Guillaume Bourque

List of Publications by Citations

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	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. *Nucleic Acids Research*, **2018**, 46, W486-W494	20.1	2157
133	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. *Cell*, **2008**, 133, 1106-17	56.2	1978
132	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. *Nature Genetics*, **2006**, 38, 431-40	36.3	1920
131	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004** , 428, 493-521	50.4	1689
130	An oestrogen-receptor-alpha-bound human chromatin interactome. *Nature*, **2009**, 462, 58-64	50.4	1243
129	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
128	K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. *Acta Neuropathologica*, **2012**, 124, 439-47	14.3	629
127	Transposable elements have rewired the core regulatory network of human embryonic stem cells. *Nature Genetics*, **2010**, 42, 631-4	36.3	546
126	CTCF-mediated functional chromatin interactome in pluripotent cells. *Nature Genetics*, **2011**, 43, 630-8	36.3	503
125	Whole-genome mapping of histone H3 Lys4 and 27 trimethylations reveals distinct genomic compartments in human embryonic stem cells. *Cell Stem Cell*, **2007**, 1, 286-98	18	489
124	Dynamics of mammalian chromosome evolution inferred from multispecies comparative maps. *Science*, **2005**, 309, 613-7	33.3	447
123	Transposable elements are major contributors to the origin, diversification, and regulation of vertebrate long noncoding RNAs. *PLoS Genetics*, **2013**, 9, e1003470	6	437
122	Genomic analysis of diffuse intrinsic pontine gliomas identifies three molecular subgroups and recurrent activating ACVR1 mutations. *Nature Genetics*, **2014**, 46, 451-6	36.3	411
121	Evolution of the mammalian transcription factor binding repertoire via transposable elements. *Genome Research*, **2008**, 18, 1752-62	9.7	378
120	Ten things you should know about transposable elements. *Genome Biology*, **2018**, 19, 199	18.3	372
119	Whole-genome cartography of estrogen receptor alpha binding sites. *PLoS Genetics*, **2007**, 3, e87	6	352
118	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	56.2	339

117	Genome-scale evolution: reconstructing gene orders in the ancestral species. *Genome Research*, **2002**, 12, 26-36	9.7	282
116	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. *Nature Structural and Molecular Biology*, **2014**, 21, 423-5	17.6	250
115	Initial sequence and comparative analysis of the cat genome. *Genome Research*, **2007**, 17, 1675-89	9.7	248
114	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
113	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. *American Journal of Human Genetics*, **2017**, 101, 664-685	11	214
112	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. *Genome Research*, **2011**, 21, 1328-38	9.7	211
111	The majority of primate-specific regulatory sequences are derived from transposable elements. *PLoS Genetics*, **2013**, 9, e1003504	6	204
110	Reconstructing the genomic architecture of ancestral mammals: lessons from human, mouse, and rat genomes. *Genome Research*, **2004**, 14, 507-16	9.7	177
109	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. *Cancer Cell*, **2016**, 30, 891-908	24.3	135
108	Comparative architectures of mammalian and chicken genomes reveal highly variable rates of genomic rearrangements across different lineages. *Genome Research*, **2005**, 15, 98-110	9.7	128
107	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. *Nature Communications*, **2014**, 5, 5135	17.4	123
106	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
105	Transposable elements in gene regulation and in the evolution of vertebrate genomes. *Current Opinion in Genetics and Development*, **2009**, 19, 607-12	4.9	116
104	Computational tools to unmask transposable elements. *Nature Reviews Genetics*, **2018**, 19, 688-704	30.1	102
103	The International Human Epigenome Consortium Data Portal. *Cell Systems*, **2016**, 3, 496-499.e2	10.6	100
102	Molecular and genetic crosstalks between mTOR and ERR are key determinants of rapamycin-induced nonalcoholic fatty liver. *Cell Metabolism*, **2013**, 17, 586-98	24.6	100
101	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. *Nature Communications*, **2016**, 7, 13555	17.4	95
100	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. *Nature Communications*, **2020**, 11, 3406	17.4	88

