

Education:

Postdoctoral Fellowship (2010 - 2012)—University of Texas Southwestern Medical Center
Ph.D. Microbiology (2005 - 2010)—University of Alabama at Birmingham
B.S. Microbiology (1999 - 2005)—Brigham Young University

Research Experience:

Assistant Professor, Brigham Young University (October 2019 – Present)

- Mentor undergraduate students in applying modern computational biology methods to mining raw public transcriptomic and genomic sequencing data
- Use transcriptomics to identify host factors that play a role in pathogenesis during infectious, genetic, and other diseases
- Apply comparative genomics methods to understand evolutionary history and genotype-phenotype correlations in influenza A virus
- Develop machine learning-based data mining techniques to identify biomarkers and relevant trends from publicly available data
- Develop and teach courses in Molecular Biology, Genomics, and Bioinformatics

Lead Scientist, Booz Allen Hamilton (November 2018-October 2019)

- Constructed a computational process to identify activated intracellular signaling pathways, identify protein targets, and predict drugs to reverse observed phenotype
- Preprocessed ~500 RNAseq datasets for storage in NIH-funded database
- Developed CHIPseq analysis pipeline on high-performance computing infrastructure to identify transcriptional start site and histone modification patterns

Assistant Professor, J. Craig Venter Institute (October 2016-November 2018)

- Quantified single-cell intracellular viral transcripts during influenza virus infection
- Supervised effort to integrate lung microbiome, influenza genome variants, host RNAseq, and clinical metadata for computational data mining
- Examined genotype-phenotype correlations between virus sequence and clinical data
- Oversaw submission of over 10,000 virus sequence records to GenBank
- Constructed a bioinformatics workflow to predict sequence alterations in influenza viruses that affect three-dimensional protein structure
- Developed sets of serodiagnostic peptides for multiple mosquito-borne viral pathogens
- Identified host factors that differentiate anti-viral response in multiple cell types during Zika virus infection

Staff Scientist, J. Craig Venter Institute (February 2016-September 2016)

- Developed computational methods to predict antibody cross-neutralization between Rhinovirus strains
- Performed phylodynamic and genotype-phenotype genomic analyses on Chikungunya and Zika viruses
- Predicted Influenza vaccine strains prior to semi-annual WHO meeting
- Identified regions in Zika genome for qRT-PCR reagents

Solution Scientist, Thomson Reuters (May 2014-February 2016)

- Predicted human transcriptional markers and protein targets for cancer, infectious diseases, rare diseases, and other indications

- Applied bioinformatics algorithms to enable: target and biomarker identification, mechanism of action reconstruction, pathway enrichment, interconnectivity, and reverse causal reasoning analysis
- Constructed bioinformatics workflow to prioritize human genetic variants associated with rare autosomal-recessive diseases

Bioinformatics Analyst, J. Craig Venter Institute (June 2012 – May 2014)

- Enhanced the Virus Pathogen Resource (vprbrc.org) and Influenza Research Database (fludb.org) bioinformatics resource centers
- Constructed an analytical method to identify significant host factors involved in Dengue virus replication through a siRNA experiment
- Developed algorithms to predict sequence of newly discovered influenza proteins in all strains (e.g. PA-X, PB1-N40, PA-N155, PA-N182, M42, NS3)
- Performed research on genotype-phenotype correlations in: Dengue, West Nile, Herpes Simplex 1, SARS-CoV, MERS-CoV, Influenza A, and other viruses

Postdoctoral Researcher, University of Texas Southwestern Medical Center (May 2010-May 2012). Mentor: Dr. Richard Scheuermann

- Identified and developed new statistical, analysis, and visualization tools for the NIH-funded Virus Pathogens Resource (ViPRbrc.org) Bioinformatics Database website
- Conceived, designed, and implemented an automated comparative genomics method to identify significant genotype-phenotype correlations
- Performed analysis to identify regions or positions of the viral genome evolving between two dengue virus outbreaks
- Contributed to an approach to identify ancestral evolution of H1N1 influenza pandemic strains

Graduate Student Assistant, University of Alabama at Birmingham (Aug 2005-May 2010)
Mentor: Dr. Elliot J. Lefkowitz

- Dissertation title: “The Contribution of Different Mechanisms of Viral Sequence Variation to the Evolution of Positive-sense Single-stranded RNA Viruses.”
- Detected recombination in West Nile virus using computational methods
- Determined phylogenetic diversity within Hepatitis C virus subtype 1a and relation to drug resistance between clades
- Identified genetic variations between Dengue viruses from two Venezuelan outbreaks and two hemispheres

Undergraduate Research Assistant, Brigham Young University (Aug 2003-Apr 2005)
Mentor: Dr. Donald P. Breakwell

- Characterization and Diversity of antimicrobial-resistance integrons in gram-negative bacteria and their effect on Minimum Inhibitory Concentration of antibiotics.
- Identification of halophilic bacteria present in the Great Salt Lake.

