

Guillaume Bourque

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

134
papers

19,948
citations

57
h-index

141
g-index

157
ext. papers

24,341
ext. citations

12.7
avg, IF

6.32
L-index

#	Paper	IF	Citations
134	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations.. <i>Genome Biology</i> , 2022 , 23, 13	18.3	1
133	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022 , 2, 100129		4
132	Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. <i>Cell Reports</i> , 2021 , 37, 109909	10.6	0
131	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029		20
130	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. <i>Cell Genomics</i> , 2021 , 1, 100033		2
129	IHEC Data Portal 2021 , 77-94		
128	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. <i>Genome Medicine</i> , 2021 , 13, 169	14.4	6
127	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021 , 31, 713-720	3.7	2
126	Cell-free DNA tissues of origin by methylation profiling reveals significant cell, tissue, and organ-specific injury related to COVID-19 severity. <i>Med</i> , 2021 , 2, 411-422.e5	31.7	13
125	A coordinated progression of progenitor cell states initiates urinary tract development. <i>Nature Communications</i> , 2021 , 12, 2627	17.4	5
124	The Cowpea Kinome: Genomic and Transcriptomic Analysis Under Biotic and Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2021 , 12, 667013	6.2	2
123	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	25
122	Distinct roles of androgen receptor, estrogen receptor alpha, and BCL6 in the establishment of sex-biased DNA methylation in mouse liver. <i>Scientific Reports</i> , 2021 , 11, 13766	4.9	0
121	Single Cell Transcriptomics of Ependymal Cells Across Age, Region and Species Reveals Cilia-Related and Metal Ion Regulatory Roles as Major Conserved Ependymal Cell Functions. <i>Frontiers in Cellular Neuroscience</i> , 2021 , 15, 703951	6.1	0
120	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. <i>Cell Reports</i> , 2021 , 36, 109418	10.6	7
119	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. <i>Neuro-Oncology</i> , 2021 , 23, 1470-1480	1	10
118	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. <i>Methods in Molecular Biology</i> , 2021 , 2381, 285-303	1.4	

117	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. <i>Scientific Data</i> , 2020 , 7, 376	8.2	4
116	Single-cell analysis of childhood leukemia reveals a link between developmental states and ribosomal protein expression as a source of intra-individual heterogeneity. <i>Scientific Reports</i> , 2020 , 10, 8079	4.9	9
115	Sex Chromosomes and Sex Phenotype Contribute to Biased DNA Methylation in Mouse Liver. <i>Cells</i> , 2020 , 9,	7.9	5
114	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. <i>Nature Communications</i> , 2020 , 11, 3406	17.4	88
113	Developmental genome-wide DNA methylation asymmetry between mouse placenta and embryo. <i>Epigenetics</i> , 2020 , 15, 800-815	5.7	4
112	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190332	5.8	8
111	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
110	Personalized and graph genomes reveal missing signal in epigenomic data. <i>Genome Biology</i> , 2020 , 21, 124	18.3	13
109	Cell-Free DNA in Blood Reveals Significant Cell, Tissue and Organ Specific injury and Predicts COVID-19 Severity 2020 ,		8
108	Failure to replicate the association of rare loss-of-function variants in type I IFN immunity genes with severe COVID-19 2020 ,		5
107	Single-cell analysis of human adipose tissue identifies depot and disease specific cell types. <i>Nature Metabolism</i> , 2020 , 2, 97-109	14.6	88
106	A point mutation in the linker domain of mouse STAT5A is associated with impaired NK-cell regulation. <i>Genes and Immunity</i> , 2020 , 21, 136-141	4.4	2
105	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. <i>Bioinformatics</i> , 2019 , 35, 4767-4769	7.2	32
104	GenPipes: an open-source framework for distributed and scalable genomic analyses. <i>GigaScience</i> , 2019 , 8,	7.6	46
103	The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of user datasets with thousands of public epigenomic datasets. <i>Bioinformatics</i> , 2019 , 35, 674-676	7.2	5
102	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. <i>Environmental Health Perspectives</i> , 2019 , 127, 87002	8.4	10
101	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. <i>Nature Communications</i> , 2019 , 10, 4856	17.4	15
100	Benefits and barriers in the design of harmonized access agreements for international data sharing. <i>Scientific Data</i> , 2019 , 6, 297	8.2	9

