

McGill University, Faculty of Medicine

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A. IDENTIFICATION

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B. APPOINTMENTS

2022 – ...	Board Director Digital Research Alliance of Canada	<i>Ottawa, On</i>
2019 – ...	Professor Department of Human Genetics, McGill University	<i>Montréal, Qc</i>
2019 – ...	Principal Investigator Institute for the Advanced Study of Human Biology (ASHBi)	<i>Kyoto, Japan</i>
2015 – ...	Director Canadian Center for Computational Genomics (C3G)	<i>Montréal, Qc</i>
2010 – ...	Director of Bioinformatics Dahdaleh Institute of Genomic Medicine of McGill University	<i>Montréal, Qc</i>
2020 – 2021	Chair, Researcher Council National Digital Research Infrastructure Organization	<i>Ottawa, On</i>
2019 – 2020	Applicant Board Director National Digital Research Infrastructure Organization	<i>Ottawa, On</i>
2010 – 2019	Associate Professor Department of Human Genetics, McGill University	<i>Montréal, Qc</i>

- 2007 – 2010 Senior Group Leader & Assoc Director *Singapore*
Computational & Mathematical Biology, Genome Institute of Singapore
- 2009 – 2010 Adjunct Associate Professor *Singapore*
Mathematics Department, National University of Singapore
- 2005 – 2009 Adjunct Assistant Professor *Singapore*
Mathematics Department, National University of Singapore
- 2004 – 2007 Group Leader *Singapore*
Computational & Mathematical Biology, Genome Institute of Singapore

C. EDUCATION

- 2002 – 2004 Postdoctoral researcher *Montréal, QC*
Centre de Recherches Mathématiques
Université de Montréal
Advisor: David Sankoff
Title : Gene regulatory network inference from gene
expression time-series
- 2000 – 2002 Ph.D. in Applied Mathematics *Los Angeles, CA*
University of Southern California
Advisor: Pavel Pevzner
Title: Algorithms for phylogenetic tree reconstruction
based on genome rearrangements
- 1998 – 2000 M.A. in Applied Mathematics *Los Angeles, CA*
University of Southern California
Advisor: Pavel Pevzner
- 1995 – 1998 B.Sc. in Computer Science and Mathematics *Montréal, QC*
Université de Montréal
Advisor: David Sankoff

D. SPECIAL HONORS, AWARDS, RECOGNITION

- 2020 – 2027 Canada Research Chair (Tier 1)
Computational Genomics and Medicine
- 2020 – 2024 Chercheurs-boursiers de mérite
Fonds de recherche Santé Québec (FRSQ)
- 2015 – 2024 Distinguished Visiting Professor

Kyoto University, Japan

- 2017 – 2020 Chercheurs-boursiers Senior
Fonds de recherche Santé Québec (FRSQ)
- 2012 – 2016 Chercheurs-boursiers Junior 2
Fonds de recherche Santé Québec (FRSQ)
- 2002 – 2004 Postdoctoral Research Fellowship
Nature and Technology Quebec Research Fund (FCAR)
- 2000 – 2002 Postgraduate Scholarship (PGS B)
Natural Sciences and Engineering Research Council of Canada (NSERC)
- 1998 – 2000 Postgraduate Scholarship (PGS A)
Natural Sciences and Engineering Research Council of Canada (NSERC)
- 1999 – 2001 Outstanding Academic Achievement
Office of International Services, University of Southern California
- 2000 Trigg Summer Fellowship
Department of Mathematics, University of Southern California
- 1997 CREPUQ scholarship to study abroad
San Francisco State University

E. TEACHING

1. University Courses

a. Graduate courses

- 2022 INDS426, Computer Applications in Medicine, Lecturer (3 hours)
- 2020 INDS426, Computer Applications in Medicine, Lecturer (3 hours)
- 2018 HGEN663, Beyond the Human Genome, Lecturer (6 hours)
- 2018 EXMD602, Advanced Techniques in Molecular Genetics, Lecturer (2 hours)
- 2017 QLS600, Quantitative Life Sciences Foundation Course, Lecturer – jointly with Jacek Majewski (12 hours)

- 2016 HGEN663, Beyond the Human Genome, Lecturer (*6 hours*)
- 2016 EXMD602, Advanced Techniques in Molecular Genetics, Lecturer (*2 hours*)
- 2016 HGEN693, Using Bioinformatics Resources, Lecturer (*6 hours*)
- 2016 BMO7043, Utilisation des ressources bioinformatiques et données publiques (Laval University), Lecturer (*3 hours*)
- 2016 HGEN676, Laboratory Course in Next Generation Sequencing based Genomics, Lecturer (*6 hours*)
- 2015 HGEN663, Beyond the Human Genome, Co-coordinator (*15 hours*)
- 2015 EXMD602, Advanced Techniques in Molecular Genetics, Lecturer (*2 hours*)
- 2015 HGEN698, Laboratory Course in Next Generation Sequencing based Genomics, Lecturer (*6 hours*)
- 2014 HGEN698, Advanced Readings in Human Genetics: Cancer Genomics (*12 hours*)
- 2014 HGEN670, Advanced Readings in Human Genetics: Disease Epigenomics (*6 hours*)
- 2014 BINF621, Bioinformatics: Molecular Biology, Lecturer (*4 hours*)
- 2014 HGEN693, Using Bioinformatics Resources, Lecturer (*9 hours*)
- 2014 HGEN698, Laboratory Course in Next Generation Sequencing based Genomics, Lecturer (*9 hours*)
- 2014 EXMD602, Advanced Techniques in Molecular Genetics, Lecturer (*2 hours*)
- 2013 BINF621, Bioinformatics: Molecular Biology, Lecturer (*4 hours*)
- 2013 HGEN663, Beyond the Human Genome, Lecturer (*3 hours*)
- 2013 COMP618, Bioinformatics: Functional Genomics, Lecturer (*4 hours*)

- 2012 BINF621, Bioinformatics: Molecular Biology, Lecturer (*4 hours*)
- 2012 COMP616, Systems Biology seminar series, Lecturer (*1 hours*)
- 2011 HGEN670, Advances in Human Genetics Theme Course, Coordinator (*15 hours*)

b. Undergraduate courses

- 2018 BIOL568, Topics on the Human Genome, Lecturer (*3 hours*)
- 2017 BIOL395, Quantitative Biology Seminar, Lecturer (*2 hours*)
- 2017 BIOL568, Topics on the Human Genome, Lecturer (*6 hours*)
- 2016 BIOL568, Topics on the Human Genome, Lecturer (*6 hours*)
- 2015 BIOL568, Topics on the Human Genome, Lecturer (*6 hours*)
- 2014 BIOL395, Quantitative Biology Seminar, Lecturer (*2 hours*)
- 2014 Montreal Spring School of Population Genomics and Genetic Epidemiology, Lecturer (*2 hours*)
- 2014 BIOL568, Topics on the Human Genome, Lecturer (*6 hours*)
- 2013 COMP561, Computational Biology Methods and Research, Lecturer (*2 hours*)
- 2013 Montreal Spring School of Population Genomics and Genetic Epidemiology, Lecturer (*2 hours*)
- 2013 BIOL395, Quantitative Biology Seminar, Lecturer (*2 hours*)
- 2013 BIOL568, Topics on the Human Genome, Lecturer (*6 hours*)
- 2012 Montreal Spring School of Population Genomics and Genetic Epidemiology, Lecturer (*2 hours*)
- 2012 BIOL568, Topics on the Human Genome, Lecturer (*3 hours*)

c. Other teaching activities

- 2015-... McGill University Genome Center, Advances and Thoughts at the Genome Center, Coordinator (*weekly meetings*)

- 2023 Kyoto Course on Bioinformatics for Genomic Medicine. *Kyoto, Japan (6 hours)*
- 2021 Canadian Bioinformatics Workshop, Epigenomics Data Analysis (*4 hours*)
- 2020 Canadian Bioinformatics Workshop, Epigenomics Data Analysis (*4 hours*)
- 2019 Kyoto-McGill Course on Bioinformatics for Genomic Medicine. Montréal, Québec (*3 hours*)
- 2019 Canadian Bioinformatics Workshop, Informatics on High Throughput Sequencing Data, Montréal, Québec (*3 hours*)
- 2018 Kyoto Course on Bioinformatics for Genomic Medicine. *Kyoto, Japan (3 hours)*
- 2018 Canadian Bioinformatics Workshop, Epigenomics Data Analysis, Vancouver, British-Columbia (*4 hours*)
- 2018 Canadian Bioinformatics Workshop, Bioinformatics for Genomic Medicine, Montréal, Québec (*4 hours*)
- 2017 Bioinformatics and Genome Analysis Course. Institut Pasteur Tunis, Tunisia. (*6 hours*)
- 2017 Canadian Bioinformatics Workshop, Epigenomics Data Analysis, Montréal, Québec (*4 hours*)
- 2017 Canadian Bioinformatics Workshop, Bioinformatics for Genomic Medicine, Toronto, Ontario (*4 hours*)
- 2016 Canadian Bioinformatics Workshop, Epigenomics Data Analysis, Toronto, Ontario (*4 hours*)
- 2016 Canadian Bioinformatics Workshop, Informatics on High-throughput Sequencing Data, Montréal, Québec (*4 hours*)
- 2016 Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics. *Kyoto, Japan (3 hours)*

- 2015 Canadian Bioinformatics Workshop, Informatics on High-throughput Sequencing Data, Toronto, Ontario (*4 hours*)
- 2015 Canadian Bioinformatics Workshop, High-throughput Biology: From Sequence to Networks, New-York, USA (*4 hours*)
- 2015 Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics. *Kyoto, Japan. (6 hours)*
- 2014 Montreal Genomics, Co-organizer (*monthly meetings*)
- 2014 Machine Learning for Personalized Medicine, Summer School, Paris, France (*2 hours*)
- 2014 Réseau Québécois en reproduction Bioinformatics workshop, Lecturer (*1 hour*)
- 2013 Montreal Genomics, Co-organizer (*monthly meetings*)
- 2013 Rendez-vous Génome Québec 2013, Organized one workshop:
- Bioinformatics analysis using HPC (*3 hours*)
- 2013 High-Performance Computing Symposium 2013, organized a tutorial on:
- High-Performance Computing in Genomics (*4 hours*)
- 2013 Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics. *Kyoto, Japan. (6 hours)*
- 2012 Rendez-vous Génome Québec 2012, Organized two workshops:
- Analysis of genome/exome sequencing data (*3 hours*)
- Functional genomics data analysis (*3 hours*)
- 2012 Rendez-vous Bioinformatique 2012, Organized two workshops:
- Next-generation sequence analysis (*3 hours*)
- Introduction to differential expression analysis (*3 hours*)
- 2011 Rendez-vous Bioinformatique 2011, Organized three workshops:
- Next-generation sequence analysis (*3 hours*)
- Introduction to differential expression analysis (*3 hours*)
- Pathway and network analysis of gene lists (*3 hours*)

