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Education:

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

Experience:

Assistant Professor, Brigham Young University (October 2019 – Present)
- Mentor undergraduate students in applying modern computational biology methods to mining raw public sequencing data
- Use transcriptomics to identify host factors that play a role in pathogenesis during infection
- Apply comparative genomics methods to understand evolutionary history and genotype-phenotype correlations
- Develop data mining techniques to identify biomarkers and relevant trends from publicly available data
- Develop and teach courses on Microbiology, 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
- Contributed to data mining and analysis efforts for the NIH-funded Placental Atlas Tool (https://pat.nichd.nih.gov)
- Increased processed RNAseq datasets by 50% and microarray datasets by 10%
- Implemented a data processing workflow to map and analyze NGS reads from genomic and transcriptomic experiments
- Developed ChIPseq analysis pipeline to identify transcriptional start site and histone modification patterns

Assistant Professor, J. Craig Venter Institute (October 2016-November 2018)
- Used single-cell RNAseq to quantify 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
- Managed work to predict causative agent of non-flu viral respiratory infections in children
- 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 viruses
- Designed peptide array screens to identify immunodominant epitopes among Zika-infected patients
- Constructed a random forest machine learning pipeline to identify immunodominant epitopes recognized by human convalescent sera after infection by flaviviruses

- Identified host factors that differentiate anti-viral response in multiple cell types during Zika virus infection
- Constructed bioinformatics pipeline to analyze minor variants in viral genomes
- Lead biweekly bioinformatics training courses
- Drafted and submitted successful proposals for external grants and contracts

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)
- Used 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
- Predicted human transcriptional markers and protein targets for cancer, infectious diseases, rare diseases, and other indications
- Wrote white papers on targets related to oral microbiome and viral infection
- Constructed workflows using Application Programming Interfaces (APIs) for precision medicine applications

Bioinformatics Analyst, J. Craig Venter Institute (June 2012 – May 2014)
- Enhanced the Virus Pathogen Resource (viprbrc.org) and Influenza Research Database (fludb.org) bioinformatics resource centers
  - Developed infrastructure and workflows to receive, mine, analyze, and visualize data from various influenza-based "-omics" experiments
  - Created analytical pipeline to categorize somatic and germline sequence variations detected by NGS in human induced pluripotent stem cells
  - Implemented analytical workflows in high-performance computing environment
  - 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
  - Developed first phylogenetic tree viewer for Apple iOS mobile devices
  - Conceived, designed, and implemented an automated comparative genomics method to identify significant genotype-phenotype correlations

- o Manually curated existing resources and literature to define Sequence Feature Variant Types for Hepatitis C Virus, Dengue Virus, and Poxviruses
- o Performed analysis to identify regions or positions of the viral genome evolving between two dengue virus outbreaks
- o Contributed to an approach to identify ancestral evolution of H1N1 influenza pandemic strains
- o Participate in outreach efforts, training, and activities to expand user base of the resource

Graduate Student Assistant, <u>University of Alabama at Birmingham</u> (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."
  - o Detected first known recombination in West Nile virus using bioinformatics
  - o Determined phylogenetic diversity within Hepatitis C virus subtype 1a and relation to drug resistance between clades
  - o Identified genetic variations between Dengue viruses from two Venezuelan outbreaks and two hemispheres
  - o Evaluated phylogenetic relationships between Eastern Equine Encephalitis whole genomes
  - o Constructed dengue virus genotyping web algorithm and application

Undergraduate Research Assistant, <u>Brigham Young University</u> (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:

Adjunct Professor in Microbiology and Human Genetics (BIOL 205, BIOL 130) (Jan 2013 – May 2014) San Diego City College; Department chairs: Dr. Donna DiPaolo & Erin Rempala

- Organized syllabi
- Prepared and present lectures on scheduled material in general Human Genetics (non-majors) and Microbiology (pre-professional)
- Presented background information, and facilitated learning in a laboratory setting
- Developed, administered and corrected written assignments, and examinations

Adjunct Professor in Biology and Microbiology (BIOL 1408, BIOL 2420) (Jan 2011-Dec 2011) North Central Texas College; Department chair: Dr. Sam Dunlap

- Organized syllabi
- Prepared and presented lectures on scheduled material in general introductory biology (non-majors) and microbiology (pre-nursing)
- Prepared lab reagents, presented background information, and facilitated learning in a laboratory setting
- Created new bioinformatics-based virtual lab module
- Developed, administered and corrected assignments, virtual labs, and examinations