99	Stalled developmental programs at the root of pediatric brain tumors. <i>Nature Genetics</i> , 2019 , 51, 1702-1713	16.3	58
98	A hidden markov model for identifying differentially methylated sites in bisulfite sequencing data. <i>Biometrics</i> , 2019 , 75, 210-221	1.8	3
97	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. <i>Circulation Research</i> , 2019 , 124, 553-563	15.7	62
96	Identifying co-opted transposable elements using comparative epigenomics. <i>Development Growth and Differentiation</i> , 2018 , 60, 53-62	3	8
95	Loss of the zona pellucida-binding protein 2 (Zpbb2) gene in mice impacts airway hypersensitivity and lung lipid metabolism in a sex-dependent fashion. <i>Mammalian Genome</i> , 2018 , 29, 281-298	3.2	6
94	Very long intergenic non-coding RNA transcripts and expression profiles are associated to specific childhood acute lymphoblastic leukemia subtypes. <i>PLoS ONE</i> , 2018 , 13, e0207250	3.7	7
93	Ten things you should know about transposable elements. <i>Genome Biology</i> , 2018 , 19, 199	18.3	372
92	Computational tools to unmask transposable elements. <i>Nature Reviews Genetics</i> , 2018 , 19, 688-704	30.1	102
91	Human copy number variants are enriched in regions of low mappability. <i>Nucleic Acids Research</i> , 2018 , 46, 7236-7249	20.1	25
90	Comparing Apples to Apples and Oranges to Oranges. <i>Trends in Genetics</i> , 2018 , 34, 571-572	8.5	
89	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. <i>Nucleic Acids Research</i> , 2018 , 46, W486-W494	20.1	2157
88	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. <i>PLoS Genetics</i> , 2018 , 14, e1007285	6	29
87	Morphological differentiation in northern pike (<i>Esox lucius</i>): the influence of environmental conditions and sex on body shape. <i>Canadian Journal of Zoology</i> , 2017 , 95, 383-391	1.5	4
86	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017 , 18, 50	18.3	57
85	Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. <i>Scientific Reports</i> , 2017 , 7, 44876	4.9	24
84	Identification of Elongated Primary Cilia with Impaired Mechanotransduction in Idiopathic Scoliosis Patients. <i>Scientific Reports</i> , 2017 , 7, 44260	4.9	32
83	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. <i>Molecular Psychiatry</i> , 2017 , 22, 1119-1125	15.1	39
82	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. <i>American Journal of Human Genetics</i> , 2017 , 101, 664-685	11	214

81	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. <i>Bioinformatics</i> , 2017 , 33, 491-499	7.2	11
80	Nuclear mTOR acts as a transcriptional integrator of the androgen signaling pathway in prostate cancer. <i>Genes and Development</i> , 2017 , 31, 1228-1242	12.6	64
79	Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1, and ABCA7 in 1779 cases and 1273 controls. <i>Neurobiology of Aging</i> , 2017 , 59, 220.e1-220.e9	5.6	83
78	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. <i>BMC Genomics</i> , 2017 , 18, 214	4.5	30
77	Retrotransposon-Derived Regulatory Regions and Transcripts in Stemness 2017 , 195-213		
76	Screening of dementia genes by whole-exome sequencing in early-onset Alzheimer disease: input and lessons. <i>European Journal of Human Genetics</i> , 2016 , 24, 710-6	5.3	61
75	SORL1 rare variants: a major risk factor for familial early-onset Alzheimer's disease. <i>Molecular Psychiatry</i> , 2016 , 21, 831-6	15.1	71
74	Functional features of EVI1 and EVI1B24 isoforms of MECOM gene in genome-wide transcription regulation and oncogenicity. <i>Oncogene</i> , 2016 , 35, 2311-21	9.2	12
73	RNA-Seq as a Tool to Study the Tumor Microenvironment. <i>Methods in Molecular Biology</i> , 2016 , 1458, 311-37	1.4	6
72	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016 , 17, 2137-2150	12.6	70
71	The International Human Epigenome Consortium Data Portal. <i>Cell Systems</i> , 2016 , 3, 496-499.e2	10.6	100
70	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016 , 167, 1415-1429.e19	56.2	637
69	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
68	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016 , 167, 1398-1414.e24	56.2	534
67	Control of embryonic stem cell self-renewal and differentiation via coordinated alternative splicing and translation of YY2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12360-12367	11.5	37
66	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. <i>BMC Medical Genomics</i> , 2016 , 9, 59	3.7	16
65	In Silico Methods to Identify Exapted Transposable Element Families. <i>Methods in Molecular Biology</i> , 2016 , 1400, 33-45	1.4	2
64	The PGC-1 β /ERR α Axis Represses One-Carbon Metabolism and Promotes Sensitivity to Anti-folate Therapy in Breast Cancer. <i>Cell Reports</i> , 2016 , 14, 920-931	10.6	58

