

# **Effect of Site-Specific Lysine Acetylation on Tau Binding to Microtubules: Mechanistic Insights from All-Atom Molecular Dynamics Simulation**

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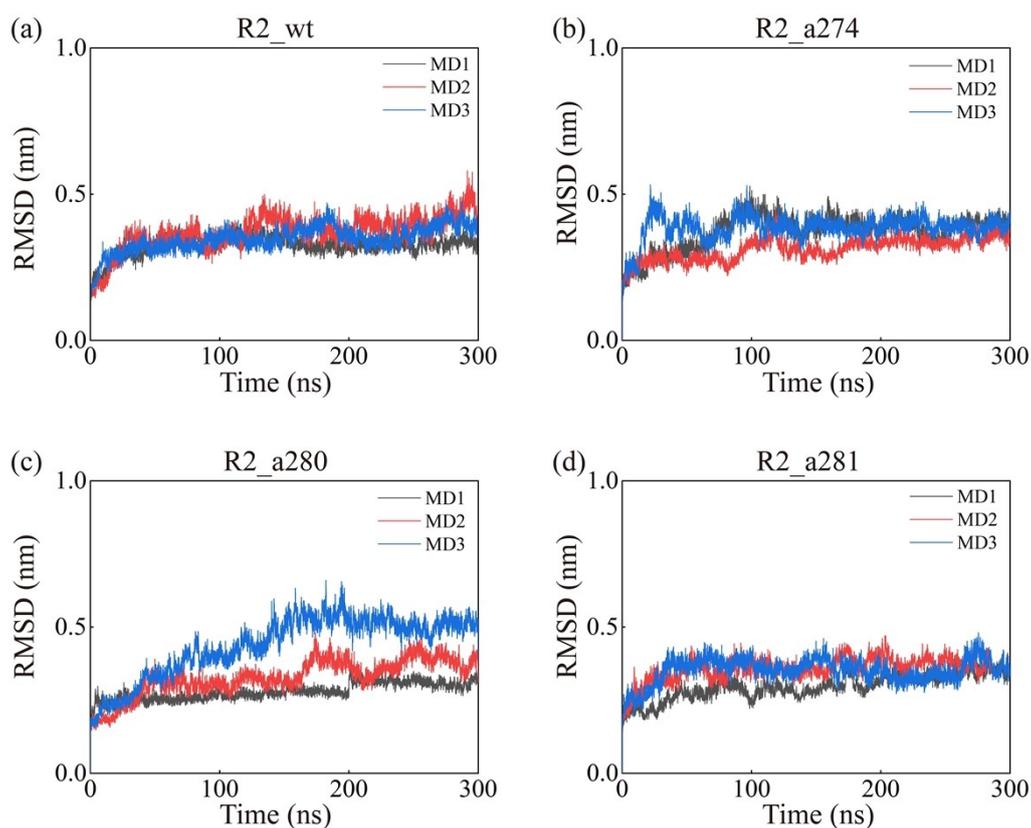
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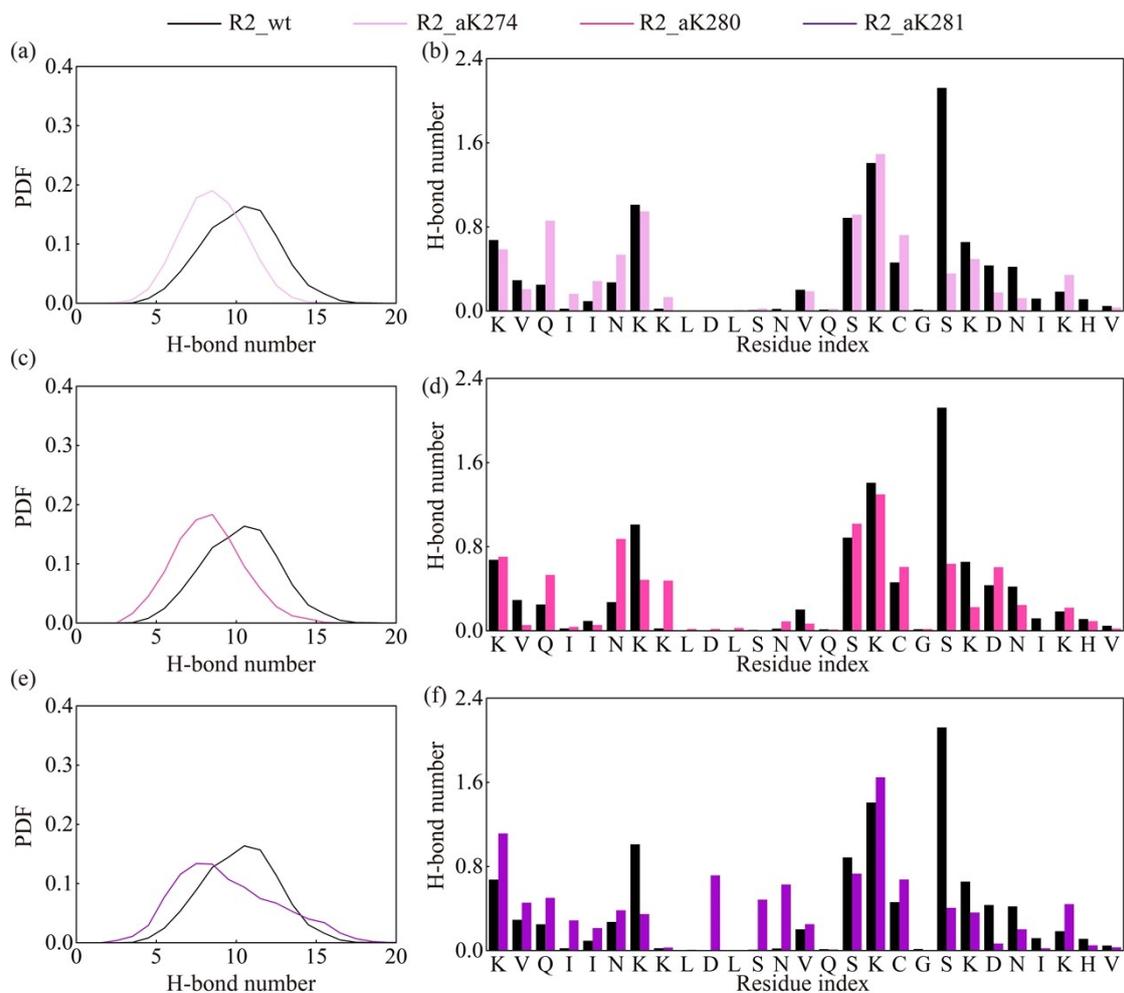
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**Table S1.** Setup details of All MD Simulations.