- 2011 4 à 7 carrières en bioinformatique, Université de Montréal,
Lecturer (*1 hour*)
- 2011 Computational Analysis of Genomic Information. Human Genome
Meeting. *Dubai, UAE.*

2. Research Trainees Supervised

Current:

1. Ms. Yuxin Zhou (PhD McGill/Kyoto joint program, 2023 - present)
2. Ms. Nhi Nguyen (PhD McGill/Kyoto joint program, 2023 - present)
3. Ms. Yizhi (Nicole) Yan (PhD McGill/Kyoto joint program, 2022 – present)
4. Mr. Rong Ma (co-supervisor, PhD McGill/Kyoto joint program, 2021 – present)
5. Dr. Clement Goubert (Research Associate, 2022 – present)
6. Dr. Xun Chen (Program-specific Assistant Professor, 2020 – present)
7. Mr. Cristian Groza (PhD QLS, 2019 – present)
8. Mr. Qinwei Zhuang (PhD McGill/Kyoto joint program, 2019 – present)
9. Ms. Mio Shibata (PhD McGill/Kyoto joint program, 2018 – present)
10. Mr. Jeffrey Hyacinthe (PhD QLS, 2018 – present)
11. Ms. Patricia Goerner-Potvin (PhD in Human Genetics, 2015 – present)

Completed

1. Clare Stephens (BSc undergrad Summer internship, 2023)
2. Jie Ying Huang (BSc – DESS undergrad Summer internship, 2023)
3. Solène Pety (MSc in Bioinformatics and Statistics, Winter, Summer internship, 2023)
4. Matteo Leguen (MSc in Biomedical Engineering, Winter, Summer internship, 2023)
5. Mr. David Lougheed (MSc in Human Genetics, 2020 – 2023)
6. Ms. Yuxin Zhou (BSc undergrad Fall internship, 2022)
7. Dr. Clement Goubert (PostDoc, 2021 – 2022)
8. Mr. Maxime Caron (PhD in Human Genetics, 2017 – 2022)
9. Mr. Nafiz Islam (BSc undergrad Summer internship, 2022 & Summer internship, 2023)
10. Mr. Sanjeev Lakhwani (BSc undergrad Summer 2022, Fall 2022, Winter 2023, Summer 2023 internship)
11. Mr. Justin Bellavance (BSc undergrad Summer internship, 2022)
12. Mr. Julian Willett (PhD candidate QLS Summer internship, 2021)

13. Ms. Yumika Shiba (BSc undergrad Summer internship, 2021)
14. Mr. Jinkun Chen (BSc undergrad Summer internship, 2021)
15. Ms. Audrey Baquette (MSc in Human Genetics, 2018 – 2020)
16. Ms. Jinchu Vijay (PhD in Human Genetics, 2016 – 2020)
17. Mr. Cristian Groza (BSc undergrad internship, 2017 – 2019)
18. Mr. Alexis Nolin-Lapalme (BSc undergrad internship 2018 – 2019)
19. Mr. David Loughheed (BSc undergrad internship, 2018 – 2019)
20. Ms. Lucia Bogdan (BSc undergrad internship, 2017 – 2019)
21. Mr. Zhaohui Su (MSc in Human Genetics, 2015 – 2018)
22. Mr. David Venuto (BSc undergraduate internship, 2015 – 2018)
23. Mr. Jean Monlong (PhD in Human Genetics, 2012 – 2018)
24. Dr. Toby Hocking (PDF in Human Genetics, 2014 – 2018)
25. Ms. Katherina Radan (MSc in Human Genetics, 2017 – 2018)
26. Ms. Leila Feng (BSc undergrad internship, 2017)
27. Mr. Nestor Nebesio (BSc undergraduate internship, 2016 – 2017)
28. Ms. LeeAnn Ramsay (MSc in Human Genetics, 2014 – 2016)
29. Dr. Simon Girard (PDF in Human Genetics, 2013 – 2015)
30. Mr. Bogdan Mazoure (Undergraduate summer internship, 2015)
31. Ms. Patricia Goerner-Potvin (Master summer internship, 2014 – 2015)
32. Dr. Eric Audemard (PDF in Human Genetics, 2012 – 2014)
33. Ms. Maty Samba (Master summer internship, 2013)
34. Mr. Laurent Bourque (Undergraduate summer internship, 2013)
35. Mr. Masoud Karzand (MSc in Computer Science, 2012 – 2013),
co-supervisor M. Blanchette
36. Ms. LeeAnn Ramsay (BSc in Biology, 2012 – 2013)
37. Dr. Pierre-Étienne Jacques (PDF in Genomics 2010 – 2011)
38. Mr. Ying Ka Ho (BSc in Computer Science, 2009)
39. Mr. Zhang Mengqi (BSc in Mathematics, 2009)
40. Ms. Sharon Tan (BSc in Mathematics, 2008)
41. Mr. Chew Tian We. (BSc in Mathematics, 2008). Project won a Gold medal at
the Singapore Science and Engineering Fair (SSEF).
42. Ms. Thidathip Wongsurawat (MSc in Biology, 2006-2007)
43. Mr. Melvin ZhiYong (BSc in Computer Science, 2005),
co-supervisor H-W Leong
44. Mr. Do Hoang (BSc in Computer Science, 2005),
co-supervisor H-W Leong

Rotation:

1. Mr. Jeffery Hyacinthe (PhD in Quantitative Life Sciences, Winter 2018)
2. Mr. Matthew D'Iorio (PhD in Quantitative Life Sciences, Fall 2017)

Thesis Committee

1. Mr. Rodrigo Lopez Gutierrez (PhD QLS, McGill, 2023 – ...)
2. Ms. Cecile Poulain (PhD Bioinfo, UdeM, 2022 – ...)
3. Ms. Peyton McClelland (MSc Human Genetics, McGill, 2022 – ...)
4. Mr. Ariel Aguirre (MSc Human Genetics, McGill, 2019 – ...)
5. Ms. Zoe Schmilovich (MSc Human Genetics, McGill, 2018 – ...)
6. Ms. Malosree Maitra (PhD Neurosciences, McGill, 2018 – ...)
7. Mr. Luke Anderson-Trocmé (PhD in Human Genetics, McGill, 2017 – 2022)
8. Mr. Pubudu Nawarathna (MSc in Human Genetics, McGill, 2017 – 2019)
9. Mr. Charles Couturier (PhD Neurosciences, McGill, 2016 – 2021)
10. Mr. Mohamed Fahmy (PhD Bioinfo, UdeM, 2016 – 2021)
11. Mr. Marc-Aurèle Chay (MSc Neurology, McGill, 2016 – 2019)
12. Ms. Sarai Mola (PhD Bioinfo, UdeM, 2015 – 2018)
13. Ms. Maia Kaplan (PhD in Biochemistry, McGill, 2015 – 2018)
14. Mr. Alain Pacis (PhD in Biochemistry, UdeM, 2015 – 2018)
15. Mr. Alain Bateman (MSc in Human Genetics, 2015 – 2018)
16. Mr. Matthew Osmond (MSc in Human Genetics, 2015 – 2016)
17. Mr. Mickael Leclercq (PhD in Computer Science, 2014 – 2016)
18. Ms. Ingrid Tam (PhD in Experimental Medicine, 2013 – 2015)
19. Mr. Pablo Cingolani (PhD in Computer Science, 2013 – 2015)
20. Ms. Amanpreet Kaur (MSc in Human Genetics, 2013 – 2015)
21. Ms. Alicia Schiavi (MSc in Human Genetics, 2012)
22. Mr. James Wagner (PhD in Computer Science, 2011 – 2012)
23. Mr. Jean-François Spinella (PhD in Molecular Biology, 2012)

Internal Reviewer for PhD/MSc Theses:

1. Ms. Natalia Aidé López Lugo (MSc in Biology), McGill University, 2023
2. Mr. Airin Ahia-Tabibi, (PhD in Computer Science), McGill University, 2021
3. Mr. David Romero (PhD in Computer Science), McGill University, 2017
4. Mr. Pablo Cingolani (PhD in Computer Science), McGill University, 2016
5. Mr. Carl Murie (PhD in Human Genetics), McGill University, 2013
6. Mr. Mathieu Rousseau (PhD in Computer Science), McGill University, 2012
7. Ms. Emilie Lalonde (MSc in Human Genetics), 2011

External Reviewer for PhD/MSc Theses:

1. Ms. Elsa Claude, Université Laval, 2023
2. Mr. Liangxi Wang, University of Toronto, 2023
3. Ms Catherine Proulx, Université de Montréal, 2022

4. Mr. Antoine Bodein, Université Laval, 2021
5. Mr. Maxime Déraspe, Université Laval, 2021
6. Mr. Vincent Mérel, Université Claude Bernard - Lyon 1, 2021
7. Ms. Laura Francesca Campitelli, University of Toronto, 2020
8. Ms. Parisa Mazrooei, University of Toronto, 2019
9. Mr. Brent Saylor, Guelph University, 2019
10. Ms. Florence Mailhot-Léonard, Université de Montréal, 2017
11. Ms. Assya Trofimov, Université de Montréal, 2017
12. Mr. Charles Joly Beuparlant, Université Laval, 2017
13. Mr. Yu-Jui Ho, Cold Spring Harbor Laboratory, USA, 2017
14. Mr. David Becerra, McGill University, 2017
15. Mr. Gireesh Kumar Bogu, Universitat Pompeu Fabra, Spain, 2017
16. Mr. Maxime Cadieux-Dion, Université de Montréal, 2016
17. Mr. Robert Lesurf, McGill University, 2014
18. Ms. Zibo Wang, McGill University, 2014
19. Ms. Jacklyn Quinlan, Université de Montréal, 2014
20. Mr. Sebastien Boisvert, Université Laval, 2014
21. Mr. Louis-Philippe Lemieux-Perreault, Université de Montréal, 2013
22. Mr. Philippe Serhal, Université de Montréal, 2013
23. Mr. Charles Joly-Beuparlant, Université Laval, 2013
24. Ms. Marie Scott-Boyer, Université de Montréal, 2013
25. Ms. Julie Hussein, Université de Montréal, 2012
26. Ms. Malaika Aïd, Université de Montréal, 2012
27. Mr. Wishva Bandara Herath, National University of Singapore, 2011
28. Ms. Maryam Haghighi, University of Ottawa, 2011
29. Mr. Glenn Hickey, McGill University, 2011
30. Mr. Emilio Vello, Université de Montréal, 2011