63	Evolving data access policy: The Canadian context. <i>Facets</i> , 2016 , 1, 138-147	2.3	12
62	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016 , 7, 13555	17.4	95
61	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , 2016 , 30, 891-908	24.3	135
60	ERR α mediates metabolic adaptations driving lapatinib resistance in breast cancer. <i>Nature Communications</i> , 2016 , 7, 12156	17.4	68
59	Using fish guilds to assess community responses to temperature and flow regimes in unregulated and regulated Canadian rivers. <i>Freshwater Biology</i> , 2016 , 61, 1759-1772	3.1	9
58	A regional analysis of the impact of dams on water temperature in medium-size rivers in eastern Canada. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2016 , 73, 1885-1897	2.4	27
57	A replication study for association of 53 single nucleotide polymorphisms in ScolioScore test with adolescent idiopathic scoliosis in French-Canadian population. <i>Spine</i> , 2015 , 40, 537-43	3.3	18
56	Transient DNMT1 suppression reveals hidden heritable marks in the genome. <i>Nucleic Acids Research</i> , 2015 , 43, 1485-97	20.1	28
55	Epigenome data release: a participant-centered approach to privacy protection. <i>Genome Biology</i> , 2015 , 16, 142	18.3	30
54	High-dose folic acid supplementation alters the human sperm methylome and is influenced by the MTHFR C677T polymorphism. <i>Human Molecular Genetics</i> , 2015 , 24, 6301-13	5.6	64
53	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015 , 6, 13	4.4	60
52	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. <i>Genome Biology</i> , 2015 , 16, 290	18.3	70
51	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 423-5	17.6	250
50	Genomic analysis of diffuse intrinsic pontine gliomas identifies three molecular subgroups and recurrent activating ACVR1 mutations. <i>Nature Genetics</i> , 2014 , 46, 451-6	36.3	411
49	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. <i>Nature Communications</i> , 2014 , 5, 5135	17.4	123
48	Molecular convergence of neurodevelopmental disorders. <i>American Journal of Human Genetics</i> , 2014 , 95, 490-508	11	51
47	Tissue factor expression provokes escape from tumor dormancy and leads to genomic alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 3544-9	11.5	78
46	Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples, and Perspectives. <i>Genes</i> , 2014 , 5, 887-925	4.2	19

45	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. <i>Nature Cell Biology</i> , 2013 , 15, 1141-1152	23.4	62
44	Optimization of temporal versus spatial replication in the development of habitat use models to explain among-reach variations of fish density estimates in rivers. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013 , 70, 600-609	2.4	4
43	Molecular and genetic crosstalks between mTOR and ERK are key determinants of rapamycin-induced nonalcoholic fatty liver. <i>Cell Metabolism</i> , 2013 , 17, 586-98	24.6	100
42	Transposable elements are major contributors to the origin, diversification, and regulation of vertebrate long noncoding RNAs. <i>PLoS Genetics</i> , 2013 , 9, e1003470	6	437
41	The majority of primate-specific regulatory sequences are derived from transposable elements. <i>PLoS Genetics</i> , 2013 , 9, e1003504	6	204
40	K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. <i>Acta Neuropathologica</i> , 2012 , 124, 439-47	14.3	629
39	Ecotopic viral integration site 1 (EVI1) regulates multiple cellular processes important for cancer and is a synergistic partner for FOS protein in invasive tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2168-73	11.5	61
38	PPARG binding landscapes in macrophages suggest a genome-wide contribution of PU.1 to divergent PPARG binding in human and mouse. <i>PLoS ONE</i> , 2012 , 7, e48102	3.7	15
37	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011 , 43, 630-8	36.3	503
36	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011 , 21, 665-75	9.7	68
35	Transcriptional consequences of genomic structural aberrations in breast cancer. <i>Genome Research</i> , 2011 , 21, 676-87	9.7	67
34	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. <i>Genome Research</i> , 2011 , 21, 1328-38	9.7	211
33	CpG deamination creates transcription factor-binding sites with high efficiency. <i>Genome Biology and Evolution</i> , 2011 , 3, 1304-11	3.9	31
32	Transposable elements have rewired the core regulatory network of human embryonic stem cells. <i>Nature Genetics</i> , 2010 , 42, 631-4	36.3	546
31	Success in the DREAM3 signaling response challenge using simple weighted-average imputation: lessons for community-wide experiments in systems biology. <i>PLoS ONE</i> , 2010 , 5, e8417	3.7	3
30	An oestrogen-receptor-alpha-bound human chromatin interactome. <i>Nature</i> , 2009 , 462, 58-64	50.4	1243
29	Inferring direct regulatory targets of a transcription factor in the DREAM2 challenge. <i>Annals of the New York Academy of Sciences</i> , 2009 , 1158, 215-23	6.5	2
28	Transposable elements in gene regulation and in the evolution of vertebrate genomes. <i>Current Opinion in Genetics and Development</i> , 2009 , 19, 607-12	4.9	116