Teaching Experience:

BYU: Assistant Professor in Microbiology and Molecular Biology

- MMBIO 240, *Molecular Biology* (lecture)
- MMBIO 667, *Quantitative Genomics* (lab & lecture)

- MMBIO 294R, *Mentored Research* (lab)
- MMBIO 494R, *Advanced Mentored Research* (lab)
- MMBIO 695R, *Graduate Research* (lab)

San Diego City College: Adjunct Professor in Microbiology (BIOL 205) and Human Genetics (Jan 2013 – May 2014)

- Prepared and present lectures on scheduled material in general Human Genetics (BIOL 205; non-majors) and Microbiology (BIOL 205pre-professional)
- Developed, administered and corrected assignments, labs, and examinations

North Central Texas College: Adjunct Professor in Biology and Microbiology (BIOL 1408, BIOL 2420) (Jan 2011-Dec 2011)

- Prepared and presented lectures on scheduled material in general introductory biology (non-majors) and microbiology (pre-nursing)
- Prepared and corrected assignments, virtual labs, labs, and examinations

UT Southwestern: Lecturer for Introduction to Applied Bioinformatics course (BSCI 5096-02) (Spring 2011)

- Prepared material for lectures including: phylogenetic tree reconstruction, genetic recombination detection, and statistical sequence analyses

UT Southwestern: Lecturer for Virology module of Core Concepts in Molecular Microbiology (MM5481) (Sept 2010)

- Constructed, organized, and presented lecture and exam on RNA virus replication

University of Alabama at Birmingham: Facilitator for UAB-CORD GENEius and BioTeach Laboratories (CB501) (Jun 2008-May 2010)

- Taught each group of students and teachers from underprivileged areas to:
 - Understand basic theories of Molecular Biology
 - Comprehend in-depth molecular causes of disease (HIV, Parkinson's, PCR, and sickle-cell anemia)
 - Perform various Molecular Biology techniques (PCR, western blots, DNA isolation, brain dissection)

Mentoring Experience:

- Brigham Young University
 - 31 Undergraduate students
 - 1 Masters graduate student
 - 1 PhD graduate student
 - 1 undergraduate summer intern
- Other Institutions:
 - Elizabeth Gachanja, doctoral student committee member (2018-2020)
 - Stephen Panossian, undergraduate intern (2018)
 - Emma Roth, undergraduate summer intern (2017)
 - Pilar Viedma, postdoctoral fellow and staff scientist (2017-2020)
- Graduate Committees
 - 7 PhD Committees (1 as Chair)
 - 11 Masters Committees (1 as Chair)

Professional Honors and Awards:

- BYU Inspiring Learning Award (April 2021)
- UAB Department of Microbiology Hiramoto Travel Awardee (Jul 2009)
- T32 NIH Training Grant for Basic Mechanisms of Virology, 5T32AI007150-29 (Jun 2007-Aug 2008)
- Recipient Cold Spring Harbor Laboratory Student Travel Award (Nov 2007)

Other Honors and Awards:

- Honorable completion of religious mission to Dominican Republic (Jul 2000-Jun 2002)
- Eagle Scout, Boy Scouts of America (Jun 1995)

Peer Review Experience:

- Reviewer, ASM mBio (2021-present)
- Reviewer, ASM mSystems (2021-present)
- Reviewer, Biostatistics & Epidemiology (2020-present)
- Reviewer, Gigascience (2020-present)
- Editorial Board Member, PeerJ (2019-present)
- Reviewer, Virology Journal (2010-present)
- Reviewer, Research Grants Council (2014-present)
- Reviewer, NIH study section: Rapid Assessment of Zika Virus Complications (2016)
- Reviewer, BMC Microbiology (2016-present)
- Reviewer, PLoS Neglected Tropical Diseases (2017-present)
- Reviewer, Computational Biology and Chemistry (2018-present)
- Reviewer, Virus Research (2018-present)
- Reviewer, Viruses (2018-present)

Extracurricular Activities:

