

Peer-Reviewed Publications *Authors contributed equally

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	All	Since 2020
Citations	14009	6132
h-index	43	33
i10-index	79	67

112. Lauren Coombe, **René L Warren**, Inanc Birol. 2025. ntSynt-viz: Visualizing syntenic patterns across multiple genomes. *bioRxiv* 2025.01.15.633221; <https://doi.org/10.1101/2025.01.15.633221>
111. **René L Warren**, Lauren Coombe, Johnathan Wong, Parham Kazemi, Inanc Birol. 2024. Human ancestry inference at scale, from genomic data *bioRxiv* 2024.03.26.586646; <https://doi.org/10.1101/2024.03.26.586646>
110. Lauren Coombe, Parham Kazemi, Johnathan Wong, Inanc Birol, **René L Warren**. 2024. Multi-genome syntenic detection using minimizer graph mappings *bioRxiv* 2024.02.07.579356; <https://doi.org/10.1101/2024.02.07.579356>
109. Ali Salehi, Anat Yanai, Amelia Richter, Chenkai Li, Darcy Sutherland, Lauren Coombe, Monica Kotkoff, **René L Warren**, Linda M.N. Hoang, Inanc Birol. Antimicrobial Peptides with High Bioactivity Against MDR Isolates: Addressing Public Health Concerns. *TBD*
108. Langlois, Valerie; Lopez, M. Louie; Allison, Michael; Imbery, Jacob; Couillard, Julie; Acharya-Patel, Neha; Bergman, Lauren; Bonderud, Matthew; Brochu, Marie-Pier; Castonguay, Marie-Lee; Coombe, Lauren; Dema, Anna; Groenwold, Emma; Lee, Hajeong; Ma, Isabel; Ren, Yilin; Knowles, Graeme; Sandre, Fidji; To, Tuan Anh; **Warren, Rene**; Yang, Cecilia; Birol, Inanc; Helbing, Caren. Roadmap for the Application of Environmental DNA (eDNA) Standards for Surveying 117 Taxa using Quantitative Polymerase Chain Reaction-Based Assays. *Environmental DNA. Accepted DOI TBD*
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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

WARREN, René

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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. 27th 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. 29th Intelligent Systems for Molecular Biology (ISMB), Virtual/online. July 2021 (Speed talk: **SARS-CoV-2 variant timemaps**)
17. 27th Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland. July 2019 (Poster: **ntEdit: ultra fast, scalable genome sequence polishing**)
16. 22nd 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. 21st 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. 24th Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA. July 2016 (Invited talk – highlights track : **A scalable genome assembly toolkit**)
12. 23rd 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**)