3. High-qualified Personnel Supervised

Current:

1. Justin Marcelino (Web Application Developer, 2023 – present)
2. David Lougheed (Web Application Specialist, 2023 – present)
3. Wilian Correa de Macedo (Bioinformatics Analyst, 2023 – present)
4. Victor Rocheleau (Scientific Data Architect, 2023 – present)
5. Mareike Janiak (Bioinformatics Analyst, 2023 – present)
6. Jean-Michel Garant (Bioinformatics Specialist, 2022 – present)
7. Julian Martinez Henao (Web Application Specialist, 2022 – present)
8. Christopher Kostiw (Web Application Specialist, 2022 – present)
9. Félix Guingant (SD4Health SW infrastructure developer, 2022 – present)

10. Nathalie Aerens (SD4Health Platform Manager, 2022 – present)
11. Gerardo Zapata (Bioinformatics Consultant, 2021 – present)
12. Gordon Krieger (Web Design Consultant, 2021 – present)
13. Danielle Perley (Bioinformatics Consultant, 2021 – present)
14. Solomia Yanishevsky (Data Administrator, 2021 – present)
15. Andres Tocasuche (System Analyst, 2020 – present)
16. Haiyong You (System Specialist Linux, 2020 – present)
17. David Brownlee (Database Analyst, 2019 – present)
18. Senthil Kumar D. Kailasam (Bioinformatics Consultant, 2019 – present)
19. Paul Stretenowich (Bioinformatics Consultant, 2019 – present)
20. Ulysse Fortier-Gauthier (Bioinformatics Software Developer, 2019 – present)
21. Alain Pacis (Bioinformatics Consultant, 2018 – present)
22. Pierre-Olivier Quirion (Software Developer, 2018 – present)
23. Marie-Michelle Simon (Research Assistant, 2018 – present)
24. Bing Ge (Bioinformatics Specialist, 2018 – present)
25. Jose Hector Galvez (Bioinformatics Specialist, 2017 – present)
26. Emmanuel Gonzalez (Bioinformatics Specialist, 2016 – present)
27. Raul Baldin (System Specialist Linux, 2016 – present)
28. Gary Leveque (Bioinformatics Specialist, 2015 – present)
29. Francois Lefebvre (Bioinformatics Manager, 2015 – present)
30. Pascale Marquis (Bioinformatics Consultant, 2015 – present)
31. Frankel Andras (Systems Officer, 2012 – present)
32. Robert Eveleigh (Bioinformatics Specialist, 2012 – present)
33. David Bujold (Bioinformatics Manager, 2012 - present)
34. Tony Kwan (Research Associate, 2012 – present)
35. Terrance McQuilkin (IT Manager, 2012 – present)

Previous:

1. Edouard Henrion (Bioinformatics Software Developer, 2015 – 2023)
2. Fatima Tokhmafshan (Project Administrator, 2020 – 2022)
3. Paul Pillot (Software Developer, 2022 – 2022)
4. Mary Ann Kizhakechethipuza (Administrator, 2020 – 2022)
5. Daniel Poppleton (Bioinformatics Manager, 2021 – 2022)
6. Sebastian Ballesteros (Web Design Consultant, 2021 – 2022)
7. Robert Syme (Bioinformatics Consultant, 2019 – 2022)
8. Mathieu Bourgey (Bioinformatics Manager, 2015 – 2022)
9. Pubudu Manoj Nawarathna Nawarathna Mudiyanse (Bioinformatics Consultant, 2019 – 2022)
10. Brennan Brouillette (Bioinformatics Software Developer, 2020 – 2022)
11. Ksenia Zaytseva (Software Infrastructure Developer, 2019 – 2022)

12. David Anderson (Web Design Consultant, 2016 – 2022)
13. Romain Gregoire (Software Developer, 2017 – 2021)
14. Jasmine Leblond-Chartrand (Web Design Consultant, 2020 – 2021)
15. Adrielle Houweling (Business Analyst, 2019 – 2021)
16. Rola Dali (Bioinformatics Specialist, 2017 – 2020)
17. Simon Chenard (Software Developer, 2019 – 2020)
18. John Wheeler (System Specialist Linux, 2019 – 2020)
19. David Lougheed (Web Application Developer, 2019 – 2020)
20. Alexandru Guja (System Specialist Linux, 2013 – 2020)
21. Sebastian Shah (Web Developer, 2019 – 2019)
22. Eloi Mercier (Bioinformatics Consultant, 2016 – 2019)
23. Julien Tremblay (Bioinformatics Consultant, 2014 – 2016)
24. Johanna Sandoval (Bioinformatics Consultant, 2012 – 2016)
25. Joel Fillon (Bioinformatics Consultant, 2012 – 2015)
26. Geneviève Dancausse (IT Specialist, 2010 – 2016)
27. Marc-André Labonté (System Specialist Linux, 2010 – 2015)
28. Louis Létourneau (Team Leader, 2010 – 2015)

4. Invited Lectures

1. Human genome 2.0 : why a pangenome graph is better for genetic and epigenetic analyses. *University of Toronto, Canada*. June 2023.
2. Graph genomes reveal missing signal in epigenomic data. Gordon Conference: Cancer Genetics and Epigenetics. *Tuscany, Italy*. May 2023.
3. Human genome 2.0 : why a pangenome graph is better for genetic and epigenetic analyses. University of Chicago. *Chicago, USA*. April 2023.
4. Human genome 2.0 : why a pangenome graph is better for genetic and epigenetic analyses. ASHBI seminar. *Kyoto, Japan*. March 2023.
5. Transposable elements are a source of innovation and variability in the human genome. The 3rd Barbados meeting on Transposable Elements. *Bellairs, Barbados*. Jan 2023.
6. Transposable elements are a source of innovation and variability in our response to infection. IHEC-CEEHRC 2022, *Estérel, Canada*. Oct 2022.
7. Transposable elements are a source of innovation and variability in our response to infection. JOBIM 2022. *Rennes, France*. June 2022.
8. Role of TEs in gene regulation and cancer. Forbeck Forum: Cancer and the Dark Matter. *Asilomar, USA*. May 2022.
9. Applications of genomic and epigenomic to understand diseases. INRS. *Virtual*. Jan 2022.

10. Data Repository-based Approaches in Comparative and Functional Epigenomics. FASEB Autumn School : The Epigenome in Human Health and Diseases. *Virtual*. Oct 2021.
11. SARS-CoV2 data sharing. National Leadership Group for Variants of Concerns. *Virtual*. Oct 2021.
12. VirusSeq Data Portal. International Discussion Group on COVID. *Virtual*. July 2021.
13. Une approche fédérée pour organiser et partager les données génomiques malgré les frontières. Table Nationale des Directeurs de Recherches. *Virtual*. June 2021.
14. Une approche fédérée pour organiser et partager les données génomiques malgré les frontières. ACFAS. *Virtual*. May 2021.
15. Genomic data infrastructure projects in Canada. Genome Canada workshop. *Virtual*. March 2021.
16. Méthodes pour organiser et partager les données génomiques. Table Nationale des Directeurs de Recherches. *Virtual*. Nov 2020.
17. Impact of transposable elements on human gene regulatory networks. IRCM. *Virtual*. Nov 2020.
18. Personalized and graph genomes reveal missing signal in epigenomic data. T2T/HPRC consortium meeting. *Virtual, USA*. Sep 2020.
19. Scalable methods for genomic analysis and comparative epigenomics. Hiroshima University. *Hiroshima, Japan*. Feb 2020.
20. Intra and inter-species epigenomic comparisons to understand non-coding DNA. ASHBi Colloquium. *Kyoto, Japan*. Jan 2020.
21. Personal genomes and global data sharing. Bellairs Workshop on clinical implementation of genomics and epigenomics. *Bellairs, Barbados*. Jan 2020.
22. Graph-genomes and global data sharing for epigenomic data. UCSC. *Santa Cruz, USA*. Dec 2019.
23. Canadian data sharing landscape. CIHR – UK data sharing workshop. *Ottawa, Ontario*. Nov 2019.
24. Scalable methods for genomics analyses and the McGill initiative in Computational Medicine. Bioengineering Department, McGill University. *Montréal, Québec*. October 2019.
25. Using comparative epigenomics to understand human gene regulation. ASHBi meeting. *Kyoto, Japan*. Aug 2019.
26. Personalized and graph genomes reveal missing signal in epigenomic data. University of Toronto. *Toronto, Ontario*. Aug 2019.
27. Genomics and epigenomics data sharing and the McGill initiative in Computational Medicine. Génome Québec Science Symposium. *Montréal, Québec*. June 2019.

28. Human copy number variants are enriched in regions of low mappability. Canadian Human and Statistical Genetics Meeting. *Montebello, Québec*. June 2019.
29. Unmasking transposable elements in regulation and disease. Royal Society Transposable Element meeting. *London, UK*. May 2019.
30. Scalable methods for genomics analyses and the McGill initiative in Computational Medicine. National Research Council. *Ottawa, Ontario*. March 2019.
31. Scalable methods for genomic and epigenomic data analyses. Concordia University. *Montréal, Québec*. March 2019.
32. Using comparative epigenomics to better understand non-coding DNA. RIKEN Institute. *Yokohama, Japan*. March 2019.
33. Understanding non-coding DNA using comparative epigenomics. ASHBi kickoff symposium. *Kyoto, Japan*. March 2019.
34. Unmasking transposable elements. Université Laval. *Québec, Québec*. February 2019.
35. Scalable methods for genomics analyses and the McGill initiative in Computational Medicine. UQAM. *Montréal, Québec*. January 2019.
36. Scalable methods for genomics and epigenomics data analyses. CANARIE Board Meeting. *Montréal, Québec*. January 2019.
37. The impact of transposable elements (and other genetic changes) on the epigenome. Bellairs Workshop on Transposable Elements. *Bellairs, Barbados*. January 2019.
38. Unmasking transposable elements. Molecular Genetics departmental seminar, University of Toronto. *Toronto, Ontario*. December 2018.
39. GA4GH, CanDIG and EpiShare. Terry Fox Research Institute workshop. *Montréal, Québec*. November 2018.
40. Genomics, epigenomics and the McGill initiative in Computational Medicine. Department of Physiology seminar. *Montréal, Québec*. November 2018.
41. Integrated genomics and bioinformatics. 3rd RIKEN – McGill symposium. *Montréal, Québec*. November 2018.
42. Understanding human genomes. Kyoto University. *Kyoto, Japan*. October 2018.
43. Understanding Impact of transposable elements on gene regulatory networks. Evolutionary Roles of Transposable Elements and Non-coding DNA: The Science and the Philosophy. *Halifax, Nova Scotia*. October 2018.
44. McGill Initiative in Computational Medicine. MUHC Symposium on Computational Medicine. *Montréal, Québec*. June 2018.