- Member, College Genetics/Genomics/Molecular Biology Committee (2020-present)
- Faculty advisor, Operation Outbreak Student Academic Association (2020-present)
- Member, Undergraduate Curriculum Committee, BYU (2019-present)
- Chair, Departmental Scientific Review Committee, BYU (2019-present)
- Smithsonian National Museum of Natural History docent for *Outbreak* exhibit (2018-2019)
- J. Craig Venter Institute External Seminar Committee Member (2016-2018)
- UT Southwestern Postdoctoral Association Symposium Subcommittee co-chair of committee (Apr 2011 – May 2012), member (Aug 2010 – May 2012),
- UT Southwestern Postdoctoral Career Development Subcommittee member (Nov 2010 – May 2012)
- Vice President and member of Board of Directors for UAB Scientists and Engineers for America chapter (Jun 2009- May 2010)
- Chairperson mentor of UAB Industry Roundtable (Aug 2008-Aug 2009)
- Co-chairperson of UAB Industry Roundtable (April 2007-Aug 2008)
- Member of the UAB Industry Roundtable Planning Committee (2005-2010)
- Author for UAB's Graduate Student Newsletter (2009)

Additional Skills:

- Computer programming
 - Proficient with programming in R
 - Experience with Docker, Conda, Java, perl, python, mySQL, and Oracle
 - Slurm-based high-performance computing environments

Memberships:

- American Society for Microbiology (2017-present)
- European Virus Bioinformatics Center (2017-present)
- American Society for Virology (2009-present)
- UAB chapter of Scientists and Engineers for America (2009-2010)
- Sigma Delta Pi (2004-present)

Courses Attended:

- Virus Evolution and Molecular Evolution (Berlin, Germany 2018)
- GABRIEL Network: Applications of Genomics & Bioinformatics to Infectious Diseases (Lyon, France 2017)
- Hamilton Robotics: Programming Course (La Jolla, CA 2017)
- Immune Epitope Database: User Workshop (La Jolla, CA 2016)
- San Diego SuperComputer Center: 1st Workshop on bioKepler Tools and its Applications (San Diego, CA, 2012)
- Texas Advanced Computing Center Workshop: High Performance Computing for Next-Generation Sequence Analysis (Austin, TX, 2011)
- First Annual NSF-funded Short Course on Statistical Genetics & Statistical Genomics (Birmingham, AL, 2008)

Meetings Attended:

- Annual American Society for Microbiology Intermountain Branch Meeting (Virtual / Ogden, UT, 2021)
- Annual American Mosquito Control Association Meeting (Virtual / Salt Lake City, UT, 2021)
- 20th Annual American Society for Microbiology Regional Meeting (Weber State University, 2020)
- 37th Annual American Society for Virology meeting (College Park, Maryland, 2018)
- 2nd Annual European Virus Bioinformatics Center meeting (Utrecht, Netherlands, 2018)
- 36th Annual American Society for Virology meeting (Madison, Wisconsin, 2017)
- 19th Genomic Standards Consortium meeting (Brisbane, Australia, 2017)
- Molecular Medicine Tri Conference (San Francisco, CA, 2015)
- 38th Annual International Herpesvirus Workshop (Grand Rapids, MI, 2013)
- 37th Annual International Herpesvirus Workshop (Calgary, Alberta, Canada, 2012)
- 6th Annual NIAID Centers of Excellence for Influenza Research and Surveillance (CEIRS) Network Meeting (New York, NY, 2012)
- 31st American Society for Virology Annual Meeting (Madison, Wisconsin, 2012)

- XV International Union of Microbiological Societies, Congress of Virology Meeting. (Sapporo, Japan, 2011)
- 30th American Society for Virology Annual Meeting (Minneapolis, Minnesota, 2011)
- A Re-Emerging Challenge in the Americas: Opportunities for Dengue Research Collaboration Meeting (San Juan, Puerto Rico, 2011)
- 9th Annual ASM Biodefense and Emerging Diseases Research Meeting (Washington D.C. 2011)
- 29th American Society for Virology Annual Meeting (Bozeman, Montana, 2010)
- 28th American Society for Virology Annual Meeting (Vancouver, Canada, 2009)
- 15th Annual International Symposium on Hepatitis C Virus and Related Viruses (San Antonio, TX, 2008)
- 7th Cold Spring Harbor Laboratory/Wellcome Trust conference on Genome Informatics (Cold Spring Harbor, NY, 2007)
- 8th International Symposium on Positive-Strand RNA Viruses (Washington DC, 2007)
- 9th Annual Conference for Computational Genomics (Baltimore, MD, 2006).
- 53rd Annual ASM Regional Meeting (Ogden, UT, 2005)

Poster Presentations:

