George A. Pantelopulos
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1991 May 28 Birthdate
USA Nationality
Single with no children
Graduate Student

Education

2015-Current	Ph.D of Chemistry. *Boston University, USA.* Expected Graduation : 2019/5/19
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

2017	NSF GROW/JSPS Fellow.
2015-Current	NSF Graduate Research Fellowship.
2015	PECO Scholar.
2015	Feynman Memorial Scholar.
2014-2015	Undergraduate Research Fellow, *Temple University.*
2014	Diamond Scholar Summer Fellow, *Temple University.*
2013	Hellenic University Club Scholar.
2013	NSF Research Experience for Undergraduates, *Boston University.*
2013	AHEPA Scholar.
2013	Community College of Philadelphia Volunteer Service Award.

Service

2015	Writing Mentor, Boston University Chemical Writing Program.
2015-2016	High School Science Outreach Instructor, Boston University Women in Chemistry.
2014-2015	Science Instructor, TeenSHARP.
2013	Chemistry Tutor, *Community College of Philadelphia.*

Extracurricular Training

2017	Fronteirs in Computational Biophysics and Biochemistry, *RIKEN, Japan.*
2016	Erice School : Exploring and Quantifying Rough Free Energy Landscapes, *International School of Statistical Physics, Ettore Majorana Foundation and Centre for Scientific Culture, Erice, Sicily, Italy.*
2015	Alan Alda Communicating Science Workshop, *Boston University, USA.*
2015	School on Molecular Dynamics and Enhanced Sampling Methods, *Institute for Computational Molecular Science, Temple University, USA.*

Presentations

2017	Poster : "Tempering in OpenMM and GENESIS," *Temple Univerity; Current trends in molecular dynamics software design*.
2017	Talk : "Critical investigation of finite size and cholesterol effects in lipid domain formation," *RIKEN, Japan; Boston University Chemistry Graduate Student Seminar Series*.
2016	Poster : "Exploring phase separation and domain formation in lipid bilayers through molecular simulation," *Boston University Graduate Research Symposium; ACS 252nd National Meeting*.
2015	Poster : "Examining the conformational dynamics of the N-terminal region of mdm2 using markov state model approaches," *ACS 250th National Meeting*.
2015	Talk : "Microsecond simulations of mdm2 and its complex with p53 yield insight into force field accuracy and conformational dynamics," *Temple University Undergraduate Research Forum and Creative Works Symposium*.
2014-2015	Poster : "Microsecond simulations of mdm2 and its complex with p53 yield insight into force field accuracy and conformational dynamics," *ACS Philadelphia Younger Chemists Committee Conference; Emory STEM Research Symposium*.
2013-2014	Poster : "Molecular Dynamics Simulations of the p53-MDM2 Binding Interface," *ACS Philadelphia Younger Chemists Committee Conference; ACS 248th National Meeting*.

Publications

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, *Submitted* (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, *Submitted* (2016).

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.* (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.* **27** 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).