

Margaret E. Johnson

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Education:

University of California, Berkeley 2004-2009
Ph.D in Bioengineering, Thesis Adviser: Teresa Head-Gordon
Thesis title: *Understanding the interplay of structure and dynamics in liquids using coarse-grained models and experiment*

Columbia University 2000-2004
B.S. in Applied Math *Magna Cum Laude*
Minor in Bioengineering

Professional Experience:

Assistant Professor, Department of Biophysics, Johns Hopkins University. 2013-Present

National Institutes of Health (NIH) 2009-2013
Postdoctoral Researcher, Laboratory of Chemical Physics. Research Adviser: Dr. Gerhard Hummer

Research Support:

Current:
NIH R00 Pathway to Independence Award R00GM098371 *Modeling the nucleation of clathrin coated vesicles at the membrane.* \$249,000/year. 2013-2016

Prior:
NIH K99 Pathway to Independence Award: *Modeling the nucleation of clathrin coated vesicles at the membrane.* 2011-2013

Publications:

Holland, D.O., Shapiro, B.H., Xue, P., & **Johnson, M.E.*** Positive selection for scale-free protein networks from motifs in protein binding interface networks. *In preparation* (2016).

Yogurtcu, O.N. & **Johnson, M.E.*** Theory of bi-molecular association dynamics in 2D for accurate model and experimental parameterization of binding rates. *J. Chem. Phys.* **143**, 084117 (2015).

Johnson, M.E.* & Hummer, G. Free propagator reweighting integrator for single-particle dynamics in reaction-diffusion models of heterogeneous protein-protein interaction systems. *Phys. Rev. X* **4**, 031037 (2014). PMC4440698, PMID: 26005592.

Johnson, M.E. & Hummer, G. Evolutionary pressure on the topology of protein interface interaction networks. *J. Phys. Chem. B* **117**, 13098-13106 (2013). PMC3808520 PMID: 23701316

Johnson, M.E.* & Hummer, G. Interface resolved network of protein-protein interactions. *PLoS Comput Biol.* **9**, e1003065 (2013). PMC3656101 PMID: 23701316

Johnson, M.E. & Hummer, G. Characterization of a Dynamic string method for the construction of transition pathways in molecular systems. *J. Phys. Chem. B* **116**, 8573-8583 (2012). PMC3406241 PMID: 22616575

Johnson, M.E. & Hummer, G. Nonspecific binding limits the number of proteins in a cell and shapes their interaction networks. *Proc. Nat. Acad. Sci. USA.* **108**, 603-608 (2011). PMC3021073 PMID: 21187424

Ponder, J.W., Wu, C.J., Ren, P.Y., Pande, V.S., Chodera, J.D., Schnieders, M.J., Haque, I., Mobley, D.L., Lambrecht, D.S., DiStasio, R.A., Head-Gordon, M., Clark, G.N.I., **Johnson, M.E.**, Head-Gordon, T. Current status of the AMOEBA polarizable force field. *J. Phys. Chem. B.* **114**, 2549-2564 (2010). PMC2918242 PMID: 20136072

Johnson, M.E.*, Malardier-Jugroot, C. & Head-Gordon, T*. Effects of co-solvents on peptide hydration water structure and dynamics. *Phys. Chem. Chem. Phys.* **12**, 393-405 (2010).

Malardier-Jugroot, C., Bowron, D.T., Soper, A.K., **Johnson, M.E.**, & Head-Gordon, T. Structure and water dynamics of aqueous peptide solutions in the presence of co-solvents. *Phys. Chem. Chem. Phys.* **12**, 382-392 (2010).

Johnson, M.E. & Head-Gordon, T. Assessing thermodynamic-dynamic relationships for waterlike liquids. *J. Chem. Phys.* **130**, 214510 (2009).

Johnson, M.E., Malardier-Jugroot, C., Murarka, R.K. & Head-Gordon, T. Hydration water dynamics near biological interfaces. *J. Phys. Chem. B.* **113**, 4080-4092 (2009).

Malardier-Jugroot, C., **Johnson, M.E.**, Murarka, R.K. & Head-Gordon, T. Aqueous peptides as experimental models for hydration water dynamics near protein surfaces. *Phys. Chem. Chem. Phys.* **10**, 4903-4908 (2008).

