

Guillaume Bourque

List of Publications by Year in descending order

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Version: 2024-02-01

130
papers

27,136
citations

20759

60
h-index

12233

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. <i>Nucleic Acids Research</i> , 2018, 46, W486-W494.	6.5	3,199
2	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. <i>Cell</i> , 2008, 133, 1106-1117.	13.5	2,279
3	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006, 38, 431-440.	9.4	2,162
4	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
5	An oestrogen-receptor- $\hat{\pm}$ -bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	13.7	1,537
6	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	13.5	1,052
7	Ten things you should know about transposable elements. <i>Genome Biology</i> , 2018, 19, 199.	3.8	817
8	K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. <i>Acta Neuropathologica</i> , 2012, 124, 439-447.	3.9	799
9	Transposable elements have rewired the core regulatory network of human embryonic stem cells. <i>Nature Genetics</i> , 2010, 42, 631-634.	9.4	698
10	Transposable Elements Are Major Contributors to the Origin, Diversification, and Regulation of Vertebrate Long Noncoding RNAs. <i>PLoS Genetics</i> , 2013, 9, e1003470.	1.5	574
11	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573
12	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	9.4	567
13	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. <i>Science</i> , 2005, 309, 613-617.	6.0	542
14	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, 286-298.	5.2	536
15	Genomic analysis of diffuse intrinsic pontine gliomas identifies three molecular subgroups and recurrent activating ACVR1 mutations. <i>Nature Genetics</i> , 2014, 46, 451-456.	9.4	525
16	Evolution of the mammalian transcription factor binding repertoire via transposable elements. <i>Genome Research</i> , 2008, 18, 1752-1762.	2.4	501
17	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
18	Whole-Genome Cartography of Estrogen Receptor $\hat{\pm}$ Binding Sites. <i>PLoS Genetics</i> , 2007, 3, e87.	1.5	400

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19	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 423-425.	3.6	347
20	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. <i>American Journal of Human Genetics</i> , 2017, 101, 664-685.	2.6	337
21	Initial sequence and comparative analysis of the cat genome. <i>Genome Research</i> , 2007, 17, 1675-1689.	2.4	311
22	Genome-scale evolution: reconstructing gene orders in the ancestral species. <i>Genome Research</i> , 2002, 12, 26-36.	2.4	308
23	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. <i>Nature Communications</i> , 2020, 11, 3406.	5.8	300
24	The Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements. <i>PLoS Genetics</i> , 2013, 9, e1003504.	1.5	293
25	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	9.4	275
26	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. <i>Nature Metabolism</i> , 2020, 2, 97-109.	5.1	272
27	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. <i>Genome Research</i> , 2011, 21, 1328-1338.	2.4	247
28	Reconstructing the Genomic Architecture of Ancestral Mammals: Lessons From Human, Mouse, and Rat Genomes. <i>Genome Research</i> , 2004, 14, 507-516.	2.4	210
29	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , 2016, 30, 891-908.	7.7	191
30	Computational tools to unmask transposable elements. <i>Nature Reviews Genetics</i> , 2018, 19, 688-704.	7.7	173
31	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. <i>Nature Communications</i> , 2014, 5, 5135.	5.8	158
32	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.	2.4	150
33	Transposable elements in gene regulation and in the evolution of vertebrate genomes. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 607-612.	1.5	143
34	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142
35	The International Human Epigenome Consortium Data Portal. <i>Cell Systems</i> , 2016, 3, 496-499.e2.	2.9	140
36	Stalled developmental programs at the root of pediatric brain tumors. <i>Nature Genetics</i> , 2019, 51, 1702-1713.	9.4	136