45. Latest developments in genomics and the McGill initiative in Computational Medicine. McGill Medical Genetics Departmental Rounds. *Montréal, Québec*. March 2018.
46. Scalable methods for genomics and epigenomics data analyses. McGill-RIKEN joint symposium. *Yokohama, Japan*. February 2018.
47. Transposable elements, tools to analyze epigenomics data and copy number aberrations. Bellairs Workshop on Cancer Epigenomics. *Bellairs, Barbados*. January 2018.
48. Updates from the Genome Center and from the McGill Initiative in Computational Medicine. Department of Pharmacology, McGill. *Montréal, Québec*. December 2017.
49. Comprendre l'ADN non-codant chez l'humain à l'aide de la génomique et de l'épigénomique. Université de Tunis. *Tunis, Tunisia*. December 2017.
50. Scalable methods for genomic and epigenomic data analyses. GeXc Symposium. *Montréal, Québec*. December 2017.
51. Updates from the Genome Center and from the McGill Initiative in Computational Medicine. Goodman Cancer Center Retreat. *Saint-Jean-sur-Richelieu, Québec*. December 2017.
52. Update from the CEEHRC Epigenomes mapping centers. CEEHRC annual meeting. *Whistler, British-Columbia*. November 2017.
53. Updates from the Genome Center, Epigenetics, the McGill Initiative in Computational Medicine and MI4. Department of Human Genetics, McGill. *Montréal, Québec*. November 2017.
54. Updates from the Genome Center, Epigenetics, the McGill Initiative in Computational Medicine and MI4. Hôpital Sainte-Justine. *Montréal, Québec*. November 2017.
55. Scalable methods for genomic and epigenomic data analyses. QLS Seminar. *Montréal, Québec*. October 2017.
56. Data Challenges in Genomics. Conférence internationale sur les méthodes d'enquêtes en transport (ISCTSC 2017). *Estérel, Québec*. Septembre 2017.
57. Next-generation sequencing: applications and data analysis. Kyoto University. *Kyoto, Japan*. August 2017.
58. Understanding the impact of transposable elements using comparative epigenomics. FASEB Mobile DNA in Mammalian Genomes. *Big Sky, Montana*. June 2017.
59. Using visual labels and supervised machine learning to mine epigenomics data. Canadian Human and Statistical Genetics Meeting. *Québec, Canada*. April 2017.

60. Using comparative epigenomics to better understand non-coding DNA. Center for Developmental Biology (CDB) Symposium 2017. *Kobe, Japan*. March 2017.
61. Using comparative epigenomics to better understand non-coding DNA. Center for Regulatory Genomics. *Barcelona, Spain*. January 2017.
62. Transposable elements stories. Bellairs Workshop on Transposable Elements. *Bellairs, Barbados*. January 2017.
63. International Human Epigenome Consortium (IHEC) Data Portal. CSHL Biological Data Science Meeting. *Cold Spring Harbor, USA*. October 2016.
64. Using comparative epigenomics to better understand non-coding DNA. Simons Center for Quantitative Biology Seminar Series. *Cold Spring Harbor, USA*. October 2016.
65. Comparative Epigenomics. 14th RECOMB Comparative Genomics Satellite Workshop. *Montréal, Canada*. October 2016.
66. A primer on DNA sequencing technologies and on whole-genome sequence analysis. Alzheimer meeting. *Lille, France*. October 2016.
67. Epigenomic resources to better understand human non-coding DNA. Spotlight at the Goodman Cancer Center. *Montréal, Canada*. September 2016.
68. Scalable hardware and software solutions for genomic and epigenomic data analyses, National Cancer Center Research Institute. *Tokyo, Japan*. July 2016.
69. The Enemy Within..., Pint of Science. *Montréal, Canada*. May 2016.
70. Genome Analysis, 1st Canadian Computational Biology Workshop Conference. *Toronto, Canada*. May 2016.
71. Impact of endogenous retroviruses on the evolution of primate embryonic stem cells, Epigenomics 2016. *Puerto Rico, USA*. February 2016.
72. Impact of endogenous retroviruses on the evolution of primate embryonic stem cells, Pasteur Institute. *Paris, France*. January 2016.
73. Transposable elements, copy number variants, and... , 2nd Epigenomics workshop in Barbados. *Bellairs, Barbados*. January 2016.
74. Impact of endogenous retroviruses on the evolution of primate embryonic stem cells, Kyoto University. *Kyoto, Japan*. December 2015.
75. Scalable hardware and software solutions for genomic and epigenomic data analyses, Shanghai Center for Bioinformation Technology. *Shanghai, China*. November 2015.
76. Scalable hardware and software solutions for genomic and epigenomic data analyses, CIHR-MOST Symposium. *Taipei, Taiwan*. November 2015.
77. Challenges and opportunities with genomic data analysis, 1st Joint Symposium of Top Global University Project. *Kyoto, Japan*. October 2015.

78. Impact of transposable elements on transcription regulation in human, The Mobile Genome: Genetic and Physiological Impacts of Transposable Elements. *Heidelberg, Germany*. September 2015.
79. Big Data in Genomics, Compute Canada MSI review. *Ottawa, Ontario*. May 2015.
80. Évolution de la régulation transcriptionnelle dans le génome humain, Department of Biochemistry 21st Symposium. *Sherbrooke, Québec*. April 2015.
81. The IHEC Data Portal and Analysis Tools for Epigenomics, The Alberta Epigenomics Network Annual Meeting. *Banff, Alberta*. March 2015.
82. Landscape and evolution of transcription regulation in the human genome, Excellence in Genetics and Immunology Seminar Series at McGill University. *Montréal, Québec*. January 2015.
83. Innovation and Biochemical Noise in the Human Genome, Understanding non-coding DNA through intra and inter-species epigenomic variation. *Bellairs, Barbados*. January 2015.
84. Understanding human non-coding DNA through functional genomics, Concordia University. *Montréal, Québec*. November 2014.
85. La Bioinformatique au Centre d'Innovation Génome Québec et Université McGill, POP! Université de Montréal. *Montréal, Québec*. November 2014.
86. Le data tsunami en génomique, Assemblée Générale Annuelle du RISQ. *Montréal, Québec*. November 2014.
87. Next-Generation Sequencing, Annual Congress of the Canadian Association of Medical Biochemists. *Montréal, Québec*. October 2014.
88. Building an open and scalable analysis platform for genomics, Best Practices for Big Data in Genomics Workshop. *Boston, USA*. October 2014.
89. Epigenome Data Coordination, International Human Epigenome Consortium (IHEC) Annual Meeting. *Vancouver, Canada*. October 2014.
90. Decoding human non-coding DNA, Genome Institute of Singapore. *Singapore, Singapore*. September 2014.
91. International Human Epigenome Consortium (IHEC), Cagekid Meeting. *Leeds, United Kingdom*. June 2014.
92. Evolution of gene regulation in the human genome. Rendez-vous Génome Québec. *Québec, Canada*. May 2014.
93. Impact of transposable elements on the human genome. Barbados Workshop on the Computational Identification and Analysis of Transposable Elements. *Bellairs, Barbados*. April 2014.
94. Transposable elements: innovation and biochemical noise in the human genome. Keystone meeting on Mobile Genetic Elements and Genome Evolution. *Santa Fe, USA*. March 2014.

95. Mapping the functional elements in the human genome. TorBUG meeting. *Toronto, Canada*. Feb 2014.
96. Genetics and genomics Analysis Platform (GenAP). Journée Bioinformatique Calcul Québec. *Montréal, Canada*. Jan 2014.
97. Microbial Meta-omics Resource Center. NSERC Discovery Frontiers reverse-site visit. *Ottawa, Canada*. Jan 2014.
98. The role of transposable elements in genome evolution. Workshop on Mathematics of Sequence Evolution: Biological Models and Applications. *Montréal, Canada*. Sept 2013.
99. The Data Tsunami in Biomedical Research. McGill – RIKEN workshop. *Montréal, Canada*. June 2013.
100. The Data Tsunami in Biomedical Research. High-Performance Computing Symposium. *Ottawa, Canada*. June 2013.
101. The role of genomic repeats in host gene regulation. Workshop on gene regulatory networks. *Bellairs, Barbados*. Apr 2013.
102. The majority of primate-specific regulatory sequences are derived from transposable elements. CHU de Québec. *Québec, Canada*. Apr 2013.
103. Role of genomic repeats in host gene regulation. Kyoto Symposium on Bioinformatics for Next-Generation Sequencing with Applications in Human Genetics. *Kyoto, Japan*. Jan 2013.
104. Role of genomic repeats in host gene regulation. Genome Institute of Singapore. *Singapore, Singapore*. Jan 2013.
105. Next-generation sequence analysis. Rendez-vous Génome Québec. *Montréal, Canada*. Dec 2012.
106. Role of genomic repeats in host gene regulation. Brown University. *Providence, USA*. Nov 2012.
107. Role of genomic repeats in host gene regulation. Center for Regulatory Genomics. *Barcelona, Spain*. Aug 2012.
108. Opportunities and challenges in genomics. High Performance Computing Symposium 2012. *Vancouver, Canada*. May 2012.
109. Role of genomic repeats in host gene regulation. International Congress on Transposable Elements (ICTE). *Saint-Malo, France*. May 2012.
110. Opportunities and challenges in genomics. Université de Sherbrooke Biology Seminar Series. *Sherbrooke, Canada*. Mar 2012.
111. Opportunities and challenges in genomics. McGill Urology Research Seminar Series. *Montréal, Canada*. Mar 2012.
112. Computational challenges in genomics. Computer Science Seminar, McGill University. *Montréal, Canada*. Mar 2012.
113. Role of genomic repeats in gene regulation. 11th Annual McGill Workshop on Bioinformatics. *Bellairs, Barbados*. Jan 2012.

