

## Regulatory interactions between APOBEC3B N- and C-terminal domains

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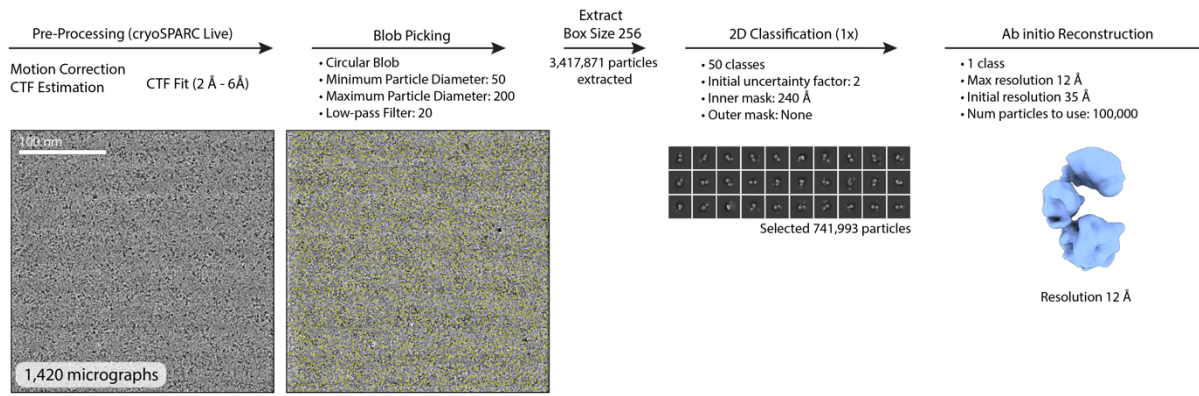
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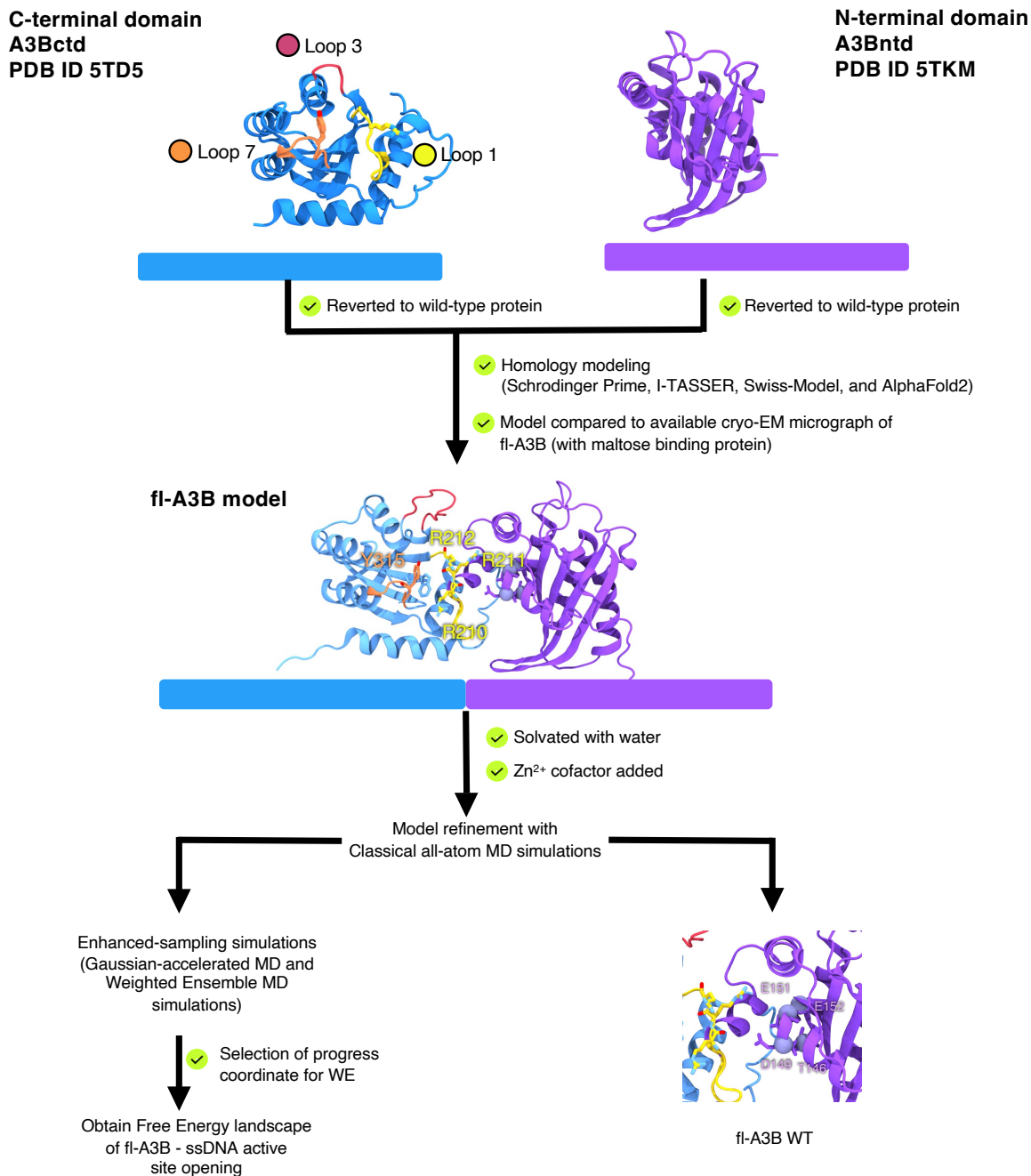
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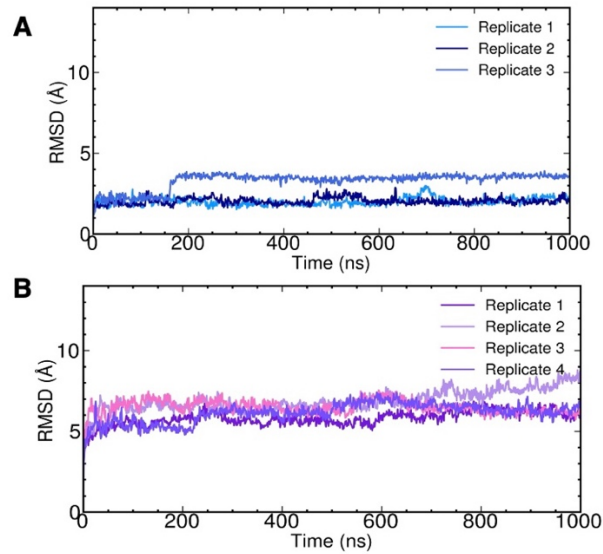
**SI Movie 2.** fl-A3B dynamics from classical MD simulations.



