Jordan A. Berg

CONTACT INFORMATION	Department of Biochemistry, University of Utah 15 N Medical Drive East Rm. 4100 Salt Lake City, UT 84112	ORCID: 0000-0002-5096-0558 Website: https://j-berg.github.io/ Email: jordan.berg@biochem.utah.edu

RESEARCH INTERESTS

Cancer Metabolism, Biological Networks, Software Development, Open Source/Open Access

EDUCATION

2016-present	Ph.D. in Biochemistry, University of Utah
2010-2016	B.S. in Molecular Biology, Brigham Young University

RESEARCH EXPERIENCE

2016-present	Graduate Research Assistant, Jared Rutter Lab, University of Utah
2013-2016	Undergraduate Research Assistant, Julianne Grose Lab, Brigham Young University

SERVICE AND PROFESSIONAL MEMBERSHIPS

2020-present	*Codechecker*, CODECHECK organization
2020-present	*Member*, ISCB
2018-present	*Web Designer/Social Media Outreach Officer*, University of Utah SACNAS chapter
2018-present	*Member*, SACNAS
2018	*Lead Recruitment Host*, Molecular Biology Graduate Program, University of Utah
2018	*Volunteer*, Adventure Scientists
2014-2016	*Volunteer*, Provo Youth Mentoring, Provo, UT
2015	*Member*, American Society for Microbiology

Reviewer (ad hoc) for Bioinformatics, NAR Genomics and Bioinformatics, F1000 Research, and Journal of Emerging Investigators.
See Publons record.

TEACHING EXPERIENCE

2018, 2020	MBIOL 6200: Lit. & Problem Solving, University of Utah (3CR; 4 class hours/week; TA)
2015-2016	MMBIOL194B: Phage Hunters Genomics, Brigham Young University (2CR; 6 lab hours/week; TA)
2014-2015	MMBIOL194A: Phage Hunters Discovery, Brigham Young University (2CR; 6 lab hours/week; TA)

HONORS, AWARDS, AND FELLOWSHIPS

2020-2022	*F99 Predoctoral Fellow*, National Cancer Institute
2018-2020	*T32 Graduate Trainee*, National Institute of Diabetes and Digestive and Kidney Diseases
2016	*Outstanding Research Award*, Department of Microbiology and Molecular Biology, Brigham Young University
2014	*iGem Silver Medal*, iGEM World Jamboree, Boston, MA

WORKS IN PROGRESS

"Metaboverse: Metabolic network pattern recognition tools contextualizemulti-omic data and reveal disease-relevant signatures"
(working manuscript)

"Electrum: An online portal to visualizing and interpreting MIDAS protein-metabolite interaction data"
(with Kevin Hicks and Youjia Zhou)

"Natural Language Processing models for contextualizing and validating MIDAS protein-metabolite interaction data"
(with Ian George and Kevin Hicks)

SELECTED PUBLICATIONS

Berg JA[&], Zhou Y, Waller TC, Ouyang Y, Nowinski SM, Van Ry T, Cox JE, Wang B, Rutter J[&]. Gazing into the Metaboverse: Automated exploration and contextualization of metabolic data. (2020) *bioRxiv.* https://doi.org/10.1101/2020.06.25.171850.

Berg JA[&], Belyeu JR, Morgan JT, Ouyang Y, Bott AJ, Quinlan AR, Gertz J, Rutter J[&]. XPRESSyourself: Enhancing, Standardizing, and Automating Ribosome Profiling Computational Analyses Yields Improved Insight into Data. (2020) *PLoS Comp. Biol.* https://doi.org/10.1371/journal.pcbi.1007625.

Berg JA, Merrill BD, Breakwell DP, Grose JH, Hope S. A PCR-based method for distinguishing between two common beehive bacteria, *Paenibacillus larvae* and *Brevibacillus laterosporus.* (2018) *Journal of Appl Environ Microbiol.* https://doi.org/10.1128/AEM.01886-18.

Berg JA, Merrill BD, Crockett JT, Esplin KP, Evans MR, Heaton KE, Hilton JA, Hyde JR, McBride MS, Schouten JT, Simister AR, Thurgood TL, Ward AT, Breakwell DP, Burnett SH, Grose JH. Characterization of five novel *Brevibacillus* bacteriophages and genomic comparison of *Brevibacillus* phages. (2016) *PLoS ONE.* https://doi.org/10.1371/journal.pone.0156838.