114. Enabling integrative analyses for genomics and genetics. McGill University and Génome Québec annual research update. *Montréal, Canada*. Jan 2012.
115. The role of genomic repeats in transcriptional regulation. Université Laval. *Québec, Canada*. Dec 2011.
116. Paired-End Sequencing Reveals Characteristic Patterns of Structural Variations in Epithelial Cancer Genomes. Environmental Mutagen Society Annual Meeting. *Montréal, Canada*. Oct 2011.
117. The role of genomic repeats in transcriptional regulation. monBUG symposium. *Montréal, Canada*. Sep 2011.
118. The role of genomic repeats in gene regulation. UCSD. *San Diego, USA*. Aug 2011.
119. Human endogenous retroviruses have contributed thousands of tissue-specific regulatory elements. Salk Institute. *San Diego, USA*. Aug 2011.
120. Human endogenous retroviruses have contributed thousands of tissue-specific regulatory elements. FASEB summer school: Mobile DNA in mammalian genomes. *Aspen, USA*. Aug 2011.
121. The role of genomic repeats in gene regulation. McGill University and University of Toronto Computer Science retreat. *Montréal, Canada*. May 2011.
122. The role of genomic repeats in gene regulation, diversity and disease. Human Genome Meeting 2011. *Dubai, UAE*. April 2011.
123. Impact of transposable elements on mammalian gene regulatory networks. Montréal Heart Institute. *Montréal, Canada*. Oct 2010.
124. Functional genomics in stem cells and in cancer. IRCM. *Montréal, Canada*. April 2010.
125. Functional genomics in stem cells and in cancer. McGill University. *Montréal, Canada*. April 2010.
126. Transposable elements have rewired the core regulatory network of human embryonic stem cells. CSHL Systems Biology Meeting. *Cold Spring Harbor USA*. Mar 2010.
127. Genomics : New Computational Challenges. NCSA - XPRIZE – HUGO. *Illinois USA*. Mar 2010.
128. Functional genomics in stem cells and in cancer. J. Craig Venter Institute, *Georgetown, USA*. Jan 2010.
129. Functional genomics in stem cells and in cancer. Memorial Sloan Kettering Cancer Center. *New York, USA*. Jan 2010.
130. Functional genomics in stem cells and in cancer. Albert Einstein College of Medicine. *New York, USA*. Jan 2010.

131. Functional genomics in stem cells and in cancer. Université de Montréal & CHU Sainte-Justine. *Montréal, Canada*. Jan 2010.
132. Extensive binding site turnover in the core regulatory network of embryonic stem cells. Stanford University. *Stanford, USA*. Oct 2009.
133. Evolution of the mammalian transcription factor binding repertoire via transposable elements. Max Planck Institute for Molecular Genetics. *Berlin, Germany*. June 2009.
134. Evolution of the mammalian transcription factor binding repertoire via transposable elements. Systems Biology: Global Regulation of Gene Expression. *Cold Spring Harbor, USA*. March 2009.
135. Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genomic Impact of Transposable Elements. *Asilomar, USA*. Feb 2009.
136. Evolution of the mammalian transcription factor binding repertoire via transposable elements. Frontiers in Bioinformatics and Systems Biology Colloquium. *San Diego, USA*. Feb 2009.
137. Informatics Solution to Medical Genomics. HUGO-Asia meeting. *Cebu, Philippines*. April 2008.
138. The Hitchhikers guide to mammalian transcription factors binding sites. Systems Biology: Global Regulation of Gene Expression. *Cold Spring Harbor, USA*. April 2008.
139. Decoding the human genome and implications for human health. *Bharathidasan University, India*. March 2008.
140. Genome-wide binding site map of mammalian transcription factors reveals rapid evolutionary turnover. Systems Biology: Global Regulation of Gene Expression. *Cold Spring Harbor, USA*. March 2007.
141. New paired-end sequencing technologies for the characterization of transcription factor binding sites and mRNA populations. IRCM. *Montréal, Canada*. Sept 2006.
142. Chromosome rearrangements in evolution and cancer. Workshop on Genomics. IMS, NUS. *Singapore, Singapore*. Nov 2005.
143. Maximizing synteny blocks to identify ancestral homologs. 3rd RECOMB Comparative Genomics Satellite Workshop. *Dublin, Ireland*. Sept 2005.
144. Improving gene network inference by comparing expression time-series across species, developmental stages or tissues. Statistical Methods in Microarray Data Analysis. Institute for Mathematical Sciences. *Singapore, Singapore*. Jan 2004.
145. A Comparative Approach for Multiple Gene Network Inference Using Time-Series Gene Expression Data. IMA/RECOMB Satellite Workshop on Comparative Genomics. *Minneapolis, USA*. October 2003.

146. Gene network inference using time-series gene expression data.
Conference organized by RBMC. *Montréal, Canada*. May 2003.

F. OTHER CONTRIBUTIONS

1. Journals

Editorial board:

- Algorithms for Molecular Biology, Member Editorial Board, 2010 – present
- Mobile DNA, Member Editorial Board, 2014 – 2022
- Mobile Genetics Elements, Member Editorial Board, 2010 – 2018
- PLoS ONE, Academic Editor, 2007 – 2014

Ad hoc reviews:

- Nature
- Nature Genetics
- Nature Communications
- eLife
- Nature Biotechnology
- Cell Reports
- Genome Research
- Bioinformatics
- Mobile DNA
- PLoS Genetics
- PNAS
- Molecular Biology and Evolution
- EMBO Journal
- Biology Direct
- PLoS Computational Biology
- NAR
- Physiological Genomics
- IEEE Transactions on Computational Biology and Bioinformatics

2. Grant Reviews

Permanent service:

- CIHR Genomics Panel, Nov 2012 – 2015, 2020 – 2021
- CIHR College of Reviewers, 2017 – ...
- FRQ, Chercheurs-Boursiers Junior 1, 2018 – 2019
- Compute Canada, Resource Allocation Committee, Nov 2012 – 2018

Ad Hoc:

- Genome BC, Data Access, Integration and Analysis (DAIA), Oct 2022.
- Medical Research Council, UK, September 2022.
- NIH R01, Elucidating the Roles of Transposable Elements in AD/ADRD and Aging, March 2022.
- NSERC, Discovery Grants, January 2019, January 2022
- NIH P01 Cancer grant panel, May 2018.
- University of Toronto, tenure dossier, December 2017.
- Shanghai Jiao Tong University, tenure track review, June 2017.
- CANARIE, Software Platform, April 2017.
- Université Cote d'Azur, Data Sciences initiative, March 2017.
- The Intelligent Systems for Molecular Biology (ISMB) Conference, Feb 2017
- CIHR Foundation Grants, January 2017
- NSERC, Discovery Grants, March 2016
- GLBIOCCBC Conference, February 2016
- The Intelligent Systems for Molecular Biology (ISMB) Conference, Jan 2016
- Laval University Bioinformatics graduate program, Oct 2015
- MITACS, Accelerate program, Sept 2015
- Michael Smith Foundation, Scholar Competition, Apr 2014
- NSERC, Discovery Grants, Jan 2014
- The Intelligent Systems for Molecular Biology (ISMB) Conference, Jan 2014
- CFI, Leaders Opportunity Fund, Nov 2013
- CANARIE, Research Middleware Program, Sept 2013
- Portuguese Foundation for Science and Technology, Sep 2013
- NCI, Early Stage Development of Informatics Technology, June 2013
- Swiss National Science Foundation, June 2013
- Agence National de la Recherche, France, May 2013
- NIH, Development and Application of Systems Approachs for Analyzing the Impact of Genomic Variation on Tissue Transcritomes (R01), Apr 2013
- NSERC, Collaborative Research and Training Experience Program, Jan 2013
- Ontario Research Fund – CFI Scientific Review, Aug 2012
- Portuguese Foundation for Science and Technology, Sep 2012
- NIH/NIGMS New Methods for Understanding the Functional Role of Human DNA Sequence Variants in Complex Phenotypes, July 2012
- The Knut and Alice Wallenberg Foundation, Sweden. Sept 2011

- NIH-NCI panel on The Cancer Genome Atlas initiative for Cancer Genome Characterization Centers^[17] and Cancer Genome Data Analysis Centers, June 2009

3. Administrative Responsibilities and University Committees

- Lead, McGill Initiative in Computational Medicine. 2016 – present.
- Member, Faculty of Medicine Standing Internal Review Committee for CRCs and Internal Awards. 2022 – present.
- Interim Scientific Director, McGill High-Performance Computing center. 2019.
- Member, Department of Human Genetics, Tenure Track Committee, 2018 – present.
- Member, Healthy Brains and Healthy Lives Neurohub subcommittee. 2016 – present.
- Member, Cross-faculty committee to develop a new Graduate program in Quantitative Life-Sciences. 2014 – 2017.
- Director of Bioinformatics at the McGill University Genome Center, 2010 – present. Responsibilities include:
 - co-PI of the Genome Canada Platform Renewal for McGill University and Genome Quebec Innovation Centre (2010, 2012, 2015 and 2017).
 - Responsible for the planning and the organization of the bioinformatics platform to increase its analysis capabilities. I Currently manage 26 staffs on the platform split between: IT (1 Manager + 4 staffs), Software Development (1 Manager + 8 staffs) and Analysis Team (12 staffs).
 - Plan, write Request For Proposal, evaluate proposals, supervise renovations and installation of equipment for the Compute Server room for the Innovation Center (located in the Ferrier building, \$3M in 2012 and \$5M to be spent in 2017).
 - Responsible for the overall quality control and analyses of datasets generated on the high-throughput platforms at the Innovation Center.
 - Participate and lead regular meetings at the Innovation Center:
 - Weekly meetings with Director of Operations
 - Bi-weekly meetings with Platform Directors
 - Monthly meetings with Platform Managers
 - Weekly meetings with Data Analysis team

- Member, McGill University Genome Center Internal Management Committee (IMC). 2013 – 2020.
- Member, McGill University Genome Center Education Committee. 2013 – 2020.
- Member, McGill University Genome Center Recruitment Committee. 2011 – 2020.

