

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

Bioinformatics Coordinator

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

Technical Officer

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

EDUCATION

Certificate Computer Science | **Concordia U.**

MSc Biochemistry & Molecular Biology | **UBC**

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

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

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 USA **talk**
2007 **Synthetic Biology**, Zürich **talk**

PUBLICATIONS

Selected from 61 peer-reviewed [23 lead author]

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

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

References available upon request