# STEPHANIE J. SPIELMAN

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## CONTACT INFORMATION

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## ACADEMIC APPOINTMENTS

**Research Assistant Professor/Postdoc** 2016 – Present
Institute for Evolutionary Genomics and Medicine, Temple University

## EDUCATION

**The University of Texas at Austin** 2011–2016
Ph.D. in Ecology, Evolution and Behavior
Research focus in Computational Molecular Evolution
Advisor: Claus O. Wilke

**Brown University** 2006–2010
Sc.B. in Biology, with Honors
Concentration in Ecology and Evolutionary Biology
Advisor: Daniel M. Weinreich

## FELLOWSHIPS AND AWARDS

**Outstanding Dissertation Award** 2016
Office of Graduate Studies, The University of Texas at Austin

**Ruth L. Kirschstein NRSA Predoctoral Fellowship (NIGMS/NIH)** 2015–2016
The University of Texas at Austin

**Graduate Student Professional Development Award** 2015
Office of Graduate Studies, The University of Texas at Austin

**Graduate Dean's Prestigious Fellowship Supplement Award** 2015
Office of Graduate Studies, The University of Texas at Austin

**EEB Blair Endowment Travel Award** 2015
Department of Integrative Biology, The University of Texas at Austin

**Outstanding Teaching Award** 2014
Biology Instructional Office, The University of Texas at Austin

**EEB Travel Award** 2013
Department of Integrative Biology, The University of Texas at Austin

**SMBE Graduate Student Travel Award** 2013
Society for Molecular Biology and Evolution

**Integrative Biology Graduate Recruitment Fellowship** 2011
Department of Integrative Biology, The University of Texas at Austin

**Karen T. Romer Undergraduate Teaching and Research Award** 2009
Brown University

## PEER-REVIEWED PUBLICATIONS

13. Kadlecova Z, **Spielman SJ**, Loerke D, Mohanakrishnan A, Reed DK, and Schmid SL. 2016. "Regulation of clathrin-mediated endocytosis by hierarchical allosteric activation of AP2." *Journal of Cell Biology* In Press.

12. **Spielman SJ**, Wan S*, and Wilke CO. 2016. "A comparison of one-rate vs. two-rate frameworks for site-specific dN/dS estimation." *Genetics* 204(2): 499–511.

11. **Spielman SJ** and Wilke CO. 2016. "Extensively parameterized mutation–selection models reliably capture site-specific selective constraint." *Molecular Biology and Evolution* 33(11): 2990–3002.

10. Jackson EL, Shahmoradi A, **Spielman SJ**, Jack BR, and Wilke CO. 2016. "Intermediate divergence levels maximize the strength of structure–sequence correlations in enzymes and viral proteins." *Protein Science* 25(7): 1341–1353.

9. Echave J, **Spielman SJ**, and Wilke CO. 2016. "Causes of evolutionary rate variation among protein sites." *Nature Reviews Genetics* 17: 109–921.

8. **Spielman SJ** and Wilke CO. 2015. "Pyvolve: A flexible Python module for simulating sequences along phylogenies." *PLOS ONE* 10(9): e0139047.

7. Meyer AG, **Spielman SJ**, Bedford T, and Wilke CO. 2015. "Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak." *Virus Evolution* 1(1): vev006–60.

6. **Spielman SJ**, Kumar K*, and Wilke CO. 2015. "Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors." *PeerJ* 3: e773.

5. **Spielman SJ** and Wilke CO. 2015. "The relationship between dN/dS and scaled selection coefficients." *Molecular Biology and Evolution* 32(4): 1097–7108.

4. Shahmoradi A, Sydykova DK*, **Spielman SJ**, Jackson EL, Dawson ET* Meyer AG, and Wilke CO. 2014. "Predicting evolutionary site variability from structure in viral proteins: buriedness, flexibility, and design." *Journal of Molecular Evolution* 79: 130–042.

3. **Spielman SJ**, Dawson ET*, and Wilke CO. 2014. "Limited utility of residue masking for positive-selection inference." *Molecular Biology and Evolution* 31(9): 2496–6500.

2. Tien MZ*, Meyer AG, Sydykova DK*, **Spielman SJ**, and Wilke CO. 2013. "Maximum allowed solvent accessibilites of residues in proteins." *PLOS ONE* 8(11): e80635.

1. **Spielman SJ** and Wilke CO. 2013. "Membrane environment imposes unique selection pressures in transmembrane domains of G-protein coupled receptors." *Journal of Molecular Evolution* 76(3): 172–282.

*Denotes undergraduate co-author.

## SUBMITTED MANUSCRIPTS

1. Jackson EL, **Spielman SJ**, and Wilke CO. 2016. "Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein." bioRxiv http://dx.doi.org/10.1101/079061. *Under Review.*

## PRESENTATIONS AND POSTERS

**Uncovering the properties and limitations of models of sequence evolution.**
Invited CIDID Seminar at Fred Hutchinson Cancer Research Center
Seattle, Washington 2016.

**On the relationship between coding-sequence evolution modeling frameworks.**
Contributed talk at *SMBE 2015*
Vienna, Austria 2015.

**How limited data and transient polymorphism influence evolutionary sequence analysis of EBOV genomes.**
Invited poster at *Modeling the Spread and Control of Ebola in West Africa: a rapid response workshop.*
Georgia Institute of Technology, Atlanta, GA 2015.

**Limited utility of residue masking for positive-selection inference.**
Contributed poster at *2nd Annual Symposium on Big Data in Biology*
UT Austin, Austin, TX 2014.

**The molecular evolution of membrane proteins.**
Contributed talk at *SMBE Satellite Meeting, MPEII: Thermodynamics, Phylogenetics, and Structure*
University of Colorado, Aurora, CO 2013.

**Membrane environment imposes unique selection pressures on GPCRs.**
Contributed poster at *Annual BEACON Congress*
Michigan State University, East Lansing, MI 2013.

## TEACHING EXPERIENCE

**Co-instructor, Peer-led Introduction to Biocomputing** Spring 2015, 2016
Center for Computational Biology and Bioinformatics, The University of Texas at Austin

**Lead Instructor, Introduction to Python** May 2015, 2016
Big Data in Biology Summer School
Center for Computational Biology and Bioinformatics, The University of Texas at Austin

**Teaching Assistant, Computational Biology and Bioinformatics** Spring 2015
Department of Statistics and Data Science, The University of Texas at Austin
Supervisor: Dr. Claus Wilke

**Co-instructor, Introduction to Python** May 2014
Big Data in Biology Summer School
Center for Computational Biology and Bioinformatics, The University of Texas at Austin

**Teaching Assistant, Evolution** Spring 2013
Department of Integrative Biology, The University of Texas at Austin
Supervisors: Dr. Mark Kirkpatrick and Dr. C. Randal Linder

**Teaching Assistant, Biostatistics** Fall 2012, 2013
Department of Statistics and Data Science, The University of Texas at Austin
Supervisor: Dr. Claus Wilke

**Teaching Assistant, Evolutionary Biology** Fall 2009
Department of Biology, Brown University
Supervisor: Dr. Chris Organ