

Aurelie Labbe

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,590
citations

279798

23
h-index

214800

47
g-index

59
all docs

59
docs citations

59
times ranked

6641
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional normalization of 450k methylation array data improves replication in large cancer studies. <i>Genome Biology</i> , 2014, 15, 503.	8.8	665
2	Trajectories of cortical thickness maturation in normal brain development – The importance of quality control procedures. <i>NeuroImage</i> , 2016, 125, 267-279.	4.2	251
3	Transcriptional Profiling Implicates Novel Interactions between Abiotic Stress and Hormonal Responses in <i>Thellungiella</i> , a Close Relative of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2006, 140, 1437-1450.	4.8	227
4	An evaluation of methods correcting for cell-type heterogeneity in DNA methylation studies. <i>Genome Biology</i> , 2016, 17, 84.	8.8	137
5	Synergistic interaction between amyloid and tau predicts the progression to dementia. <i>Alzheimer's and Dementia</i> , 2017, 13, 644-653.	0.8	79
6	Measuring and Estimating the Effect Sizes of Copy Number Variants on General Intelligence in Community-Based Samples. <i>JAMA Psychiatry</i> , 2018, 75, 447.	11.0	77
7	VoxelStats: A MATLAB Package for Multi-Modal Voxel-Wise Brain Image Analysis. <i>Frontiers in Neuroinformatics</i> , 2016, 10, 20.	2.5	73
8	Alternative Risk Models for Ranking Locations for Safety Improvement. <i>Transportation Research Record</i> , 2005, 1908, 1-8.	1.9	69
9	Cohort Profile: The Nicotine Dependence in Teens (NDIT) Study. <i>International Journal of Epidemiology</i> , 2015, 44, 1537-1546.	1.9	62
10	Stage-specific links between plasma neurofilament light and imaging biomarkers of Alzheimer's disease. <i>Brain</i> , 2020, 143, 3793-3804.	7.6	60
11	Characterization of age/sex and the regional distribution of mGluR5 availability in the healthy human brain measured by high-resolution [11C]ABP688 PET. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2016, 43, 152-162.	6.4	58
12	Bayesian multiple testing procedures for hotspot identification. <i>Accident Analysis and Prevention</i> , 2007, 39, 1192-1201.	5.7	56
13	Transmission ratio distortion: review of concept and implications for genetic association studies. <i>Human Genetics</i> , 2013, 132, 245-263.	3.8	53
14	Effect Sizes of Deletions and Duplications on Autism Risk Across the Genome. <i>American Journal of Psychiatry</i> , 2021, 178, 87-98.	7.2	50
15	Plasma neurofilament light associates with Alzheimer's disease metabolic decline in amyloid-positive individuals. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2019, 11, 679-689.	2.4	48
16	Transcriptomic and metabolomic analysis of Yukon <i>Thellungiella</i> plants grown in cabinets and their natural habitat show phenotypic plasticity. <i>BMC Plant Biology</i> , 2012, 12, 175.	3.6	44
17	Trajectories of cortical surface area and cortical volume maturation in normal brain development. <i>Data in Brief</i> , 2015, 5, 929-938.	1.0	43
18	Refining psychiatric phenotypes for response to treatment: Contribution of LPHN3 in ADHD. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 776-785.	1.7	41