1. Scott TM, Solis-Leal A, Lopez JB, Robison RA, Berges BK, **Pickett BE**. *Analysis of differential host cell response to infection with Washington and New York strains of SARS-CoV-2*. BYU College Undergraduate Research Awards Annual Presentation. November, 2021.
2. Gray M, Guerrero-Arguero I, Solis Leal A, Robison RA, Berges BA, **Pickett BE**. *Chikungunya Virus Time Course Infection of Human Macrophages*. BYU College Undergraduate Research Awards Annual Presentation. November, 2021.
3. Velazquez EJ, Bellini DM, Skabelund RA, Humpherys TB, Skidmore JR, **Pickett BE**, Piccolo SR, O'Neill KL. *Bioinformatic analysis of the tumor biomarker thymidine kinase 1: Elucidating its cancer gene network and membrane expression across all cancers*. American Association for Cancer Research Annual Meeting. April, 2021.
4. Howell J, Jackson C, Scott TM, Lowen AC, Tan GS, **Pickett BE**. *A Single-Cell Bioinformatics Analysis of the Host Transcriptional Response to Infection Consisting of Natural Combinations of Influenza A Virus Gene Segments*. BYU College of Life Sciences Virtual Poster Competition. Provo, UT. March, 2021.
5. Gray M, Guerrero-Arguero I, Solis Leal A, Robison RA, Berges BA, **Pickett BE**. *Chikungunya Virus Time Course Infection of Human Macrophages*. BYU College of Life Sciences Virtual Poster Competition. Provo, UT. March, 2021.
6. Downey JL, Griffin BT, Jensen AR, Ludwig A, Spencer JB, Scott TM, Vander Werff KS, **Pickett BE**, Grose JH, Breakwell DP. *Comparative Genomic Analysis of Microbacterium foliorum Cluster EE Phages*. American Society for Microbiology Intermountain Branch Meeting. December, 2020.
7. Miller A, Knowles A, Hill JT, **Pickett BE**, Nielsen BL. *Gene Expression Changes in Plants Inoculated with Halophilic Bacteria and Grown in Salty Soil*. American Society for Microbiology Intermountain Branch Meeting. December, 2020.
8. Ferrarini MG, Lal A, Rebollo R, Gruber A, Guarracino A, Martinez-Gonzalez I, Floyd T, Siqueira de Oliveira D, Pusa T, **Pickett BE**, Aguiar-Pulido V.

- Comprehensive analysis of human SARS-CoV-2 infection and host-virus interaction.* International Society of Computational Biology Annual Meeting (Virtual). July 13-16, 2020.
9. Parham L, **Pickett BE**, Tan GS, Lorenzana I. *Sequencing of a Zika virus isolate from the amniotic fluid of a fetus with microcephaly during an outbreak in Honduras-2016.* American Society for Tropical Medicine and Hygiene annual meeting. National Harbor, MD. November 20-24, 2019.
 10. Viedma Martinez MP, **Pickett BE**. *Placenta and Microglia Cells Immune Response After Zika Virus Infection.* American Society for Virology annual meeting. College Park, MD. July 14-18, 2018.
 11. **Pickett BE**, Willis CD. *Oral Microbiome: Potential Mechanisms and Drug Targets for Differential Host Response During Infection with Pathogenic and Commensal Bacteria.* Molecular Medicine Tri Conference. San Francisco, CA. March 6-9, 2016.
 12. **Pickett BE**. *Functional Analysis of Infection with Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and a Possible Therapeutic Target.* Molecular Medicine Tri Conference. San Francisco, CA. February 16-18, 2015.
 13. Aevermann BD, Greer DS, **Pickett BE**, Kumar S, Zhang Y, Quesenberry B, Zhou L, Gu Z, Zaremba S, Klem EB, and Scheuermann RH. *Exploration and Comparison of Host Factor Responses to Viral Infection in the Influenza Research Database (IRD)* Centers of Excellence for Influenza Research and Surveillance (CEIRS) annual meeting. Memphis, TN. July 8-10, 2013.
 14. Zhang Y, **Pickett BE**, Greer DS, Aevermann BD, Stewart L, Zhou L, Kumar S, Zaremba S, Gu Z, Sun G, Larsen C, Jen W, Klem EB, Scheuermann RH. *Virus Pathogen Resource (ViPR): Bioinformatics Database and Analysis Resource for Human Virus Pathogen Research.* ASM Biodefense and Emerging Diseases Research Meeting. Washington, D.C. February 25-27, 2013.
 15. Zhang Y, **Pickett BE**, Sadat E, Squires RB, Noronha J, Kumar S, Zaremba S, Gu Z, Zhou L, Larsen C, Jen W, Klem EB, Scheuermann RH. *Integrated Bioinformatics Data and Analysis Tools for Herpesviridae Viruses in the Virus Pathogen Resource (ViPR).* 37th Annual International Herpesvirus Workshop. Calgary, Alberta, Canada. August 4-9, 2012.
 16. **Pickett BE**, Sadat E, Zhang Y, Hunt V, Noronha JM, Squires RB, Law L, Katze M, Klem EB, Scheuermann RH. *Integration of Host Factor Data into the Virus Pathogen Database and Analysis Resource (ViPR) and the Influenza Research Database (IRD).* 2012 American Society for Virology Annual Meeting. Madison, WI, USA. July 21-25, 2012.
 17. **Pickett BE**, Sadat E, Zhang Y, Noronha J, Squires RB, Hunt V, Liu M, Zhou L, Larson C, Dietrich J, Klem EB, Scheuermann RH. *ViPR: An Open Comprehensive Bioinformatics Database and Analysis Resource for the Virology Research Community.* 2011 International Union of Microbiological Societies (International Congress of Virology). Sapporo, Japan. September 11-17, 2011.
 18. **Pickett BE**, Noronha J, Squires RB, Hunt V, Liu M, Zhou L, Larson C, Dietrich J, Klem EB, Scheuermann RH. *Genomic sequence analysis tools and a genotype-phenotype association platform in the virus pathogen resource.* 30th American Society for Virology Annual Meeting. Minneapolis, Minnesota. July 16-20, 2011.

