

## Guillaume Bourque

Associate Professor, Department of Human Genetics, McGill University  
 Director of Bioinformatics, McGill University & Genome Quebec Innovation Center

### Academic and Training Background

Degree	Year awarded	Discipline	Institution, Country
Ph.D.	2002	Applied Mathematics	University of Southern California, USA
M.A.	2000	Applied Mathematics	University of Southern California, USA
B.Sc.	1998	Computer Science and Mathematics	Université de Montréal, Canada

### Work Experience

Position	Organization	Dept./Division	Start Date	End Date
Director	Canadian Center for Computational Genomics, Montreal, QC		2015	present
Associate Professor	McGill University, Montreal, QC	Human Genetics	2010	present
Director	McGill University and Génome Québec Innovation Center, Montreal, QC	Bioinformatics	2010	present
Senior Group Leader & Assoc Director	Genome Institute of Singapore, Singapore	Computational & Mathematical Biology	2007	2010
Adjunct Associate Professor	National University of Singapore, Singapore	Mathematics	2009	2010
Postdoctoral Fellow	Centre de Recherches Mathématiques, Montreal, QC		2002	2004

### Selected Peer-Reviewed Publications

1. Bourgey M, Dali R, Eveleigh RJM, Chen KC, Letourneau L, Fillon J, Michaud M, Caron M, Sandoval J, Lefebvre F, Leveque G, Mercier E, Bujold D, Marquis P, Tran Van P, Morais DAL, Tremblay J, Shao XJ, Henrion E, Caron B, **Bourque G@**. GenPipes: an open-source framework for scalable genomic analyses. *GigaScience*. *In press*.
2. Page DJ, Miossec MJ, Williams SG, Monaghan RM, Fotiou E, Cordell HJ, Sutcliffe L, Topf A, Bourgey M, **Bourque G**, Eveleigh R, Dunwoodie SL, Winlaw DS, Bhattacharya S, Breckpot J, Devriendt K, Gewillig M, Brook JD, Setchfield KJ, Bu'Lock FA, O'Sullivan J, Stuart G, Bezzina CR, Mulder BJM, Postma AV, Bentham JR, Baron M, Bhaskar SS, Black GC, Newman WG, Hentges KE, Lathrop GM, Santibanez-Koref M & Keavney BD. Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. *Circ Res*. 2019 Feb 15;124(4):553-563. doi: 10.1161/CIRCRESAHA.118.313250.
3. Laperle J, Hebert-Deschamps S, Raby J, de Lima Morais DA, Barrette M, Bujold D, Bastin C, Robert MA, Nadeau JF, Harel M, Nordell-Markovits A, Veilleux A, **Bourque G**. & Jacques PE. The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison