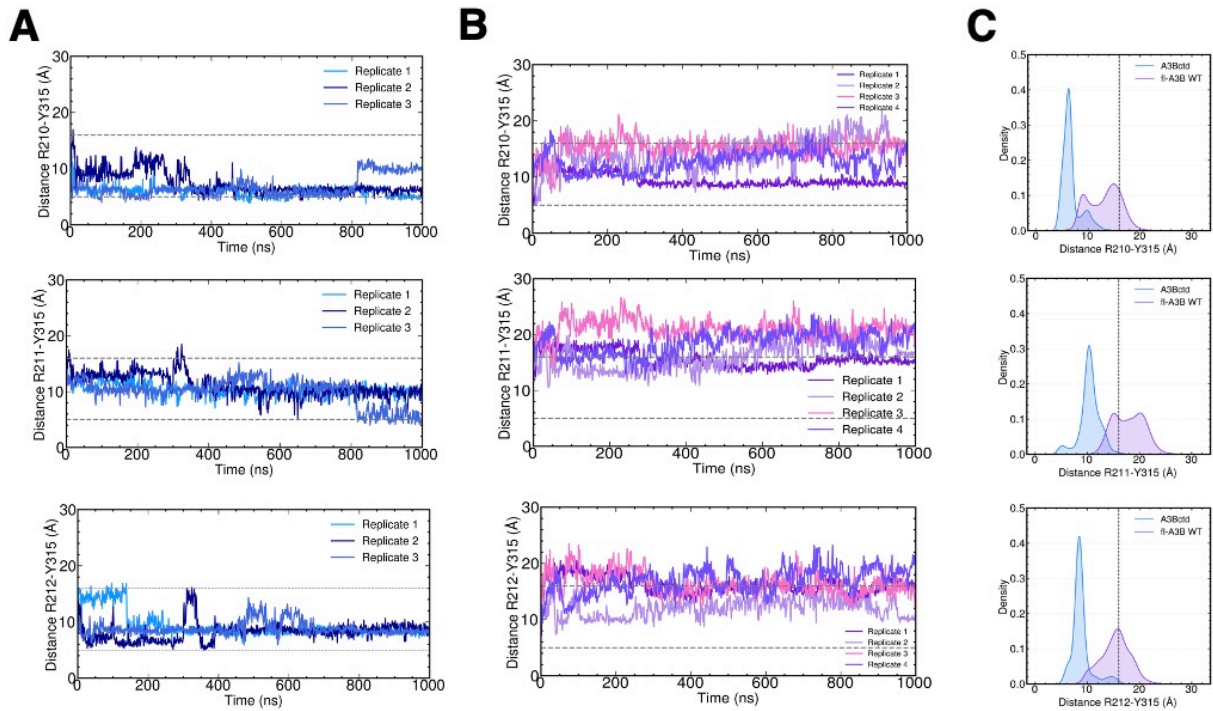
**SI Figure 1.** CryoEM data processing of the full-length APOBEC3B and maltose binding protein complex. See main text Methods section for detailed explanation of cryoEM data processing.