19. Joslin S, Pybus C, Brautigham C, **Pickett BE**, Noronha J, Scheuermann R, Ahmed A, Erlich G, Hansen E. *Involvement of the MesR response regulator in Moraxella catarrhalis biofilm formation*. Annual Hemophilus-Moraxella Meeting. Curacao. June 2011.
20. **Pickett BE**, Ponraj P, Hunt V, Liu M, Zhou L, Kumar S, Dietrich J, Zaremba S, Larson C, Klem EB, Scheuermann RH. *Tool for Identifying Sequence Variations that Correlate with Virus Phenotypic Characteristics*. 9th Annual ASM Biodefense and Emerging Diseases Research Meeting. Washington D.C. February 6-9, 2011.
21. Ponraj P, **Pickett BE**, Squires RB, Noronha JM, Hunt V, McClellan EA, Zhou L, Kumar S, Liu Z, Su H, Dietrich J, Zaremba S, Larsen C, Klem EB, and Scheuermann RH. *Virus Pathogen Resource (ViPR): Applications for Studying Virus Variation and Host-Virus Interactions*. 29th American Society for Virology Annual Meeting. Bozeman, Montana. July 17-21, 2010.
22. **Pickett BE**, Lefkowitz EJ. *West Nile virus: analysis of covariance and recombination*. 28th Annual American Society for Virology meeting. Vancouver, Canada. July 11-15, 2009.
23. **Pickett BE**, Striker RT, Lefkowitz EJ. *Evidence for separation of HCV Genotype 1, Subtype A into Two Distinct Clades*. 15th International Symposium on Hepatitis C Virus & Related Viruses. San Antonio TX. Oct 5-9, 2008.
24. SS Drysdale, L Tazi, **BE Pickett**, SB Dahlquist, KA Crandall, DP Breakwell, and AR Harker. 2005. *Microbial Diversity in the Great Salt Lake, Utah*. 105th American Society for Microbiology General Meeting. Atlanta, GA. June 5-9, 2005.

Oral Presentations:

1. Gray M, Ahlborn G, **Pickett BE**. *Quantifying the Effects of Potential CHIKV Therapeutics in Human Macrophage Cells*. American Society for Microbiology Intermountain Branch Annual Meeting. Ogden, UT (virtual). December, 2021.
2. Moreno C, Whitley K, Freitas C, **Pickett BE**, Weber KS. *CD5 signaling inhibits the transcription of metabolic enzymes and metabolite transporters at the transcriptomic level*. Autumn Immunology Conference 49th Annual Meeting. Chicago, IL. November, 2021.
3. Rapiere-Sharman NL, **Pickett BE**. *A Transcriptomic Meta-Analysis of B-cell Lymphomas*. 2nd International Webinar on Cancer Research and Oncology Aug 2021.
4. Gray M, Guerrero-Arguero I, Solis Leal A, Robison RA, Berges BA, **Pickett BE**. *Chikungunya Virus Time Course Infection of Human Macrophages*. American Society for Virology. July, 2021.
5. Jackson CA, Scott TM, Howell J, Tan GS, Lowen A, **Pickett BE**. *A single-cell bioinformatics analysis of the host transcriptional response to infection consisting of natural combinations of influenza A virus gene segments*. American Society for Virology. July, 2021.
6. Scott TM, Jensen S, **Pickett BE**. *A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases*. American Society for Virology. Virtual Meeting. July, 2021.
7. Gray M, Guerrero-Arguero I, Solis Leal A, Robison RA, Berges BA, **Pickett BE**. *Chikungunya Virus Time Course Infection of Human Macrophages*. World Society for Virology Annual Conference (virtual). June, 2021.

