## Supporting Information For

## HIV-1 Capsid Function is Regulated by Dynamics: Quantitative Atomic-Resolution Insights by Integrating Magic-Angle-Spinning NMR, QM/MM, and MD

Huilan Zhang<sup>1,2,#</sup>, Guangjin Hou<sup>1,2,#</sup>, Manman Lu<sup>1,2</sup>, Jinwoo Ahn<sup>2,3</sup>, In-Ja L. Byeon<sup>2,3</sup>, Christopher J. Langmead<sup>4</sup>, Juan R. Perilla<sup>5</sup>, Ivan Hung<sup>6</sup>, Peter L. Gor'kov<sup>6</sup>, Zhehong Gan<sup>6</sup>, William W. Brey<sup>6</sup>, David A. Case<sup>7</sup>, Klaus Schulten<sup>5</sup>, Angela M. Gronenborn<sup>2,3\*</sup>, and Tatyana Polenova<sup>1,2\*</sup>

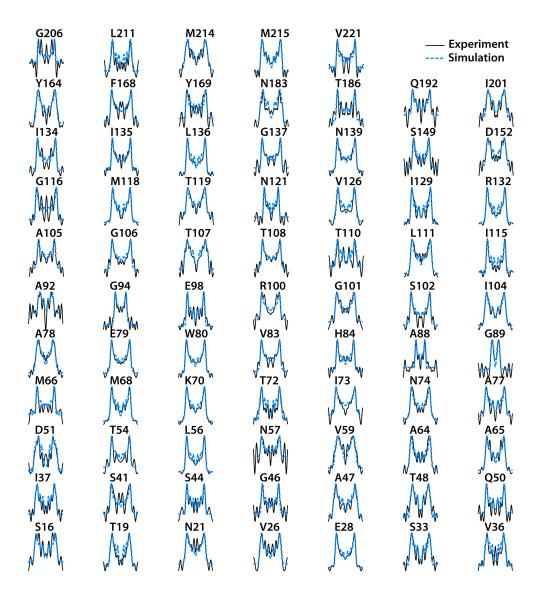
Classification: Biological Sciences-Biophysics and Computational Biology

**Keywords:** magic-angle spinning NMR, HIV-1 capsid, CA protein assemblies, HIV-AIDS, conformational dynamics, chemical shift anisotropy, quantum mechanics/molecular mechanics

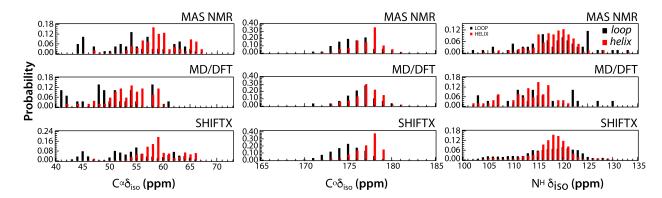
Department of Chemistry and Biochemistry, University of Delaware, Newark, Delaware 19716, United States;
Pittsburgh Center for HIV Protein Interactions, University of Pittsburgh School of Medicine, 1051 Biomedical Science Tower 3, 3501 Fifth Ave., Pittsburgh, PA 15261, United States;
Department of Structural Biology, University of Pittsburgh School of Medicine, 3501 Fifth Ave., Pittsburgh, PA 15261, United States;
Carnegie Mellon University, Gates Hillman Center, 5000 Forbes Avenue, Pittsburgh, PA, United States;
Department of Physics and Beckman Institute for Advanced Science and Technology University of Illinois at Urbana-Champaign, Urbana, Illinois 61801;
National High Magnetic Field Laboratory, Florida State University, Tallahassee, FL, 32310, United States;
Department of Chemistry and Chemical Biology, Rutgers University, 174 Frelinghuysen Road, Piscataway, NJ 08854-8087, United States

