

Lambertus Klei

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9347719/publications.pdf>

Version: 2024-02-01

31
papers

10,883
citations

331538

21
h-index

434063

31
g-index

37
all docs

37
docs citations

37
times ranked

15003
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. <i>Translational Psychiatry</i> , 2021, 11, 171.	2.4	13
2	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. <i>Molecular Psychiatry</i> , 2021, 26, 5797-5811.	4.1	30
3	How rare and common risk variation jointly affect liability for autism spectrum disorder. <i>Molecular Autism</i> , 2021, 12, 66.	2.6	20
4	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. <i>Molecular Autism</i> , 2021, 12, 65.	2.6	22
5	Cohort profile: Epidemiology and Genetics of Obsessive-compulsive disorder and chronic tic disorders in Sweden (EGOS). <i>Social Psychiatry and Psychiatric Epidemiology</i> , 2020, 55, 1383-1393.	1.6	13
6	Age dependent association of inbreeding with risk for schizophrenia in Egypt. <i>Schizophrenia Research</i> , 2020, 216, 450-459.	1.1	1
7	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <i>Cell</i> , 2020, 180, 568-584.e23.	13.5	1,422
8	Maternal Effects as Causes of Risk for Obsessive-Compulsive Disorder. <i>Biological Psychiatry</i> , 2020, 87, 1045-1051.	0.7	18
9	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. <i>Cell Reports</i> , 2020, 31, 107489.	2.9	91
10	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
11	Semisoft clustering of single-cell data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 466-471.	3.3	71
12	Joint evaluation of serum C-Reactive Protein levels and polygenic risk scores as risk factors for schizophrenia. <i>Psychiatry Research</i> , 2018, 261, 148-153.	1.7	6
13	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. <i>Nature Genetics</i> , 2018, 50, 727-736.	9.4	235
14	Heritable Variation, With Little or No Maternal Effect, Accounts for Recurrence Risk to Autism Spectrum Disorder in Sweden. <i>Biological Psychiatry</i> , 2018, 83, 589-597.	0.7	38
15	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. <i>Science</i> , 2018, 362, .	6.0	234
16	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. <i>Nature Genetics</i> , 2018, 50, 1032-1040.	9.4	64
17	A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohn's Disease and Human Gut Microbiome Composition. <i>Gastroenterology</i> , 2016, 151, 724-732.	0.6	109
18	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. <i>Nature Communications</i> , 2015, 6, 6404.	5.8	316

#	ARTICLE	IF	CITATIONS
19	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. <i>Neuron</i> , 2015, 87, 1215-1233.	3.8	1,219
20	A Genome-wide Association Study of Autism Using the Simons Simplex Collection: Does Reducing Phenotypic Heterogeneity in Autism Increase Genetic Homogeneity?. <i>Biological Psychiatry</i> , 2015, 77, 775-784.	0.7	133
21	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. <i>American Journal of Human Genetics</i> , 2014, 94, 677-694.	2.6	819
22	Most genetic risk for autism resides with common variation. <i>Nature Genetics</i> , 2014, 46, 881-885.	9.4	977
23	Rare deleterious mutations of the gene EFR3A in autism spectrum disorders. <i>Molecular Autism</i> , 2014, 5, 31.	2.6	27
24	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. <i>American Journal of Human Genetics</i> , 2014, 94, 870-883.	2.6	116
25	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. <i>Cell</i> , 2013, 155, 997-1007.	13.5	825
26	Refining genetically inferred relationships using treelet covariance smoothing. <i>Annals of Applied Statistics</i> , 2013, 7, 669-690.	0.5	9
27	Common genetic variants, acting additively, are a major source of risk for autism. <i>Molecular Autism</i> , 2012, 3, 9.	2.6	357
28	Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. <i>Statistics in Medicine</i> , 2010, 29, 2932-2945.	0.8	15
29	Functional impact of global rare copy number variation in autism spectrum disorders. <i>Nature</i> , 2010, 466, 368-372.	13.7	1,803
30	Pleiotropy and principal components of heritability combine to increase power for association analysis. <i>Genetic Epidemiology</i> , 2008, 32, 9-19.	0.6	123
31	On the Use of General Control Samples for Genome-wide Association Studies: Genetic Matching Highlights Causal Variants. <i>American Journal of Human Genetics</i> , 2008, 82, 453-463.	2.6	120