

René



Warren

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20+ years experience in biotechnology, genomics & informatics

Developed the first *de novo* genome assembly software (SSAKE) with short DNA sequences
Discovered *Fusobacterium* in colon cancer, one of Time Magazine's 2011 top ten breakthrough
Coordinated bioinformatics analyses of *Rhodococcus*, *Cryptococcus*, bullfrog & spruce genomes

Seeking new challenges & additional leadership

EXPERIENCE

Group Leader

BC Cancer – Genome Sciences Centre, Vancouver
Research project concept, management, guidance
Interview, supervise, mentor staff / students

Bioinformatics Coordinator

BC Cancer – Genome Sciences Centre, Vancouver
Lead bioinformatics R&D
Interviewed, taught, trained, supervised staff

Technical Officer

NRC – Biotechnology Research Institute, Montréal
Engineered gene expression regulation technology
Collaborated with stakeholders / scientists

2017-current

2002-17

2000-01

ACCOLADES

2015, 16 **Awarded John Jambor Knowledge Fund**
2011 NTN24 **Interview**, *Fusobacterium* cancer discovery
2009 **Genome Technology interview**, next-gen. seq.
2007 **GenomeWeb interview**, SSAKE development
1998 **Awarded MSc UBC Graduate Fellowship**
1997 **Awarded BSc FRSQ bursary**
1996 **Awarded BSc FRSQ** for honour's research project
1995 **Worked at NASA**, CMIX-4 payload protein crystal.

PRESENTATIONS

Selected from 17 lead author

2017, 18 **RECOMB** Hong Kong / Paris **talks**
2015, 16, 19 **ISMB** Dublin / Orlando / Basel **talks**
2008, 12, 15 **Pac. Symp. Biocomputing** Hawaii **posters**
2010 **SFAF** Santa Fe **talk**
2007 **Synthetic Biology** Zürich **talk**

EDUCATION

Certificate Computer Science
Concordia University

MSc Biochemistry & Molecular Biology
University of British Columbia

BSc Biochemistry (*Honours*)
Université de Montréal

2000

1997

1994

PUBLICATIONS

Selected from 63 peer-reviewed | 23 lead author

Warren RL, et al. 2019. ntEdit: scalable genome sequence polishing. *Bioinformatics*. doi: 10.1093/bioinformatics/btz400
Warren RL, et al. 2015. LINKS: Scalable, alignment-free scaffolding [...] genomes with long reads. *GigaScience*. 4:35
Warren RL, et al. 2012. Derivation of HLA types from shotgun sequence datasets. *Genome Med*. 4:95
Castellarin M*, **Warren RL***, et al. 2012. *Fusobacterium* infection [...] in colorectal carcinoma. *Genome Res*. 22:299
Warren RL, et al. 2007. Assembling millions of short DNA sequences using SSAKE. *Bioinformatics*. 23:500

IT Skills Python PERL R MySQL HTML/js Git unix/mac/win Office

Projects SAM SSAKE TASR HLAMiner LINKS XMV RAILS ARCS ntEdit

References available upon request