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

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

2017-current

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

2002-2017

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

2000-2001

EDUCATION

Certificate Computer Science | **Concordia U.**
2000

MSc Biochemistry & Molecular Biology | **UBC**
1997

BSc Biochemistry *(Honours)* | **U. de Montréal**
1994

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

*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

IT Skills: *Python, PERL, R, MySQL, HTML/js, Git, unix/mac/win, MSoffice*   **Projects**: *SAM, SSAKE, TASR, HLAminer, LINKS, XMV, RAILS, ARCS, ntEdit*

References available upon request