8. Gifford K, **Pickett BE**. *A Cell Under Siege: the Mechanisms of Streptococcus Pneumoniae Infection*. BYU College of Physical and Mathematical Sciences - Student Research Conference. Provo, UT. February 2021.
9. Scott TM, Jensen S, **Pickett BE**. *A Signaling Pathway-Driven Bioinformatics Pipeline for Predicting Therapeutics against Emerging Infectious Diseases*. American Society for Microbiology Intermountain Branch Meeting. December, 2020
10. Gray M, **Pickett BE**. *Chikungunya Virus Time Course Infection of Human Macrophages*. American Society for Microbiology Intermountain Branch Meeting. December, 2020.
11. Grose, JH, Downey JL, Griffin BT, Jensen AR, Ludwig A, Spencer JB, Scott TM, Wander Werff KS, **Pickett BE**, Breakwell DP. *Comparative Genomic Analysis of Microbacterium foliorum Cluster EE phages*. Intermountain Branch American Society for Microbiology. Ogden, UT. December, 2020.
12. Ferrarini MG, Lal A, Rebollo R, Gruber A, Guarracino A, Martinez-Gonzalez I, Floyd T, Siqueira de Oliveira D, Pusa T, **Pickett BE**, Aguiar-Pulido V. *Genome-wide Bioinformatic Analyses Predict Key Host and Viral Factors in SARS-CoV-2 Pathogenesis*. Cold Spring Harbor Laboratory COVID/SARS CoV2 Rapid Research Reports #3. Cold Spring Harbor, NY (Virtual). August 25-26, 2020.
13. Gifford K, **Pickett BE**. *Understanding the Mechanisms of Streptococcus Pneumoniae Infection*. BYU College of Physical and Mathematical Sciences - Student Research Conference. Provo, UT. February 29, 2020.
14. **Pickett BE**. *Identification and Validation of Diagnostic Peptides to Differentiate Serum Antibody Patterns Between Zika and Other Mosquito-Borne Viruses*. 37th Annual American Society for Virology meeting. College Park, Maryland. July 14-18, 2018.
15. **Pickett BE**. *Deep-sequencing Analysis of coding-complete Zika virus genomes*. 36th Annual American Society for Virology meeting. Madison, Wisconsin. June 24-28, 2017.
16. **Pickett BE**. *Peptide array technology: an opportunity for standardization*. 19th Genomic Standards Consortium meeting. Brisbane, Queensland, Australia. May 15-17, 2017 .
17. **Pickett BE**, Zhang Y, Scheuermann R. *ViPR Resource Workshop*. 37th Annual International Herpesvirus Workshop. Calgary, Alberta, Canada. August 4-9, 2012.
18. **Pickett BE**, Schmidt D, Camacho D, Comach G, Bosch I, Lefkowitz EJ. *Analysis of Dengue Type 3 Sequences from Two Venezuelan Outbreaks*. 29th American Society for Virology Annual Meeting. Bozeman, Montana. July 17-21, 2010.
19. **Pickett BE**, Lefkowitz EJ. *Separating HCV genotype 1a into 2 clades and implications for drug resistance*. University of Alabama at Birmingham Virology Discussion Group. Birmingham, Alabama. November 7, 2008.
20. **Pickett BE**, Lefkowitz EJ. *CovarView—A program for visual display of genome-wide covariance analyses*. 7th Cold Spring Harbor Laboratory/Wellcome Trust conference on Genome Informatics. Cold Spring Harbor, New York. November 1-5, 2007.
21. **Pickett BE**, Breakwell DP. *Antibiotic Resistance Gene Cassettes Associated With Integrons in Escherichia coli*. 53rd Annual meeting of the American Society for Microbiology regional meeting. Weber State University, Ogden, Utah. March 12th, 2005.

