Guillaume Bourque

List of Publications by Year
in descending order

130 papers	27,136 citations	20817 60 h-index	12272 133 g-index
158 all docs	158 docs citations	158 times ranked	45131 citing authors

#	Article	IF	Citations
1	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. Genome Biology, 2022, 23, 13.	8.8	19
2	Application of ATAC-Seq for genome-wide analysis of the chromatin state at single myofiber resolution. ELife, 2022, 11, .	6.0	11
3	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
4	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	6.5	72
5	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. Science Advances, 2022, 8, .	10.3	14
6	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. Genome Research, 2021, 31, 713-720.	5.5	15
7	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
8	A coordinated progression of progenitor cell states initiates urinary tract development. Nature Communications, 2021, 12, 2627.	12.8	19
9	The Cowpea Kinome: Genomic and Transcriptomic Analysis Under Biotic and Abiotic Stresses. Frontiers in Plant Science, 2021, 12, 667013.	3.6	12
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. Cell Reports, 2021, 37, 109909.	6.4	14
18	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94

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19	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. Cell Genomics, 2021, 1, 100033.	6.5	10
20	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
21	IHEC Data Portal. , 2021, , 77-94.		0
22	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
23	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. Nature Metabolism, 2020, 2, 97-109.	11.9	272
24	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
25	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
26	Sex Chromosomes and Sex Phenotype Contribute to Biased DNA Methylation in Mouse Liver. Cells, 2020, 9, 1436.	4.1	13
27	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. Nature Communications, 2020, 11, 3406.	12.8	300
28	Developmental genome-wide DNA methylation asymmetry between mouse placenta and embryo. Epigenetics, 2020, 15, 800-815.	2.7	10
29	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
30	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
31	Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biology, 2020, 21, 124.	8.8	29
32	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
33	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
34	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. Nature Communications, 2019, 10, 4856.	12.8	22
35	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. Bioinformatics, 2019, 35, 4767-4769.	4.1	84
36	GenPipes: an open-source framework for distributed and scalable genomic analyses. GigaScience, 2019, 8, .	6.4	121

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37	Benefits and barriers in the design of harmonized access agreements for international data sharing. Scientific Data, 2019, 6, 297.	5.3	18
38	Stalled developmental programs at the root of pediatric brain tumors. Nature Genetics, 2019, 51, 1702-1713.	21.4	136
39	A Hidden Markov Model for Identifying Differentially Methylated Sites in Bisulfite Sequencing Data. Biometrics, 2019, 75, 210-221.	1.4	9
40	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. Circulation Research, 2019, 124, 553-563.	4.5	118
41	Identifying coâ€opted transposable elements using comparative epigenomics. Development Growth and Differentiation, 2018, 60, 53-62.	1.5	14
42	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
43	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
44	Ten things you should know about transposable elements. Genome Biology, 2018, 19, 199.	8.8	817
45	Computational tools to unmask transposable elements. Nature Reviews Genetics, 2018, 19, 688-704.	16.3	173
46	Human copy number variants are enriched in regions of low mappability. Nucleic Acids Research, 2018, 46, 7236-7249.	14.5	36
47	Comparing Apples to Apples and Oranges to Oranges. Trends in Genetics, 2018, 34, 571-572.	6.7	0
48	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. Nucleic Acids Research, 2018, 46, W486-W494.	14.5	3,199
49	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. PLoS Genetics, 2018, 14, e1007285.	3.5	50
50	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. Bioinformatics, 2017, 33, 491-499.	4.1	28
51	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
52	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
53	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
54	Identification of Elongated Primary Cilia with Impaired Mechanotransduction in Idiopathic Scoliosis Patients. Scientific Reports, 2017, 7, 44260.	3.3	44

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55	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. Molecular Psychiatry, 2017, 22, 1119-1125.	7.9	57
56	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. American Journal of Human Genetics, 2017, 101, 664-685.	6.2	337
57	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
58	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
59	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. BMC Genomics, 2017, 18, 214.	2.8	40
60	Evolving data access policy: The Canadian context. Facets, 2017, 1, 138-147.	2.4	13
61	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	12.8	142
62	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. Cancer Cell, 2016, 30, 891-908.	16.8	191
63	ERRÎ± mediates metabolic adaptations driving lapatinib resistance in breast cancer. Nature Communications, 2016, 7, 12156.	12.8	98
64	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
65	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
66	RNA-Seq as a Tool to Study the Tumor Microenvironment. Methods in Molecular Biology, 2016, 1458, 311-337.	0.9	7
67	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	6.4	102
68	The International Human Epigenome Consortium Data Portal. Cell Systems, 2016, 3, 496-499.e2.	6.2	140
69	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
70	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
71	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
72	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