27	Recovering genome rearrangements in the mammalian phylogeny. <i>Genome Research</i> , 2009 , 19, 934-42	9.7	62
26	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. <i>Cell</i> , 2008 , 133, 1106-17	56.2	1978
25	Evolution of the mammalian transcription factor binding repertoire via transposable elements. <i>Genome Research</i> , 2008 , 18, 1752-62	9.7	378
24	Regulation of estrogen receptor-mediated long range transcription via evolutionarily conserved distal response elements. <i>Journal of Biological Chemistry</i> , 2008 , 283, 32977-88	5.4	74
23	A comparative synteny map of Burkholderia species links large-scale genome rearrangements to fine-scale nucleotide variation in prokaryotes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 549-58	8.3	23
22	Whole-genome cartography of estrogen receptor alpha binding sites. <i>PLoS Genetics</i> , 2007 , 3, e87	6	352
21	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , 2007 , 17, 828-38	9.7	80
20	Whole-genome mapping of histone H3 Lys4 and 27 trimethylations reveals distinct genomic compartments in human embryonic stem cells. <i>Cell Stem Cell</i> , 2007 , 1, 286-98	18	489
19	Initial sequence and comparative analysis of the cat genome. <i>Genome Research</i> , 2007 , 17, 1675-89	9.7	248
18	Epizoic Algae from Freshwater Turtles in Nova Scotia. <i>Journal of Freshwater Ecology</i> , 2007 , 22, 677-685	1.4	18
17	Genomewide expression profiling in the zebrafish embryo identifies target genes regulated by Hedgehog signaling during vertebrate development. <i>Genetics</i> , 2006 , 174, 735-52	4	36
16	The convergence of cytogenetics and rearrangement-based models for ancestral genome reconstruction. <i>Genome Research</i> , 2006 , 16, 311-3	9.7	30
15	Models and Methods in Comparative Genomics. <i>Advances in Computers</i> , 2006 , 68, 59-104	2.9	1
14	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006 , 38, 431-40	36.3	1920
13	Dynamics of mammalian chromosome evolution inferred from multispecies comparative maps. <i>Science</i> , 2005 , 309, 613-7	33.3	447
12	A population-based LD map of the human chromosome 6p. <i>Immunogenetics</i> , 2005 , 57, 559-65	3.2	6
11	Comparative architectures of mammalian and chicken genomes reveal highly variable rates of genomic rearrangements across different lineages. <i>Genome Research</i> , 2005 , 15, 98-110	9.7	128
10	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689

9	Detailed four-way comparative mapping and gene order analysis of the canine ctvm locus reveals evolutionary chromosome rearrangements. <i>Genomics</i> , 2004 , 83, 1053-62	4-3	13
8	Reconstructing the genomic architecture of ancestral mammals: lessons from human, mouse, and rat genomes. <i>Genome Research</i> , 2004 , 14, 507-16	9-7	177
7	Improving gene network inference by comparing expression time-series across species, developmental stages or tissues. <i>Journal of Bioinformatics and Computational Biology</i> , 2004 , 2, 765-83	1	14
6	Genome-scale evolution: reconstructing gene orders in the ancestral species. <i>Genome Research</i> , 2002 , 12, 26-36	9-7	282
5	The omics of our lives: practices and policies of direct-to-consumer epigenetic and microbiomic testing companies. <i>New Genetics and Society</i> , 1-29	1-9	1
4	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection		1
3	precisionFDA Truth Challenge V2: Calling variants from short- and long-reads in difficult-to-map regions		25
2	RobusTAD: A Tool for Robust Annotation of Topologically Associating Domain Boundaries		4
1	Personalized and graph genomes reveal missing signal in epigenomic data		4