

CURRICULUM VITAE

BENJAMIN K. JOHNSON

Bioinformatics Research Scientist

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Education

Ph.D.	Michigan State University	2016	Microbiology and Molecular Genetics
B.S.	Calvin College	2011	Biology; Biochemistry

Positions

2017-	Bioinformatics Research Scientist, Van Andel Research Institute, Grand Rapids, MI
2016-2017	Bioinformatics Scientist, Van Andel Research Institute, Grand Rapids, MI
2011-2016	Graduate Research Assistant, Michigan State University, East Lansing, MI
2007-2011	Undergraduate Research Assistant, Calvin College, Grand Rapids, MI

Awards and Honors

2016	Hsiung-Kimball Award, Michigan State University
2015	Rudolph Hugh Fellowship, Michigan State University
2010-2011	National Science Foundation Scientific Computing Scholarship
2010-2011	Henry Bengelink Scholarship, Department of Biology, Calvin College
2007-2011	Knollcrest Scholarship, Calvin College
2010	Teaching Assistant selected to train faculty involved in the Science Education Alliance (SEA) HHMI Mycobacteriophage Research Laboratory, HHMI Janelia Farms Research Campus
2007	Presidential Scholarship, Calvin College

Publications and Book Chapters

1. Senchuk MM, Dues DJ, Schaar CE, **Johnson BK**, Madaj ZM, Bowman MJ, Winn ME, Van Raamsdonk JM. Activation of DAF-16/FOXO by reactive oxygen species contribute to longevity in long-lived mitochondrial mutants in *C. elegans*. **PLoS Genetics**. 2018 (In Press)
2. Coulson GB*, **Johnson BK***, Zheng H, Colvin CJ, Fillinger RJ#, Haiderer ER#, Hammer ND, Abramovitch RB. Targeting *Mycobacterium tuberculosis* Sensitivity to Thiol Stress at Acidic pH Kills the Bacterium and Potentiates Antibiotics. **Cell Chem Biol**. 2017 Aug 17;24(8):993-1004.e4. doi: 10.1016/j.chembiol.2017.06.018. Epub 2017 Aug 3. PubMed PMID: 28781126; PubMed Central PMCID: PMC5562523. Times cited: 4

*contributed equally #undergraduate co-author

3. Dues DJ, Schaar CE, **Johnson BK**, Bowman MJ, Winn ME, Senchuk MM, Van Raamsdonk JM. Uncoupling of oxidative stress resistance and lifespan in long-lived isp-1 mitochondrial mutants in *Caenorhabditis elegans*. **Free Radic Biol Med**. 2017 Jul;108:362-373. doi: 10.1016/j.freeradbiomed.2017.04.004. Epub 2017 Apr 7. PubMed PMID: 28392283; PubMed Central PMCID: PMC5493208. Times cited: 2
4. **Johnson BK**, Abramovitch RB. Small Molecules That Sabotage Bacterial Virulence. **Trends Pharmacol Sci**. 2017 Apr;38(4):339-362. doi: 10.1016/j.tips.2017.01.004. Epub 2017 Feb 14. Review. PubMed PMID: 28209403. Times cited: 17

Featured Review and received the cover for April issue.