<sup>\*</sup>These authors have contributed equally

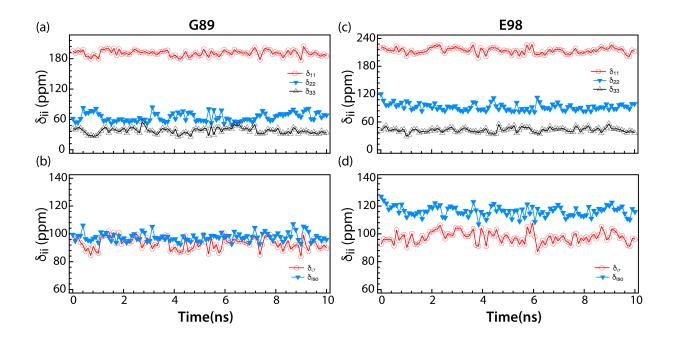
<sup>\*</sup>Corresponding authors: Tatyana Polenova, Department of Chemistry and Biochemistry, University of Delaware, Newark, DE, USA, Tel.: (302) 831-1968; Email: tpolenov@udel.edu; Angela M. Gronenborn, Department of Structural Biology, University of Pittsburgh School of Medicine, 3501 Fifth Ave., Pittsburgh, PA 15260, USA, Tel.: (412) 648-9959; Email: amg100@pitt.edu



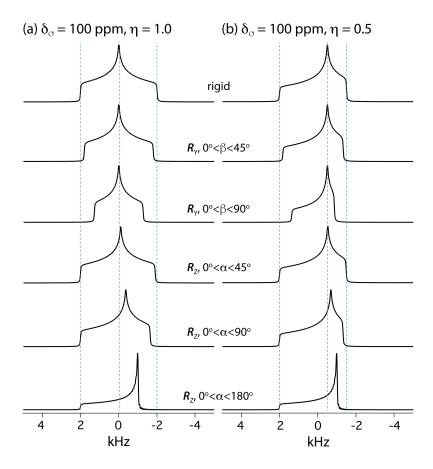
**Figure S1.** Experimental (solid black lines) and simulated (dashed blue lines)  $^{15}$ N CSA lineshapes for different residues in tubular assemblies of CA HXB2 extracted from the R8 $_1$  $^3$ -RNCSA 3D spectra, recorded at the magnetic field of 21.1 T and the MAS frequency of 14 kHz.



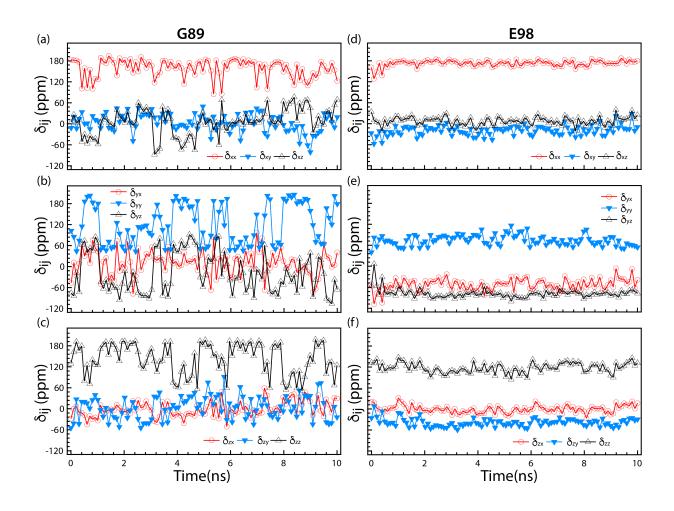
*Figure S2.* Distribution plots for the isotropic  $^{13}$ C $^{\alpha}$  (left),  $^{13}$ C $^{\circ}$  (middle), and  $^{15}$ N $^{H}$  (right) chemical shifts in HIV-1 CA assemblies. Top: experimental MAS NMR; middle, calculated from MD/DFT; bottom, calculated by SHIFTX as the averaged values over the MD trajectory. The distributions for helical regions are shown in red, for loops- in black.



