## Protecting High Energy Barriers: A New Equation to Regulate Boost Energy in Accelerated Molecular Dynamics Simulations

William Sinko<sup>l,†\*</sup>, César Augusto F. de Oliveira<sup>2,3,†\*</sup>, Levi C. T. Pierce<sup>2</sup> and J. Andrew McCammon<sup>1,2,3</sup>

<sup>1</sup>Biomedical Sciences Program, University of California San Diego, La Jolla, California 92093-0365.

<sup>2</sup>Department of Chemistry & Biochemistry, Department of Pharmacology, and NSF Center for Theoretical Biological Physics, University of California San Diego, La Jolla, California 92093-0365.

<sup>3</sup>Howard Hughes Medical Institute, University of California San Diego, La Jolla, CA 92093-0365.

*† These Authors contributed equally.* 

\* Corresponding Author

AUTHOR EMAIL ADDRESS: wsinko@ucsd.edu; cesar@mccammon.ucsd.edu

CORRESPONDING AUTHOR FOOTNOTE William Sinko and César Augusto F. de Oliveira Department of Chemistry & Biochemistry University of California San Diego 9500 Gilman Drive, Mail Code 0365 La Jolla, CA 92093-0365 858-822-1083 (Office) 858-534-4974 (Fax)

TITLE RUNNING HEAD: New Boost Equation for Accelerated MD



**Figure S1:** Decalanine Phi( $\Phi$ )-Psi( $\Psi$ ) angles distribution obtained from aMD simulations with  $\Delta V^c$ . Parameters were set to E<sub>1</sub>=74, E<sub>2</sub>= E<sub>1</sub>+35,  $\alpha_2$ =5 and  $\alpha_1$ =15. All values are in kcal/mol.



**Figure S2:** Decalinine root mean square (RMS) deviation from  $\alpha$ -helix conformation calculated along: A) 350ns of cMD and 50 ns of aMD simulations, and B) the first 50ns of simulations displayed in (A). Solid lines correspond to MD (black) and aMD with parameters set to E<sub>1</sub>=74,  $\alpha_2$ =5 (all aMD simulations) E<sub>2</sub>= E<sub>1</sub>+25 and  $\alpha_1$ =30 (cyan); E<sub>2</sub>= E<sub>1</sub>+25 and  $\alpha_1$ =15 (red); E<sub>2</sub>= E<sub>1</sub>+35 and  $\alpha_1$ =15 (green). All values are in kcal/mol.