4. National and International Committees

National committees:

- Variant of Concerns Leadership Group, 2020 – present.
- Member of the Conseil Scientifique de Calcul Québec, 2015 – present.
- Member of Researcher Council, Digital Research Alliance, 2021 – 2022.
- Member of Genome Canada/CIHR Pan-Canadian Population Cohort Working Group, 2020 – 2022.
- Member of CIHR Institute Advisory Board for the Institute of Genetics, 2017 – 2021.
- Member of CIHR Institute Advisory Board on Research Excellence, Policy and Ethics, 2016 – 2017.
- Member of Compute Canada Research Advisory Council, 2013 – 2019.
- Member of CANARIE Research Advisory Council, 2013 – 2019.

International committees:

- Member, Somatic Mosaicism Across Human Tissues (SMaHT), External Consultants Panel, NIH-NHGRI program, 2023 – present.
- Member, Impact of Genomic Variation on Function (IGVF), External Consultants Panel, NIH-NHGRI program, 2022 – present.
- Member, Global Alliance for Genomics and Health (GA4GH), Steering Committee, 2018 – present.
- Chair, International Human Epigenome Consortium, Integrative Analysis Workgroup, 2016 – present.
- Member, ENCODE External Consultants Panel, NIH-NHGRI program, 2017 – 2022.
- FAANG Data Coordination Centre Strategic Management Board, EBI project, UK. 2017 – 2021.

- Member, International Human Epigenome Consortium, International Scientific Steering Committee, 2015 – present.
- Member, International Human Epigenome Consortium, Metadata Standards and Data Ecosystem Workgroups, 2012 – present.
- Member, International Cancer Genome Consortium, Data Coordination Committee, 2011 – 2018.

5. Professional and/or Learned Societies

Member, American Society of Human Genetics, 2011 – 2015.

6. Other Professional and Scientific Contributions

- Letters of recommendation for promotions:
 - University of Southern California, USA, August 2023.
 - King's College London, UK, March 2023.
 - University Western Ontario, Canada, July 2022.
 - Nanyang Technological University, Singapore, July 2022.
 - The Jackson Laboratory, USA, June 2022.
 - Southern University of Science and Technology (SUSTech), China, Sept 2021.
 - Université de Montpellier, France, Sept 2021.
 - Université de Montréal, Canada, Sept 2021.
- Conference organization
 - 9th Annual Canadian Conference on Epigenetics. *Banff, Canada*. November 2023.
 - The 3rd Barbados meeting on Transposable Elements. *Bellairs, Barbados*. Jan 2023.
 - 8th Canadian Conference on Epigenetics. *Esterel, Québec*. October 2022.
 - 7th Canadian Conference on Epigenetics. *Esterel, Québec*. November 2021.
 - Barbados Workshop on Clinical Implementation of Genomics and Epigenomics. *Bellairs, Barbados*. January 2020.
 - 6th Canadian Conference on Epigenetics/IHEC Annual Meeting, *Banff, Canada*. November 2019.
 - 2nd Barbados Workshop on Transposable Elements. *Bellairs, Barbados*. January 2019.
 - McGill initiative in Computational Medicine (MiCM) 2nd symposium. *Montréal, Québec*. November 2018.
 - 5th Canadian Conference on Epigenetics. *Esterel, Québec*. September 2018.

- Barbados Workshop on Cancer Epigenomics. *Bellairs, Barbados*. January 2018.
- McGill initiative in Computational Medicine (MiCM) symposium. *Montréal, Québec*. December 2017.
- 4th Canadian Conference on Epigenetics: Mechanisms of Disease. *Whistler, British-Colombia*. November 2017.
- Barbados Workshop on Transposable Elements and Gene Regulation. *Bellairs, Barbados*. January 2017.
- 3rd Canadian Conference on Epigenetics: Epigenomics in Development and Disease. *Esterel, Québec*. September 2016.
- 2nd Epigenomics Workshop in Barbados. *Bellairs, Barbados*. January 2016.
- Rendez-vous Génome Québec 2015, Organized a workshop on Next-generation sequence analysis. *Montréal, Québec*. Dec 2015.
- Understanding non-coding DNA through intra and inter-species epigenomic variation. *Bellairs, Barbados*. January 2015.
- Rendez-vous Génome Québec 2014, Organized a workshop on Next-generation sequence analysis. *Montréal, Québec*. May 2014.
- Rendez-vous Génome Québec 2013, Organized one workshop on Next-generation sequence analysis. *Montréal, Québec*. Nov 2013.
- Challenges and Opportunities in Microbiome Research. *Montréal, Québec*. Sept 2013.
- Rendez-vous Génome Québec 2012, Organized two workshops on Next-generation sequence analysis. *Montréal, Québec*. Dec 2012.
- Rendez-vous Bioinformatique 2012. Organized three workshops on data analysis. *Montréal, Québec*. May 2012.
- Genome Canada 2011 Bioinformatics and Computational Biology Workshop. *Toronto, Ontario*. Dec 2011.
- Rendez-vous Bioinformatique 2011 (chair). *Montréal, Québec*. Dec 2011.
- RECOMB'2008, *Singapore, Singapore*. Mar 2008.
- Genome Informatics Workshop (GIW'07). *Singapore, Singapore*. Dec 2007.
- GEM4 Conference on Cancer (Co-chair). *Singapore, Singapore*. July 2007.
- 4th RECOMB Satellite Workshop on Comparative Genomics (Co-chair). *Montreal, Canada*. Sep 2006.
- Workshop on BioAlgorithms. *Singapore, Singapore*. July 2006.
- Workshop on Genomics. Institute for Mathematical Sciences, *Singapore, Singapore*. Nov 2005.
- Participated in a 2-day Digital Infrastructure Summit organized by Leadership Council for Digital Infrastructure. *Ottawa, Ontario*. Jan 2014.

- Participated in a 2-day workshop organized by CFI on Cyber-infrastructure. *Toronto, Ontario*. Jan 2014.
- Participated in a 3-day workshop organized by the International Human Epigenome Consortium. *Berlin, Germany*. Nov 2013.
- Participated in a 3-day workshop organized by the International Cancer Genome Consortium. *Toronto, Ontario*. Oct 2013.
- Participated in 2-day workshop organized by CIFAR on “Cyber-Infrastructure in Advanced Research: Needs, Challenges and Opportunities.” *Ottawa, Ontario*. May 2012.

G. RESEARCH

1. Research Activities

The goal of the lab is to understand mammalian genomes using comparative genomic and epigenomic analyses. Areas of interest include: the evolution of regulatory sequences, the role of transposable elements in gene regulation and the impact of genome rearrangements in evolution and cancer.

As a computational genomicists our work involves examining the billions of DNA base pairs and interpreting how variation impacts basic biology and disease. We develop computational methods and resources for the functional annotation of genomes with a special emphasis on sequencing-based assays (e.g. ChIP-seq, RNA-Seq, exome- and whole-genome sequencing, single-cell analysis).

2. Personal Support Awards

2020 – 2027	Canada Research Chair (Tier 1) Title : Computational Genomics and Medicine	\$ 1,400,000
2020 – 2024	Fonds de la recherche en santé du Québec Chercheurs-boursiers de merite (<i>partially accepted</i>)	\$ 400,000
2017 – 2020	Fonds de la recherche en santé du Québec Chercheurs-boursiers Senior	\$ 240,000
2012 – 2016	Fonds de la recherche en santé du Québec Chercheurs-boursiers Junior 2	\$ 287,000

3. Research Grants

Current (as PI in blue):

- 2023 – 2030 Ministry of Science Technology and Innovation, Canada First
Research Excellence Fund (CFREF) *\$165,307,000*
Role: Principal Investigator
Title: DNA to RNA: An inclusive Canadian Approach to
Genomic-based RNA Therapeutics
- 2020 – 2025 CFI, Innovation Fund 2020 *\$22,752,000*
Role: Project Lead
Title: SecureData4Health
- 2017 – 2024 CIHR, CEEHRC Epigenomics Platform *\$4,400,000*
Role: Project Lead (transferred from Tomi Pastinen)
Title: Multidimensional Epigenomics Mapping Centre
(EMC) at McGill
- 2021 – 2024 Genome Canada, Genome Quebec *\$1,100,000*
Role: Project Lead
Title: The National VirusSeq Data Portal (Covid-19)
- 2019 – 2024 CIHR, CEEHRC Consortium Network (phase 2) *\$1,000,000*
Role: Principal Applicant (NPA Hirst, share 7%)
Title: Canadian Epigenetics, Environment and Health Research
Consortium Network
- 2018 – 2024 CIHR, CIHR Team CEEHRC Phase II *\$1,497,750*
Role: Principal Applicant (PL Dilworth, share 5%)
Title: Epigenetic changes affecting muscle stem cell function in
the aging population

Past:

- 2017 – 2023 Genome Canada, Genomics Technology Platforms *\$6,890,786*
Role: Project Lead
Title: Canadian Center for Computational Genomics (C3G)
- 2018 – 2022 Genome Canada, B/CB competition,
\$1,035,024
Role: Project Lead

	Title: Epigenomics Secure Data Sharing Platform for Integrative Analyses (EpiShare)	
2017 – 2022	CIHR, 4D Nucleome Collaborative Projects	\$800,000
	Role: Project Lead (transferred from Tomi Pastinen)	
	Title: Accessing chromatin interactions by high-resolution analyses of correlated regulatory element variation	
2016 – 2022	CIHR/FRQS, Epigenomics of Complex Diseases	\$646,170
	Role: Project Lead (transferred from Elin Grundberg)	
	Title: Integrative epigenomics of obesity and metabolic complications	
2018 – 2020	CANARIE, Research Data Management,	\$447,000
	Role: Project Lead	
	Title: CanDIG CHORD: Canadian Health Omics Repository, Distributed	
2015 – 2017	Genome Canada, Genomics Innovation Network	\$ 1,050,000
	Role: Project Lead	
	Title: Canadian Center for Computational Genomics (C3G)	
2015 – 2017	Genome Canada, GIN – Tech. Development	\$ 527,000
	Role: Project Lead	
	Title: Canadian Center for Computational Genomics (C3G)	
2012 – 2017	CIHR, CEEHRC Epigenomics Platform	\$ 1,500,000
	Role: Principal Investigator	
	Title: Integrative Epigenomic Data Coordination Centre (EDCC) at McGill	
2011 – 2016	CIHR, Operating Grant	\$ 426,482
	Role: Principal Investigator	
	Title: Functional characterization of the endogenous retrovirus HERV-H family in human embryonic stem cells	
2013 – 2015	CANARIE, Research Middleware Program	\$ 771,000
	Role: Principal Investigator	
	Title: Genetics and Genomics Analysis Platform (GenAP)	
2006 – 2010	GIS Internal Grant (GIS05-114101), Singapore	S\$ 1,000,000
	Role: Principal Investigator	
	Title: Comparative Genomics: Theory and Application Platform.	