Johnson, M.E., Head-Gordon, T. & Louis, A.A. Representability problems for coarse-grained water potentials. *J. Chem. Phys.* **126**, 144509 (2007).

Head-Gordon, T. & **Johnson, M.E.** Tetrahedral Structure or chains for liquid water. *Proc. Nat. Acad. Sci. USA* **103**, 7973-7977 (2006).

***Corresponding Author**

Pubmed link:

<http://www.ncbi.nlm.nih.gov/sites/myncbi/1XCwaYfWsa15f/bibliography/46177854/public/?sort=date&direction=ascending>

Google Scholar:

<https://scholar.google.com/citations?user=PWWKcAMAAAJ&hl=en&oi=pll>

Awards and Honors:

NIH K99/R00 Pathway to Independence Award: <i>Modeling the nucleation of clathrin coated vesicles at the membrane</i>	2011
Mini Statistical Mechanics Meeting, Berkeley, CA: Grand Prize Poster Award	2011
NIH Fellows Award for Research Excellence (FARE)	2010
American Chemical Society Conference San Francisco, CA: Physical Chemistry Outstanding Poster Award	2006
Nominated by Columbia Dept. of Applied Math and Physics for George Vincent Wendell Memorial Award	2004

Teaching Experience:

Johns Hopkins University

Undergraduate teaching: Models and Algorithms in Biophysics. AS 250.302, Spring semester. 2015-Present

Graduate teaching: Biophysics Graduate Program Introductory Computer Bootcamp. Organizer and instructor, Fall semester. 2014

Previous teaching experience

Creator and co-leader of Biophysics journal club for summer undergraduate researchers, Bethesda, NIH. 2012

Graduate Student Instructor, UC Berkeley, Computational Methods in Biophysics BE243/143 2007

Graduate Student Instructor, UC Berkeley, Freshman Physics 7A 2005

Leadership and Service:

NIMBioS Working Group, “Improving Tools for Spatially-Realistic Cell Simulations”. PIs: Robert F Murphy, CMU and James Faeder, Univ. Pittsburgh 2015-2017

Faculty mentor, STEM Achievement for Baltimore Elementary Schools (SABES). Johns Hopkins NSF Funded program. 2014-2015

Workshop Chair, Artificial Cells: Understanding and Engineering, Biophysical Society Meeting, Baltimore. 2015

Graduate Board Oral exam committee, Program in Molecular Biophysics 2014, 2016

Thesis Committee member, Biology Department, Chemical and Biological Engineering Department. 2014-2015

Judge for NIH-NIDDK Fellows retreat 2011-2013

Judge for NIH Graduate student research symposium 2012

Invited Seminars:

“*Mechanisms of protein assembly at the membrane: Insights from theory and reaction-diffusion simulation*” Center for Cell Analysis and Modeling, University of Connecticut Health Center, Farmington, CT. May 2016

“*Modeling protein interactions and assembly at the cell-scale*” NIMBioS Working Group on “Improving Tools for Spatially Realistic Cell Simulations”, Knoxville, TN. Mar. 2016 & Dec. 2015

<i>(Declined-Maternity)</i> CECAM Workshop on Molecular and Chemical Kinetics, Free University, Berlin, Germany.	Sept. 2015
<i>“Optimizing protein interactions for the crowded cell”</i> Telluride Science Research Center, Workshop on Macromolecular Crowding, Telluride, CO.	June 2015
<i>“Modeling protein interactions and assembly at the cellular length and timescales”</i> Department of Computational and Systems Biology, Univ. of Pittsburgh, Pittsburgh, PA.	March 2015
<i>“Modeling protein interactions and assembly with single particle reaction diffusion and multi-scale methods”</i> Krasnow Institute for Advanced Study, George Mason University, VA.	Feb. 2015
<i>“Free-propagator reweighting integrator (FPR) for single particle reaction diffusion in solution and on the membrane”</i> Banff International Research Station workshop on Single Particle Reaction Diffusion Methods, Banff, Canada.	Nov. 2014
<i>“Modeling protein interactions and assembly processes in the cell”</i> IBR Retreat, Johns Hopkins University, Baltimore, MD.	Sept. 2013
<i>“Connecting protein network topology to specificity and regulation in protein-protein interactions”</i> School of Public Health, Johns Hopkins Univ. Baltimore, MD.	March 2013
<i>“Connecting protein network topology to specificity and regulation in protein-protein interactions”</i> NIDDK Fellows Retreat, NIH, Bethesda, MD.	March 2013
<i>“Evolutionary pressure on interface-interface topology in protein interaction networks”</i> Laboratory of Chemical Physics, NIH, Bethesda, MD.	Nov 2012
<i>“Evolutionary pressure on interface-interface topology in protein interaction networks”</i> NIDDK Fellows Retreat, NIH, Bethesda, MD.	April 2012
<i>“Refining protein interaction networks with interface structure and protein expression levels”</i> Laboratory of Chemical Physics, NIH, Bethesda, MD.	Feb. 2012
<i>“Refining protein interaction networks with interface structure and protein expression levels”</i> Biophysical Society Meeting platform presentation, San Diego, CA.	Feb. 2012
<i>“How nonspecific binding between proteins shapes their interaction networks and expression levels”</i> Biophysics Department, Johns Hopkins	Jan. 2012