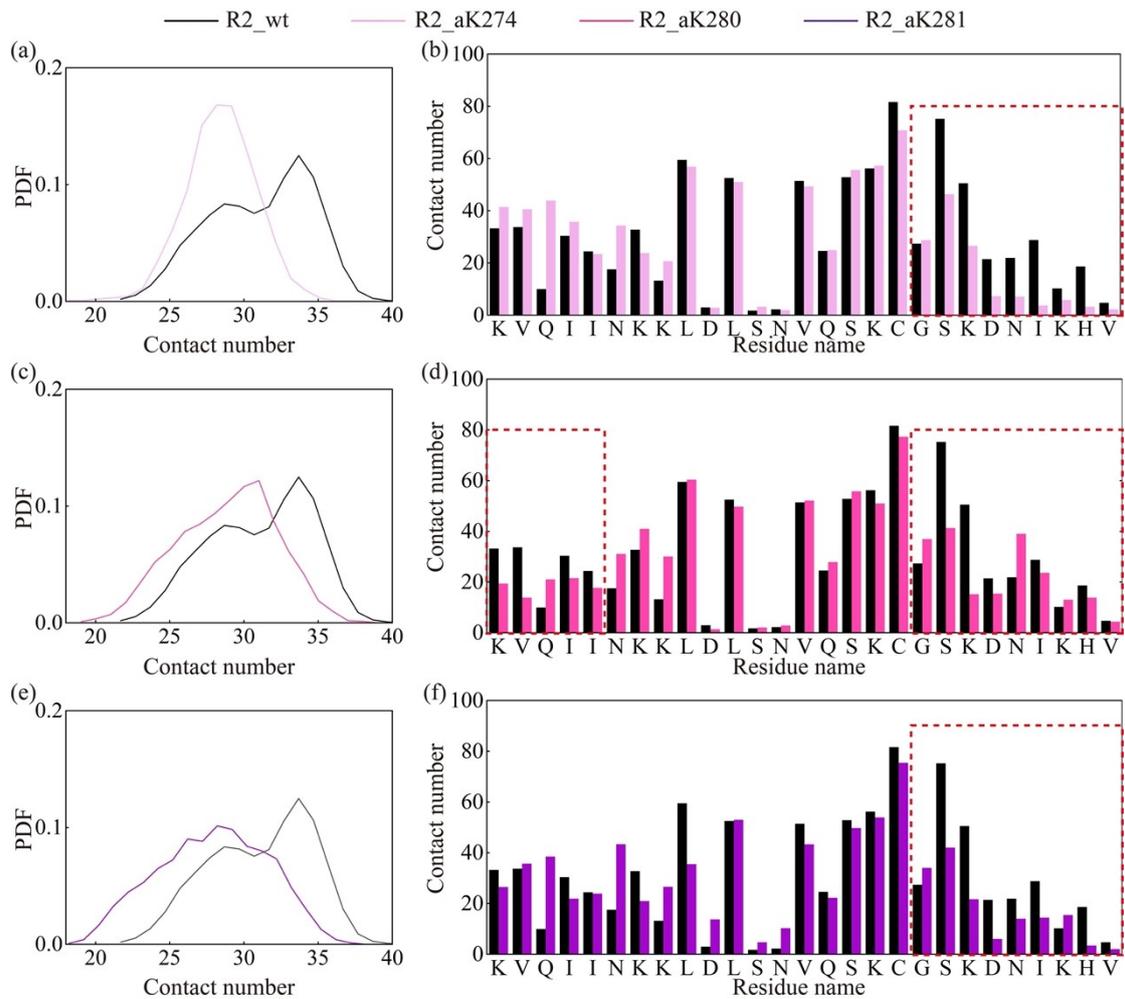
Systems	Simulation time (ns)	Number of trajectories	Box sizes (nm <sup>3</sup> )	Number of atoms
R2_wt	300	3	9.86*9.86*15.85	153728
R2_aK274	300	3	9.86*9.86*15.85	153733
R2_aK280	300	3	9.86*9.86*15.85	153736
R2_aK281	300	3	9.86*9.86*15.85	153742



