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 *Rhodococus, Cryptococcus*, Bullfrog, Spruce genomes

seeking new challenges & additional leadership

EXPERIENCE   now

Group Leader
BC Cancer – Genome Sciences Centre, Vancouver
Lead group, project management & guidance
Conceptualize, lead, develop genome technologies
Interview, supervise, mentor staff / students

2017

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

2002

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

2000

EDUCATION

2000

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

1997

MSc Biochemistry & Molecular Biology | **UBC**

1994

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

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	
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