Pierre-Luc Germain

List of Publications by Year
in descending order

38 papers	2,656 citations	331259 21 h-index	377514 34 g-index
57 all docs	57 docs citations	57 times ranked	4383 citing authors

#	Article	IF	Citations
1	Exploratory rearing: a context- and stress-sensitive behavior recorded in the open-field test. Stress, 2018, 21, 443-452.	0.8	280
2	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	9.4	254
3	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. Nature Communications, 2020, 11, 6077.	5.8	223
4	Germinal center dysregulation by histone methyltransferase EZH2 promotes lymphomagenesis. Journal of Clinical Investigation, 2013, 123, 5009-5022.	3.9	215
5	Doublet identification in single-cell sequencing data using scDblFinder. F1000Research, 0, 10, 979.	0.8	179
6	Alterations in sperm long RNA contribute to the epigenetic inheritance of the effects of postnatal trauma. Molecular Psychiatry, 2020, 25, 2162-2174.	4.1	130
7	From cohorts to molecules: Adverse impacts of endocrine disrupting mixtures. Science, 2022, 375, eabe8244.	6.0	129
8	YY1 Haploinsufficiency Causes an Intellectual Disability Syndrome Featuring Transcriptional and Chromatin Dysfunction. American Journal of Human Genetics, 2017, 100, 907-925.	2.6	125
9	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. Nature Communications, 2017, 8, 1212.	5.8	112
10	7q11.23 dosage-dependent dysregulation in human pluripotent stem cells affects transcriptional programs in disease-relevant lineages. Nature Genetics, 2015, 47, 132-141.	9.4	108
11	Doublet identification in single-cell sequencing data using scDblFinder. F1000Research, 0, 10, 979.	0.8	91
12	Taming Human Genetic Variability: Transcriptomic Meta-Analysis Guides the Experimental Design and Interpretation of iPSC-Based Disease Modeling. Stem Cell Reports, 2017, 8, 1784-1796.	2.3	86
13	Dosage analysis of the 7q11.23 Williams region identifies <i>BAZ1B</i> as a major human gene patterning the modern human face and underlying self-domestication. Science Advances, 2019, 5, eaaw7908.	4.7	67
14	pipeComp, a general framework for the evaluation of computational pipelines, reveals performant single cell RNA-seq preprocessing tools. Genome Biology, 2020, 21, 227.	3.8	61
15	Cell Reprogramming Requires Silencing of a Core Subset of Polycomb Targets. PLoS Genetics, 2013, 9, e1003292.	1.5	59
16	hLGDB: a database of human lysosomal genes and their regulation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat024.	1.4	48
17	RNAontheBENCH: computational and empirical resources for benchmarking RNAseq quantification and differential expression methods. Nucleic Acids Research, 2016, 44, 5054-5067.	6.5	48
18	A complete pupillometry toolbox for real-time monitoring of locus coeruleus activity in rodents. Nature Protocols, 2020, 15, 2301-2320.	5.5	46

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19	Isoform–resolved correlation analysis between <scp>mRNA</scp> abundance regulation and protein level degradation. Molecular Systems Biology, 2020, 16, e9170.	3.2	42
20	Junk or functional DNA? ENCODE and the function controversy. Biology and Philosophy, 2014, 29, 807-831.	0.7	38
21	Multiomic profiling of the acute stress response in the mouse hippocampus. Nature Communications, 2022, 13, 1824.	5.8	32
22	The Acute Stress Response in the Multiomic Era. Biological Psychiatry, 2021, 89, 1116-1126.	0.7	29
23	Cancer cells and adaptive explanations. Biology and Philosophy, 2012, 27, 785-810.	0.7	28
24	KMT2B Is Selectively Required for Neuronal Transdifferentiation, and Its Loss Exposes Dystonia Candidate Genes. Cell Reports, 2018, 25, 988-1001.	2.9	28
25	Involvement of circulating factors in the transmission of paternal experiences through the germline. EMBO Journal, 2020, 39, e104579.	3.5	28
26	The European politics of animal experimentation: From Victorian Britain to 'Stop Vivisection'. Studies in History and Philosophy of Science Part C:Studies in History and Philosophy of Biological and Biomedical Sciences, 2017, 64, 75-87.	0.8	16
27	scanMiR: a biochemically based toolkit for versatile and efficient microRNA target prediction. Bioinformatics, 2022, 38, 2466-2473.	1.8	15
28	MicroRNA-138 controls hippocampal interneuron function and short-term memory in mice. ELife, 2022, 11, .	2.8	14
29	Pervasive compartment–specific regulation of gene expression during homeostatic synaptic scaling. EMBO Reports, 2021, 22, e52094.	2.0	13
30	Metastasis as supra-cellular selection? A reply to Lean and Plutynski. Biology and Philosophy, 2017, 32, 281-287.	0.7	9
31	What mechanisms can't do: Explanatory frameworks and the function of the p53 gene in molecular oncology. Studies in History and Philosophy of Science Part C:Studies in History and Philosophy of Biological and Biomedical Sciences, 2013, 44, 374-384.	0.8	8
32	From replica to instruments: animal models in biomedical research. History and Philosophy of the Life Sciences, 2014, 36, 114-128.	0.6	7
33	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. Genome Biology, 2021, 22, 157.	3.8	7
34	Streamlining differential exon and 3′ UTR usage with diffUTR. BMC Bioinformatics, 2021, 22, 189.	1.2	5
35	<i>enrichMiR</i> predicts functionally relevant microRNAs based on target collections. Nucleic Acids Research, 2022, 50, W280-W289.	6.5	5
36	A relic of design: against proper functions in biology. Biology and Philosophy, 2022, 37, .	0.7	2

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37	Germinal center dysregulation by histone methyltransferase EZH2 promotes lymphomagenesis. Journal of Clinical Investigation, 2014, 124, 1869-1869.	3.9	1
38	Living Instruments and Theoretical Terms: Xenografts as Measurements in Cancer Research. , 2014, , 141-155.		0