Guillaume Bourque

List of Publications by Year
in descending order

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130 papers	27,136 citations	20815 60 h-index	12272 133 g-index
158 all docs	158 docs citations	158 times ranked	45131 citing authors

#	Article	IF	Citations
1	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. Nucleic Acids Research, 2018, 46, W486-W494.	14.5	3,199
2	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. Cell, 2008, 133, 1106-1117.	28.9	2,279
3	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. Nature Genetics, 2006, 38, 431-440.	21.4	2,162
4	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
5	An oestrogen-receptor-Î±-bound human chromatin interactome. Nature, 2009, 462, 58-64.	27.8	1,537
6	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
7	Ten things you should know about transposable elements. Genome Biology, 2018, 19, 199.	8.8	817
8	K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. Acta Neuropathologica, 2012, 124, 439-447.	7.7	799
9	Transposable elements have rewired the core regulatory network of human embryonic stem cells. Nature Genetics, 2010, 42, 631-634.	21.4	698
10	Transposable Elements Are Major Contributors to the Origin, Diversification, and Regulation of Vertebrate Long Noncoding RNAs. PLoS Genetics, 2013, 9, e1003470.	3.5	574
11	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
12	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	21.4	567
13	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. Science, 2005, 309, 613-617.	12.6	542
14	Whole-Genome Mapping of Histone H3 Lys4 and 27 Trimethylations Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. Cell Stem Cell, 2007, 1, 286-298.	11.1	536
15	Genomic analysis of diffuse intrinsic pontine gliomas identifies three molecular subgroups and recurrent activating ACVR1 mutations. Nature Genetics, 2014, 46, 451-456.	21.4	525
16	Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genome Research, 2008, 18, 1752-1762.	5.5	501
17	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
18	Whole-Genome Cartography of Estrogen Receptor Î± Binding Sites. PLoS Genetics, 2007, 3, e87.	3.5	400

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19	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. Nature Structural and Molecular Biology, 2014, 21, 423-425.	8.2	347
20	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. American Journal of Human Genetics, 2017, 101, 664-685.	6.2	337
21	Initial sequence and comparative analysis of the cat genome. Genome Research, 2007, 17, 1675-1689.	5.5	311
22	Genome-scale evolution: reconstructing gene orders in the ancestral species. Genome Research, 2002, 12, 26-36.	5.5	308
23	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. Nature Communications, 2020, 11, 3406.	12.8	300
24	The Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements. PLoS Genetics, 2013, 9, e1003504.	3.5	293
25	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
26	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. Nature Metabolism, 2020, 2, 97-109.	11.9	272
27	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. Genome Research, 2011, 21, 1328-1338.	5.5	247
28	Reconstructing the Genomic Architecture of Ancestral Mammals: Lessons From Human, Mouse, and Rat Genomes. Genome Research, 2004, 14, 507-516.	5.5	210
29	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. Cancer Cell, 2016, 30, 891-908.	16.8	191
30	Computational tools to unmask transposable elements. Nature Reviews Genetics, 2018, 19, 688-704.	16.3	173
31	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. Nature Communications, 2014, 5, 5135.	12.8	158
32	Comparative architectures of mammalian and chicken genomes reveal highly variable rates of genomic rearrangements across different lineages. Genome Research, 2005, 15, 98-110.	5.5	150
33	Transposable elements in gene regulation and in the evolution of vertebrate genomes. Current Opinion in Genetics and Development, 2009, 19, 607-612.	3.3	143
34	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	12.8	142
35	The International Human Epigenome Consortium Data Portal. Cell Systems, 2016, 3, 496-499.e2.	6.2	140
36	Stalled developmental programs at the root of pediatric brain tumors. Nature Genetics, 2019, 51, 1702-1713.	21.4	136