99	Single-cell analysis of human adipose tissue identifies depot and disease specific cell types. *Nature Metabolism*, **2020**, 2, 97-109	14.6	88
98	Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1, and ABCA7 in 1779 cases and 1273 controls. *Neurobiology of Aging*, **2017**, 59, 220.e1-220.e9	5.6	83
97	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). *Genome Research*, **2007**, 17, 828-38	9.7	80
96	Tissue factor expression provokes escape from tumor dormancy and leads to genomic alterations. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 3544-9	11.5	78
95	Regulation of estrogen receptor-mediated long range transcription via evolutionarily conserved distal response elements. *Journal of Biological Chemistry*, **2008**, 283, 32977-88	5.4	74
94	SORL1 rare variants: a major risk factor for familial early-onset Alzheimer's disease. *Molecular Psychiatry*, **2016**, 21, 831-6	15.1	71
93	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. *Cell Reports*, **2016**, 17, 2137-2150	8.0	70
92	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. *Genome Biology*, **2015**, 16, 290	18.3	70
91	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. *Genome Research*, **2011**, 21, 665-75	9.7	68
90	ERR mediates metabolic adaptations driving lapatinib resistance in breast cancer. *Nature Communications*, **2016**, 7, 12156	17.4	68
89	Transcriptional consequences of genomic structural aberrations in breast cancer. *Genome Research*, **2011**, 21, 676-87	9.7	67
88	High-dose folic acid supplementation alters the human sperm methylome and is influenced by the MTHFR C677T polymorphism. *Human Molecular Genetics*, **2015**, 24, 6301-13	5.6	64
87	Nuclear mTOR acts as a transcriptional integrator of the androgen signaling pathway in prostate cancer. *Genes and Development*, **2017**, 31, 1228-1242	12.6	64
86	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. *Nature Cell Biology*, **2013**, 15, 1141-1152	23.4	62
85	Recovering genome rearrangements in the mammalian phylogeny. *Genome Research*, **2009**, 19, 934-42	9.7	62
84	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. *Circulation Research*, **2019**, 124, 553-563	15.7	62
83	Screening of dementia genes by whole-exome sequencing in early-onset Alzheimer disease: input and lessons. *European Journal of Human Genetics*, **2016**, 24, 710-6	5.3	61
82	Ecotopic viral integration site 1 (EVI1) regulates multiple cellular processes important for cancer and is a synergistic partner for FOS protein in invasive tumors. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 2168-73	11.5	61

81	A call for benchmarking transposable element annotation methods. *Mobile DNA*, **2015**, 6, 13	4.4	60
80	The PGC-1/ERR Axis Represses One-Carbon Metabolism and Promotes Sensitivity to Anti-folate Therapy in Breast Cancer. *Cell Reports*, **2016**, 14, 920-931	10.6	58
79	Stalled developmental programs at the root of pediatric brain tumors. *Nature Genetics*, **2019**, 51, 1702-1713	30.5	58
78	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. *Genome Biology*, **2017**, 18, 50	18.3	57
77	Molecular convergence of neurodevelopmental disorders. *American Journal of Human Genetics*, **2014**, 95, 490-508	11	51
76	GenPipes: an open-source framework for distributed and scalable genomic analyses. *GigaScience*, **2019**, 8,	7.6	46
75	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. *Molecular Psychiatry*, **2017**, 22, 1119-1125	15.1	39
74	Control of embryonic stem cell self-renewal and differentiation via coordinated alternative splicing and translation of YY2. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 12360-12367	11.5	37
73	Genomewide expression profiling in the zebrafish embryo identifies target genes regulated by Hedgehog signaling during vertebrate development. *Genetics*, **2006**, 174, 735-52	4	36
72	Identification of Elongated Primary Cilia with Impaired Mechanotransduction in Idiopathic Scoliosis Patients. *Scientific Reports*, **2017**, 7, 44260	4.9	32
71	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. *Bioinformatics*, **2019**, 35, 4767-4769	7.2	32
70	CpG deamination creates transcription factor-binding sites with high efficiency. *Genome Biology and Evolution*, **2011**, 3, 1304-11	3.9	31
69	Epigenome data release: a participant-centered approach to privacy protection. *Genome Biology*, **2015**, 16, 142	18.3	30
68	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. *BMC Genomics*, **2017**, 18, 214	4.5	30
67	The convergence of cytogenetics and rearrangement-based models for ancestral genome reconstruction. *Genome Research*, **2006**, 16, 311-3	9.7	30
66	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. *PLoS Genetics*, **2018**, 14, e1007285	6	29
65	Transient DNMT1 suppression reveals hidden heritable marks in the genome. *Nucleic Acids Research* , **2015**, 43, 1485-97	20.1	28
64	A regional analysis of the impact of dams on water temperature in medium-size rivers in eastern Canada. *Canadian Journal of Fisheries and Aquatic Sciences*, **2016**, 73, 1885-1897	2.4	27