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37	Molecular and Genetic Crosstalks between mTOR and ERR α Are Key Determinants of Rapamycin-Induced Nonalcoholic Fatty Liver. <i>Cell Metabolism</i> , 2013, 17, 586-598.	7.2	132
38	GenPipes: an open-source framework for distributed and scalable genomic analyses. <i>GigaScience</i> , 2019, 8, .	3.3	121
39	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. <i>Circulation Research</i> , 2019, 124, 553-563.	2.0	118
40	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.	1.5	116
41	Nuclear mTOR acts as a transcriptional integrator of the androgen signaling pathway in prostate cancer. <i>Genes and Development</i> , 2017, 31, 1228-1242.	2.7	103
42	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	2.9	102
43	ERR α mediates metabolic adaptations driving lapatinib resistance in breast cancer. <i>Nature Communications</i> , 2016, 7, 12156.	5.8	98
44	SORL1 rare variants: a major risk factor for familial early-onset Alzheimer's disease. <i>Molecular Psychiatry</i> , 2016, 21, 831-836.	4.1	96
45	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
46	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, 3544-3549.	3.3	90
47	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.	3.8	90
48	Regulation of Estrogen Receptor-mediated Long Range Transcription via Evolutionarily Conserved Distal Response Elements. <i>Journal of Biological Chemistry</i> , 2008, 283, 32977-32988.	1.6	89
49	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , 2007, 17, 828-838.	2.4	86
50	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, 6301-6313.	1.4	86
51	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. <i>Nature Cell Biology</i> , 2013, 15, 1141-1152.	4.6	84
52	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. <i>Bioinformatics</i> , 2019, 35, 4767-4769.	1.8	84
53	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.	1.3	83
54	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, 710-716.	1.4	77

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55	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011, 21, 665-675.	2.4	74
56	Transcriptional consequences of genomic structural aberrations in breast cancer. <i>Genome Research</i> , 2011, 21, 676-687.	2.4	74
57	Ecotopic viral integration site 1 (EV11) 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, 2168-2173.	3.3	74
58	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.	2.9	73
59	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022, 2, 100129.	3.0	72
60	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.	3.8	71
61	Recovering genome rearrangements in the mammalian phylogeny. <i>Genome Research</i> , 2009, 19, 934-942.	2.4	66
62	Molecular Convergence of Neurodevelopmental Disorders. <i>American Journal of Human Genetics</i> , 2014, 95, 490-508.	2.6	64
63	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. <i>Molecular Psychiatry</i> , 2017, 22, 1119-1125.	4.1	57
64	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, .	3.9	56
65	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.	3.3	54
66	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. <i>PLoS Genetics</i> , 2018, 14, e1007285.	1.5	50
67	CpG Deamination Creates Transcription Factor Binding Sites with High Efficiency. <i>Genome Biology and Evolution</i> , 2011, 3, 1304-1311.	1.1	45
68	Identification of Elongated Primary Cilia with Impaired Mechanotransduction in Idiopathic Scoliosis Patients. <i>Scientific Reports</i> , 2017, 7, 44260.	1.6	44
69	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.	1.6	42
70	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.	2.2	41
71	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. <i>BMC Genomics</i> , 2017, 18, 214.	1.2	40
72	Genomewide Expression Profiling in the Zebrafish Embryo Identifies Target Genes Regulated by Hedgehog Signaling During Vertebrate Development. <i>Genetics</i> , 2006, 174, 735-752.	1.2	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. <i>Scientific Reports</i> , 2020, 10, 8079.	1.6	37
74	Human copy number variants are enriched in regions of low mappability. <i>Nucleic Acids Research</i> , 2018, 46, 7236-7249.	6.5	36
75	Transient DNMT1 suppression reveals hidden heritable marks in the genome. <i>Nucleic Acids Research</i> , 2015, 43, 1485-1497.	6.5	35
76	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.	0.7	35
77	The convergence of cytogenetics and rearrangement-based models for ancestral genome reconstruction. <i>Genome Research</i> , 2006, 16, 311-313.	2.4	34
78	Epigenome data release: a participant-centered approach to privacy protection. <i>Genome Biology</i> , 2015, 16, 142.	3.8	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. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 703951.	1.8	31
80	Personalized and graph genomes reveal missing signal in epigenomic data. <i>Genome Biology</i> , 2020, 21, 124.	3.8	29
81	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. <i>Bioinformatics</i> , 2017, 33, 491-499.	1.8	28
82	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, 537-543.	1.0	27
83	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.	0.7	26
84	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.	2.9	25
85	Epizoic Algae from Freshwater Turtles in Nova Scotia. <i>Journal of Freshwater Ecology</i> , 2007, 22, 677-685.	0.5	24
86	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, 549-558.	3.5	23
87	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. <i>Nature Communications</i> , 2019, 10, 4856.	5.8	22
88	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.	2.8	20
89	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.	1.8	20
90	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.	1.1	20

