

Annique A J Claringbould

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6798527/publications.pdf>

Version: 2024-02-01

24
papers

3,662
citations

471371

17
h-index

580701

25
g-index

35
all docs

35
docs citations

35
times ranked

6855
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
2	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	9.4	590
3	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019, 51, 245-257.	9.4	536
4	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
5	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
6	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
7	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	9.4	97
8	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. <i>Science Advances</i> , 2019, 5, eaaw3095.	4.7	86
9	Enhancers in disease: molecular basis and emerging treatment strategies. <i>Trends in Molecular Medicine</i> , 2021, 27, 1060-1073.	3.5	84
10	Gender differences in the mental health impact of the COVID-19 lockdown: Longitudinal evidence from the Netherlands. <i>SSM - Population Health</i> , 2021, 15, 100878.	1.3	53
11	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. <i>BMJ Open</i> , 2021, 11, e044474.	0.8	49
12	A SNP panel for identification of DNA and RNA specimens. <i>BMC Genomics</i> , 2018, 19, 90.	1.2	47
13	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. <i>BMC Bioinformatics</i> , 2020, 21, 243.	1.2	38
14	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. <i>European Journal of Human Genetics</i> , 2020, 28, 253-263.	1.4	29
15	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. <i>Genome Biology</i> , 2019, 20, 235.	3.8	26
16	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	1.2	23
17	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. <i>Nature Communications</i> , 2020, 11, 4930.	5.8	20
18	Systematic Prioritization of Candidate Genes in Disease Loci Identifies TRAFD1 as a Master Regulator of IFN γ Signaling in Celiac Disease. <i>Frontiers in Genetics</i> , 2020, 11, 562434.	1.1	20

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19	Sex and Gender-Related Differences in COVID-19 Diagnoses and SARS-CoV-2 Testing Practices During the First Wave of the Pandemic: The Dutch Lifelines COVID-19 Cohort Study. <i>Journal of Women's Health</i> , 2021, 30, 1686-1692.	1.5	20
20	Genome-wide identification of directed gene networks using large-scale population genomics data. <i>Nature Communications</i> , 2018, 9, 3097.	5.8	18
21	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. <i>Biological Psychiatry</i> , 2020, 88, 470-479.	0.7	14
22	The genetic architecture of molecular traits. <i>Current Opinion in Systems Biology</i> , 2017, 1, 25-31.	1.3	6
23	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. <i>Human Genetics</i> , 2019, 138, 375-388.	1.8	6
24	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. <i>PLoS ONE</i> , 2021, 16, e0255402.	1.1	6