Lecturer for Introduction to Applied Bioinformatics course (BSCI 5096-02) (Spring 2011) UT Southwestern; Course master: Dr. Richard Scheuermann
- Prepared material for lectures covering: phylogenetic tree reconstruction, genetic recombination detection, and statistical sequence analyses
- Used capabilities in ViPR web-based resource to solidify concepts being taught

Lecturer for Virology module of Core Concepts in Molecular Microbiology (MM5481) (Sept 2010) UT Southwestern; Supervisor: Dr. Julie Pfeiffer
- Constructed, organized, and presented lecture on RNA virus replication
- Developed questions and graded evaluations

Facilitator for UAB-CORD GENEius and BioTeach Laboratories (CB501) (Jun 2008-May 2010) University of Alabama at Birmingham; Supervisors: Dr. Vanessa Williams, Dr. Sabrina Walthall
- Taught each group of students to:
  - 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)
- Taught high school teachers and students from underprivileged areas to:
  - Understand basic theories of Molecular Biology
  - Perform Molecular Biology techniques (genetic engineering, bacterial culture)
  - Assess their own improvement

Teaching Assistant for Advanced Molecular Biology Lab (MMBIO 441) (Jan-Apr 2005) Brigham Young University; Supervisor: Dr. Brent Nielsen
- Prepared laboratory materials before each class
- Taught undergraduate class members how to perform protocols
- Graded evaluations

Teaching Assistant for Advanced Lab Methods (MMBIO 365) (Aug 2004-Apr 2005) Brigham Young University; Supervisor: Dr. Sandra Burnett (Hope)
- Prepared protocols before each class
- Demonstrated protocols for members of class
- Taught undergraduate class members how to perform protocols
- Constructed online evaluations of student knowledge

Professional Honors and Awards:
- UAB Department of Microbiology Hiramoto Travel Awardee (Jul 2009)
- T32 NIH Training Grant for Basic Mechanisms of Virology (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)

Mentor Experience:
- Elizabeth Gachanja, doctoral student committee member (2018-present)
- Stephen Panossian, undergraduate intern (2018)
- Emma Roth, undergraduate summer intern (2017)
- Pilar Viedma, postdoctoral fellow and staff scientist (2017-present)

Peer Review Experience:
- 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:
- Smithsonian National Museum of Natural History docent for *Outbreak* exhibit (2018-present)
- Treasurer for local non-profit organization (2012-2016)
- J. Craig Venter Institute External Seminar Committee Member (2016-present)
- UT Southwestern Postdoctoral Association Symposium Subcommittee co-chair of committee (Apr 2011 – May 2012), member (Aug 2010 – May 2012),
  - Contact vendors for fundraising budget ($5,000/yr)
  - Plan and execute annual event for presentations attended by over 500 people
- UT Southwestern Postdoctoral Career Development Subcommittee member (Nov 2010 – May 2012)
  - Evaluate career preparation needs of postdoctoral researchers
  - Identify and invite monthly speakers to address those career needs
- Vice President and member of Board of Directors for UAB Scientists and Engineers for America chapter (Jun 2009- May 2010)
  - Perform administrative duties (funding, identifying speakers, website, etc.)
  - Oversee education initiatives undertaken by student body
- Chairperson mentor of UAB Industry Roundtable (Aug 2008-Aug 2009)
  - Obtain funding for annual Career Development workshop ($13,000/yr)
  - Assist and train new chairpersons to perform administrative tasks
- Co-chairperson of UAB Industry Roundtable (April 2007-Aug 2008)
  - Obtain and supervise spending of budget funds ($20,000/yr)
  - Write funding applications, seminar synopses
  - Manage 12 members of planning committee
  - Identify and invite 6 monthly speakers
  - Plan and execute annual Career Development workshop to inform attendees (14 speakers and 86 students) about career opportunities after graduation
- Member of the UAB Industry Roundtable Planning Committee (2005-2010)

- Referee for various journals (2009-present)
- Author for UAB's Graduate Student Newsletter (2009)

Additional Skills:
- Computer programming
  - Proficient with programming in Perl, R
  - Experience with Docker, Conda, Java, mySQL, and Oracle
- Proficient with Microsoft Office environment
- Comfortable with online classroom environments such as Blackboard

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:
- 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:

- 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.
- 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.
- **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.
- **Pickett BE**. *Functional Analysis of Infection with Meddle East Respiratory Syndrome Coronavirus (MERS_CoV) and a Possible Therapeutic Target.* Molecular Medicine Tri Conference. San Francisco, CA. February 16-18, 2015.
- 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.
- 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.
- Zhang Y, **Pickett BE**, Sadat E, Squires RB, Noronha J, Kumar S, Zaremba S, Gu Z, Zhou L, Larsen C, Jen W, Klem EB, Scherumann 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.