63	precisionFDA Truth Challenge V2: Calling variants from short- and long-reads in difficult-to-map regions		25
62	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. *Journal of Clinical Investigation*, **2021**, 131,	15.9	25
61	Human copy number variants are enriched in regions of low mappability. *Nucleic Acids Research*, **2018**, 46, 7236-7249	20.1	25
60	Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. *Scientific Reports*, **2017**, 7, 44876	4.9	24
59	A comparative synteny map of Burkholderia species links large-scale genome rearrangements to fine-scale nucleotide variation in prokaryotes. *Molecular Biology and Evolution*, **2008**, 25, 549-58	8.3	23
58	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
57	Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples, and Perspectives. *Genes*, **2014**, 5, 887-925	4.2	19
56	A replication study for association of 53 single nucleotide polymorphisms in ScoliScore test with adolescent idiopathic scoliosis in French-Canadian population. *Spine*, **2015**, 40, 537-43	3.3	18
55	Epizoic Algae from Freshwater Turtles in Nova Scotia. *Journal of Freshwater Ecology*, **2007**, 22, 677-685	1.4	18
54	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. *BMC Medical Genomics*, **2016**, 9, 59	3.7	16
53	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. *Nature Communications*, **2019**, 10, 4856	17.4	15
52	PPARG binding landscapes in macrophages suggest a genome-wide contribution of PU.1 to divergent PPARG binding in human and mouse. *PLoS ONE*, **2012**, 7, e48102	3.7	15
51	Improving gene network inference by comparing expression time-series across species, developmental stages or tissues. *Journal of Bioinformatics and Computational Biology*, **2004**, 2, 765-83	1	14
50	Detailed four-way comparative mapping and gene order analysis of the canine ctvm locus reveals evolutionary chromosome rearrangements. *Genomics*, **2004**, 83, 1053-62	4.3	13
49	Personalized and graph genomes reveal missing signal in epigenomic data. *Genome Biology*, **2020**, 21, 124	18.3	13
48	Cell-free DNA tissues of origin by methylation profiling reveals significant cell, tissue, and organ-specific injury related to COVID-19 severity. *Med*, **2021**, 2, 411-422.e5	31.7	13
47	Functional features of EVI1 and EVI1Δ324 isoforms of MECOM gene in genome-wide transcription regulation and oncogenicity. *Oncogene*, **2016**, 35, 2311-21	9.2	12
46	Evolving data access policy: The Canadian context. *Facets*, **2016**, 1, 138-147	2.3	12

45	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. *Bioinformatics*, **2017**, 33, 491-499	7.2	11
44	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. *Environmental Health Perspectives*, **2019**, 127, 87002	8.4	10
43	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. *Neuro-Oncology*, **2021**, 23, 1470-1480	1	10
42	Single-cell analysis of childhood leukemia reveals a link between developmental states and ribosomal protein expression as a source of intra-individual heterogeneity. *Scientific Reports*, **2020**, 10, 8079	4.9	9
41	Using fish guilds to assess community responses to temperature and flow regimes in unregulated and regulated Canadian rivers. *Freshwater Biology*, **2016**, 61, 1759-1772	3.1	9
40	Benefits and barriers in the design of harmonized access agreements for international data sharing. *Scientific Data*, **2019**, 6, 297	8.2	9
39	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2020**, 375, 20190332	5.8	8
38	Identifying co-opted transposable elements using comparative epigenomics. *Development Growth and Differentiation*, **2018**, 60, 53-62	3	8
37	Cell-Free DNA in Blood Reveals Significant Cell, Tissue and Organ Specific injury and Predicts COVID-19 Severity **2020**,		8
36	Very long intergenic non-coding RNA transcripts and expression profiles are associated to specific childhood acute lymphoblastic leukemia subtypes. *PLoS ONE*, **2018**, 13, e0207250	3.7	7
35	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. *Cell Reports*, **2021**, 36, 109418	10.6	7
34	Loss of the zona pellucida-binding protein 2 (Zpbp2) gene in mice impacts airway hypersensitivity and lung lipid metabolism in a sex-dependent fashion. *Mammalian Genome*, **2018**, 29, 281-298	3.2	6
33	RNA-Seq as a Tool to Study the Tumor Microenvironment. *Methods in Molecular Biology*, **2016**, 1458, 311-37	1.4	6
32	A population-based LD map of the human chromosome 6p. *Immunogenetics*, **2005**, 57, 559-65	3.2	6
31	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. *Genome Medicine*, **2021**, 13, 169	14.4	6
30	Sex Chromosomes and Sex Phenotype Contribute to Biased DNA Methylation in Mouse Liver. *Cells*, **2020**, 9,	7.9	5
29	The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of user datasets with thousands of public epigenomic datasets. *Bioinformatics*, **2019**, 35, 674-676	7.2	5
28	Failure to replicate the association of rare loss-of-function variants in type I IFN immunity genes with severe COVID-19 **2020**,		5

