Jean-FranÃ§ois Deleuze

List of Publications by Year
in descending order

31 papers	3,739 citations	567281 15 h-index	414414 32 g-index
40 all docs	40 docs citations	40 times ranked	8344 citing authors

#	Article	IF	Citations
1	Different Pigmentation Risk Loci for High-Risk Monosomy 3 and Low-Risk Disomy 3 Uveal Melanomas. Journal of the National Cancer Institute, 2022, 114, 302-309.	6.3	5
2	PIntMF: Penalized Integrative Matrix Factorization method for multi-omics data. Bioinformatics, 2022, 38, 900-907.	4.1	5
3	Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures. Science Translational Medicine, 2022, 14, eabg3083.	12.4	5
4	A high-throughput real-time PCR tissue-of-origin test to distinguish blood from lymphoblastoid cell line DNA for (epi)genomic studies. Scientific Reports, 2022, 12, 4684.	3.3	2
5	Fatty acid desaturase genetic variations and dietary omega-3 fatty acid intake associate with arterial stiffness. European Heart Journal Open, 2022, 2, .	2.3	6
6	Discovery of a genetic module essential for assigning leftâ€“right asymmetry in humans and ancestral vertebrates. Nature Genetics, 2022, 54, 62-72.	21.4	16
7	Methylated ccfDNA from plasma biomarkers of Alzheimer's disease using targeted bisulfite sequencing. Epigenomics, 2022, , .	2.1	1
8	Novel role of the synaptic scaffold protein Dlgap4 in ventricular surface integrity and neuronal migration during cortical development. Nature Communications, 2022, 13, 2746.	12.8	4
9	Heritability of a resting heart rate in a 20-year follow-up family cohort with GWAS data: Insights from the STANISLAS cohort. European Journal of Preventive Cardiology, 2021, 28, 1334-1341.	1.8	12
10	Selective loss of a LAP1 isoform causes a muscle-specific nuclear envelopathy. Neurogenetics, 2021, 22, 33-41.	1.4	3
11	Genomic insights into population history and biological adaptation in Oceania. Nature, 2021, 592, 583-589.	27.8	100
12	Heterogeneity of SARS-CoV-2 virus produced in cell culture revealed by shotgun proteomics and supported by genome sequencing. Analytical and Bioanalytical Chemistry, 2021, 413, 7265-7275.	3.7	7
13	Papua New Guinean Genomes Reveal the Complex Settlement of North Sahul. Molecular Biology and Evolution, 2021, 38, 5107-5121.	8.9	11
14	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. Nature Communications, 2021, 12, 6031.	12.8	34
15	Reclaiming digital democracy: A need for inauguration of regulated digital sovereignty. Journal of Digital Media and Policy, 2021, 12, 521-529.	0.6	1
16	Clustering and variable selection evaluation of 13 unsupervised methods for multi-omics data integration. Briefings in Bioinformatics, 2020, 21, 2011-2030.	6.5	54
17	cGAS-mediated induction of type I interferon due to inborn errors of histone pre-mRNA processing. Nature Genetics, 2020, 52, 1364-1372.	21.4	105
18	Loss of MTX2 causes mandibuloacral dysplasia and links mitochondrial dysfunction to altered nuclear morphology. Nature Communications, 2020, 11, 4589.	12.8	30

#	Article	IF	Citations
19	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	12.6	534
20	<scp>The importance of naturally attenuated SARSâ€CoV</scp>â€2<scp>in the fight against COVID</scp>â€19. Environmental Microbiology, 2020, 22, 1997-2000.	3.8	54
21	Comparison of commercially available whole-genome sequencing kits for variant detection in circulating cell-free DNA. Scientific Reports, 2020, 10, 6190.	3.3	13
22	Mutations in the Heterotopia Gene Eml1/EML1 Severely Disrupt the Formation of Primary Cilia. Cell Reports, 2019, 28, 1596-1611.e10.	6.4	28
23	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
24	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
25	Genome-Wide Association Study Identifies a Novel Genetic Risk Factor for Recurrent Venous Thrombosis. Circulation Genomic and Precision Medicine, 2018, 11, .	3.6	10
26	Whole-Genome Bisulfite Sequencing Using the OvationÂ® Ultralow Methyl-Seq Protocol. Methods in Molecular Biology, 2018, 1708, 83-104.	0.9	15
27	A GWAS in uveal melanoma identifies risk polymorphisms in the CLPTM1L locus. Npj Genomic Medicine, 2017, 2, .	3.8	17
28	Mutations in the HECT domain of NEDD4L lead to AKTâ€“mTOR pathway deregulation and cause periventricular nodular heterotopia. Nature Genetics, 2016, 48, 1349-1358.	21.4	101
29	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	6.2	222
30	MMP21 is mutated in human heterotaxy and is required for normal left-right asymmetry in vertebrates. Nature Genetics, 2015, 47, 1260-1263.	21.4	65
31	Mutations in Eml1 lead to ectopic progenitors and neuronal heterotopia in mouse and human. Nature Neuroscience, 2014, 17, 923-933.	14.8	137