University, Baltimore, MD.

“Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology” Chemistry Department, University of Chicago, Chicago, IL. Jan. 2012

“How nonspecific binding between proteins shapes their interaction networks and expression levels” Stadtman Seminar, NIH, Bethesda, MD. Dec. 2011

“Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology” NHLBI Systems Biology research seminar, NIH, Bethesda, MD. Oct. 2011

“Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology” Gordon Research Conference: Cellular Systems Biology. Davidson, NC July 2011

“Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology” NIDDK Fellows Retreat, NIH, Bethesda, MD. April 2011

“Nonspecific binding limits the number of proteins in a cell and shapes their interaction topology” Biophysical Society Meeting platform presentation, Baltimore, MD. March 2011

“How many proteins are too many?” Laboratory of Chemical Physics, NIH, Bethesda, MD. 2010

“Assessing theories of liquid dynamics” Prof. Ken Dill Research Group, UCSF, San Francisco, CA. 2008

“Evaluating theories of liquid dynamics” Prof. Jhih-Wei Chu Research Group, UC Berkeley, Berkeley, CA. 2008

Recent Contributed Talks/Posters:

“Governing principles of multiprotein complex formation on the cell membranes” Biophysical Society Meeting, Los Angeles, CA Feb 2016

“Computational investigation of membrane adaptor proteins under different cellular conditions” Biophysical Society Meeting, Baltimore, MD Feb 2015

“Modeling reaction-diffusion processes in 2D and 3D with a novel single-particle integrator” GRC on Stochastic Physics in Biology, Ventura, CA Jan 2015

“ <i>Modeling reaction-diffusion processes in 2D and 3D with a novel single-particle integrator</i> ” Berkeley Mini Statistical Mechanics Meeting, Berkeley, CA	2007-2015
“ <i>Multi-scale modeling of protein assembly in clathrin-mediated endocytosis</i> ” Biophysical Society Thematic Meeting, Modeling of Biomolecular Systems Interactions, Istanbul, Turkey	Nov 2014
“ <i>Multi-scale modeling of protein assembly in clathrin-mediated endocytosis</i> ” GRC on Lysosomes and Endocytosis, Andover, NH	June 2014
“ <i>Free propagator reweighting algorithm for reaction-diffusion simulations of heterogeneous protein systems</i> ” Biophysical Society Meeting, San Francisco, CA	Feb 2014

Advisees:

David Holland: Graduate student in Biomedical Engineering, Johns Hopkins University. October 2013-Present.

Osman Yogurtcu, PhD: Post-doctoral fellow. December 2013-Present.

Dariush Mohammadyani, PhD: Post-doctoral fellow. May 2016-Present.

Benjamin Shapiro, MS: Undergraduate then Master’s student in Applied Math, Johns Hopkins University. 2014-May 2016.

Raza Ul-Haq, PhD: Post-doctoral fellow, March 2015-Feb 2016.

Undergraduate Researchers:

Rohan Tilva: Johns Hopkins University, 2015-Present.

Athena Chen: Biophysics and Mathematics, Johns Hopkins University, 2015-Present.

Pei Xue: Biophysics, Johns Hopkins University, 2014-2015.