27	A coordinated progression of progenitor cell states initiates urinary tract development. *Nature Communications*, **2021**, 12, 2627	17.4	5
26	Morphological differentiation in northern pike (Esox lucius): the influence of environmental conditions and sex on body shape. *Canadian Journal of Zoology*, **2017**, 95, 383-391	1.5	4
25	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. *Scientific Data*, **2020**, 7, 376	8.2	4
24	Developmental genome-wide DNA methylation asymmetry between mouse placenta and embryo. *Epigenetics*, **2020**, 15, 800-815	5.7	4
23	Optimization of temporal versus spatial replication in the development of habitat use models to explain among-reach variations of fish density estimates in rivers. *Canadian Journal of Fisheries and Aquatic Sciences*, **2013**, 70, 600-609	2.4	4
22	RobusTAD: A Tool for Robust Annotation of Topologically Associating Domain Boundaries		4
21	Personalized and graph genomes reveal missing signal in epigenomic data		4
20	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. *Cell Genomics*, **2022**, 2, 100129		4
19	Success in the DREAM3 signaling response challenge using simple weighted-average imputation: lessons for community-wide experiments in systems biology. *PLoS ONE*, **2010**, 5, e8417	3.7	3
18	A hidden markov model for identifying differentially methylated sites in bisulfite sequencing data. *Biometrics*, **2019**, 75, 210-221	1.8	3
17	In Silico Methods to Identify Exapted Transposable Element Families. *Methods in Molecular Biology*, **2016**, 1400, 33-45	1.4	2
16	Inferring direct regulatory targets of a transcription factor in the DREAM2 challenge. *Annals of the New York Academy of Sciences*, **2009**, 1158, 215-23	6.5	2
15	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. *Cell Genomics*, **2021**, 1, 100033		2
14	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. *Genome Research*, **2021**, 31, 713-720	9.7	2
13	The Cowpea Kinome: Genomic and Transcriptomic Analysis Under Biotic and Abiotic Stresses. *Frontiers in Plant Science*, **2021**, 12, 667013	6.2	2
12	A point mutation in the linker domain of mouse STAT5A is associated with impaired NK-cell regulation. *Genes and Immunity*, **2020**, 21, 136-141	4.4	2
11	Models and Methods in Comparative Genomics. *Advances in Computers*, **2006**, 68, 59-104	2.9	1
10	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations.. *Genome Biology*, **2022**, 23, 13	18.3	1

9	The omics of our lives: practices and policies of direct-to-consumer epigenetic and microbiomic testing companies. *New Genetics and Society*,1-29	1.9	1
8	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection		1
7	Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. *Cell Reports*, **2021**, 37, 109909	10.6	0
6	Distinct roles of androgen receptor, estrogen receptor alpha, and BCL6 in the establishment of sex-biased DNA methylation in mouse liver. *Scientific Reports*, **2021**, 11, 13766	4.9	0
5	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. *Frontiers in Cellular Neuroscience*, **2021**, 15, 703951	6.1	0
4	IHEC Data Portal **2021**, 77-94		
3	Retrotransposon-Derived Regulatory Regions and Transcripts in Stemness **2017**, 195-213		
2	Comparing Apples to Apples and Oranges to Oranges. *Trends in Genetics*, **2018**, 34, 571-572	8.5	
1	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. *Methods in Molecular Biology*, **2021**, 2381, 285-303	1.4	