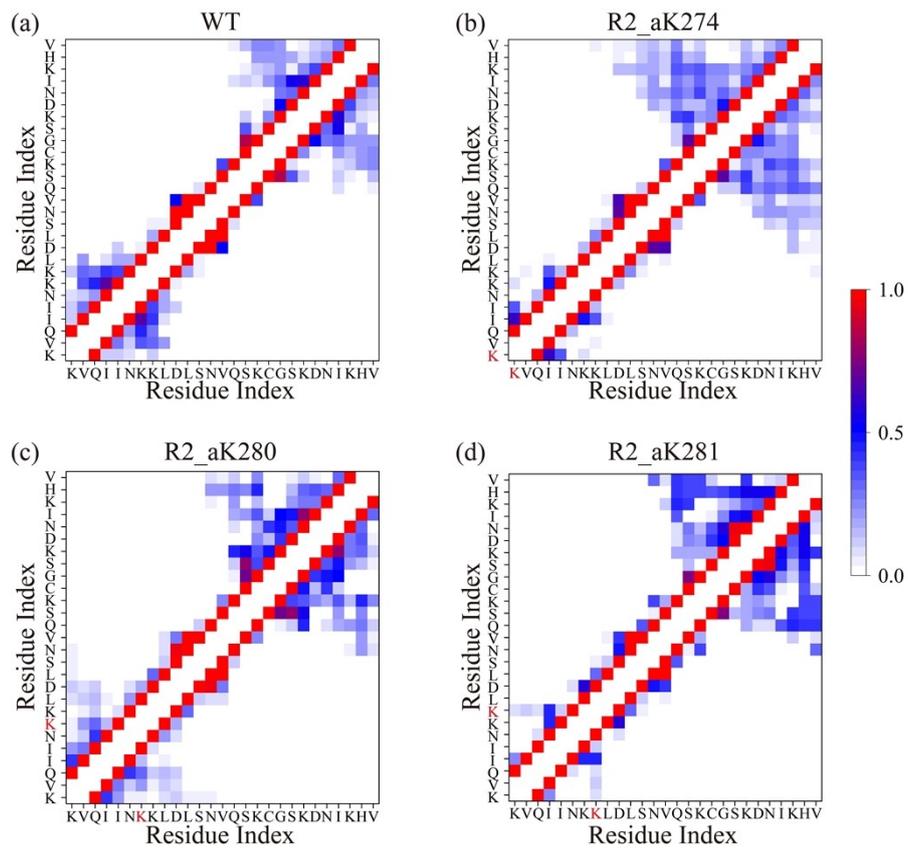
**Figure S1.** Time evolution of all-atom RMSD of the four systems (R2\_wt, R2\_aK274, R2\_aK280, and R2\_aK281), respectively.



**Figure S2.** Analysis of hydrogen bonding interactions between Tau\_R2 and microtubules. (a, c, e) Probability distribution functions of the number of hydrogen bonds formed between Tau\_R2 and microtubules in four simulation systems (R2\_wt, R2\_aK274, R2\_aK280, and R2\_aK281). (b, d, f) Residue-level hydrogen bond counts between Tau\_R2 and microtubules for each of the four systems.



**Figure S3.** Analysis of the contact between Tau\_R2 and MT. (a, c, e) PDFs of contact number between Tau\_R2 and MT in the R2\_aK274, R2\_aK280, and R2\_aK281 systems, compared to R2\_wt. (b, d, f) Contact numbers between individual residues of Tau\_R2 and MT in the corresponding systems.



**Figure S4.** Residue-residue interaction analyses. (a-d) The intrachain residue-residue contact probabilities for each simulation of the four systems, respectively