Invited Oral Presentations:

1. *Using Bioinformatics to Better Understand Molecular Mechanisms of Cancer*. Simmons Center for Cancer Research Weekly Seminar Series. May, 2021.
2. *Using a simulated campus SARS-CoV-2 outbreak to inform better decision making*. MMBIO Department Weekly Seminary. Provo, UT, 2021.
3. *Developing a peptide-based diagnostic platform to detect past infection with mosquito-borne viruses using human convalescent serum*. Annual American Mosquito Control Association Meeting; Salt Lake City, UT, 2021.
4. *Reference-based assembly and variant calling in NGS data*. Virus Evolution and Molecular Epidemiology; Berlin, Germany, 2018.
5. *Genome Sequencing, serodiagnostics, and the intracellular host response: making sense of -omics data for Zika virus*. European Virus Bioinformatics Center; Utrecht, Netherlands, 2018.
6. *Applications of next generation sequencing technologies to viral infectious diseases*. GABRIEL Network; Fondation Merieux; Lyon, France, 2017.
7. *Next generation sequencing technologies for host response*. GABRIEL Network; Fondation Merieux; Lyon, France, 2017.
8. *Molecular Evolution of Viral Genomes and the Host Response*. Dept of Biology; Brigham Young University; Provo, UT, 2014.
9. *Using siRNA Screens to Identify Host Genes Important for Dengue Virus Replication*. Dept of Microbiology and Molecular Biology; Brigham Young University; Provo, UT, 2014.
10. *Introduction to the Metadata-driven Comparative Analysis Tool for Sequences (meta-CATS)*. Dept of Microbiology and Molecular Biology; Brigham Young University; Provo, UT, 2013.
11. *Influenza Research Database / Virus Pathogen Resource Hands-on Workshop at annual Pork Board Meeting*. US Dept of Agriculture; Ames, IA, 2013.
12. *Influenza Research Database / Virus Pathogen Resource Hands-on Workshop*. Emory University. October 5, 2012.
13. *Features and Capabilities of the Virus Pathogen Database and Analysis Resource (ViPR)*. Purdue University. September 7, 2011.

Patents:

1. U.S. Patent Application: "COMPOSITIONS AND METHODS FOR THE DETECTION OF ANTI-VIRAL ANTIBODIES". Serial No.: 16/033,117. Submission date: July 11, 2018.

Peer-Reviewed Publications:

1. Guerrero-Arguero I, Tellez-Freitas CM, Weber KS, Berges BK, Robison RA, **Pickett BE**. *Alphaviruses: Host pathogenesis, immune response, and vaccine & treatment updates*. J Gen Virol. 2021 Aug;102(8). DOI: 10.1099/jgv.0.001644. PMID: 34435944.
2. Rapier-Sharman N, Krapohl J, Beausoleil EJ, Gifford KTL, Hinatsu BR, Hoffmann CS, Komer M, Scott TM, **Pickett BE**. *Preprocessing of Public RNA-Sequencing Datasets to Facilitate Downstream Analyses of Human Diseases*. Data. 2021; 6(7):75. DOI: 10.3390/data6070075.

