George A. PANTELOPULOS Laboratory of Chemical Physics NIH-NIDDK Bethesda, MD, USA

 $Email: \verb"george.pantelopulos@nih.gov;" gpantelopulos@gmail.com" \\$

Education

| 2015-2022 | Ph.D of Chemistry. Boston University, USA. |
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| | m Graduation: 2022/1/25 |
| 2013-2015 | B.S. OF CHEMISTRY. Temple University, Philadelphia, USA. |
| | Graduation: 2015/5/8 |
| 2011-2013 | A.S. OF SCIENCE. Community College of Philadelphia, Philadelphia, USA. |
| | Graduation: 2013/5/4 |

Honors

| 2019 | LICHTIN AWARD FOR EXCELLENCE IN RESEARCH. |
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| 2018 | RIKEN SHORT-TERM INTERNATIONAL PROGRAM ASSOCIATE. |
| 2017 | NSF GROW/JSPS Fellow. |
| 2015-2020 | NSF Graduate Research Fellowship. |
| 2015 | PECO Scholar, <i>PECO</i> . |
| 2015 | FEYNMAN MEMORIAL SCHOLAR, Temple University. |
| 2014 | DIAMOND SCHOLAR SUMMER FELLOW, Temple University. |
| 2013 | NSF RESEARCH EXPERIENCE FOR UNDERGRADUATES, Boston University. |
| | |

Service and Teaching

| 2018-2019 | Teaching Fellow, Boston University $\mathrm{CH225}$ - Mathematical Me- |
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| | THODS FOR CHEMISTS. |
| 2016-2018 | Graduate Fellowships Mentorship and Workshops, Boston Univer- |
| | SITY CHEMISTRY DEPARTMENT. |
| 2015-2016 | WRITING MENTOR, BOSTON UNIVERSITY CHEMICAL WRITING PROGRAM. |
| 2015-2016 | HIGH SCHOOL SCIENCE OUTREACH INSTRUCTOR, BOSTON UNIVERSITY WO- |
| | MEN IN CHEMISTRY. |
| 2014-2015 | SCIENCE INSTRUCTOR, TEENSHARP. |
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Presentations 2015-

| 2023 | "PARAMETERIZATION OF A SEQUENCE-SPECIFIC COARSE-GRAINED COLLAGEN |
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| າດາາ | "Similiating Atomistic Structure of Collacen · Force Field Cor |
| 2022 | PECTIONS AND REVOND." Protein Folding Dynamics Cordon Research Confe- |
| | rence (Poster) |
| 2022 | "ATOMISTIC STRUCTURE OF COLLACEN · VALIDATION OF ATOMISTIC FORCE |
| 2022 | FIELDS " Roston University Physical Chemistry Lecture Series (Talk) |
| 0000 | "Developing a guerically perined coapse grained room for the form |
| 2022 | DEVELOPING A CHEMICALLY-DEFINED COARSE-GRAINED FORCE FIELD FOR |
| | "INTERNAL AND A DISORDERED MEMORANE PROTEIN ANYLOID RECURSOR |
| | INTRINSICALLY DISORDERED MEMBRANE PROTEIN AMYLOID PRECORSOR |
| | TION WITH CHOLDERTEDOL " Desifichers (Virtual Talk) |
| 2020 | "EVELOPING ADD COMPLEXES IN LIDE DU AVERS AND THEIR DOLE IN |
| 2020 | EXPLORING APP-C99 COMPLEXES IN LIPID BILAYERS AND THEIR ROLE IN |
| 2010 | ALZHEIMER'S DISEASE, ACS Annual Meeting, Philadelphia (Virtual Poster). |
| 2019 | PHASE SEPARATIONS IN LIPID MEMBRANES, WHAT THEY HAVE TO DO WITH |
| | PROTEINS, AND RECENT DEVELOPMENTS IN MD-BASED MODELING, <i>Doston</i> |
| 2010 | University Physical Chemistry Lecture Series (Talk). |
| 2019 | "PROBING THE ROLES OF MEMBRANE AND CHOLESTEROL ON A BIOGENESIS |
| 0010 | AND TOXICITY," ACS Annual Meeting, Orianao (Taik). |
| 2018 | UNDERSTANDING AN INTRINSICALLY DISORDERED MEMBRANE PROTEIN |
| | IN ALZHEIMER'S DISEASE VIA MOLECULAR SIMULATION," RIKEN Summer |
| | School (Poster); Computational Biophysics at the Molecular and Meso Scales, |
| 2017 | IUISE Vietnam (Iaik). |
| 2017 | STRUCTURE OF APP-099 1-99 AND IMPLICATIONS FOR ITS ROLE IN AMY- |
| 9017 | LOIDOGENESIS, <i>Kyolo University (101k)</i> . "Pole of cholesterol in ternary lind, Memorane phase serar atton |
| 2017 | ODGEDUED VIA COADGE ODAINED GIVIN ATIONS" American Theoretical Cha |
| | mietry Conference (Poster): Jananese Bionhusical Society (Poster) |
| 2017 | "TEMPERING IN OPENMM AND CENESIS" Temple University Comment |
| | Tempering in Opennimi and Genesis, Temple University Current |
| 2017 | "Contract investigation of finite size and choicesterol references in the |
| 2017 | DID DOMAIN FORMATION " RIKEN Wake shi (Talk): Roston University Cha |
| | mietry Student Craduate Seminar Series Nacova University ICER Seminar |
| | Series (Talk) |
| 2016 | FUELORING DUAGE SEDADATION AND DOMAIN FORMATION IN LIDID DUAVEDS |
| 2010 | THOUCH MOLECULAR SIMULATION " Boston University Craduate Research |
| | Sumnovium · ACS National Meeting Philadelphia (Poster) |
| | "Examining the concornational pynamics of the N terminal pecion |
| 2015 | DE MDM2 USING MADROV STATE MODEL ADDROACHES "ACS National Macting |
| | Boston (Poston) |
| | "Microsecond simulations of MDM2 and its complex with p52 vield |
| 2010 | MIGROSECOND SIMULATIONS OF MDM2 AND 115 COMPLEX WITH P35 YIELD |
| | Tomala University Undergraduate Research Forum and Creative Works Commo |
| | sium (Talk) |
| | sum (10m). |

