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 *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

2017-current

Bioinformatics Coordinator
BC Cancer – Genome Sciences Centre, Vancouver
Lead bioinformatics R&D
Interviewed, taught, trained, supervised staff

2002-17

Technical Officer
NRC – Biotechnology Research Institute, Montréal
Engineered gene expression regulation technology
Collaborated with stakeholders / scientists

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

2000

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

1997

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

1994

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

References Available