2020 – 2023	Genome Canada Role: co-Applicant (share ~5%) Title: Canadian COVID Genomics Network (CanCOGeN)	\$20,000,000
2017 – 2023	Genome Canada, Genomics Technology Platforms Role: co-Lead (PL Lathrop, share 15%) Title: McGill University and Génome Québec Innovation Center	\$9,866,249
2018 – 2023	Genome Canada, LSARP Competition, Role: co-Applicant (PI Jabado, share 2.5%) Title: Tackling Childhood Brain Cancer at the root to improve survival and quality of life	\$12,997,397
2018 – 2023	CFI, Cyberinfrastructure: Challenge, Role: co-Applicant (PI Stein, share 10%) Title: The Cancer Genome Collaboratory	\$4,995,318
2019 – 2023	EU-H2020-CIHR Collaboration on data sharing Role: co-Applicant (PI Brinkman, share 23%) Title: Common Infrastructure for National Cohorts in Europe, Canada, and Africa (CINECA)	\$800,000
2019 – 2023	EU-H2020-CIHR Collaboration on data sharing Role: co-Applicant (PI Emerson, share 20%) Title: Integrated Human data repositories for infectious disease-related international cohorts to facilitate personalized medicine approaches to infectious disease research (ReCoDID)	\$800,000
2022 – 2023	Public Health Agency of Canada (PHAC) Role: co-PI (PI Mooser, Rousseau, share 5%) Title: Biobanque québécoise de la COVID-19. Sero-Surveillance and Research (COVID-19 Immunity Task Force Initiative)	\$7,935,000
2022 – 2023	Public Health Agency of Canada (PHAC) Role: co-PI (PI Durand, Rousseau, share 5%) Title: Determining the impact of hybrid immunity on the evolving landscape of host responses to SARS-CoV-2 in the Biobanque Québécoise de la COVID-19 (BQC19)	\$1,174,608
2022 – 2023	Fonds de recherche du Québec - Santé (FRQS) Role: co-PI (PI Durand, Mooser, Rousseau, share 5%) Title: Biobanque québécoise de la COVID-19	\$200,000

2020 – 2022	CANARIE, Research Management Call 2 Role: co-PI (PI Brudno, share 28%) Title: ClinDig: A distributed system for clinical and genomics data	<i>\$699,843</i>
2018 – 2022	Terry Fox, Cancer Centre Consortium Network Role: co-PI (PI Watson, share 6%) Title: Montreal Cancer Consortium (MCC) - Pilot Project	<i>\$2,480,000</i>
2018 – 2022	Genome Canada, B/CB, Role: co-Project Leader (PI Xia) Title: An integrative platform for metabolomics and systems biology	<i>\$1,094,607</i>
2018 – 2022	Genome Canada, B/CB, Role: co-Applicant (PI Xia) Title: Development and Validation of a Web-Based Platform for Environmental Omics and Toxicology	<i>\$999,019</i>
2018 – 2021	Genome Canada, B/CB, Role: co-Applicant (PI Borchers, share 0%) Title: Proteogenomics -Improved and -Guided Quantification Pipeline (PIGQpipe)	<i>\$556,472</i>
2016 – 2021	CFI, Cyber-infrastructure Role: co-Lead (PL Brudno, share 40%) Title: CanDIG: Canadian Distributed cyber-Infrastructure for Genomics	<i>\$5,000,000</i>
2018 – 2020	CANARIE, Research Software Program, Role: co-PI (PI Jacques, share 12%) Title: Generalization of GenAP toward the growing single-cell and metabolomic communities	<i>\$224,626</i>
2015 – 2019	CIHR, CEEHRC Consortium Network Role: Principal Applicant (NPA Hirst, share 7%) Title: Canadian Epigenetics, Environment and Health Research Consortium Network	<i>\$2,000,000</i>
2015 – 2019	CFI, Innovation Fund Role: Principal User (PL Jones, share 8%)	<i>\$ 58,435,000</i>

	Title: Canada's Genomics Enterprise (CGEn): A national genomic tools network for transforming life science research	
2015 – 2019	CFI, Innovation Fund	\$2,893,000
	Role: Principal User (PL Meaney, share 0%)	
	Title: Treatment Outcomes in Mood Disorders	
2014 – 2018	NSERC, Discovery Frontiers	\$6,000,000
	Role: co-Investigator (PI Stein, share 7%)	
	Title: The Cancer Genome Collaboratory	
2015 – 2017	Genome Canada, Genomics Innovation Network	\$ 2,000,000
	Role: co-Lead (PL Lathrop, share 15%)	
	Title: McGill University and Génome Québec Innovation Center	
2015 – 2017	Genome Canada, GIN – Tech. Development	\$ 1,000,000
	Role: co-Lead (PL Lathrop, share 10%)	
	Title: McGill University and Génome Québec Innovation Center	
2012 – 2017	CIHR, CEEHRC Epigenomics Platform	\$ 6,000,000
	Role: co-Investigator (PI Lathrop, share 15%)	
	Title: Multidimensional Epigenomics Mapping Centre (EMC) at McGill	
2013 – 2017	Genome Canada, Large-scale Applied Research	\$ 6,000,000
	Role: co-Investigator (PIs Jabado – Majewski, share 5%)	
	Title: Biomarkers for Pediatric Glioblastoma through Genomics and Epigenomics	
2013 – 2016	Brain Canada	\$ 1,494,900
	Role: co-Investigator (PI Meaney, share 0%)	
	Title: Epigenetics and Mental Health	
2011 – 2016	CIHR, Team Grant: Childhood Cancer	\$ 2,445,054
	Role: co-Investigator (PI Sinnett, share 0%)	
	Title: Genomic determinants of common long-term treatment effects in childhood acute lymphoblastic leukemia survivors	
2011 – 2014	Genome Quebec, Human Health Competition	\$ 2,000,000
	Role: co-Inv (PI Moreau, share 10%)	
	Title: Development of comprehensive diagnostic assays for scoliosis	

- 2011 – 2012 CIHR, Advancing Technology Innovation \$ 1,550,000
 Role: co-Inv (PI Sorensen, share 10%)
 Title: The Canadian Pediatric Cancer Genome Consortium:
 Translating next-generation sequencing technologies into
 improved therapies for high-risk childhood cancer.
- 2006 – 2010 A*STAR-SSCC Grant, *Singapore* S\$ 850,000
 Role: co-Inv (PI Robson, share 10%)
 Title: Improved Derivations of Human Embryonic Stem Cells
 via Modelling of the Preimplantation Genetic Regulatory Network
- 2006 – 2010 BMRC-NMRC Grant, *Singapore* S\$ 1,500,000
 Role: co-Inv (PI Tan, share 10%)
 Title: Systematic Identification of Oncogenic Cellular Pathways
 and Processes in Gastric Can- cer for Patient Stratification and
 Personalized Therapy.
- 2007 – 2009 NIH RFA Grant (RFA-CA-07-001), *USA* US\$ 1,000,000
 Role: co-Inv (PI Liu, share 15%)
 Title: Pair-end-ditag technologies for the complete annotation of
 fusion genes.

4. Publications

* Papers where the first (or co-first) author is from my group

@ Corresponding author

Students and group members are underlined.

Refereed Journal Papers

2023

1. *Chen X, *Pacis A, Aracena KA, Gona S, *Kwan T, *Groza C, Lin YL, Sindeaux R, Yotova V, *Pramatarova A, *Simon MM, Pastinen T, Barreiro LB, **Bourque G@**. Transposable elements are associated with the variable response to influenza infection. *Cell Genom.* 2023 Apr 7;3(5):100292. doi: 10.1016/j.xgen.2023.100292.
2. *Groza C, *Chen X, *Pacis A, *Simon MM, *Pramatarova A, Aracena KA, Pastinen T, Barreiro LB, **Bourque G@**. Genome graphs detect human polymorphisms in active epigenomic state during influenza infection. *Cell Genom.* 2023 Apr 7;3(5):100294. doi: 10.1016/j.xgen.2023.100294.

3. [*Groza C](#), Schwendinger-Schreck C, Cheung WA, Farrow EG, Thiffault I, Lake J, Rizzo WB, Evrony G, Curran T, **Bourque G@**, Pastinen T. Pangenome graphs improve the analysis of rare genetic diseases. *medRxiv* 2023.05.31.23290808; doi: <https://doi.org/10.1101/2023.05.31.23290808>
4. N'Guessan A, [*Kailasam S](#), Mostefai F, Poujol R, Grenier JC, Ismailova, N, Contini P, De Palma R, Haber C, Stadler V, **Bourque G**, Hussin JG, Shapiro BJ, Fritz JH, Piccirillo CA. Selection for immune evasion in SARS-CoV-2 revealed by high-resolution epitope mapping and sequence analysis., *iScience*. 2023 Aug 18;26(8):107394. doi: <https://doi.org/10.1016/j.isci.2023.107394>.
5. [*Lougheed DR](#), Liu H, Aracena KA, Grégoire R, [*Pacis A](#), Pastinen T, Barreiro LB, Joly Y, [*Bujold D](#), **Bourque G**. EpiVar Browser: advanced exploration of epigenomics data under controlled access. *bioRxiv: the preprint server for biology*. 2023 Aug 5. doi: <https://doi.org/10.1101/2023.08.03.551309>
6. Tav C, Fournier É, Fournier M, Khadangi F, Baguette A, Côté MC, Silveira MAD, Bérubé-Simard FA, **Bourque G**, Droit A, Bilodeau S. Glucocorticoid stimulation induces regionalized gene responses within topologically associating domains. *Front Genet*. 2023 Jul 27;14:1237092. doi: [10.3389/fgene.2023.1237092](https://doi.org/10.3389/fgene.2023.1237092).
7. Graham-Paquin AL, Saini D, Sirois J, Hossain I, Katz MS, [*Zhuang QK](#), Kwon SY, Yamanaka Y, **Bourque G**, Bouchard M, Pastor WA. ZMYM2 is essential for methylation of germline genes and active transposons in embryonic development. *Nucleic Acids Res*. 2023 Jul 3:gkad540. doi: [10.1093/nar/gkad540](https://doi.org/10.1093/nar/gkad540). Epub ahead of print.
8. Kuzmin E, Baker T, Lesluyes T, Monlong J, Abe KT, Coelho PP, Schwartz M, Zou D, Morin G, [*Pacis A](#), Yang Y, Martinez C, Barber J, Kuasne H, Li R, Bourgey M, Fortier AM, Davison PG, Omeroglu A, Guiot MC, Morris Q, Kleinman CL, Huang S, Gingras AC, Ragoussis J, **Bourque G**, Van Loo P, Park M. Evolution of chromosome arm aberrations in breast cancer through genetic network rewiring. *bioRxiv*. 2023 Jun 12:2023-06. doi: <https://doi.org/10.1101/2023.06.10.544434>
9. Rahimi S, Shao X, Chan D, Martel J, Bérard A, Fraser WD, [*Simon MM](#), [*Kwan T](#), **Bourque G**, Trasler J. Capturing sex-specific and hypofertility-linked effects of assisted reproductive technologies on the cord blood DNA methylome. *Clin Epigenetics*. 2023 May 11;15(1):82. doi: [10.1186/s13148-023-01497-7](https://doi.org/10.1186/s13148-023-01497-7).
10. Yoo S, Garg E, Elliott LT, Hung RJ, Halevy AR, Brooks JD, Bull SB, Gagnon F, Greenwood C, Lawless JF, Paterson AD, Sun L, Zawati MH, Lerner-Ellis J,