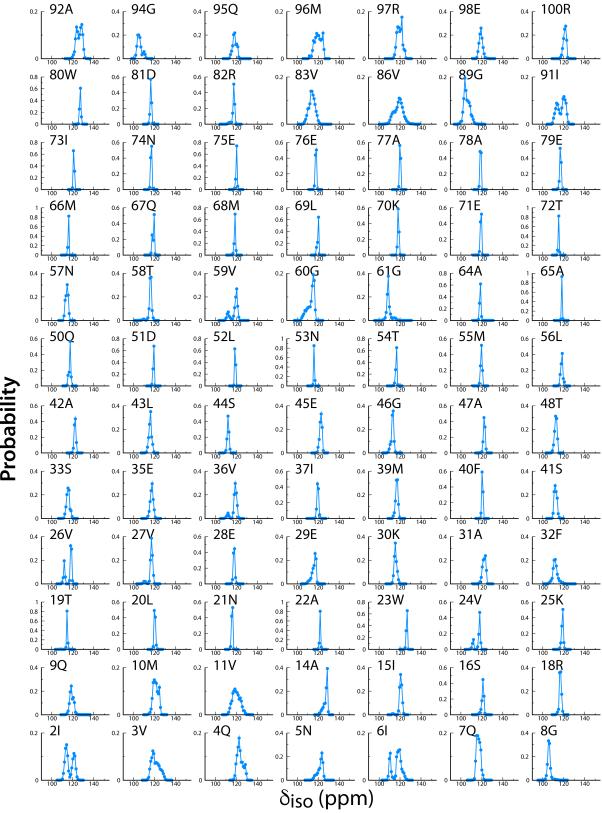
**Figure S3.** Principal components of  $^{15}N$  CSA tensor,  $\delta_{ii}$ ,  $\delta_{\sigma}$ , and  $\delta_{iso}$ , calculated along the MD trajectory, for selected CA residues: G89 (a, c) and E98 (b, d). For the calculations, 100 frames were used from the first 10 ns of the 100-ns MD trajectory.



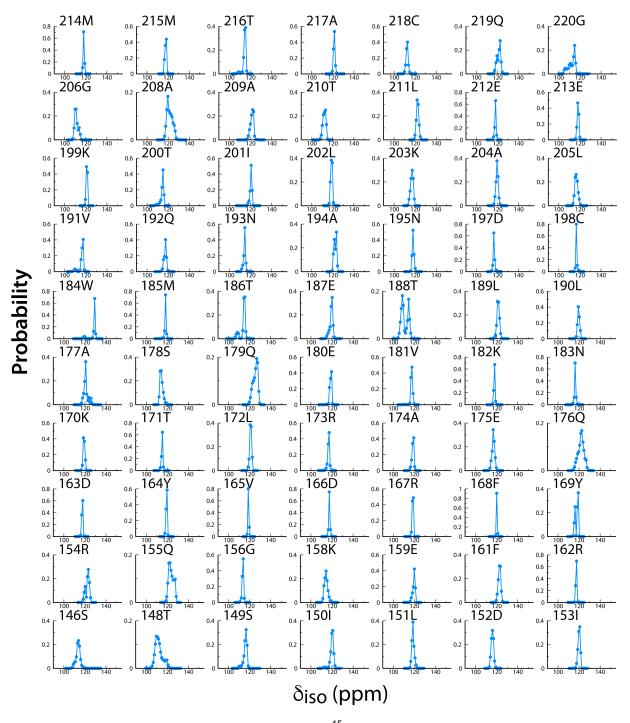
**Figure S4.** Simulated rigid and motionally reduced  $^{15}N$  CSA line shapes for the sites with the following CSA NMR parameters: (a)  $\delta_{\sigma}$  = 100 ppm and  $\eta$  = 1.0; (b)  $\delta_{\sigma}$  = 100 ppm and  $\eta$  = 0.5. The Euler angles are indicated next to each line shape.



