

MEETING ABSTRACTS

PROTEIN DYNAMICS OF PHOSPHOTRIESTERASE: TWO CATIONS REQUIRED FOR ENZYME CATALYSIS

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To investigate how protein dynamics facilitates substrate entering and product exiting the phosphotriesterase active site, over 60 distinct, independent, unrestricted, unbiased, isobaric–isothermal, microsecond molecular dynamics simulations of zinc-containing phosphotriesterase in complex with a substrate analog¹ were performed using the second-generation cationic dummy atom model for the zinc divalent cation, forcefield FF12MC², and PMEMD of AMBER 16 with a periodic boundary condition at 1 atm and 277 K, 300 K, and 340 K. In-depth conformational analysis of these simulations with an aggregated simulation time of over 76 microseconds revealed atomic and dynamic details on the phosphtriesterase catalysis and its requirement of two cations, which offers insight into re-engineering of phosphotriesterase to develop an improved scavenger against phosphorous-containing inhibitors of acetylcholinesterase.

Keywords: phosphotriesterase; protein dynamics; zinc; scavenger; protein engineering

References

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- 2. Pang, Y.-P. FF12MC: a revised AMBER forcefield and new protein simulation protocol. *Proteins* **84**, 1490–1516 (2016).