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37	Molecular and Genetic Crosstalks between mTOR and ERRÎ± Are Key Determinants of Rapamycin-Induced Nonalcoholic Fatty Liver. Cell Metabolism, 2013, 17, 586-598.	16.2	132
38	GenPipes: an open-source framework for distributed and scalable genomic analyses. GigaScience, 2019, 8, .	6.4	121
39	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. Circulation Research, 2019, 124, 553-563.	4.5	118
40	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.	3.1	116
41	Nuclear mTOR acts as a transcriptional integrator of the androgen signaling pathway in prostate cancer. Genes and Development, 2017, 31, 1228-1242.	5.9	103
42	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	6.4	102
43	ERRÎ± mediates metabolic adaptations driving lapatinib resistance in breast cancer. Nature Communications, 2016, 7, 12156.	12.8	98
44	SORL1 rare variants: a major risk factor for familial early-onset Alzheimerâ€™s disease. Molecular Psychiatry, 2016, 21, 831-836.	7.9	96
45	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
46	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, 3544-3549.	7.1	90
47	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology, 2015, 16, 290.	8.8	90
48	Regulation of Estrogen Receptor-mediated Long Range Transcription via Evolutionarily Conserved Distal Response Elements. Journal of Biological Chemistry, 2008, 283, 32977-32988.	3.4	89
49	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). Genome Research, 2007, 17, 828-838.	5.5	86
50	High-dose folic acid supplementation alters the human sperm methylome and is influenced by theMTHFRC677T polymorphism. Human Molecular Genetics, 2015, 24, 6301-6313.	2.9	86
51	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. Nature Cell Biology, 2013, 15, 1141-1152.	10.3	84
52	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. Bioinformatics, 2019, 35, 4767-4769.	4.1	84
53	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
54	Screening of dementia genes by whole-exome sequencing in early-onset Alzheimer disease: input and lessons. European Journal of Human Genetics, 2016, 24, 710-716.	2.8	77

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55	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research, 2011, 21, 665-675.	5.5	74
56	Transcriptional consequences of genomic structural aberrations in breast cancer. Genome Research, 2011, 21, 676-687.	5.5	74
57	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, 2168-2173.	7.1	74
58	The PGC-1Î±/ERRÎ± Axis Represses One-Carbon Metabolism and Promotes Sensitivity to Anti-folate Therapy in Breast Cancer. Cell Reports, 2016, 14, 920-931.	6.4	73
59	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	6.5	72
60	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	8.8	71
61	Recovering genome rearrangements in the mammalian phylogeny. Genome Research, 2009, 19, 934-942.	5.5	66
62	Molecular Convergence of Neurodevelopmental Disorders. American Journal of Human Genetics, 2014, 95, 490-508.	6.2	64
63	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. Molecular Psychiatry, 2017, 22, 1119-1125.	7.9	57
64	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. Journal of Clinical Investigation, 2021, 131, .	8.2	56
65	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.	7.1	54
66	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. PLoS Genetics, 2018, 14, e1007285.	3.5	50
67	CpG Deamination Creates Transcription Factorâ€“Binding Sites with High Efficiency. Genome Biology and Evolution, 2011, 3, 1304-1311.	2.5	45
68	Identification of Elongated Primary Cilia with Impaired Mechanotransduction in Idiopathic Scoliosis Patients. Scientific Reports, 2017, 7, 44260.	3.3	44
69	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.	3.3	42
70	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.	4.4	41
71	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. BMC Genomics, 2017, 18, 214.	2.8	40
72	Genomewide Expression Profiling in the Zebrafish Embryo Identifies Target Genes Regulated by Hedgehog Signaling During Vertebrate Development. Genetics, 2006, 174, 735-752.	2.9	39

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73	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.	3.3	37
74	Human copy number variants are enriched in regions of low mappability. Nucleic Acids Research, 2018, 46, 7236-7249.	14.5	36
75	Transient DNMT1 suppression reveals hidden heritable marks in the genome. Nucleic Acids Research, 2015, 43, 1485-1497.	14.5	35
76	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.	1.4	35
77	The convergence of cytogenetics and rearrangement-based models for ancestral genome reconstruction. Genome Research, 2006, 16, 311-313.	5.5	34
78	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	8.8	34
79	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.	3.7	31
80	Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biology, 2020, 21, 124.	8.8	29
81	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. Bioinformatics, 2017, 33, 491-499.	4.1	28
82	A Replication Study for Association of 53 Single Nucleotide Polymorphisms in ScoliScore Test With Adolescent Idiopathic Scoliosis in French-Canadian Population. Spine, 2015, 40, 537-543.	2.0	27
83	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.	1.5	26
84	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.	6.4	25
85	Epizoic Algae from Freshwater Turtles in Nova Scotia. Journal of Freshwater Ecology, 2007, 22, 677-685.	1.2	24
86	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, 549-558.	8.9	23
87	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. Nature Communications, 2019, 10, 4856.	12.8	22
88	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. Environmental Health Perspectives, 2019, 127, 87002.	6.0	20
89	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.	4.0	20
90	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.	2.5	20

