

# Jonathon Edward Mohl

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## *Education*

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2019, Expected Spring, PhD in Computational Science, University of Texas—El Paso, El Paso, TX 79968

2012, Graduate Certificate in Public Health, University of Texas—Houston, Houston, TX 77030

2009, M.S. in Bioinformatics, University of Texas—El Paso, El Paso, TX 79968

2002, B.S. in Microbiology and Biochemistry, Colorado State University, Fort Collins, CO 80523

## *Work Experience*

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### UTEP Border Biomedical Research Center

September 2014 to Present—Systems Analyst in the Bioinformatics Program—Maintain Bioinformatics network (including webpages), and assist undergraduate, graduate students and faculty in research activities by analyzing biological data using a variety of bioinformatics and statistical programs. Developed programs for use in analysis of biological data.

### UTEP Department of Computational Sciences

September 2013 to August 2014—Graduate Teaching Assistant for Bioinformatics I/II courses and UPBiT Workshop

### Texas Tech University Health Sciences Center-El Paso

September 2012 to August 2013—Research Aide in the Genomics Core Facility—Performed DNA sequencing reactions. Maintained Genomics Core webpages. Performed bioinformatic analysis.

December 2010 to August 2012—Research Aide in the Center of Excellence Infectious Disease Group— Performed cell fusion assays. Maintained tissue cultures and prepared viral stocks. Performed bacterial transformations and isolated plasmid DNA. Prepared media and buffers. Ordered laboratory supplies.

### City of El Paso Department of Public Health

September 2009 to November 2010—Microbiologist—Performed RNA extractions and RT-PCR for Flu testing. Worked with Select Agent as an LRN lab and with BioWatch in a Surge capacity. Ran diagnostic tests related to food and environmental samples. Validated new protocols and machinery within the laboratory. Trained laboratory personnel in different areas of the lab. Performed general lab duties including ordering, QC/QA, and media prep. Performed Proficiency Tests for all related areas.

### UTEP Department of Mathematics

January 2010 to May 2010—Program Analyst—Wrote programs using Java, HTML and other programming languages for use in RNA research.

September 2007 to August 2009—Graduate Research Assistant in the RNAVLab—Developed a Graphical User Interface for desktop utilization of RNA folding algorithms.

September 2008 to May 2009—Graduate Teaching Assistant for Bioinformatics I/II courses

#### Texas Tech University Health Sciences Center

June 2009 to August 2009—Intern for the Biostatistics & Epidemiology Consulting Lab—Worked with researchers in analyzing Next Generation Sequencing data and developed computer programs to help with this analysis. I provided basic molecular biology and current technological presentations as reviews for people within the group

#### CSU Department of Microbiology

May 2002 to May 2004, October 2006 to January 2007—Graduate Research Assistant —Phage isolation, analysis of RNA, DNA, and organics within different *Mycobacterium avium* subspecies.

August 2000 to May 2002—Undergraduate Research Assistant—Performed general lab prep and projects while studying *M. avium*.

January 2000 to May 2003—Undergraduate/Graduate Teaching Assistant--Set up the general microbiology, immunology, and molecular biology labs, answered questions students had on procedures and graded homework assignments.

#### CSU Morgan Libraries

October 2001 to January 2007—Access Services Assistant Coordinator—Supervised Reserve systems (Electronic and Traditional), monitored student budget expenditures, helped with general library functions, served on inter-departmental committees

August 1999 to October 2001—Access Services Monitor (Student Desk Manager)

August 1996 to May 1997, January 1999 to August 1999—Student worker

#### Monsanto

May 2001 to June 2001—Bioinformatics Intern—Entered data into a genomics database from journal articles and wrote simple PERL scripts.

