Supporting Information for: Conformation and Domain Movement Analysis of Human Matrix Metalloproteinase-2: role of associated Zn²⁺ and Ca²⁺ ions.

Leah Voit-Ostricki¹, Sándor Lovas², and Charles R. Watts^{1,3},*

- ¹ Department of Neurosurgery, Mayo Clinic Health System-Franciscan Healthcare in La Crosse, Wisconsin, 54601, USA; voitost.leah@gmail.com
- Department of Biomedical Sciences, Creighton University, Omaha, Nebraska, 68178, USA; SandorLovas@creighton.edu
- ³ Department of Neurologic Surgery, Mayo Clinic, Rochester, Minnesota, 55905, USA; charles.watts@parknicollet.com
- * Correspondence: charles.watts@parknicollet.com; Tel.: +1-952-993-3200, Fax: +1-952-993-7407 Received: date; Accepted: date; Published: date

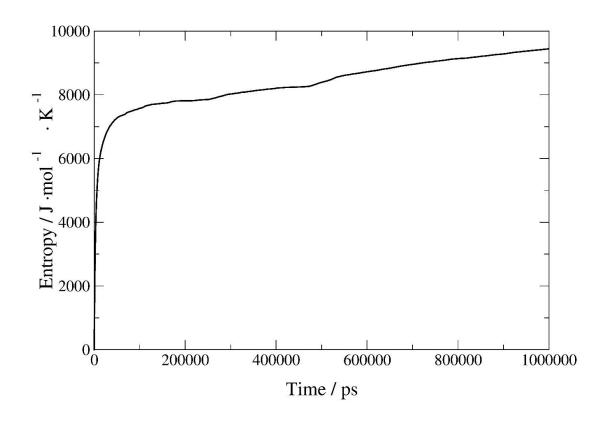


Figure S1. Configurational entropy of MMP-2 (calculated from the $C\alpha$ -trace, Zn^{2+} and Ca^{2+} coordinates) as a function of time, demonstrating the 200000 ps necessary for system equilibration.

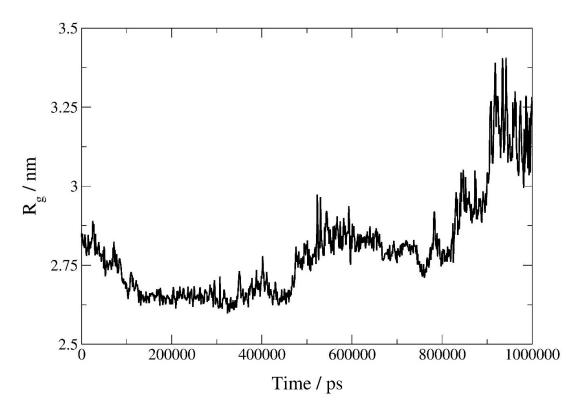


Figure S2. The radius of gyration $(R_{\rm g})$ as a function of time.

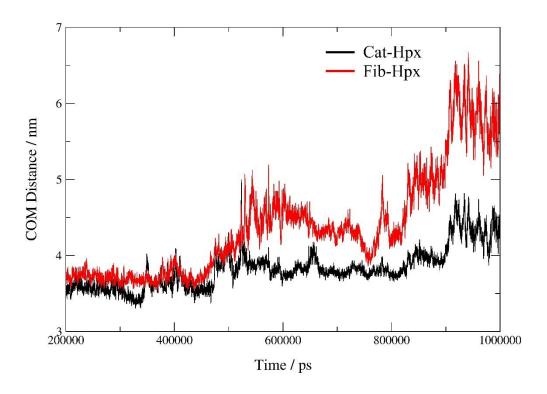


Figure S3. The Center of mass (COM) distance as a function of time between the Cat and Hpx (black) and Fib and Hpx (red) domains, respectively.

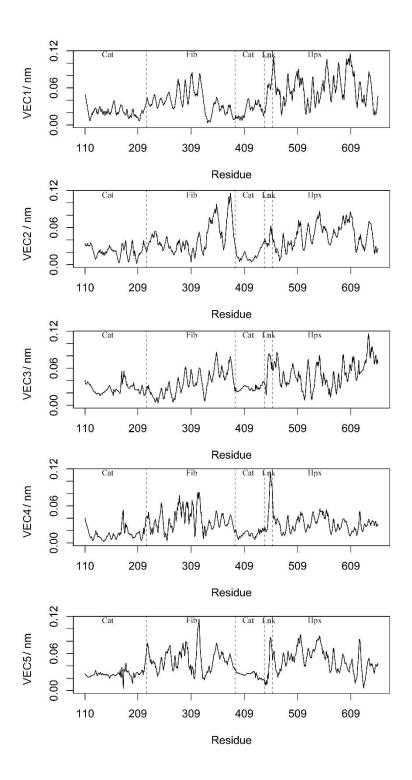


Figure S4. Cα-trace RMSF plots of the top 5 eigenvectors.