- Abraham R, Birol I, **Bourque G**, Garant JM, Gosselin C, Li J, Whitney J, Thiruvahindrapuram B, Herbrick JA, Lorenti M, Reuter MS, Adeoye OO, Liu S, Allen U, Bernier FP, Biggs CM, Cheung AM, Cowan J, Herridge M, Maslove DM, Modi BP, Mooser V, Morris SK, Ostrowski M, Parekh RS, Pfeffer G, Suchowersky O, Taher J, Upton J, Warren RL, Yeung R, Aziz N, Turvey SE, Knoppers BM, Lathrop M, Jones S, Scherer SW, Strug LJ. HostSeq: a Canadian whole genome sequencing and clinical data resource. *BMC Genom Data*. 2023 May 2;24(1):26. doi: 10.1186/s12863-023-01128-3.
11. Liao WW, Asri M, Ebler J, Doerr D, Haukness M, Hickey G, Lu S, Lucas JK, Monlong J, Abel HJ, Buonaiuto S, Chang XH, Cheng H, Chu J, Colonna V, Eizenga JM, Feng X, Fischer C, Fulton RS, Garg S, *Groza C, Guarracino A, Harvey WT, Heumos S, Howe K, Jain M, Lu TY, Markello C, Martin FJ, Mitchell MW, Munson KM, Mwaniki MN, Novak AM, Olsen HE, Pesout T, Porubsky D, Prins P, Sibbesen JA, Sirén J, Tomlinson C, Villani F, Vollger MR, Antonacci-Fulton LL, Baid G, Baker CA, Belyaeva A, Billis K, Carroll A, Chang PC, Cody S, Cook DE, Cook-Deegan RM, Cornejo OE, Diekhans M, Ebert P, Fairley S, Fedrigo O, Felsenfeld AL, Formenti G, Frankish A, Gao Y, Garrison NA, Giron CG, Green RE, Haggerty L, Hoekzema K, Hourlier T, Ji HP, Kenny EE, Koenig BA, Kolesnikov A, Korbel JO, Kordosky J, Koren S, Lee H, Lewis AP, Magalhães H, Marco-Sola S, Marijon P, McCartney A, McDaniel J, Mountcastle J, Nattestad M, Nurk S, Olson ND, Popejoy AB, Puiu D, Rautiainen M, Regier AA, Rhie A, Sacco S, Sanders AD, Schneider VA, Schultz BI, Shafin K, Smith MW, Sofia HJ, Abou Tayoun AN, Thibaud-Nissen F, Tricoli FF, Wagner J, Walenz B, Wood JMD, Zimin AV, **Bourque G**, Chaisson MJP, Flicek P, Phillippy AM, Zook JM, Eichler EE, Haussler D, Wang T, Jarvis ED, Miga KH, Garrison E, Marschall T, Hall IM, Li H, Paten B. A draft human pangenome reference. *Nature*. 2023 May;617(7960):312-324. doi: 10.1038/s41586-023-05896-x. Epub 2023 May 10.
12. Bhérer C, *Eveleigh R, Trajanoska K, St-Cyr J, Paccard A, Nadukkalam Ravindran P, Caron E, Bader Asbah N, Wei C, Baumgartner I, Schindewolf M, Döring Y, *Perley D, *Lefebvre F, Lepage P, Bourgey M, **Bourque G**, Ragoussis J, Mooser V, Taliun D. WEGS: a cost-effective sequencing method for genetic studies combining high-depth whole exome and low-depth whole genome. *bioRxiv*. 2023.04.27.538531; doi: <https://doi.org/10.1101/2023.04.27.538531>
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15. Duperron MG, Knol MJ, Le Grand Q, Evans TE, Mishra A, Tsuchida A, Roshchupkin G, Konuma T, Trégouët DA, Romero JR, Frenzel S, Luciano M, Hofer E, *Bourgey M, Dueker ND, Delgado P, Hilal S, Tankard RM, Dubost F, Shin J, Saba Y, Armstrong NJ, Bordes C, Bastin ME, Beiser A, Brodaty H, Bülow R, Carrera C, Chen C, Cheng CY, Deary IJ, Gampawar PG, Himali JJ, Jiang J, Kawaguchi T, Li S, Macalli M, *Marquis P, Morris Z, Muñoz Maniega S, Miyamoto S, Okawa M, Paradise M, Parva P, Rundek T, Sargurupremraj M, Schilling S, Setoh K, Soukarieh O, Tabara Y, Teumer A, Thalamuthu A, Trollor JN, Valdés Hernández MC, Vernooij MW, Völker U, Wittfeld K, Wong TY, Wright MJ, Zhang J, Zhao W, Zhu YC, Schmidt H, Sachdev PS, Wen W, Yoshida K, Joutel A, Satizabal CL, Sacco RL, **Bourque G**; CHARGE consortium; Lathrop M, Paus T, Fernandez-Cadenas I, Yang Q, Mazoyer B, Boutinaud P, Okada Y, Grabe HJ, Mather KA, Schmidt R, Joliot M, Ikram MA, Matsuda F, Tzourio C, Wardlaw JM, Seshadri S, Adams HHH, Debette S. Genomics of perivascular space burden unravels early mechanisms of cerebral small vessel disease. *Nat Med*. 2023 Apr;29(4):950-962. doi: 10.1038/s41591-023-02268-w. Epub 2023 Apr 17.
16. Batdorj E, AlOgayil N, *Zhuang QK, *Galvez JH, Bauermeister K, Nagata K, Kimura T, Ward MA, Taketo T, **Bourque G**, Naumova AK. Genetic variation in the Y chromosome and sex-biased DNA methylation in somatic cells in the mouse. *Mamm Genome*. 2023 Mar;34(1):44-55. doi: 10.1007/s00335-022-09970-z. Epub 2022 Dec 1.

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17. Aracena KA, Lin Y-L, Luo K, [Pacis A](#), Gona S, Mu Z, Yotova V, Sindeaux R, [Pramatarova A](#), [Simon M-M](#), [Chen X](#), [Groza C](#), [Lougheed D](#), [Gregoire R](#), [Brownlee D](#), Li Y, He X, [Bujold D](#), Pastinen T, **Bourque G@**, Barreiro LB. Epigenetic variation impacts ancestry-associated differences in the transcriptional response to influenza infection. *bioRxiv* 2022.05.10.491413; doi: <https://doi.org/10.1101/2022.05.10.491413>
18. da Silva SD, Morand GB, Diesel L, de Lima JM, Bijian K, [Kailasam S](#), [Lefebvre F](#), **Bourque G**, Hier M, Alaoui-Jamali MA. Identification of R-Spondin Gene Signature Predictive of Metastatic Progression in BRAFV^{600E}-Positive Papillary Thyroid Cancer. *Cells*. 2022 Dec 29;12(1):139. doi: 10.3390/cells12010139.
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20. Butler-Laporte G, Povysil G, Kosmicki JA, Cirulli ET, Drivas T, Furini S, Saad C, Schmidt A, Olszewski P, Korotko U, Quinodoz M, Çelik E, Kundu K, Walter K, Jung J, Stockwell AD, Sloofman LG, Jordan DM, Thompson RC, Del Valle D, Simons N, Cheng E, Sebra R, Schadt EE, Kim-Schulze S, Gnjatic S, Merad M, Buxbaum JD, Beckmann ND, Charney AW, Przychodzen B, Chang T, Pottinger TD, Shang N, Brand F, Fava F, Mari F, Chwialkowska K, Niemira M, Pula S, Baillie JK, Stuckey A, Salas A, Bello X, Pardo-Seco J, Gómez-Carballea A, Rivero-Calle I, Martínón-Torres F, Ganna A, Karczewski KJ, Veerapen K, [Bourgey M](#), **Bourque G**, [Eveleigh RJ](#), Forgetta V, Morrison D, Langlais D, Lathrop M, Mooser V, Nakanishi T, Frithiof R, Hultström M, Lipcsey M, Marincevic-Zuniga Y, Nordlund J, Schiabor Barrett KM, Lee W, Bolze A, White S, Riffle S, Tanudjaja F, Sandoval E, Neveux I, Dabe S, Casadei N, Motameny S, Alaamery M, Massadeh S, Aljawini N, Almutairi MS, Arabi YM, Alqahtani SA, Al Harthi FS, Almutairi A, Alqubaishi F, Alotaibi S, Binowayn A, Alsolm EA, El Bardisy H, Fawzy M, Cai F, Soranzo N, Butterworth A; COVID-19 Host Genetics Initiative; DeCOI Host Genetics Group; GEN-COVID Multicenter Study (Italy); Mount Sinai Clinical Intelligence Center; GEN-COVID consortium (Spain); GenOMICC Consortium; Japan COVID-19 Task Force; Regeneron Genetics Center; Geschwind DH, Arteaga S, Stephens A, Butte MJ, Boutros PC, Yamaguchi TN, Tao S, Eng S, Sanders T, Tung PJ, Broudy ME, Pan Y, Gonzalez A, Chavan N, Johnson R, Pasaniuc B, Yaspan B, Smieszek S, Rivolta C, Bibert S, Bochud PY, Dabrowski M, Zawadzki P,

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