**SI Figure 2.** Workflow in modeling and refining the human full-length APOBEC3B (fl-A3B). Reference structures for homology modeling of fl-A3B PDB ID 5TD5 (ssDNA substrate removed)<sup>3</sup> and 5TKM have several mutations. We reverted them to the wild-type A3Bctd and A3Bntd. Models were refined with conventional all-atom MD simulations and were used for further modeling and simulations work (i.e., Gaussian accelerated and WE method MD simulations and mutations study on fl-A3B N-terminal domain residues).

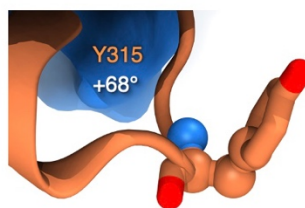
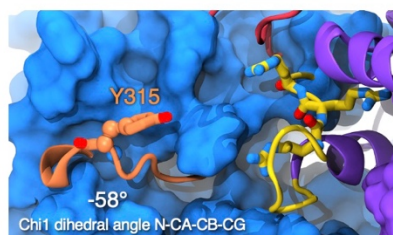


**SI Figure 3.** Protein backbone root-mean-square deviation (RMSD). (A) A3Bctd and (B) fl-A3B Wild-type.

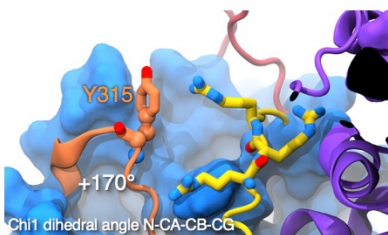
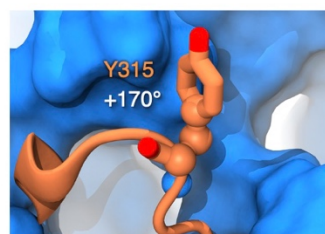
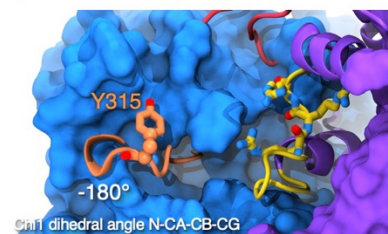


**SI Figure 4.** R210-Y315, R211-Y315, and R212-Y315 distances (A) A3Bctd; (B) fl-A3B; and (C) Kernel Density Estimates of the distances.

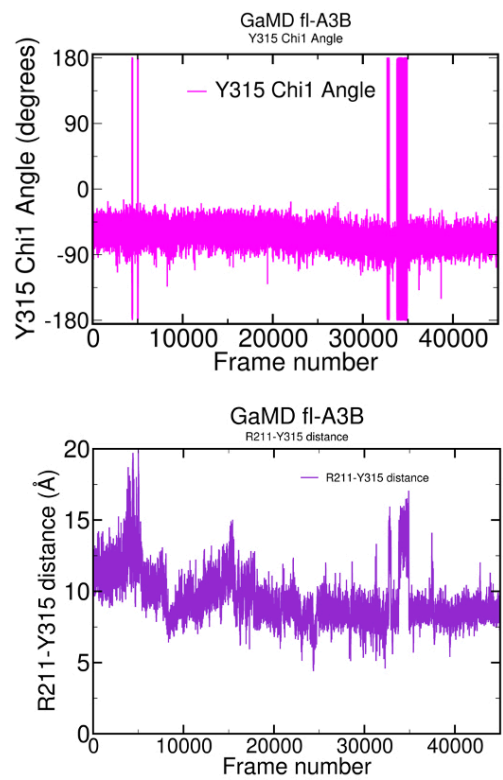
Partially-open state A3B active site



open-state A3B active site



**SI Figure 5.** Representative conformation of the Y315 Chi1 dihedral angle in a partially open and open states active site.



**SI Figure 6.** GaMD simulations of fl-A3B. Y315 Chi1 dihedral angle values (top) and R211-Y315 distance values (bottom).