- **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.
- **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.
- **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.
- 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.
- **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.
- 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.
- **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.
- **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.
- 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:

- **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.
- **Pickett BE**. *Deep-sequencing Analysis of coding-complete Zika virus genomes*. 36th Annual American Society for Virology meeting. Madison, Wisconsin. June 24-28, 2017

- **Pickett BE**. *Peptide array technology: an opportunity for standardization*. 19th Genomic Standards Consortium meeting. Brisbane, Queensland, Australia. May 15-17, 2017
- **Pickett BE**, Zhang Y, Scheuermann R**. *ViPR Resource Workshop*. 37th Annual International Herpesvirus Workshop. Calgary, Alberta, Canada. August 4-9, 2012.
- **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.
- **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.
- **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.
- **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:
- Reference-based assembly and variant calling in NGS data. Virus Evolution and Molecular Epidemiology; Berlin, Germany, 2018
- Genome Sequencing, serodiagnostics, and the intracellular host response: making sense of –omics data for Zika virus. European Virus Bioinformatics Center; Utrecht, Netherlands, 2018
- Applications of next generation sequencing technologies to viral infectious diseases. GABRIEL Network; Fondation Merieux; Lyon, France, 2017
- Next generation sequencing technologies for host response. GABRIEL Network; Fondation Merieux; Lyon, France, 2017
- Molecular Evolution of Viral Genomes and the Host Response. Dept of Biology; Brigham Young University; Provo, UT, 2014
- Using siRNA Screens to Identify Host Genes Important for Dengue Virus Replication. Dept of Microbiology and Molecular Biology; Brigham Young University; Provo, UT, 2014
- Introduction to the Metadata-driven Comparative Analysis Tool for Sequences (meta-CATS). Dept of Microbiology and Molecular Biology; Brigham Young University; Provo, UT, 2013
- Influenza Research Database / Virus Pathogen Resource Hands-on Workshop at annual Pork Board Meeting. US Dept of Agriculture; Ames, IA, 2013
- Influenza Research Database / Virus Pathogen Resource Hands-on Workshop. Emory University. October 5, 2012
- Features and Capabilities of the Virus Pathogen Database and Analysis Resource (ViPR). Purdue University. September 7, 2011.

Patents:

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

Publications:

- Bitter EE, Townsend MH, Tsai KYF, Allen CI, Erickson RI, **Pickett BE**, Arroyo JA, O'Neill K. TK1 in Cancer Progression: elucidating its influence on cellular invasion and survival. (In Submission)
- 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 BioRxiv 736108; doi: https://doi.org/10.1101/736108. (In Submission).
- 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. BioRxiv, 325324. doi: https://doi.org/10.1101/325324. (In Submission).
- Viedma MPM, Kose N, Parham L, Balmaseda A, Kuan G, Lorenzana I, Harris E, Crowe JE, **Pickett BE**. Peptide Arrays of Three Collections of Human Sera from Patients Infected with Mosquito-Borne Viruses. BioRxiv 650796; doi: https://doi.org/10.1101/650796. (In Submission).
- 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.
- 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.
- Viedma Martinez MP, **Pickett BE**. Characterizing the Different Effects of Zika Virus Infection in Placenta and Microglia Cells. *Viruses* 2018, 10(11), 649. https://doi.org/10.3390/v10110649. PMID: 30453684.
- Moser LA, Boylan BT, Moreira FR, Myers LJ, Svenson EL, Fedorova NB, **Pickett BE**, Bernard KA. Growth and adaptation of Zika virus in mammalian and mosquito cells. *PLoS Negl Trop Dis*. 2018 Nov 12;12(11):e0006880. doi: 10.1371/journal.pntd.0006880. PMID: 30418969.
- Shrivastava S, Puri V, Dilley KA, Ngouajio E, Shifflett J, Oldfield L, Fedorova N, Hu L, Williams T, Durbin A, Amedeo P, Rashid S, Shabman RS, **Pickett BE**. Whole genome sequencing, variant analysis, phylogenetics, deep sequencing, and development of diagnostic assays for Zika virus strains. *Nature Sci Rep*. 2018 Oct 26;8(1):15843. doi: 10.1038/s41598-018-34147-7. PMID: 30367096.