### *Classes Taught*

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#### UTEP

CS Seminar for Bioinformatics (Spring 2016)

### *Community and University Service*

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UTEP Annual COURI Symposium -- Judge 2014 to 2018

### *Skills*

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#### Bioinformatics

Use of software related to sequence alignments, sequence searches, primer design, RNA folding, protein prediction, protein folding, statistical analysis

Knowledge of the Java, SQL, Perl, Python, SQL, and HTML programming languages

#### General Molecular Biology

Viral and Cell Culture Maintenance, Biochemical tests, Bacterial growth optimization, phage isolation, sterile laboratory techniques, QC/QA, cell fusion assays, DNA, RNA, protein and organic extractions, PCR, prokaryotic cloning, real-time PCR, DNA sequencing

#### General Computer

Word, Excel, PowerPoint, UNIX, Windows, Mac and HPC systems

#### Management

Staff training, policy making, monitoring budgets, writing and reviewing goals, analysis and optimization of workflows

## Fields of Interest

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Genomics, Multi-omics, Molecular Biology, Bioinformatics, Gene Regulatory Networks, Machine Learning Applications in Molecular Biology, Distributive Computing

## Organizations and Groups:

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International Society of Computation Biology  
February 2013 to Present—Member  
Society for Industrial and Applied Mathematics  
September 2013 to Present—Member  
UTEP College of Science Graduate Student Council  
Spring 2008 to Spring 2009—Member  
BioInTx (UTEP Bioinformatics Club)  
Fall 2007 to Spring 2008—Member  
Summer 2008 to Spring 2009—Elected President  
Microbiology Student Organization at Colorado State University  
Fall 2002 to Summer 2003—Member  
Fall 2003 to Spring 2004—Executive committee

## Attended Workshops

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Microbiology  
FERN National Training Conference — June 2010  
Bioinformatics  
Summer Institute in Bioinformatics (MARC) — July 2008

## Publications

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1. Gorry, PR., Ahmad, F., **Mohl, J.**, and Alkhatib, G. (2018) Low levels of HIV-1 envelope-mediated fusion are associated with long-term survival of an infected CCR5-/- patient. *AIDS* (Accepted Manuscript)
2. Vasquez, M., **Mohl, J.**, and Leung, MY. (2018) STUDENT PAPER: Parsing Next Generation Sequencing Data in Parallel Environments for Downstream Genetic Variation Analysis. *Journal of Computational Science Education* (Accepted Manuscript)
3. Rivas, J., **Mohl, J.**, Van Pelt, R., Leung, MY., Wallace, R., Gill, T., and Walsh, E. (2018) Evidence for regional Aeolian transport of freshwater micrometazoans in arid regions. *Limnology and Oceanography Letters* **3**(4):320-330
4. Joshi, A., Lee, RTC., **Mohl, J.**, Sedano, M., Xin, KW., Tek, NO., Maurer-Stroh, S. and Garg, H. (2014) Genetic Signatures of HIV-1 Envelope-mediated Bystander Apoptosis. *Journal of Biological Chemistry* **289**(5): 2497-514
5. Garg, H., **Mohl, J.** and Joshi, A. (2012) HIV-1 Induced Bystander Apoptosis. *Viruses* **4**(11) 3020-43

## Talks

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1. **Mohl, J.**, Brown, P. and Walsh, E. (2018) “Sequencing and annotation of the *Sinantherina socialis* genome.” XV International Rotifer Symposium. El Paso, TX.
2. **Mohl, J.** (2015) “Constructing an iterative method in predicting O-glycosylation modification sites of a protein with different ppGalNAc-transferases working in concert.” UTEP Graduate Expo, El Paso, TX

## Posters

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1. **Mohl, J.**, Gerken, T., and Leung, MY. (2018) "Making sense of the complexity in GalNAc glycosylation prediction through a mix of laboratory experiments and data mining." 2018 ISCB Intelligent Systems for Molecular Biology, Chicago, IL
2. **Mohl, J.E.**, Gerken, T., Leung, MY (2018). "GalNAc glycosylation prediction and effects of surrounding O-glycosylation sites" 13<sup>th</sup> Annual New Mexico Bioinformatics, Science, and Technology Symposium: Genome Editing. Santa Fe, NM.
3. **Mohl, J.**, Gerken, T., Leung, MY (2017). "A kinetic approach to predicting O-glycosylation by ppGalNAc-Ts." 3rd Border Biomedical Research Center Symposium on Health Disparities: From Molecules to Disease, El Paso, Texas.
4. **Mohl, J.**, Gerken, T., and Leung, MY (2016) "Constructing an iterative method in predicting O-glycosylation sites of a protein with different GalNAc-transferases working in concert." 2016 ISCB Intelligent Systems for Molecular Biology, Orlando, FL
5. **Mohl, J.**, Cardenas, G., Gerken, T and Leung, MY (2014) "ISOGlyP: Protein O-glycosylation Prediction Using Results From Random Peptide Studies". Dynamica Expo, El Paso, TX
6. **Mohl, J.**, Licon, A., Martz, R., Taufer, M., Johnson, KL. and Leung, MY. (2009) "The RNAVLab Web-server and Graphical User Interface". New Mexico Bioinformatics Symposium. Santa Fe, NM