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91	IMPROVING GENE NETWORK INFERENCE BY COMPARING EXPRESSION TIME-SERIES ACROSS SPECIES, DEVELOPMENTAL STAGES OR TISSUES. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 765-783.	0.3	19
92	Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples, and Perspectives. <i>Genes</i> , 2014, 5, 887-925.	1.0	19
93	A coordinated progression of progenitor cell states initiates urinary tract development. <i>Nature Communications</i> , 2021, 12, 2627.	5.8	19
94	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. <i>Genome Medicine</i> , 2021, 13, 169.	3.6	19
95	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. <i>Genome Biology</i> , 2022, 23, 13.	3.8	19
96	Benefits and barriers in the design of harmonized access agreements for international data sharing. <i>Scientific Data</i> , 2019, 6, 297.	2.4	18
97	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.	0.6	18
98	Functional features of EVI1 and EVI1 ³²⁴ isoforms of MECOM gene in genome-wide transcription regulation and oncogenicity. <i>Oncogene</i> , 2016, 35, 2311-2321.	2.6	17
99	Detailed four-way comparative mapping and gene order analysis of the canine ctvm locus reveals evolutionary chromosome rearrangements. <i>Genomics</i> , 2004, 83, 1053-1062.	1.3	15
100	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.	2.4	15
101	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021, 31, 713-720.	2.4	15
102	Identifying co-opted transposable elements using comparative epigenomics. <i>Development Growth and Differentiation</i> , 2018, 60, 53-62.	0.6	14
103	Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. <i>Cell Reports</i> , 2021, 37, 109909.	2.9	14
104	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. <i>Science Advances</i> , 2022, 8, .	4.7	14
105	Sex Chromosomes and Sex Phenotype Contribute to Biased DNA Methylation in Mouse Liver. <i>Cells</i> , 2020, 9, 1436.	1.8	13
106	Evolving data access policy: The Canadian context. <i>Facets</i> , 2017, 1, 138-147.	1.1	13
107	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.	1.2	12
108	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.	1.1	12

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109	The Cowpea Kinome: Genomic and Transcriptomic Analysis Under Biotic and Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2021, 12, 667013.	1.7	12
110	Application of ATAC-Seq for genome-wide analysis of the chromatin state at single myofiber resolution. <i>ELife</i> , 2022, 11, .	2.8	11
111	Glioblastoma scRNA-seq shows treatment-induced, immune-dependent increase in mesenchymal cancer cells and structural variants in distal neural stem cells. <i>Neuro-Oncology</i> , 2022, 24, 1494-1508.	0.6	11
112	Developmental genome-wide DNA methylation asymmetry between mouse placenta and embryo. <i>Epigenetics</i> , 2020, 15, 800-815.	1.3	10
113	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. <i>Cell Genomics</i> , 2021, 1, 100033.	3.0	10
114	A Hidden Markov Model for Identifying Differentially Methylated Sites in Bisulfite Sequencing Data. <i>Biometrics</i> , 2019, 75, 210-221.	0.8	9
115	RNA-Seq as a Tool to Study the Tumor Microenvironment. <i>Methods in Molecular Biology</i> , 2016, 1458, 311-337.	0.4	7
116	Loss of the zona pellucida-binding protein 2 (<i>Zpbp2</i>) gene in mice impacts airway hypersensitivity and lung lipid metabolism in a sex-dependent fashion. <i>Mammalian Genome</i> , 2018, 29, 281-298.	1.0	7
117	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.	1.6	7
118	The omics of our lives: practices and policies of direct-to-consumer epigenetic and microbiomic testing companies. <i>New Genetics and Society</i> , 2021, 40, 541-569.	0.7	7
119	A population-based LD map of the human chromosome 6p. <i>Immunogenetics</i> , 2005, 57, 559-565.	1.2	6
120	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.	1.8	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. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013, 70, 600-609.	0.7	4
122	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.	0.4	4
123	Inferring Direct Regulatory Targets of a Transcription Factor in the DREAM2 Challenge. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 215-223.	1.8	3
124	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.	1.1	3
125	In Silico Methods to Identify Exapted Transposable Element Families. <i>Methods in Molecular Biology</i> , 2016, 1400, 33-45.	0.4	2
126	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.	2.2	2

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127	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.	0.4	2
128	Models and Methods in Comparative Genomics. <i>Advances in Computers</i> , 2006, 68, 59-104.	1.2	1
129	Comparing Apples to Apples and Oranges to Oranges. <i>Trends in Genetics</i> , 2018, 34, 571-572.	2.9	0
130	IHEC Data Portal. , 2021, , 77-94.		0