Publications

20. "Characterizing the transmembrane domains of ADAM10 and BACE1 and the impact of membrane composition" C. Abraham, L. Xu, **G.A. Pantelopulos**, J.E. Straub, *Biophys. J.* Submitted (2023)

19. "MolPainter : A Tool for Painting and Solvating Layered Molecular Systems" **G.A. Pantelopulos**, A. Liberatore, *J. Open Source Softw.* Accepted (2023)

18. "Formation of extramembrane β -strands controls dimerization of transmembrane helices in amyloid precursor protein C99" G.A. Pantelopulos, D. Matsuoka, J.M. Hutchison, C.R. Sanders, Y. Sugita, J.E. Straub, D. Thirumalai, *Proc. Natl. Acad. Sci. USA* 119, 52 (2023)

"Efficient calculation of the free energy for protein partitioning using restraining potentials," S. Kwon, G.A. Pantelopulos, J.E. Straub, *Biophys. J.* 122, 1 (2023)

"Finite-size effects and optimal system sizes in simulations of surfactant micelle self-assembly," J. Harris,
 G.A. Pantelopulos, J.E. Straub, J. Phys. Chem. B 19, 125 (2021)

"Direct Observation of Cholesterol Dimers and Tetramers in Lipid Bilayers," M.R. Elkins, A. Bandara, G.A. Pantelopulos, J.E. Straub, M. Hong, J. Phys. Chem. B 7, 125 (2021)

14. "Impact of Cholesterol Concentration and Lipid Phase on Structure and Fluctuation of Amyloid Precursor Protein," G.A. Pantelopulos, A. Panahi, J.E. Straub, J. Phys. Chem. B 45, 124, (2020)

13. "Bicelles Rich in both Sphingolipids and Cholesterol and Their Use in Studies of Membrane Proteins," J. Hutchinson, K. Shih, H. Scheidt, S. Fantin, G.A. Pantelopulos, H. Harrington, K. Mittendorf, S. Qian, R. Stein, S. Collier, M. Chambers, J. Kastaras, M. Voehler, B. Ruotolo, D. Huster, R. McFeeters, J. Straub, M. Neih, C. Sanders J. Am. Chem. Soc., 29, 142 (2020)

"Exploring the impact of line tension on the spatial localization of protein in phase-separated lipid bilayers,"
 A. Bandara, A. Panahi, G.A. Pantelopulos, T. Nagai, J. E. Straub, J. Phys. Chem. B, 20, 204702 (2019)

"Aerosol-OT Surfactant Forms Stable Reverse Micelles in Aploar Solvent in the Absence of Water," R. Urano,
 G.A. Pantelopulos, J. E. Straub, J. Chem. Phys. 14, 149 (2019).

 "Structural Role of Cholesterol in Complex Lipid Bilayer Phases Observed via MD Simulation," G.A. Pantelopulos, J. E. Straub, *Biophys. J.* 115, 2167-2178 (2018).

"Characterization of dynamics and mechanism in the self-assembly of AOT reverse micelles," R. Urano, G.A. Pantelopulos, S. Song, J. E. Straub, J. Chem. Phys. 14, 144901 (2018).

8. "Structure of APP-C99₁₋₉₉ and Implications for Role of Extra-Membrane Domains in Function and Oligomerization," **G.A. Pantelopulos**, J. E. Straub, D. Thirumalai, Y. Sugita, *Biochim. Biophys. Acta - Biomembranes* **1860**, 1698-1708 (2018).

7. "Critical size dependence of domain formation observed in coarse-grained simulations of bilayers composed of ternary lipid mixtures," G.A. Pantelopulos, T. Nagai, A. Bandara, A. Panahi, J. E. Straub, *J. Chem. Phys.* 147 095101 (2017).

6. "Bridging microscopic and macroscopic mechanisms of p53-MDM2 binding using molecular simulations and kinetic network models," G. Zhou, G.A. Pantelopulos, S. Mukherjee, V. Voelz, *Biophys. J.* 113, 785-793 (2017).
5. "Exploring the structure and stability of cholesterol dimer formation in multicomponent lipid bilayers," A. Bandara, A. Panahi, G.A. Pantelopulos, J.E. Straub *J. Comp. Chem.* 38, 1479-1488 (2016).

4. "Specific binding of cholesterol to C99 domain of Amyloid Precursor Protein depends critically on charge state of protein," A. Panahi, A. Bandara, G.A. Pantelopulos, L. Dominguez and J.E. Straub, *J. Phys. Chem. Lett.* 7, 3535-3541 (2016).

3. "On the use of mass scaling for stable and efficient simulated tempering with molecular dynamics," T. Nagai,
 G.A. Pantelopulos, T. Takahashi, J.E. Straub J. Comp. Chem. 37 2017-2028 (2016).

2. "Markov models of the apo-MDM2 lid region reveal diffuse yet two-state binding dynamics and receptor poses for computational docking," S. Mukherjee, G.A. Pantelopulos, V.A. Voelz *Sci. Rep.* 6 31631 (2016).

1. "Microsecond simulations of mdm2 and its complex with p53 yield insight into force field accuracy and conformational dynamics," G.A. Pantelopulos, S. Mukherjee, V.A. Voelz, *Proteins* 83 1665-1676 (2015).