& indicates co-corresponding authors

OTHER PUBLICATIONS

Nuebel E, Morgan JT, Fogarty S, Winter JM, Lettlova S, Berg JA, Chen Y-C, Kidwell CU, Maschek JA,Clowers KJ, Argyriou C, Chen L, Wittig I, Cox JE, Roh-Johnson M, Braverman N, Steinberg SJ, Gygi SP, Rutter J. Msp1/ATAD1 restores mitochondrial function in Zellweger Spectrum Disease. (2020) *bioRxiv.* https://doi.org/10.1101/2020.09.19.303826.

Nowinski SM, Solmonson A, Rusin SF, Maschek JA, Bensard CL, Fogarty S, Jeong M, Lettlova S, Berg JA, Morgan JT, Ouyang Y, Naylor BC, Paulo JA, Funai K, Cox JE, Gygi SP, Winge DR, Deberardinis RJ, Rutter J. Mitochondrial fatty acid synthesis coordinates oxidative metabolism in mammalian mitochondria. (2020) *eLife.* https://doi.org/10.7554/eLife.58041.

Waller TC, Berg JA, Lex A, Chapman BE, Rutter J. Compartment and Hub Definitions Tune Metabolic Networks for Metabolic Interpretations. (2020) *GigaScience.* https://doi.org/10.1093/gigascience/giz137.

Hughes CE, Coody TK, Jeong M, Berg JA, Winge DR, Hughes AL. Amino acid toxicity drives age-related mitochondrial decline by altering iron metabolism. (2020) *Cell.* https://doi.org/10.1016/j.cell.2019.12.035.

Bensard CL, Wisidigama DR, Olsen KA, Berg JA, Krah NM, Schell JC, Nowinski SM, Fogarty S, Bott AJ, Wei P, Dove KK, Tanner JM, Panic V, Cluntun A, Lettlova S, Earl CS, Namnath DF, Vázquez-Arregun K, Villanueva CJ, Tantin D, Murtaugh LC, Evason KJ, Ducker GS, Thummel

CS, Rutter J. Regulation of Tumor Initiation by the Mitochondrial Pyruvate Carrier. (2019) *Cell Metabolism.* https://doi.org/10.1016/j.cmet.2019.11.002.

Van Vranken JG, Nowinski SM, Clowers KJ, Jeong M, Ouyang Y, Berg JA, Gygi J, Gygi SP, Winge DR, Rutter JP. ACP acylation is an acetyl-CoA-dependent modification required for electron transport chain assembly. (2018) *Molecular Cell.* https://doi.org/10.1016/j.molcel.2018.06.039.

A complete list of publications can be found at Google Scholar.

ORAL PRESENTATIONS

Berg JA, Zhou Y, Wang B, Rutter J. Modeling and Identifying Regulatory Patterns within Chaotic Metabolic Networks. (2020) *Selected Short Talk.* ISMB 2020 (virtual).
  Program Slides

Berg JA, Zhou Y, Waller TC, George I, Cox J, Wang B, Rutter J. Contextualizing chaotic metabolic networks and their regulation. (2019) *Selected Talk.* EMBL/EMBO Epigenetics Meets Metabolism, Heidelberg, DE.
  Program Slides

Berg JA, Belyeu JR, Morgan JT, Ouyang Y, Bott AJ, Quinlan AR, Gertz J, Rutter J. XPRESSyourself — Enhancing, standardizing, and automating ribosome profiling computational analyses yields improved insight into data. (2019) *Lightning Talk.* Genome Informatics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA.
  Program

Berg JA. XPRESSyourself: Enhancing, Standardizing, and Automating Ribosome Profiling Computational Analyses Yields Improved Insights. (2019) *Invited Talk.* Bioinformatics Seminar Series, Center for Computational Biology & Bioinformatics, University of California San Diego, San Diego, CA, USA.
  Program Slides

Berg JA, Simister, AR, Thurgood TL, Grose JH. Characterization and analysis of six novel *Erwinia* phages reveals relationship to *Enterobacteriaceae* family members. (2015) *Selected Talk.* Tri- branch ASM meeting, Colorado State University, Fort Collins, CO.