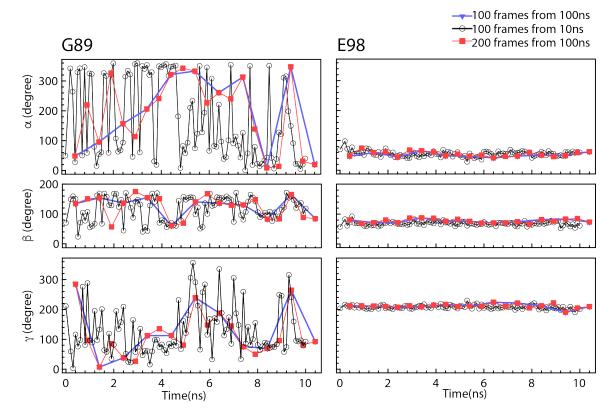
*Figure S5.* Individual components of  $^{15}$ N CSA tensor  $\delta_{ij}$  (molecular fixed frame representation), calculated along the MD trajectory, for selected CA residues: G89 (a-c) and E98 (d-f). For the calculations, 100 frames were used from the first 10 ns of the 100-ns MD trajectory.



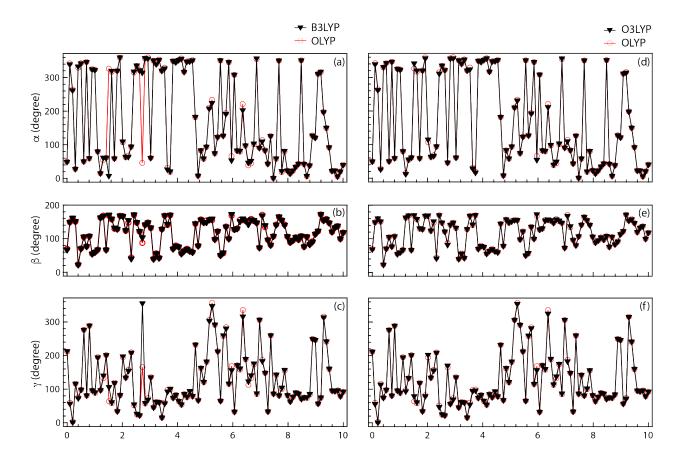
*Figure S6.* Probability distributions of <sup>15</sup>N isotropic chemical shifts of HIV-1 CA calculated by Shiftx based on 5000 frames extracted from 100 ns MD simulation.



*Figure S6.* (con'd) Probability distributions of  $^{15}$ N isotropic chemical shifts of HIV-1 CA calculated by Shiftx based on 5000 frames extracted from 100 ns MD simulation.



**Figure S7.** Euler angles of the  $^{15}N$  CSA tensors for G89 and E98 residues of CA, calculated by MD/DFT with different sampling schedules: 200 frames from 100-ns MD trajectory, red; 100 frames from 100-ns MD trajectory, blue; 100 frames from the first 10 ns of the 100-ns MD trajectory, black. The corresponding  $^{15}N$  CSA parameters for G89 are:  $\delta_\sigma$  = 28.92 ppm,  $\eta_\sigma$  = 0.11;  $\delta_\sigma$  = 23.28 ppm,  $\eta_\sigma$  = 0.10;  $\delta_\sigma$  = 23.75 ppm,  $\eta_\sigma$  = 0.12. The corresponding  $^{15}N$  CSA parameters for E98 are:  $\delta_\sigma$  = 93.83 ppm,  $\eta_\sigma$  = 0.52;  $\delta_\sigma$  = 93.00 ppm,  $\eta_\sigma$  = 0.53;  $\delta_\sigma$  = 92.94 ppm,  $\eta_\sigma$  = 0.54.



**Figure S8.** Euler angles of the <sup>15</sup>N CSA tensors for G89 residue in the molecular frame along the MD trajectory, calculated using (a-c) B3LYP and OLYP functionals (black and red symbols, respectively), and (d-f) O3LYP and OLYP functionals (black and red symbols, respectively). The angles were calculated using  $\delta_{\sigma}$  = 25.63, 23.75, and 24.66 ppm for B3LYP, OLYP, and O3LYP, respectively. Note that the differences are small for  $\delta_{\sigma}$  computed with the three functionals. For the calculations, 100 frames were used from the first 10 ns of the 100-ns MD trajectory.