5. Zheng H, Colvin CJ, **Johnson BK**, Kirchhoff PD, Wilson M, Jorgensen-Muga K, Larsen SD, Abramovitch RB. Inhibitors of *Mycobacterium tuberculosis* DosRST signaling and persistence. **Nat Chem Biol**. 2017 Feb;13(2):218-225. doi: 10.1038/nchembio.2259. Epub 2016 Dec 19. PubMed PMID: 27992879. Times cited: 15
6. Williams EA, Mba Medie F, Bosserman RE, **Johnson BK**, Reyna C, Ferrell MJ, Champion MM, Abramovitch RB, Champion PA. A Nonsense Mutation in *Mycobacterium marinum* That Is Suppressible by a Novel Mechanism. **Infect Immun**. 2017 Jan 26;85(2). pii: e00653-16. doi: 10.1128/IAI.00653-16. Print 2017 Feb. PubMed PMID: 27789543; PubMed Central PMCID: PMC5278160. Times cited: 2
7. Jeon AB, Obregón-Henao A, Ackart DF, Podell BK, Belardinelli JM, Jackson M, Nguyen TV, Blackledge MS, Melander RJ, Melander C, **Johnson BK**, Abramovitch RB, Basaraba RJ. 2-aminoimidazoles potentiate β -lactam antimicrobial activity against *Mycobacterium tuberculosis* by reducing β -lactamase secretion and increasing cell envelope permeability. **PLoS One**. 2017 Jul 27;12(7):e0180925. doi: 10.1371/journal.pone.0180925. eCollection 2017. PubMed PMID: 28749949; PubMed Central PMCID: PMC5547695.
8. Harlow ML, Maloney N, Roland J, Guillen Navarro MJ, Easton MK, Kitchen-Goosen SM, Boguslawski EA, Madaj ZB, **Johnson BK**, Bowman MJ, D'Incalci M, Winn ME, Turner L, Hostetter G, Galmarini CM, Aviles PM, Grohar PJ. Lurbinectedin Inactivates the Ewing Sarcoma Oncoprotein EWS-FLI1 by Redistributing It within the Nucleus. **Cancer Res**. 2016 Nov 15;76(22):6657-6668. doi: 10.1158/0008-5472.CAN-16-0568. Epub 2016 Oct 3. PubMed PMID: 27697767; PubMed Central PMCID: PMC5567825. Times cited: 3

9. **Johnson BK**, Scholz MB, Teal TK, Abramovitch RB. SPARTA: Simple Program for Automated reference-based bacterial RNA-seq Transcriptome Analysis. **BMC Bioinformatics**. 2016 Feb 4;17:66. doi: 10.1186/s12859-016-0923-y. PubMed PMID: 26847232; PubMed Central PMCID: PMC4743240. Times cited: 10
10. **Johnson BK**, Colvin CJ, Needle DB, Mba Medie F, Champion PA, Abramovitch RB. The Carbonic Anhydrase Inhibitor Ethoxzolamide Inhibits the *Mycobacterium tuberculosis* PhoPR Regulon and Esx-1 Secretion and Attenuates Virulence. **Antimicrob Agents Chemother**. 2015 Aug;59(8):4436-45. doi: 10.1128/AAC.00719-15. Epub 2015 May 18. PubMed PMID: 25987613; PubMed Central PMCID: PMC4505220. Times cited: 19

Highlighted in **MSU today** (July 23, 2015)

Highlighted as a News and Analysis Research Briefing in **The Pharmaceutical Journal** (August 9, 2015)

11. Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF; **Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science**.*; Phage Hunters Integrating Research and Education.; Mycobacterial Genetics Course. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. **Elife**. 2015 Apr 28;4:e06416. doi: 10.7554/eLife.06416. PubMed PMID: 25919952; PubMed Central PMCID: PMC4408529. Times cited: 89

**Teaching assistant and research contributor to the SEA-PHAGES consortium*

12. Leung W, ...**Johnson BK**, ...Elgin SC. Drosophila muller f elements maintain a distinct set of genomic properties over 40 million years of evolution. **G3 (Bethesda)**. 2015 Mar 4;5(5):719-40. doi: 10.1534/g3.114.015966. PubMed PMID: 25740935; PubMed Central PMCID: PMC4426361. Times cited: 37
13. **Johnson BK**, Abramovitch RB. Macrophage infection models for *Mycobacterium tuberculosis*. **Methods Mol Biol**. 2015;1285:329-41. doi: 10.1007/978-1-4939-2450-9_20. PubMed PMID: 25779326. Times cited: 6
14. Baker JJ, **Johnson BK**, Abramovitch RB. Slow growth of *Mycobacterium tuberculosis* at acidic pH is regulated by phoPR and host-associated carbon sources. **Mol Microbiol**. 2014 Oct;94(1):56-69. doi: 10.1111/mmi.12688. Epub 2014 Jul 13. PubMed PMID: 24975990; PubMed Central PMCID: PMC4177513. Times cited: 40

Highlighted as an Editor's Choice in **Science Translational Medicine** (July 9, 2014)

Software and Computational Proficiency

Proficient programming languages: Python, R, and bash

Programming environments: Unix/Linux, Windows, high-performance/cluster computing (PBS and SGE), and cloud-based computing (AWS EC2 and S3)