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19	Network screening for large urban road networks: Using GPS data and surrogate measures to model crash frequency and severity. <i>Accident Analysis and Prevention</i> , 2019, 125, 290-301.	5.7	37
20	Genome-wide analysis of gene dosage in 24,092 individuals estimates that 10,000 genes modulate cognitive ability. <i>Molecular Psychiatry</i> , 2021, 26, 2663-2676.	7.9	33
21	Revealing the bovine embryo transcript profiles during early in vivo embryonic development. <i>Reproduction</i> , 2009, 138, 95-105.	2.6	31
22	Surrogate safety and network screening: Modelling crash frequency using GPS travel data and latent Gaussian Spatial Models. <i>Accident Analysis and Prevention</i> , 2018, 120, 174-187.	5.7	31
23	Assessment of Overlap of Phylogenetic Transmission Clusters and Communities in Simple Sexual Contact Networks: Applications to HIV-1. <i>PLoS ONE</i> , 2016, 11, e0148459.	2.5	28
24	Identification of the most important features of knee osteoarthritis structural progressors using machine learning methods. <i>Therapeutic Advances in Musculoskeletal Disease</i> , 2020, 12, 1759720X2093346.	2.7	25
25	Symptom dimensions as alternative phenotypes to address genetic heterogeneity in schizophrenia and bipolar disorder. <i>European Journal of Human Genetics</i> , 2012, 20, 1182-1188.	2.8	23
26	funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. <i>Bioinformatics</i> , 2016, 32, 593-595.	4.1	22
27	Pedestrian safety at signalized intersections: Modelling spatial effects of exposure, geometry and signalization on a large urban network. <i>Accident Analysis and Prevention</i> , 2020, 134, 105265.	5.7	21
28	Machine Learning-Based Individualized Survival Prediction Model for Total Knee Replacement in Osteoarthritis: Data From the Osteoarthritis Initiative. <i>Arthritis Care and Research</i> , 2021, 73, 1518-1527.	3.4	21
29	Decreased expression of nociceptin/orphanin FQ in the dorsal anterior cingulate cortex of suicides. <i>European Neuropsychopharmacology</i> , 2015, 25, 2008-2014.	0.7	18
30	Real-time monitoring of aRNA production during T7 amplification to prevent the loss of sample representation during microarray hybridization sample preparation. <i>Nucleic Acids Research</i> , 2009, 37, e65-e65.	14.5	17
31	Epistatic interactions involving DRD2, DRD4, and COMT polymorphisms and risk of substance abuse in women with binge-purge eating disturbances. <i>Journal of Psychiatric Research</i> , 2016, 77, 8-14.	3.1	15
32	Genetic Variants and Early Cigarette Smoking and Nicotine Dependence Phenotypes in Adolescents. <i>PLoS ONE</i> , 2014, 9, e115716.	2.5	15
33	The association between CHRN genetic variants and dizziness at first inhalation of cigarette smoke. <i>Addictive Behaviors</i> , 2014, 39, 316-320.	3.0	14
34	Placebo response and its determinants in children with ADHD across multiple observers and settings: A randomized clinical trial. <i>International Journal of Methods in Psychiatric Research</i> , 2018, 27, .	2.1	14
35	Using disease symptoms to improve detection of linkage under genetic heterogeneity. <i>Genetic Epidemiology</i> , 2008, 32, 476-486.	1.3	13
36	Epistasis analysis links immune cascades and cerebral amyloidosis. <i>Journal of Neuroinflammation</i> , 2015, 12, 227.	7.2	10

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37	Latent class model with familial dependence to address heterogeneity in complex diseases: adapting the approach to family-based association studies. <i>Genetic Epidemiology</i> , 2011, 35, 182-189.	1.3	9
38	A Hidden Markov Model for Identifying Differentially Methylated Sites in Bisulfite Sequencing Data. <i>Biometrics</i> , 2019, 75, 210-221.	1.4	9
39	Association between COMT methylation and response to treatment in children with ADHD. <i>Journal of Psychiatric Research</i> , 2021, 135, 86-93.	3.1	9
40	Maturational trajectories of pericortical contrast in typical brain development. <i>NeuroImage</i> , 2021, 235, 117974.	4.2	9
41	CYP2C19 variant mitigates Alzheimer disease pathophysiology in vivo and postmortem. <i>Neurology: Genetics</i> , 2018, 4, e216.	1.9	8
42	DRD3 Gene and ADHD: A Pharmaco-Behavioural Genetic Study. <i>NeuroMolecular Medicine</i> , 2018, 20, 515-524.	3.4	8
43	Principal component of explained variance: An efficient and optimal data dimension reduction framework for association studies. <i>Statistical Methods in Medical Research</i> , 2018, 27, 1331-1350.	1.5	7
44	Assessing the role of transmission chains in the spread of HIV-1 among men who have sex with men in Quebec, Canada. <i>PLoS ONE</i> , 2019, 14, e0213366.	2.5	7
45	DM-PhyClus: a Bayesian phylogenetic algorithm for infectious disease transmission cluster inference. <i>BMC Bioinformatics</i> , 2018, 19, 324.	2.6	6
46	Integration of Genetic Familial Dependence Structure in Latent Class Models. <i>International Journal of Biostatistics</i> , 2009, 5, .	0.7	6
47	Solving genetic heterogeneity in extended families by identifying sub-types of complex diseases. <i>Computational Statistics</i> , 2011, 26, 539-560.	1.5	4
48	Analysis of Case-Parent Trios Using a Loglinear Model with Adjustment for Transmission Ratio Distortion. <i>Frontiers in Genetics</i> , 2016, 7, 155.	2.3	4
49	Transmission Ratio Distortion: A Neglected Phenomenon with Many Consequences in Genetic Analysis and Population Genetics. , 2013, , 265-285.		4
50	A novel statistical method for modeling covariate effects in bisulfite sequencing derived measures of DNA methylation. <i>Biometrics</i> , 2021, 77, 424-438.	1.4	3
51	Massive GNSS data for road safety analysis: Comparing crash models for several Canadian cities and data sources. <i>Accident Analysis and Prevention</i> , 2021, 159, 106232.	5.7	3
52	Analysis of case-parent trios for imprinting effect using a loglinear model with adjustment for sex-of-parent-specific transmission ratio distortion. <i>Human Genetics</i> , 2017, 136, 951-961.	3.8	2
53	Hierarchical Inverse Gaussian Models and Multiple Testing: Application to Gene Expression Data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article23.	0.6	1
54	Special Issue on Computational Statistical Methods for Genomics and Systems Biology. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, .	0.6	1

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55	Assessing transmission ratio distortion in extended families: a comparison of analysis methods. BMC Proceedings, 2016, 10, 197-202.	1.6	1