POSTER PRESENTATIONS

Berg JA, Belyeu JR, Morgan JT, Ouyang Y, Bott AJ, Quinlan AR, Gertz J, Rutter J. XPRESSyourself — Enhancing, standardizing, and automating ribosome profiling computational analyses yields improved insight into data. (2019) Genome Informatics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA.

Berg JA, Nuebel E, Rutter JP. Ribosome profiling reveals translation-level regulation of peroxins in response to loss of peroxisomes. (2018) Frontiers in Metabolism, Madison, WI, USA.

Berg, JA, Rutter JP. RiboPipe: A ribosome profiling pipeline optimized for easy assembly and data analysis. (2018) RECOMB, Paris, France.

Berg JA, Esplin IND, Brundage BM, Crockett JT, Esplin KP, Evans MR, Heaton KE, Hilton JA, Hyde JR, McBride MS, Schouten JT, Simister AR, Thurgood TL, Merrill BD, Ward AT, Breakwell DP, Burnett SH, Grose JH. Isolation of six novel *Paenibacillus larvae* bacteriophage and characterization of five *Brevibacillus laterosporus* bacteriophages to understand their evolutionary relationship to *Brevibacillus* and other bacteriophages. (2015) 7th Annual HHMI SEA-PHAGES Symposium, Janelia Farms, Ashburn, VA.

Abboud M, Berg JA, Boekweg C, Jensen G, Keele B, Linzey M, McOmber JS, Murdock MH,

Roberts J, Robinson T, Sargent C, Zenger C, DeMille D, Price P, Grose JH. Reclaiming water reclamation: Engineering microbes for enhanced sewage treatment. (2014) iGEM Giant Jamboree, Hynes Convention Center, Boston, MA.

Ransom EK, Berg JA, Grossarth SE, Smith H, Anieves D, Esplin ID, Merrill BD, Schoenhals JE, Breakwell DP, Burnett SH, Grose JH. Comparative genome analysis of seven novel *Erwinia* phages reveals orthologous proteins and allows for formation of a cluster with three known *Enterbacteriaceae* phages. (2014) ASM Intermountain Branch Meeting, Brigham Young University, Provo, UT.

GENBANK PUBLICATIONS

A complete listing of bacteriophage genome publications can be found on GenBank (60 total).

TRAINEES

Ian George* (Undergraduate, U. of Utah)
Claudia Charles (Undergraduate, U. of Utah)
Nolan Beatty (Undergraduate, Brigham Young U.)
Braden Brundage* (Undergraduate, Brigham Young U.)
Alisa Buchanan (Undergraduate, Brigham Young U.)
Minsey Choi* (Undergraduate, Brigham Young U.)
Justin Crockett* (Undergraduate, Brigham Young U.)
Kyle Esplin* (Undergraduate, Brigham Young U.)
Marlee Evans* (Undergraduate, Brigham Young U.)
Hannah Ferguson* (Undergraduate, Brigham Young U.)
Karli Heaton* (Undergraduate, Brigham Young U.)
Jared Hilton* (Undergraduate, Brigham Young U.)
Emily Hurst (Undergraduate, Brigham Young U.)
Jonathan Hyde* (Undergraduate, Brigham Young U.)
Moon Hee I (Undergraduate, Brigham Young U.)
Morgan McBride* (Undergraduate, Brigham Young U.)
Sam Pollock (Undergraduate, Brigham Young U.)
Micah Putnam* (Undergraduate, Brigham Young U.)
Jordan Schouten* (Undergraduate, Brigham Young U.)
Jeremy Severe (Undergraduate, Brigham Young U.)
Austin Simister* (Undergraduate, Brigham Young U.)
Philip (PJ) Tatlow* (Undergraduate, Brigham Young U.)
Trever Thurgood* (Undergraduate, Brigham Young U.)
Charles (CJ) Webb* (Undergraduate, Brigham Young U.)

An asterisk indicates those who presented their research at a conference or in a publication.

OTHER

Languages: English (native), Spanish (professional working proficiency), Mandarin Chinese (elementary proficiency)

Programming: Python, R, Bash, C++, Julia, HTML/CSS, Javascript, LaTeX

Citizenship: United States; Born: 1991