

# Jean-François Deleuze

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4961322/publications.pdf>

Version: 2024-02-01

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	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates APOE, tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	21.4	1,962
2	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	12.6	534
3	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.	6.2	222
4	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	1.4	162
5	Mutations in Eml1 lead to ectopic progenitors and neuronal heterotopia in mouse and human. <i>Nature Neuroscience</i> , 2014, 17, 923-933.	14.8	137
6	cGAS-mediated induction of type I interferon due to inborn errors of histone pre-mRNA processing. <i>Nature Genetics</i> , 2020, 52, 1364-1372.	21.4	105
7	Mutations in the HECT domain of NEDD4L lead to AKT/mTOR pathway deregulation and cause periventricular nodular heterotopia. <i>Nature Genetics</i> , 2016, 48, 1349-1358.	21.4	101
8	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021, 592, 583-589.	27.8	100
9	MMP21 is mutated in human heterotaxy and is required for normal left-right asymmetry in vertebrates. <i>Nature Genetics</i> , 2015, 47, 1260-1263.	21.4	65
10	Clustering and variable selection evaluation of 13 unsupervised methods for multi-omics data integration. <i>Briefings in Bioinformatics</i> , 2020, 21, 2011-2030.	6.5	54
11	The importance of naturally attenuated SARS-CoV-2 in the fight against COVID-19. <i>Environmental Microbiology</i> , 2020, 22, 1997-2000.	3.8	54
12	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. <i>Nature Communications</i> , 2021, 12, 6031.	12.8	34
13	Loss of MTX2 causes mandibuloacral dysplasia and links mitochondrial dysfunction to altered nuclear morphology. <i>Nature Communications</i> , 2020, 11, 4589.	12.8	30
14	Mutations in the Heterotopia Gene Eml1/EML1 Severely Disrupt the Formation of Primary Cilia. <i>Cell Reports</i> , 2019, 28, 1596-1611.e10.	6.4	28
15	A GWAS in uveal melanoma identifies risk polymorphisms in the CLPTM1L locus. <i>Npj Genomic Medicine</i> , 2017, 2, .	3.8	17
16	Discovery of a genetic module essential for assigning left-right asymmetry in humans and ancestral vertebrates. <i>Nature Genetics</i> , 2022, 54, 62-72.	21.4	16
17	Whole-Genome Bisulfite Sequencing Using the Ovation® Ultralow Methyl-Seq Protocol. <i>Methods in Molecular Biology</i> , 2018, 1708, 83-104.	0.9	15
18	Comparison of commercially available whole-genome sequencing kits for variant detection in circulating cell-free DNA. <i>Scientific Reports</i> , 2020, 10, 6190.	3.3	13

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19	Heritability of a resting heart rate in a 20-year follow-up family cohort with GWAS data: Insights from the STANISLAS cohort. <i>European Journal of Preventive Cardiology</i> , 2021, 28, 1334-1341.	1.8	12
20	Papua New Guinean Genomes Reveal the Complex Settlement of North Sahul. <i>Molecular Biology and Evolution</i> , 2021, 38, 5107-5121.	8.9	11
21	Genome-Wide Association Study Identifies a Novel Genetic Risk Factor for Recurrent Venous Thrombosis. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, .	3.6	10
22	Heterogeneity of SARS-CoV-2 virus produced in cell culture revealed by shotgun proteomics and supported by genome sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 7265-7275.	3.7	7
23	Fatty acid desaturase genetic variations and dietary omega-3 fatty acid intake associate with arterial stiffness. <i>European Heart Journal Open</i> , 2022, 2, .	2.3	6
24	Different Pigmentation Risk Loci for High-Risk Monosomy 3 and Low-Risk Disomy 3 Uveal Melanomas. <i>Journal of the National Cancer Institute</i> , 2022, 114, 302-309.	6.3	5
25	PlntMF: Penalized Integrative Matrix Factorization method for multi-omics data. <i>Bioinformatics</i> , 2022, 38, 900-907.	4.1	5
26	Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures. <i>Science Translational Medicine</i> , 2022, 14, eabg3083.	12.4	5
27	Novel role of the synaptic scaffold protein Dlgap4 in ventricular surface integrity and neuronal migration during cortical development. <i>Nature Communications</i> , 2022, 13, 2746.	12.8	4
28	Selective loss of a LAP1 isoform causes a muscle-specific nuclear envelopathy. <i>Neurogenetics</i> , 2021, 22, 33-41.	1.4	3
29	A high-throughput real-time PCR tissue-of-origin test to distinguish blood from lymphoblastoid cell line DNA for (epi)genomic studies. <i>Scientific Reports</i> , 2022, 12, 4684.	3.3	2
30	Reclaiming digital democracy: A need for inauguration of regulated digital sovereignty. <i>Journal of Digital Media and Policy</i> , 2021, 12, 521-529.	0.6	1
31	Methylated ccfDNA from plasma biomarkers of Alzheimer's disease using targeted bisulfite sequencing. <i>Epigenomics</i> , 2022, , .	2.1	1