh, -3σ: red mesh) electron-density map of the acetate ion in native hLZM.



Supplementary Figure S5. Interaction between the acetate ion and native hLZM. Hydrophobic interactions and hydrogen bonds are indicated by the grey dotted lines and blue lines, respectively.