Working knowledge languages: C++

1. SPARTA: Simple Program for Automated reference-based bacterial RNA-seq Transcriptome Analysis (www.github.com/biobenkj; sparta.readthedocs.org [documentation and tutorial]; sparta-teaching.readthedocs.org [teaching materials])
 2. HAARP: High-throughput screening Automated Analysis and Retrieval of Putative hits (www.github.com/biobenkj/HAARP)
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Bioinformatics Experience

Genomics (short and long read/single molecule sequencing)

1. *De novo* and reference-guided genome assembly and annotation
2. Variant calling – whole genome, exome, and targeted sequencing
3. Whole genome and reduced representation/targeted bisulfite sequencing
4. ChIP-seq and regulatory element prediction/identification/annotation
5. SNP and methylation array analysis

Transcriptomics (gene level and transcript/isoform level)

1. RNA-seq (total RNA and coding region-selected analysis)
2. Transcriptome assembly and annotation

Enrichment analyses

1. Integration of ChIP/regulatory element sequencing and expression profiling
 2. Transcription factor enrichment
 3. Pathway and reactome enrichment
 4. Weighted gene correlation network analysis (co-expression and network analysis)
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Biostatistics Experience

1. Mixed-effects modeling
 2. Beta and zero/one inflated beta modeling (genome-wide methylation modeling)
 3. Negative binomial (NB) and zero inflated NB modeling (RNA-seq and scRNA-seq, respectively)
 4. Poisson and zero inflated poisson modeling (rare event modeling)
 5. Survival analysis
 6. Empirical Bayes estimation
 7. NGS power analysis
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Genome Annotation

1. Davis,A.J., ... **Johnson,B.K.**, Wertz,J.T., DeJong,R.J. ... and Hatfull,G.F. Full Genome Annotation of Mycobacteriophage *Anaya*. NCBI Genbank: JF704106.1, 2011. J. Virol. 86 (4), 2382-2384 (2012)
 2. Osterbaan,L.J., ... **Johnson,B.K.**, DeJong,R.J., Wertz,J.T., ... and Hatfull,G.F. Full Genome Annotation of Mycobacteriophage *Oosterbaan*. NCBI Genbank: JF704109, 2011. J. Virol. 86 (4), 2382-2384 (2012)
 3. Jacobs-Sera,D., ... **Johnson,B.K.**, ... and Hatfull,G.F. Full Genome Annotation of Mycobacteriophage *Red Rock*. NCBI Genbank: NC_025444.1, 2009.
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Selected Poster Presentations

1. VanOeveren S, **Johnson B.K.**, Bernstein A.I. Parkinson's disease associated alterations in the DNA modifications, 5-methylcytosine and 5-hydroxymethylcytosine. Neuroscience, Washington D.C., District of Colombia, 2017
 2. **Johnson B.K.**, Colvin C.J., Needle D.B., Mba Medie F., Champion P.A.D., and Abramovitch R.B. The Carbonic Anhydrase Inhibitor Ethoxzolamide Inhibits the *Mycobacterium tuberculosis* PhoPR-regulon and Esx-1 Secretion and Attenuates Virulence. Microbial Pathogenesis & Host Response (Cold Spring Harbor Laboratory), Cold Spring Harbor, New York, 2015 – Abstract accepted and conference in September 2015
 3. **Johnson B.K.**, Colvin C.J., Needle D.B., Mba Medie F., Champion P.A.D., and Abramovitch R.B. The Carbonic Anhydrase Inhibitor Ethoxzolamide Inhibits the *Mycobacterium tuberculosis* PhoPR-regulon and Esx-1 Secretion and Attenuates Virulence. Midwest Microbial Pathogenesis Conference (MMPC 2015), Indianapolis, Indiana, 2015 – Abstract accepted and conference in September 2015
 4. **Johnson, B.K.**, Colvin, C.J., Abramovitch, R.B. Ethoxzolamide inhibits the *Mycobacterium tuberculosis phoPR* regulon and attenuates virulence. Midwest Microbial Pathogenesis Conference (MMPC 2014), Chicago, Illinois, 2014.
 5. **Johnson, B.K.**, Colvin, C.J., Abramovitch, R.B. High throughput screen for small molecule inhibitors of a pH-regulated fluorescent biosensor in *Mycobacterium tuberculosis*. Keystone Symposia – Tuberculosis: Understanding the enemy. Whistler, British Colombia, Canada, 2012.
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Invited Seminars

