

# René



# Warren

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20+ Years Experience - Biotechnology | Genomics | Informatics

**Developed** first *de novo* genome assembly software (SSAKE) with short DNA sequences

**Discovered** *Fusobacterium* in colon cancer, Time Magazine's 2011 top 10 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 **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 honour's research project  
1995 **Worked** at NASA, CMIX-4 protein payload

## 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** Concordia University  
Computer Science

**MSc** University of British Columbia  
Biochemistry & Molecular Biology

**BSc** Université de Montréal  
Biochemistry (*Honours*)

2000

1997

1994

## PUBLICATIONS

*Selected from 63 peer-reviewed 23 lead author*

Warren RL, et al. 2019. ntEdit: scalable genome sequence polishing. *Bioinformatics*. 35:4430  
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