

**Peer-Reviewed Publications** \*Authors contributed equally

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	All	Since 2020
Citations	14827	6895
h-index	44	36
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WARREN, René

## Patents

3. BIROL, Inanc; LIN, Diana; **WARREN, René, Louis**; SUTHERLAND, Darcy; LI, Chenkai; HOANG, Linda; YANAI, Anat; EBRAHIMIKONDORI, Hossein; RICHTER, Amelia; HELBING, Caren, C; HOF, Fraser. WIPO (PCT) Patent Appln No. CA2024/050914, ANTIMICROBIAL PEPTIDES
- 2 BIROL, Inanc, LIN, Diana, **WARREN, René, Louis**, SUTHERLAND, Darcy, LI, Chenkai, HOANG, Linda, YANAI, Anat, FRASER, Erin - U.S. Patent Application No. 63/487,920 filed March 2, 2023, and in PCT Patent Application No. PCT/CA2023/050941 filed July 13, 2023. Antimicrobial Peptides.
1. E Allen-Vercoe, R Holt, R Moore, **R Warren** - US Patent App. 13/877,421, 2011. Detection of fusobacterium in a gastrointestinal sample to diagnose gastrointestinal cancer.

## First-Author Conference Presentations

20. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2025. (Poster: **ntRoot: Human ancestry inference at scale from genomic data**)
19. 27<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB), Istanbul, Turkey, April 2023 (Poster: **Unique region identification in genomes using a k-mer approach**)
18. 29<sup>th</sup> Intelligent Systems for Molecular Biology (ISMB), Virtual/online. July 2021 (Speed talk: **SARS-CoV-2 variant timemaps**)
17. 27<sup>th</sup> Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland. July 2019 (Poster: **ntEdit: ultra fast, scalable genome sequence polishing**)
16. 22<sup>nd</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, April 2018 (Poster: **Chromosome-scale scaffolding human genomes with linked read k-mers**)
15. 21<sup>st</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB), Hong Kong, May 2017 (Selected talk: **ARCS: Genome scaffolding with linked reads**)
14. American Society of Human Genetics (ASHG), Vancouver, Canada, October 2016 (Poster: **HLAminer v2: HLA predictions by targeted assembly with ABySS**)
13. 24<sup>th</sup> Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA. July 2016 (Invited talk – highlights track : **A scalable genome assembly toolkit**)
12. 23<sup>rd</sup> Intelligent Systems for Molecular Biology (ISMB), Dublin, Ireland. July 2015 (Invited talk – late breaking research track. Selected talk - HiTSeq): **LINKS: Scaffolding genome assemblies with nanopore reads**
11. Student Biotechnology Network, Vancouver, Canada. February 2015 (Invited talk: **My bioinformatics career journey**)
10. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2015 (Poster: **High-performance computing for assembly and analysis of big genomics data**)
9. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2012 (Poster: **HLAminer: Derivation of HLA types from shotgun sequence datasets**)
8. Sequencing, Finishing and Analysis in the Future, Santa Fe, New Mexico, USA. June 2010 (Invited Talk: **Sequencing human IgH from H. mole**)
7. Advances in Genome Biology and Technology, Marco Island, Florida, USA. February 2009 (Posters: **SSAKE v3.2.1 and T Cell Receptor Sequencing**)

6. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2008 (Poster: **SSAKE v3.0**)
5. Synthetic Biology 3.0 conference, Zurich, Switzerland. June 2007 (Invited talk: ***H. influenzae* genome reconstruction in *E. coli***)
4. 5th CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. October 2005 (Poster: **Physical map-assisted whole-genome shotgun sequence assemblies**)
3. 7th Annual Conference on Computational Genomics. Reston, Virginia, USA. October 2004 (Poster: ***Rhodococcus* sp. RHA1 whole genome sequencing**)
2. Genomes 2004: International Conference on Microbial Genomes analysis. Hinxton, UK. April 2004 (Poster: ***Rhodococcus* sp. RHA1 whole genome sequencing**)
1. 3rd CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. May 2003 (Poster: **Sequence Assembly Manager**)