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| 2017 | “Hacking Disease: Using Computational Biology to Exploit Pathogenesis” Calvin College , Department of Biology. <i>Departmental seminar</i> . |
| 2017 | “What is Bioinformatics?” Innovation Central High School , Engineering class. |
| 2016 | “Disarming a Killer: Developing New Treatments for Tuberculosis” Calvin College , Department of Biology. <i>Departmental seminar</i> . |
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Department, College and University Service

2015-2016	Graduate Student Invited Speaker Organization Committee, Michigan State University
2014-2016	Graduate Representative to the Dean's Advisory Committee, College of Natural Science, Michigan State University
2011-2013	Graduate Student Workshop Organization Committee, Michigan State University

Patent applications

1. Abramovitch RB, **Johnson BK**, and Colvin CJ. Compositions and methods for inhibiting bacterial growth. U.S. Patent Application PCT/US2016/030689, WO2016179231 (Ethoxzolamide)
 2. Abramovitch RB, Zheng H, **Johnson BK**, and Colvin CJ. Compositions and methods for inhibiting bacterial growth. *Provisional patent application submitted.* (DosRST inhibitors)
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Bioinformatics Supported Research

National Institutes of Health, Daniel Vogt Ph.D., Michigan State University <i>Subaward Principal Investigator - provide integrative TRAP-seq bioinformatics support</i> Pending funding	R01	2017
National Institutes of Health, NCI, Matthew Steensma M.D., Van Andel Institute <i>Senior Key Personnel - provide integrative ChIP-seq and RNA-seq bioinformatics support</i> Pending funding	R01	2017
National Institutes of Health, Jose Teixeira Ph.D., Michigan State University <i>Senior Key Personnel - provide RNA-seq, ATAC-seq, and ChIP-seq bioinformatics support</i> Pending funding	R01	2017
National Institutes of Health, Gerd Pfeifer Ph.D., Van Andel Institute <i>Key Personnel - provide integrative scRNA-seq, ChIP-seq, targeted bisulfite sequencing, and whole genome bisulfite sequencing bioinformatics support</i> Pending funding	R01	2017
National Institutes of Health, Tao Yang Ph.D., Van Andel Institute <i>Key Personnel - provide RNA-seq bioinformatics support</i> Pending funding	R01	2017
National Institutes of Health, Stefan Jovinge M.D., Ph.D. and Bart Williams Ph.D., Van Andel Institute <i>Key Personnel - provide scRNA-seq and whole genome sequencing bioinformatics support</i> Pending funding	R01	2017

Selected Teaching Experience and Certifications

- 2017 ***Instructor, RNA-seq theory, applications and analysis, VAIGS VAI9109***
- Developed and delivered course material for bulk and scRNA-seq theory and applications
 - Guided the graduate level learner through identification of high quality publicly available RNA-seq datasets, interpretation of analysis techniques, and integration with internal and external data
 - Discussed common theory and applications to design well-powered sequencing studies
 - Integrated basic command line and R programming into data analysis
 - Assessments were based on participation in discussions and a final capstone project extending concepts to develop a robust transcriptional profiling experiment
- 2017 ***Instructor, Introductory command line workshop, VARI***
- Modified previously prepared Data Carpentry workshop materials to fit into a 4 hour workshop
 - Leveraged pre- and post-assessment tools to identify areas of learning gains and difficult concepts for iterative course material development
 - Implemented progressive learning speed modifier techniques designed by Software Carpentry
 - Course materials are available at vari-linux-workshop.readthedocs.io
- 2015 ***Co-Instructor, Microbial genomics and transcriptomics two-day workshop, UC Davis***
- Prepared workshop material to be accessible to a wide-range of learner levels (undergraduate, graduate, post-doc, and faculty)
 - Guided learners through a standard microbial RNA-seq analysis workflow to provide bioinformatics resources for future use
 - Led a discussion regarding common pitfalls and answered questions regarding project specific caveats/deviations from the presented workflow
 - Course materials are available at <http://2015-sep-microbial.readthedocs.io>
- 2015 ***Co-Instructor, Data Carpentry two-day workshop, Genentech***
- Delivered Data Carpentry genomics materials designed to build a knowledge base of tools and resources to access and manipulate genomic data in R
 - Led tutorials and discussions surrounding an introduction to R, accessing public genomics databases through R, and construction of SQL databases for data management
 - Prepared and delivered an example of a two condition RNA-seq differential gene expression analysis (<https://github.com/biobenkj/example-RNAseq>)
 - Course materials are available at <https://github.com/datacarpentry/2015-09-21-Genentech/wiki>
- 2015 ***Guest lecturer, Undergraduate Microbiology lab, MSU***
- Prepared and delivered five, four-hour laboratory lectures analyzing *Lactobacillus reuteri* data generated by the undergraduate learners and sequenced at MSU