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73	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
74	In Silico Methods to Identify Exapted Transposable Element Families. Methods in Molecular Biology, 2016, 1400, 33-45.	0.9	2
75	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
76	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
77	SORL1 rare variants: a major risk factor for familial early-onset Alzheimerâ€™s disease. Molecular Psychiatry, 2016, 21, 831-836.	7.9	96
78	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
79	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
80	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
81	Transient DNMT1 suppression reveals hidden heritable marks in the genome. Nucleic Acids Research, 2015, 43, 1485-1497.	14.5	35
82	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	8.8	34
83	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
84	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
85	Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples, and Perspectives. Genes, 2014, 5, 887-925.	2.4	19
86	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
87	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
88	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. Nature Communications, 2014, 5, 5135.	12.8	158
89	Molecular Convergence of Neurodevelopmental Disorders. American Journal of Human Genetics, 2014, 95, 490-508.	6.2	64
90	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

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91	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. Nature Cell Biology, 2013, 15, 1141-1152.	10.3	84
92	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
93	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
94	Transposable Elements Are Major Contributors to the Origin, Diversification, and Regulation of Vertebrate Long Noncoding RNAs. PLoS Genetics, 2013, 9, e1003470.	3.5	574
95	The Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements. PLoS Genetics, 2013, 9, e1003504.	3.5	293
96	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
97	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
98	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
99	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	21.4	567
100	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
101	Transcriptional consequences of genomic structural aberrations in breast cancer. Genome Research, 2011, 21, 676-687.	5.5	74
102	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. Genome Research, 2011, 21, 1328-1338.	5.5	247
103	CpG Deamination Creates Transcription Factorâ€“Binding Sites with High Efficiency. Genome Biology and Evolution, 2011, 3, 1304-1311.	2.5	45
104	Transposable elements have rewired the core regulatory network of human embryonic stem cells. Nature Genetics, 2010, 42, 631-634.	21.4	698
105	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
106	An oestrogen-receptor-Î±-bound human chromatin interactome. Nature, 2009, 462, 58-64.	27.8	1,537
107	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
108	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

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109	Recovering genome rearrangements in the mammalian phylogeny. Genome Research, 2009, 19, 934-942.	5.5	66
110	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. Cell, 2008, 133, 1106-1117.	28.9	2,279
111	Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genome Research, 2008, 18, 1752-1762.	5.5	501
112	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
113	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
114	Whole-Genome Cartography of Estrogen Receptor Î± Binding Sites. PLoS Genetics, 2007, 3, e87.	3.5	400
115	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
116	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
117	Initial sequence and comparative analysis of the cat genome. Genome Research, 2007, 17, 1675-1689.	5.5	311
118	Epizoic Algae from Freshwater Turtles in Nova Scotia. Journal of Freshwater Ecology, 2007, 22, 677-685.	1.2	24
119	Models and Methods in Comparative Genomics. Advances in Computers, 2006, 68, 59-104.	1.6	1
120	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. Nature Genetics, 2006, 38, 431-440.	21.4	2,162
121	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
122	The convergence of cytogenetics and rearrangement-based models for ancestral genome reconstruction. Genome Research, 2006, 16, 311-313.	5.5	34
123	A population-based LD map of the human chromosome 6p. Immunogenetics, 2005, 57, 559-565.	2.4	6
124	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
125	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. Science, 2005, 309, 613-617.	12.6	542
126	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943

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127	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
128	Reconstructing the Genomic Architecture of Ancestral Mammals: Lessons From Human, Mouse, and Rat Genomes. Genome Research, 2004, 14, 507-516.	5.5	210
129	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
130	Genome-scale evolution: reconstructing gene orders in the ancestral species. Genome Research, 2002, 12, 26-36.	5.5	308