## Contributed Posters and Talks(\*)

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1. \*Stunz, E., **Mohl, J.**, Fetcher, N., Tang, J., and Moody, M. (2018) "Molecular ecology of the arctic moist tundra sedge, tussock cottongrass (*Eriophorum vaginatum*), in the context of local adaptation and climate." Botany 2018, Rochester, Minnesota
2. \*Kordbacheh, A., **Mohl, J.** and Walsh, E.J. (2018) "Detecting adaptive genetic variation among cryptic species of *Euchlans dilatata* using a next generation sequencing approach." XV International Rotifer Symposium. El Paso, TX.
3. Samaniego, S., **Mohl, J.**, and Walsh, E.J. (2018) "Assessing rotifer diversity in desert wetlands through sediment rehydration and next-generation sequencing" XV International Rotifer Symposium. El Paso, TX.
4. Begum, K., **Mohl, J.E.**, Leung, MY. (2018) "Construction of the database GPCRPEndB to facilitate prediction and classification of G protein-coupled receptors." 13<sup>th</sup> Annual New Mexico Bioinformatics, Science, and Technology Symposium: Genome Editing. Santa Fe, NM.
5. Godinez Macias, K.P., **Mohl, J.E.**, Leung, MY. (2018) "A pipeline for bioinformatics analysis of RNA-seq data" 13<sup>th</sup> Annual New Mexico Bioinformatics, Science, and Technology Symposium: Genome Editing. Santa Fe, NM.
6. Grant, A., **Mohl, J.**, Rodriguez, G., Leung, MY., Kirken, R. (2017) "A borderland whole exome analysis of hematological cancers" RCMI Translational Science 2017, Washington, DC
7. \*Stunz, E., **Mohl, J.**, Fetcher, N., Tang, J., Moody, M. (2017). "Population genetics and gene flow of the arctic moist tundra sedge, tussock cottongrass (*Eriophorum vaginatum*), in the context of local adaptation and climate change" Evolution 2017, Portland, Oregon
8. Kordbacheh, A., Walsh, E., **Mohl, J.** (2017). "Detecting adaptive genetic variation among cryptic species of the microinvertebrate *Euchlanis dilatata*, using RAD-Seq" Evolution 2017, Portland, Oregon
9. \*Moody, M., **Mohl, J.**, Fetcher, N., Tang, J., Stunz, E. (2017). "Population genomics and gene flow of the dominant arctic moist tundra sedge, tussock cottongrass (*Eriophorum vaginatum*), in the context of local adaptation and climate change" Botany 2017, Fort Worth, Texas

10. Baral, M., Avila, R., **Mohl, J.**, Leung, MY., Skouta, R. (2017). "In silico evaluation of human OX2 orexin receptor (hOX2R) inhibitors using AutoDock and Glide." 2017 Great Lakes Bioinformatics Conference, Chicago, Illinois.
11. Stunz, E., **Mohl, J.**, Fetcher, N., Tang, J., and Moody, M. (2016) "Population genetics and gene flow of the arctic tussock cottongrass (*Eriophorum vaginatum*) in context of local adaptation and climate change." Evolution 2016. Austin, TX
12. Vasquez, M., **Mohl, J.**, and Leung, MY (2016) "Identification of a Dataset and Features for Ubiquitination Predictions" Advanced Computational Biology at Howard University Symposium. Washington, DC
13. \*Walsh, E., **Mohl, J.**, Rivas, JA., Leung, MY., and Gill, T (2015) "Environmental sequencing of biotic components of dust in the Chihuahuan Desert" American Geophysical Union Fall Meeting. San Francisco, CA
14. Lerma, A., **Mohl, J.**, Fetcher, N., Leung, MY., and Moody, ML (2014) "Genetic variation and genealogical structure among *Eriophorum vaginatum* ecotypes using next generation sequencing." 2014 SACNAS National Conference. Los Angeles, CA