- Introduced basic command line techniques to leverage contemporary bioinformatics tools for quality control, alignment, and transcript quantification on MSU's high performance computing cluster
- Led differential gene expression analysis and pathway enrichment approaches in R to generate hypotheses for additional experiments
- Course materials are available at mmg434.readthedocs.io

2015 ***Guest lecturer, Bioinformatics training workshop, MSU iCER***

- Led a discussion regarding my work in the Abramovitch lab in the context of microbial drug discovery that leverages NGS approaches
- Live-coded a differential gene expression analysis to a broad audience (undergraduates, graduate students, post-docs, and faculty)
- Outlined common confounding factors during analyses (e.g. batch effects) that can lead to inappropriate biological conclusions

2014 ***Guest lecturer, Summer graduate-level NGS applications and analysis, MSU***

- Prepared a 3-hour interactive, live-coding tutorial surrounding *de novo* genome assembly and quality assessment of the assembly
- Led a discussion regarding next steps following assembly (e.g. annotation)

2014 ***Certified Software Carpentry Instructor***

- Completed instructor training for effective teaching of computational approaches at the Mozilla Foundation Toronto office with Dr. Greg Wilson
- <https://software-carpentry.org/team/>

2013 ***Graduate teaching assistant, Undergraduate introductory microbiology lab, MSU***

- Guided undergraduate learners through a semester long series of microbiology experiments, culminating in identification of an unknown microbe
- Graded weekly and monthly progress and laboratory reports
- As the section teaching assistant lead, I compiled grade information from other section teaching assistants and provided the course proctor midterm and final grades

2009-2011 ***Undergraduate teaching assistant, HHMI SEA-PHAGES program, Calvin College***

- Prepared laboratory materials for lab exercises
 - Aided peers with interpretation of experimental results and next steps
 - This experience provided me the first opportunity to develop methodology to communicate complex/abstract biological concepts to my undergraduate peers and other biologists
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High school student, Undergraduate student, Graduate student, and Postdoctoral Mentoring

High school students

- 2016 Anthony Kirkland (Innovation Central High School summer research student at VAI)
- Co-mentored with Dr. Mary Winn and Dr. Megan Bowman
 - Capstone materials can be found at <http://anthonys-teaching-documentation.readthedocs.io>
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Undergraduate students

- 2017 Rachel House (Calvin College summer research student at VAI)
- 2017 YukKei Wan (MSU summer research student at VAI)
- 2017 Ricardo Burke (Claflin University summer research student at VAI)
- 2016 Philip Versluis (Hope College summer research student at VAI)
- 2014-2015 Robert Fillinger (MSU undergraduate research student)
- Mentored the development of microbial variant calling approaches (<http://www.abramovitchlab.com/#!/snp-identification-using-gatk/>)
- 2013-2015 Boitshoko Molefhi (MSU undergraduate research student)
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Graduate students

- 2017 Emily Machiela (VAI graduate student)
- RNA-seq independent study learner
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Postdoctoral researchers

- 2017 Lee Marshall, PhD (VAI postdoc in neurodegenerative disease)
- 2017 Rochelle Tiedemann, PhD (VAI postdoc in epigenetics)
- 2016-2017 Zhi-jun Huang, PhD (VAI postdoc in epigenetics)
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