3. Martinez Viedma MDP, Panossian S, Gifford K, García K, Figueroa I, Parham L, de Moraes L, Nunes Gomes L, García-Salum T, Perret C, Weiskopf D, Tan GS, Augusto Silva A, Boaventura V, Ruiz-Palacios GM, Sette A, De Silva AD, Medina RA, Lorenzana I, Akrami KM, Khouri R, Olson D, **Pickett BE**. *Evaluation of ELISA-Based Multiplex Peptides for the Detection of Human Serum Antibodies Induced by Zika Virus Infection across Various Countries*. Viruses. 2021 Jul 8;13(7):1319. DOI: 10.3390/v13071319. PMID: 34372525.
4. Scott TM, Jensen S and **Pickett BE**. *A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases*. F1000Research 2021, 10:330. DOI: 10.12688/f1000research.52412.2. PMID: 34868553.
5. Ferrarini MG, Lal A, Rebollo R, Gruber AJ, Guarracino A, Gonzalez IM, Floyd T, de Oliveira DS, Shanklin J, Beausoleil E, Pusa T, **Pickett BE**, Aguiar-Pulido V. *Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis*. Commun Biol. 2021 May 17;4(1):590. DOI: 10.1038/s42003-021-02095-0. PMID: 34002013.
6. Phipps KL, Ganti K, Carnaccini S, Manandhar M, Jacobs NT, **Pickett BE**, Tan GS, Ferreri LM, Perez DR, Lowen AC. *Collective interactions augment influenza A virus replication in a host-dependent manner*. Nat Microbiol. 2020 Jul. DOI: 10.1038/s41564-020-0749-2. PMID: 32632248.
7. Kaul D, Rathnasinghe R, Ferres M, Tan GS, Barrera A, **Pickett BE**, Methe B, Das SR, Budnik I, Halpin RA, Wentworth D, Schmolke M, Mena I, Albrecht R, Singh I, Nelson KE, Garcia-Sastre A, Dupont C, Medina R. *Microbiome disturbance and resilience dynamics of the upper respiratory tract in response to influenza A virus infection in analog hosts*. Nat Commun. 2020 May;11(1):2537. DOI: 10.1038/s41467-020-16429-9. PMID: 32439901.
8. Viedma MPM, Kose N, Parham L, Balmaseda A, Kuan G, Lorenzana I, Harris E, Crowe JE, **Pickett BE**. *Peptide Arrays Incubated with Three Collections of Human Sera from Patients Infected with Mosquito-Borne Viruses*. F1000Res. 28 Feb 2020, 8:1875. DOI: 10.12688/f1000research.20981.3. PMID: 32201571.
9. Bialosuknia SM, Tan Y, Zink SD, Koetzner CA, Maffei JG, Halpin RA, Muller E, Novatny M, Shilts M, Fedorova NB, Amedeo P, Das SR, **Pickett B**, Kramer LD, Ciota AT. *Evolutionary dynamics and molecular epidemiology of West Nile virus in New York State: 1999-2015*. Virus Evol. 2019 Jul;5(2):vez020. DOI: 10.1093/ve/vez020. PMID: 31341640.
10. Viedma Martinez MP, Puri V, Oldfield LM, Shabman RS, Tan GS, **Pickett BE**. *Optimization of qRT-PCR assay for Zika virus detection in human serum and urine*. Virus Research 2019 Feb 10; 263:173-178. DOI: 10.1016/j.virusres.2019.01.013. PMID: 30742853.
11. Viedma Martinez MP, **Pickett BE**. *Characterizing the Different Effects of Zika Virus Infection in Placenta and Microglia Cells*. Viruses 2018, 10(11), 649. DOI: 10.3390/v10110649. PMID: 30453684.
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Ongoing Funding Support

Role: Principal Investigator

Title: College of Life Sciences Startup Funds

Dates: December 2020 – Present

Sponsor: BYU-College of Life Sciences, new faculty startup funding

Amount: \$60,000

Role: Principal Investigator

Title: Department Capital Startup Funds

Dates: October 2019 - present

Sponsor: BYU-Department of Microbiology and Molecular Biology

Amount: \$75,000

Completed Funding Support:

Role: Principal Investigator

Title: Computational analysis of human transcriptomic data to predict host drug targets that reduce Influenza A virus (IAV) infection.

Dates: November 2019 – November 2020

Sponsor: BYU-College of Life Sciences, new faculty startup funding

Amount: \$20,000

Role: Principal Investigator

Title: Predicting Influenza Vaccine Strains

Dates: Dec 1, 2012-Nov 30, 2016

Sponsor: Synthetic Genomics Vaccines, Inc.

Amount: \$746,061

Role: Principal Investigator

Title: Influenza Curation Project

Dates: 01/15/2017 - 02/28/2017

Sponsor: Private funding

Amount: \$28,669

Role: Investigator

Title: Development of a Universal Rhinovirus Vaccine

Dates: 06/01/14-11/01/17

Sponsor: Private Funding

Amount: \$2,683,500

Role: Principal Investigator

Title: Implementation of an Influenza HA Sequence to Structure to Function Computational Workflow

Dates: 08/28/2017 – 12/31/2017

Sponsor: Private Funding

Amount: \$137,107

Role: Principal Investigator

Title: A Protein-Based Method to Distinguish Seroprevalence in Humans for Multiple Mosquito-Borne Flaviviruses

Dates: Oct 1, 2016 - Dec 31, 2018

Sponsor: United States Agency for International Development

Amount: \$450,670

Role: Co-Investigator

Title: Bioinformatics Resource Centers for Infectious Disease – Viral

Dates: 07/01/14-06/30/19

Sponsor: National Institute of Allergy and Infectious Diseases

Amount: \$7,302,405

Brett E. Pickett, Ph.D.

Role: Co-Project Director

Title: The J. Craig Venter Institute Genome Center for Infectious Diseases

Dates: 04/01/14-03/31/19

Sponsor: National Institute of Allergy and Infectious Diseases

Amount: \$28,288,353