René



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778.386.4192 http://renewarren.ca

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 *Rhodococus*, *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

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 Concordia UniversityComputer Science

MSC University of British Columbia

Biochemistry & Molecular Biology

BSC Université de Montréal Biochemistry (Honours)

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