- of user datasets with thousands of public epigenomic datasets. *Bioinformatics*. 2019 Feb 15; 35(4):674-676. doi: 10.1093/bioinformatics/bty655.
4. **Bourque G**, Burns KH, Gehring M, Gorbunova V, Seluanov A, Hammell M, Imbeault M, Izsvak Z, Levin HL, Macfarlan TS, Mager DL & Feschotte C. Ten things you should know about transposable elements. *Genome Biol* 19, 199 (2018). doi: 10.1186/s13059-018-1577-z.
  5. Caron M, St-Onge P, Drouin S, Richer C, Sontag T, Busche S, **Bourque G**, Pastinen T. & Sinnett D. Very long intergenic non-coding RNA transcripts and expression profiles are associated to specific childhood acute lymphoblastic leukemia subtypes. *PLoS One* 13, e0207250 (2018). doi: 10.1371/journal.pone.0207250.
  6. Goerner-Potvin P. & **Bourque G**. Computational tools to unmask transposable elements. *Nat Rev Genet* 19, 688-704 (2018). doi: 10.1038/s41576-018-0050-x.
  7. Shokoohi F, Stephens DA, **Bourque G**, Pastinen T, Greenwood CMT. & Labbe A. A hidden markov model for identifying differentially methylated sites in bisulfite sequencing data. *Biometrics* (2018). doi: 10.1111/biom.12965.
  8. \*Monlong J, Cossette P, Meloche C, Rouleau G, Girard SL, **Bourque G@**. Human copy number variants are enriched in regions of low-mappability. *NAR*. June 21 <https://doi.org/10.1093/nar/gky538>.
  9. Laperle J, Hébert-Deschamps S, Raby J, Morais DAL, Barrette M, Bujold D, Bastin C, Robert M-A, Nadeau J-F, Harel M, Nordell-Markovits A, Veilleux A, **Bourque G**, Jacques P-E. The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of private datasets with thousands of public epigenomic datasets. *Bioinformatics*. Jul 24 doi:10.1093/bioinformatics/bty65.
  10. Hirukawa A, Smith HW, Zuo D, Dufour CR, Savage P, Bertos N, Johnson RM, Bui T, **Bourque G**, Basik M, Giguère V, Park M, Muller WJ. Targeting EZH2 reactivates a breast cancer subtype-specific anti-metastatic transcriptional program. *Nat Commun*. 2018 Jun 29;9(1):2547.
  11. **Bourque G@**. Comparing Apples to Apples and Oranges to Oranges. *Trends Genet*. Aug;34(8):571-572.
  12. Chong J, Soufan O, Li C, Caurus I, Li S, **Bourque G**, Wishart D, Xia J. MetaboAnalyst 4.0 – Towards More Transparent and Integrative Metabolomic Analysis. *Nucleic Acids Res*. Jul 2;46(W1):W486-W494.
  13. \*Monlong J, \*Girard SL, Meloche C, Cadieux-Dion M, Andrade DM, Lafreniere RG, Gravel M, Spiegelman D, Dionne-Laporte A, Boelman C, Hamdan FF, Michaud JL, Rouleau G, Minassian BA, **Bourque G@**, Cossette P. Genome-wide characterization of copy number variants in epilepsy patients. *PLoS Genetics*. Apr 12;14(4):e1007285. doi: 10.1371/journal.pgen.
  14. Kanagaratham C, Chiwara V, Ho B, Moussette S, Youssef M, Venuto D, Jeannotte L, **Bourque G**, de Sanctis JB, Radzioch D, Naumova AK. Loss of the zona pellucida-binding protein 2 (Zpbp2) gene in mice impacts airway hypersensitivity and lung lipid metabolism in a sex-dependent fashion. *Mamm Genome*. Apr;29(3-4):281-298.
  15. \*Ramsay L, Marchetto MC, Caron M, Chen S-H, Busche S, Kwan T, Pastinen T, Gage FH, **Bourque G@**. Conserved expression of transposon-derived non-coding transcripts in primate stem cells. *BMC Genomics*. 2017 Feb 28;18(1):214.
  16. \*Hocking TD, Rigail G, Fearnhead P, **Bourque G**. A log-linear time algorithm for constrained changepoint detection. 2017 arXiv preprint arXiv:1703.03352.
  17. Hamdan FF, *et al.*, High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. *Am J Hum Genet*. 2017 Nov 2;101(5):664-685. doi: 10.1016/j.ajhg.2017.09.008
  18. Bellenguez C, Charbonnier C, Grenier-Boley B, Quenez O, Le Guennec K, Nicolas G, Chauhan G, Wallon D, Rousseau S, Richard AC, Boland A, **Bourque G**, Munter HM, Olaso R, Meyer V, Rollin-Sillaire A, Pasquier F, Letenneur L, Redon R, Dartigues JF, Tzourio C, Frebourg T, Lathrop M, Deleuze JF, Hannequin D, Genin E, Amouyel P, Debette S, Lambert JC, Campion D; CNR MAJ collaborators. Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1,

- and ABCA7 in 1779 cases and 1273 controls. *Neurobiol Aging*. 2017 Nov;59:220.e1-220.e9. doi: 10.1016/j.neurobiolaging.2017.07.001. Epub 2017 Jul 14.
19. Audet-Walsh É, Dufour CR, Yee T, Zouanat FZ, Yan M, Kalloghlian G, Vernier M, **Caron M, Bourque G**, Scarlata E, Hamel L, Brimo F, Aprikian AG, Lapointe J, Chevalier S, Giguère V. Nuclear mTOR acts as a transcriptional integrator of the androgen signaling pathway in prostate cancer. *Genes Dev*. 2017. doi:10.1101/gad.299958.117
  20. Arseneault M, **Monlong J**, Vasudev NS, Laskar RS, Safisamghabadi M, Harnden P, Egevad L, Nourbehesht N, Panichnantakul P, Holcatova I, Brisuda A, Janout V, Kollarova H, Foretova L, Navratilova M, Mates D, Jinga V, Zaridze D, Mukeria A, Jandaghi P, Brennan P, Brazma A, Tost J, Scelo G, Banks RE, Lathrop M, **Bourque G**, Riazalhosseini Y. Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. *Sci Rep*. 2017 Mar 23;7:44876.
  21. Oliazadeh N, Gorman KF, **Eveleigh R, Bourque G**, Moreau A. Identification of Elongated Primary Cilia with Impaired Mechanotransduction in Idiopathic Scoliosis Patients. *Sci Rep*. 2017 Mar 14;7:44260.
  22. Cheung WA, Shao X, Morin A, Siroux V, Kwan T, Ge B, Aissi D, Chen L, Vasquez L, Allum F, Guenard F, Bouzigon E, Simon MM, Boulier E, Redensek A, Watt S, Datta A, Clarke L, Flicek P, Mead D, Paul DS, Beck S, **Bourque G**, Lathrop M, Tchernof A, Vohl MC, Demenais F, Pin I, Downes K, Stunnenberg HG, Soranzo N, Pastinen T. & Grundberg E. Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. *Genome Biol* 18, 50 (2017). doi: 10.1186/s13059-017-1173-7.