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91	IMPROVING GENE NETWORK INFERENCE BY COMPARING EXPRESSION TIME-SERIES ACROSS SPECIES, DEVELOPMENTAL STAGES OR TISSUES. Journal of Bioinformatics and Computational Biology, 2004, 02, 765-783.	0.8	19
92	Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples, and Perspectives. Genes, 2014, 5, 887-925.	2.4	19
93	A coordinated progression of progenitor cell states initiates urinary tract development. Nature Communications, 2021, 12, 2627.	12.8	19
94	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in QuÃ©bec, Canada. Genome Medicine, 2021, 13, 169.	8.2	19
95	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. Genome Biology, 2022, 23, 13.	8.8	19
96	Benefits and barriers in the design of harmonized access agreements for international data sharing. Scientific Data, 2019, 6, 297.	5.3	18
97	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. Neuro-Oncology, 2021, 23, 1470-1480.	1.2	18
98	Functional features of EVI1 and EVI1Î”324 isoforms of MECOM gene in genome-wide transcription regulation and oncogenicity. Oncogene, 2016, 35, 2311-2321.	5.9	17
99	Detailed four-way comparative mapping and gene order analysis of the canine ctvm locus reveals evolutionary chromosome rearrangements. Genomics, 2004, 83, 1053-1062.	2.9	15
100	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. Scientific Data, 2020, 7, 376.	5.3	15
101	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. Genome Research, 2021, 31, 713-720.	5.5	15
102	Identifying coâ€opted transposable elements using comparative epigenomics. Development Growth and Differentiation, 2018, 60, 53-62.	1.5	14
103	Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. Cell Reports, 2021, 37, 109909.	6.4	14
104	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. Science Advances, 2022, 8, .	10.3	14
105	Sex Chromosomes and Sex Phenotype Contribute to Biased DNA Methylation in Mouse Liver. Cells, 2020, 9, 1436.	4.1	13
106	Evolving data access policy: The Canadian context. Facets, 2017, 1, 138-147.	2.4	13
107	Using fish guilds to assess community responses to temperature and flow regimes in unregulated and regulated Canadian rivers. Freshwater Biology, 2016, 61, 1759-1772.	2.4	12
108	Very long intergenic non-coding RNA transcripts and expression profiles are associated to specific childhood acute lymphoblastic leukemia subtypes. PLoS ONE, 2018, 13, e0207250.	2.5	12

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109	The Cowpea Kinome: Genomic and Transcriptomic Analysis Under Biotic and Abiotic Stresses. Frontiers in Plant Science, 2021, 12, 667013.	3.6	12
110	Application of ATAC-Seq for genome-wide analysis of the chromatin state at single myofiber resolution. ELife, 2022, 11, .	6.0	11
111	Glioblastoma scRNA-seq shows treatment-induced, immune-dependent increase in mesenchymal cancer cells and structural variants in distal neural stem cells. Neuro-Oncology, 2022, 24, 1494-1508.	1.2	11
112	Developmental genome-wide DNA methylation asymmetry between mouse placenta and embryo. Epigenetics, 2020, 15, 800-815.	2.7	10
113	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. Cell Genomics, 2021, 1, 100033.	6.5	10
114	A Hidden Markov Model for Identifying Differentially Methylated Sites in Bisulfite Sequencing Data. Biometrics, 2019, 75, 210-221.	1.4	9
115	RNA-Seq as a Tool to Study the Tumor Microenvironment. Methods in Molecular Biology, 2016, 1458, 311-337.	0.9	7
116	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.	2.2	7
117	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.	3.3	7
118	The omics of our lives: practices and policies of direct-to-consumer epigenetic and microbiomic testing companies. New Genetics and Society, 2021, 40, 541-569.	1.2	7
119	A population-based LD map of the human chromosome 6p. Immunogenetics, 2005, 57, 559-565.	2.4	6
120	The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of user datasets with thousands of public epigenomic datasets. Bioinformatics, 2019, 35, 674-676.	4.1	5
121	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.	1.4	4
122	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.	1.0	4
123	Inferring Direct Regulatory Targets of a Transcription Factor in the DREAM2 Challenge. Annals of the New York Academy of Sciences, 2009, 1158, 215-223.	3.8	3
124	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.	2.5	3
125	In Silico Methods to Identify Exapted Transposable Element Families. Methods in Molecular Biology, 2016, 1400, 33-45.	0.9	2
126	A point mutation in the linker domain of mouse STAT5A is associated with impaired NK-cell regulation. Genes and Immunity, 2020, 21, 136-141.	4.1	2

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127	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. Methods in Molecular Biology, 2021, 2381, 285-303.	0.9	2
128	Models and Methods in Comparative Genomics. Advances in Computers, 2006, 68, 59-104.	1.6	1
129	Comparing Apples to Apples and Oranges to Oranges. Trends in Genetics, 2018, 34, 571-572.	6.7	0
130	IHEC Data Portal. , 2021, , 77-94.		0