- Tan Y*, **Pickett BE***, Shrivastava S, Gresh L, Balmaseda A, Amedeo P, Hu L, Puri V, Fedorova NB, Halpin RA, LaPointe MP, Cone MR, Larson LH, Kramer LD, Ciota AT, Gordon A, Shabman RS, Das SR, Harris E. Differing epidemiological dynamics of Chikungunya virus in the Americas during 2014- 2015 epidemic. *PLoS Neglected Tropical Diseases*. 2018 Jul 30; 12(7):e0006670. PMID: 30059496

- Oldfield LM, Fedorova N, Puri V, Shrivastava S, Amedeo P, Durbin A, Rocchi I, Williams T, Shabman RS, Tan GS, Balmaseda A, Kuan G, Saborio S, Gordon A, Harris E, **Pickett BE**. Sequences of Zika Virus Genomes from a Pediatric Cohort in Nicaragua. *Genome Announc*. 2018 Jun 14;6(24). pii: e00498-18. PMID: 29903816.

- Nyaga MM, Tan Y, Seheri ML, Halpin RA, Akopov A, Stucker KM, Fedorova NB, Shrivastava S, Duncan Steele A, Mwenda JM, **Pickett BE**, Das SR, Jeffery Mphahlele M. Whole-genome sequencing and analyses identify high genetic heterogeneity and diversity of rotavirus genotype P[6] strains circulating in Africa. *Infect Genet Evol*. 2018 May 18. pii: S1567-1348(18)30286-7. PubMed PMID: 29782933.

- Ibrahim B, Arkhipova K, Andeweg AC, Posada-Céspedes S, Enault F, Gruber A, Koonin EV, Kupczok A, Lemey P, McHardy AC, McMahon DP, **Pickett BE**, Robertson DL, Scheuermann RH, Zhernakova A, Zwart MP, Schönhuth A, Dutilh BE, Marz M. Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. *Viruses*. 2018 May 14;10(5). pii: E256. PubMed PMID: 29757994.

- Moser LA, Oldfield LM, Fedorova N, Puri V, Shrivastava S, Amedeo P, Isom R, Hu L, Durbin A, Rocchi I, Williams T, Tan GS, Shabman RS, Bernard KA, **Pickett BE**. Whole-Genome Sequences of Zika Virus FLR Strains after Passage in Vero or C6/36 Cells. *Genome Announc*. 2018 Jan 25;6(4). pii: e01528-17. doi: 10.1128/genomeA.01528-17. PubMed PMID: 29371358.

- Shrivastava S, Puri V, Fedorova N, Amedeo P, Stockwell TB, Shabman RS, Rashid S, **Pickett BE**. Identification of Dezidougou virus in a DAK AR 41524 Zika virus stock. *Genome Announcements*. 2017 Jul 27;5(30). pii: e00605-17. PMID: 28751385.

- Lee AJ, Bhattacharya R, Scheuermann RH, **Pickett BE**. Identification of Diagnostic Peptide Regions that Distinguish Zika Virus from Related Mosquito-Borne Flaviviruses. *PLoS One* 2017 May 31;12(5):e0178199. PMID: 28562637.

- Zhang Y, Aevermann BD, Anderson TK, Burke DF, Dauphin G, Gu Z, He S, Kumar S, Larsen CN, Lee AJ, Li X, Macken C, Mahaffey C, **Pickett BE**, Reardon B, Smith T, Stewart L, Suloway C, Sun G, Tong L, Vincent AL, Walters B, Zaremba S, Zhao H, Zhou L, Zmasek C, Klem EB, Scheuermann RH. Influenza Research Database: An integrated bioinformatics resource for influenza virus research. *Nucleic Acids Res*. 2016 Sep 26. PMID: 27679478

- Miller MA, Schwartz T, **Pickett BE**, He S, Klem EB, Scheuermann RH, Passarotti M, Kaufman S, O'Leary MA. A RESTful API for Access to Phylogenetic Tools via the CIPRES Science Gateway. *Evol Bioinform Online*. 2015 Mar 16;11:43-8. PMID: 25861210.

- Lee AJ, Das SR, Wang W, Fitzgerald T, **Pickett BE**, Aevermann BD, Topham DJ, Falsey AR, Scheuermann RH. Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. *J Virol*. 2015 May;89(10):5427-40. PMID: 25741011.

- Squires RB, **Pickett BE**, Das S, Scheuermann RH. Toward a method for tracking virus evolutionary trajectory applied to the pandemic H1N1 2009 influenza virus. *Infect Genet Evol.* 2014 Dec;28:351-7. PMID: 25064525.
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Ongoing 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 - present
Sponsor: BYU-College of Life Sciences, new faculty startup funding
Amount: $20,000

Role: Principal Investigator
Title: Department Capital Equipment Funds
Dates: October 2019 - present
Sponsor: BYU-Department of Microbiology and Molecular Biology
Amount: $75,000

Completed Funding Support:

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

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