### Selected Research Funding

Title / Lead PI	Funding source / Program	Total grant	From	To
Epigenomics Secure Data Sharing Platform for Integrative Analyses (EpiShare)/ G Bourque	Genome Canada/ B/CB competition	\$1,000,000	2018	2021
CanDIG CHORD: Canadian Health Omics Repository, Distributed/ G Bourque	CANARIE / Research Data Management	\$447,000	2018	2020
Canadian Center for Computational Genomics (C3G) / G Bourque	Genome Canada / Genomics Technology Platforms	\$7,053,000	2017	2022
Multidimensional Epigenomics Mapping Centre (EMC) at McGill/ T Pastinen transferred to G Bourque	CIHR/ CEEHRC Epigenomics Platform	\$4,400,000	2017	2022
Accessing chromatin interactions by high-resolution analyses of correlate regulatory element variation / G Bourque	CIHR / 4D Nucleome Collaborative Projects	\$800,000	2017	2020
Integrative Epigenomics of Obesity and Metabolic Complications-The Obesity Epigenomic Trilateral Project / E Grundberg transferred to G Bourque	CIHR / Epigenomics of Complex Diseases	\$646,170	2016	2020
Common Infrastructure for National Cohorts in Europe, Canada, and Africa (CINECA)/ F	EU-H2020 / CIHR Collaboration on data sharing	\$800,000	2019	2023

Brinkman PI, G Bourque ( <b>co-Applicant, share 23%</b> )				
Integrated Human data repositories for infectious disease-related international cohorts to facilitate personalized medicine approaches to infectious disease research (CAN-SHARE)/ C Emerson PI, G Bourque ( <b>co-Applicant, share 20%</b> )	EU-H2020 / CIHR Collaboration on data sharing	\$800,000	2019	2023
Tackling Childhood Brain Cancer at the root to improve survival and quality of life/N Jabado PI, G Bourque ( <b>co-Applicant, share 2.5%</b> )	Genome Canada/ LSARP Competition	\$12,997,397	2018	2021
The Cancer Genome Collaboratory/ L Stein PI, G Bourque ( <b>co-Applicant, share 10%</b> )	CFI / Cyberinfrastructure: Challenge	\$4,995,318	2018	2021
Generalization of GenAP toward the growing single-cell and metabolomic communities/ PE Jacques PI, G Bourque ( <b>co-PI, share 12%</b> )	CANARIE / Research Software Program	\$224,626	2018	2022
Montreal Cancer Consortium (MCC) - Pilot Project/I Watson PI, G Bourque ( <b>co-PI, share 6%</b> )	Terry Fox / Cancer Centre Consortium Network	\$2,480,000	2018	2020
Development and Validation of a Web-Based Platform for Environmental Omics and Toxicology/ J Xia PI, G Bourque ( <b>co-Applicant</b> )	Genome Canada / B/CB Competition	\$999,019	2018	2021
An integrative platform for metabolomics and systems biology/ J Xia PI, G Bourque ( <b>co-Project Leader</b> )	Genome Canada / B/CB Competition	\$1,094,607	2018	2021
Epigenetic changes affecting muscle stem cell function in the aging population/ Dilworth PI, G Bourque ( <b>Principal Applicant, share 5%</b> )	CIHR / CIHR Team CEEHRC Phase II	\$1,497,750	2018	2023
McGill University and G�enome Qu�ebec Innovation Center / M Lathrop PI, G Bourque ( <b>Co-Lead, share 15%</b> )	Genome Canada / Genomics Technology Platforms	\$9,176,000	2017	2022
CanDIG: Canadian Distributed cyber-Infrastructure for Genomics / M Brudno, G Bourque ( <b>Co-Lead, share 40%</b> )	CFI / Cyber-Infrastructure	\$5,000,000	2016	2020
Canadian Epigenetics, Environment and Health Research Consortium Network / M Hirst PI, G Bourque ( <b>Principal Applicant, share 7%</b> )	CIHR / CEEHRC Consortium Network	\$2,000,000	2015	2019
Canada's Genomics Enterprise (CGEn): A national genomic tools network for transforming life science research / S Jones PI, G Bourque ( <b>Principal User, share 8%</b> )	CFI / Innovation Fund	\$58,435,000	2015	2019