

Pierre-Luc Germain

List of Publications by Year in descending order

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Version: 2024-02-01

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	From cohorts to molecules: Adverse impacts of endocrine disrupting mixtures. <i>Science</i> , 2022, 375, eabe8244.	6.0	129
2	MicroRNA-138 controls hippocampal interneuron function and short-term memory in mice. <i>ELife</i> , 2022, 11, .	2.8	14
3	Multiomic profiling of the acute stress response in the mouse hippocampus. <i>Nature Communications</i> , 2022, 13, 1824.	5.8	32
4	scanMiR: a biochemically based toolkit for versatile and efficient microRNA target prediction. <i>Bioinformatics</i> , 2022, 38, 2466-2473.	1.8	15
5	<i>enrichMiR</i> predicts functionally relevant microRNAs based on target collections. <i>Nucleic Acids Research</i> , 2022, 50, W280-W289.	6.5	5
6	A relic of design: against proper functions in biology. <i>Biology and Philosophy</i> , 2022, 37, .	0.7	2
7	Streamlining differential exon and 3â€² UTR usage with diffUTR. <i>BMC Bioinformatics</i> , 2021, 22, 189.	1.2	5
8	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. <i>Genome Biology</i> , 2021, 22, 157.	3.8	7
9	The Acute Stress Response in the Multiomic Era. <i>Biological Psychiatry</i> , 2021, 89, 1116-1126.	0.7	29
10	Pervasive compartmentâ€specific regulation of gene expression during homeostatic synaptic scaling. <i>EMBO Reports</i> , 2021, 22, e52094.	2.0	13
11	Alterations in sperm long RNA contribute to the epigenetic inheritance of the effects of postnatal trauma. <i>Molecular Psychiatry</i> , 2020, 25, 2162-2174.	4.1	130
12	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. <i>Nature Communications</i> , 2020, 11, 6077.	5.8	223
13	pipeComp, a general framework for the evaluation of computational pipelines, reveals performant single cell RNA-seq preprocessing tools. <i>Genome Biology</i> , 2020, 21, 227.	3.8	61
14	Isoformâ€resolved correlation analysis between <scp>mRNA</scp> abundance regulation and protein level degradation. <i>Molecular Systems Biology</i> , 2020, 16, e9170.	3.2	42
15	A complete pupillometry toolbox for real-time monitoring of locus coeruleus activity in rodents. <i>Nature Protocols</i> , 2020, 15, 2301-2320.	5.5	46
16	Involvement of circulating factors in the transmission of paternal experiences through the germline. <i>EMBO Journal</i> , 2020, 39, e104579.	3.5	28
17	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. <i>Nature Biotechnology</i> , 2019, 37, 314-322.	9.4	254
18	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. <i>Science Advances</i> , 2019, 5, eaaw7908.	4.7	67

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19	Exploratory rearing: a context- and stress-sensitive behavior recorded in the open-field test. <i>Stress</i> , 2018, 21, 443-452.	0.8	280
20	KMT2B Is Selectively Required for Neuronal Transdifferentiation, and Its Loss Exposes Dystonia Candidate Genes. <i>Cell Reports</i> , 2018, 25, 988-1001.	2.9	28
21	YY1 Haploinsufficiency Causes an Intellectual Disability Syndrome Featuring Transcriptional and Chromatin Dysfunction. <i>American Journal of Human Genetics</i> , 2017, 100, 907-925.	2.6	125
22	Metastasis as supra-cellular selection? A reply to Lean and Plutynski. <i>Biology and Philosophy</i> , 2017, 32, 281-287.	0.7	9
23	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017, 8, 1212.	5.8	112
24	Taming Human Genetic Variability: Transcriptomic Meta-Analysis Guides the Experimental Design and Interpretation of iPSC-Based Disease Modeling. <i>Stem Cell Reports</i> , 2017, 8, 1784-1796.	2.3	86
25	The European politics of animal experimentation: From Victorian Britain to "Stop Vivisection"™. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2017, 64, 75-87.	0.8	16
26	RNAontheBENCH: computational and empirical resources for benchmarking RNAseq quantification and differential expression methods. <i>Nucleic Acids Research</i> , 2016, 44, 5054-5067.	6.5	48
27	7q11.23 dosage-dependent dysregulation in human pluripotent stem cells affects transcriptional programs in disease-relevant lineages. <i>Nature Genetics</i> , 2015, 47, 132-141.	9.4	108
28	From replica to instruments: animal models in biomedical research. <i>History and Philosophy of the Life Sciences</i> , 2014, 36, 114-128.	0.6	7
29	Junk or functional DNA? ENCODE and the function controversy. <i>Biology and Philosophy</i> , 2014, 29, 807-831.	0.7	38
30	Germinal center dysregulation by histone methyltransferase EZH2 promotes lymphomagenesis. <i>Journal of Clinical Investigation</i> , 2014, 124, 1869-1869.	3.9	1
31	Living Instruments and Theoretical Terms: Xenografts as Measurements in Cancer Research. , 2014, , 141-155.		0
32	What mechanisms can "do": Explanatory frameworks and the function of the p53 gene in molecular oncology. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2013, 44, 374-384.	0.8	8
33	Cell Reprogramming Requires Silencing of a Core Subset of Polycomb Targets. <i>PLoS Genetics</i> , 2013, 9, e1003292.	1.5	59
34	hLGDB: a database of human lysosomal genes and their regulation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat024.	1.4	48
35	Germinal center dysregulation by histone methyltransferase EZH2 promotes lymphomagenesis. <i>Journal of Clinical Investigation</i> , 2013, 123, 5009-5022.	3.9	215
36	Cancer cells and adaptive explanations. <i>Biology and Philosophy</i> , 2012, 27, 785-810.	0.7	28

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37	Doublet identification in single-cell sequencing data using scDblFinder. F1000Research, 0, 10, 979.	0.8	179
38	Doublet identification in single-cell sequencing data using scDblFinder. F1000Research, 0, 10, 979.	0.8	91