

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
Lead group, project management, guidance
Conceptualize, lead, develop genome technologies
Interview, supervise, mentor staff / students

Coordinator

BC Cancer – Genome Sciences Centre, Vancouver
Lead bioinformatics R&D
Published research (science journals, conferences)
Interviewed, taught, trained, supervised staff

Officer

NRC Biotechnology Research Institute, Montréal
Engineered gene expression regulation technology
Designed, fabricated, tested DNA “gene switch”
Collaborated with stakeholders, scientists

EDUCATION

Certificate Comp. Science | **Concordia U.**

MSc Biochemistry & Molecular Biology | **UBC**

BSc Biochemistry (*Honours*) | **U. de Montréal**

now

2017

2002

2000

2000

1997

1994

ACCOLADES

2015, 16 Awarded the *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 **Pacific Symposium Biocomputing**, Hawaii **talks**
2010 **SFAF**, Santa Fe USA **talk**
2007 **Synthetic Biology**, Zürich **talk**

PUBLICATIONS

*61 peer-reviewed [23 lead author], *co-first*

Warren RL, et al. 2019. ntEdit: scalable genome sequence polishing. *Bioinformatics*. btz400

Warren RL, et al. 2015. LINKS: Scalable scaffolding of 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* in colorectal carcinoma. *Genome Res.* 22:299

Warren RL, et al. 2007. Assembling millions of short DNA sequences using SSAKE. *Bioinfo.* 23:500

Skills: Python, PERL, R, MySQL, HTML/js, unix/mac/win, MSOffice, Git

Projects: SAM, SSAKE, TASR, HLaminer, LINKS, XMV, RAILS, ARCS, ntEdit

References available upon request