

SHASHIDHAR RAVISHANKAR

Staff Scientist
Fred Hutchinson Cancer Center

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Summary

Staff Scientist with over 5 years of experience in bioinformatics and computational immunology. Proven track record in developing scalable NGS workflows, developing methodologies to explore the immune repertoire, and contributing to high-impact publications. Skilled in machine learning, genomic data analysis, and open-source tool development, with a strong commitment to advancing cancer and immunotherapy research.

Current Role

April 2022 - Present **Staff Scientist, Warren Lab, Translational Science and Therapeutics Division, Fred Hutchinson Cancer Center.**

- Examining the role of T-cells within the tumor micro-environment of individuals with KS. ([Manuscript in bioRxiv](#))
- Identifying the diversity of Epstein Barr Virus (EBV) and its impact on the immune response. ([Published in Blood Advances](#))
- Exploring the impact of HLA Class II genotype on mNSCLC patients undergoing ICI therapy. ([Published in Nature Scientific Reports](#))

Research Interests

- Foundational models for T-cell therapies in cancers
- 3D Structure Prediction of T-Cell Receptor-pMHC Complexes
- Machine learning for prediction of response to immuno-therapy

Research Experience

Oct 2019 - April 2022 **Bioinformatics Analyst, Warren Lab, Clinical Research Division, Fred Hutchinson Cancer Center.**

- Investigating the impact of extended ART on the T-cell repertoire in people living with HIV. ([Frontiers in Immunology](#))
- Understanding the tumor micro-environment of Kaposi Sarcoma using single-cell RNA-Seq.
- Developing tools for the analysis of [AIRR-Seq](#), [scRNA-Seq analysis](#), and [genome assembly](#).

Jan 2018 - Aug 2018 **SWEP Graduate Researcher, Malaria Branch, Centers for Disease Control and Prevention.**

- Developing a scalable NGS workflow for to identify variations associated with drug resistance in *P. falciparum*. (Published in [Antimicrobial agents and chemotherapy](#) and available on [bioRxiv](#))
- Constructing the first complete genome of the simian malaria parasite *P. brasilianum*. ([Nature Scientific Reports](#))

Jun 2015 - Aug 2015 **Bioinformatics Intern, New York Genome Center.**

- Developing a framework for Bisulfite-Seq analysis.
- Benchmarking tools for variant identification from Bisulfite-Seq data.
- Developing a tool for the detection of allele-specific methylation from Bisulfite-Seq data.

- Jul 2013 - **Junior Bioinformatics Analyst, Interpretomics India Pvt Ltd.**
- May 2014
- Design and implementation of a Python based pipeline for Whole Genome/Exome Sequencing, RNA-Seq, ChIP-Seq, microRNA-Seq, and HLA-Typing for NGS-based cloud platform called iOMICS.
 - Developing a tool for the detection of the complete spectrum of variations in WGS/WES data. ([PLOS One](#))

Publications

- Blood Advances, July 2024 **Geographic EBV variants confound disease-specific variant interpretation and predict variable immune therapy responses.**
Edward L. Briercheck, **Shashidhar Ravishankar**, Elshafa Hassan Ahmed, César Camilo Carías Alvarado, Juan Carlos Barrios Menéndez, Oscar Silva, Elizabeth Solórzano-Ortiz, Marcos Mauricio Siliézar Tala, Philip Stevenson, Yuexin Xu, Anthony Wilder Wohns, Daniel Enriquez-Vera, Carlos Barrionuevo, Shan-Chi Yu, Aharon G. Freud, Christopher Oakes, Christoph Weigel, David M. Weinstock, Haley L. Klimaszewski, Apollinaire Ngankeu, Nora Mutalima, Gabriela Samayoa-Reyes, Robert Newton, Rosemary Rochford, Fabiola Valvert, Yasodha Natkunam, Andrei Shustov, Robert A. Baiocchi, Edus H. Warren
- bioRxiv, Jan 2024 **The signature of a T-cell response to KSHV persists across space and time in individuals with epidemic and endemic KS from Uganda.**
Shashidhar Ravishankar, Andrea MH Towleron, Peter Mooka, James Kafeero, David G Coffey, Lauri D Aicher, Kelvin R Mubiru, Lazarus Okoche, Prisca Atwinirembabazi, Joseph Okonye, Warren T Phipps, Edus H Warren
- Scientific Reports, Jan 2024 **Class II HLA-DRB4 is a predictive biomarker for survival following immunotherapy in metastatic non-small cell lung cancer.**
Cindy Y Jiang, Lili Zhao, Michael D Green, **Shashidhar Ravishankar**, Andrea MH Towleron, Anthony J Scott, Malini Raghavan, Matthew F Cusick, Edus H Warren, Nithya Ramnath
- Scientific Reports, Nov 2022 **The first complete genome of the simian malaria parasite *Plasmodium brasilianum*.**
Marko Bajic*, **Shashidhar Ravishankar***, Mili Sheth, Lori Rowe, M. Andreina Pacheco, Dhruviben S. Patel, Dhvani Batra, Vladimir Loparev, Christian Olsen, Ananias Escalante, Fredrik Vannberg, Venkatachalam Udhayakumar, John W. Barnwell, Eldin Talundzic
- Front. immunol., May 2022 **Serial analysis of the T-cell receptor β -chain repertoire in people living with HIV reveals incomplete recovery after long-term antiretroviral therapy.**
Andrea M. H. Towleron*, **Shashidhar Ravishankar***, David G. Coffey, Camillie E. Puronen, Edus H. Warren
- DNA repair, Jul 2021 **RNA helicase, DDX3X, is actively recruited to sites of DNA damage in live cells.**
Michael J. Cargill, **Shashidhar Ravishankar**, Alicia Morales, Edus H. Warren
- IJID, Jun 2021 **Targeted deep amplicon sequencing of antimalarial resistance markers in *Plasmodium falciparum* isolates from Cameroon.**
Mariangela L'Episcopia, Julia Kelley, Bruna G Djeunang Dongho, Dhruviben Patel, Sarah Schmedes, **Shashidhar Ravishankar**, Edvige Perrotti, David Modiano, Naomi W Lucchi, Gianluca Russo, Eldin Talundzic, Carlo Severini
- Antimicrob Agents Chemother, May 2019 **Evolution and genetic diversity of the k13 gene associated with artemisinin delayed parasite clearance in *Plasmodium falciparum*.**
M Andreina Pacheco, Esha R Kadakia, Zainab Chaudhary, Douglas J Perkins, Julia Kelley, **Shashidhar Ravishankar**, Michael Cranfield, Eldin Talundzic, Venkatachalam Udhayakumar, Ananias A Escalante
- bioRxiv, May 2018 **Next-generation Sequence-analysis Toolkit (NeST): A standardized bioinformatics framework for analyzing Single Nucleotide Polymorphisms in next-generation sequencing data.**
Shashidhar Ravishankar, Sarah E Schmedes, Dhruviben S Patel, Mateusz Plucinski, Venkatachalam Udhayakumar, Eldin Talundzic, Fredrik Vannberg

- Antimicrob Agents **Next-Generation Sequencing and Bioinformatics Protocol for Malaria Drug Resistance Marker Surveillance.**
 Chemother , Eldin Talundzic, **Shashidhar Ravishankar**, Julia Kelly, Dhruviben Patel, Mateusz Plucinski,
 Mar 2018 Sarah Schmedes, Dragan Ljolje, Brooke Clemons, Susan Madison-Antenucci, Paul M. Arguin,
 Naomi W Lucchi, Fredrik Vannberg, Venkatachalam Udhayakumar
- Bioinformatics, **Mapping-free variant calling using haplotype reconstruction from k-mer frequen-**
 Nov 2017 **cies.**
 Peter Audano III, **Shashidhar Ravishankar**, Fredrik Vannberg
- Scientific **TLR-exosomes exhibit distinct kinetics and effector function.**
 Reports, Mar Swetha Srinivasan , Michelle Su , **Shashidhar Ravishankar** , James Moore , Pamela Sara Head ,
 2017 Brandon J Dixon, Fredrik Vannberg
- Genome **First full draft genome of *Plasmodium brasilianum*.**
 Announc., Eldin Talundzic, **Shashidhar Ravishankar**, Vishal Nayak, Dhruviben S. Patel, Christian Olsen,
 Feb 2017 Mili Sheth, Dhvani Batra, Vladimir Loparev, Fredrik O.Vannberg, Venkatachalam Udhayaku-
 mar, John W. Barnwell
- PLOS ONE, **XomAnnotate: Analysis of Heterogeneous and Complex Exome - A Step Towards**
 Apr 2015 **Translational Medicine.**
 Asoke Talukder, **Shashidhar Ravishankar**, Jyothsna Prabhukumar, Francesco Blasi

Open source tools

- Oct 2019 - **LymphoSeq2: A toolkit for exploratory data analysis of AIRR-Seq datasets**, *Dr. Edus*
 Present *H. Warren, Fred Hutchinson Cancer Center.*
- Calculate diversity and identify changes in the composition of immune repertoire from AIRR-Seq datasets.
 - Visualize and explore immune repertoire from multiple samples.
- May 2017 - **Next-generation Sequence analysis Toolkit**, *Dr. Fredrik Vannberg, Georgia Institute*
 Aug 2019 *of Technology, Dr. Venkatachalam Udhayakumar, Center for Disease Control.*
- Development of a toolkit for the rapid identification of mutations in the *Plasmodium falciparum* genome conferring drug resistance against standard anti-malaria drug regimes.
- Aug 2016 - **Hummingbird: A K-mer based, alignment-free tool for RNA Seq analysis**, *Dr.*
 May 2017 *Fredrik Vannberg, Georgia Institute of Technology.*
- k-mer based algorithm for the quantification of transcripts in RNA-Seq data.
 - k-mer frequencies across indexed transcriptome used to calculate abundances at gene and isoform level.