Johannes Waage

List of Publications by Year
in descending order

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Version: 2024-02-01

38 papers	6,532 citations	159585 30 h-index	289244 40 g-index
41 all docs	41 docs citations	41 times ranked	13617 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
2	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
3	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
4	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
5	Maturation of the gut microbiome and risk of asthma in childhood. Nature Communications, 2018, 9, 141.	12.8	380
6	Fish Oilâ€"Derived Fatty Acids in Pregnancy and Wheeze and Asthma in Offspring. New England Journal of Medicine, 2016, 375, 2530-2539.	27.0	367
7	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
8	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
9	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
10	microRNA-9 targets the long non-coding RNA MALAT1 for degradation in the nucleus. Scientific Reports, 2013, 3, 2535.	3.3	231
11	Human nonsense-mediated RNA decay initiates widely by endonucleolysis and targets snoRNA host genes. Genes and Development, 2014, 28, 2498-2517.	5.9	163
12	Prenatal vitamin D supplementation reduces risk of asthma/recurrent wheeze in early childhood: A combined analysis of two randomized controlled trials. PLoS ONE, 2017, 12, e0186657.	2.5	158
13	Large-scale benchmarking reveals false discoveries and count transformation sensitivity in 16S rRNA gene amplicon data analysis methods used in microbiome studies. Microbiome, 2016, 4, 62.	11.1	138
14	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	3.5	126
15	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. Genome Biology, 2012, 13, R35.	9.6	113
16	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
17	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
18	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	21.4	106

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19	spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics, 2014, 15, 81.	2.6	100
20	UPF2-Dependent Nonsense-Mediated mRNA Decay Pathway Is Essential for Spermatogenesis by Selectively Eliminating Longer 3'UTR Transcripts. PLoS Genetics, 2016, 12, e1005863.	3.5	94
21	Infant airway microbiota and topical immune perturbations in the origins of childhood asthma. Nature Communications, 2019, 10, 5001.	12.8	92
22	C/EBPÎ± Is Required for Long-Term Self-Renewal and Lineage Priming of Hematopoietic Stem Cells and for the Maintenance of Epigenetic Configurations in Multipotent Progenitors. PLoS Genetics, 2014, 10, e1004079.	3.5	85
23	UPF2 Is a Critical Regulator of Liver Development, Function and Regeneration. PLoS ONE, 2010, 5, e11650.	2.5	80
24	Cadherin-related Family Member 3 Genetics and Rhinovirus C Respiratory Illnesses. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 589-594.	5.6	80
25	Temporal mapping of CEBPA and CEBPB binding during liver regeneration reveals dynamic occupancy and specific regulatory codes for homeostatic and cell cycle gene batteries. Genome Research, 2013, 23, 592-603.	5.5	73
26	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	2.9	63
27	Genetics of allergy and allergic sensitization: common variants, rare mutations. Current Opinion in Immunology, 2015, 36, 115-126.	5.5	56
28	Genetic, Clinical, and Environmental Factors Associated With Persistent Atopic Dermatitis in Childhood. JAMA Dermatology, 2019, 155, 50.	4.1	50
29	The developing hypopharyngeal microbiota in early life. Microbiome, 2016, 4, 70.	11.1	46
30	Enhancer and Transcription Factor Dynamics during Myeloid Differentiation Reveal an Early Differentiation Block in Cebpa null Progenitors. Cell Reports, 2018, 23, 2744-2757.	6.4	45
31	A genome-wide association meta-analysis of diarrhoeal disease in young children identifiesFUT2locus and provides plausible biological pathways. Human Molecular Genetics, 2016, 25, 4127-4142.	2.9	35
32	Consortium-based genome-wide meta-analysis for childhood dental caries traits. Human Molecular Genetics, 2018, 27, 3113-3127.	2.9	32
33	A novel rare CUBN variant and three additional genes identified in Europeans with and without diabetes: results from an exome-wide association study of albuminuria. Diabetologia, 2019, 62, 292-305.	6.3	29
34	Amplification of pico-scale DNA mediated by bacterial carrier DNA for small-cell-number transcription factor ChIP-seq. BMC Genomics, 2015, 16, 46.	2.8	27
35	Distinct immune phenotypes in infants developing asthma during childhood. Science Translational Medicine, 2020, 12, .	12.4	19
36	CDHR3 gene variation and childhood bronchiolitis. Journal of Allergy and Clinical Immunology, 2017, 140, 1469-1471.e7.	2.9	11

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37	Incidence and Determinants of Ventilation Tubes in Denmark. PLoS ONE, 2016, 11, e0165657.	2.5	10
38	NKG2D gene variation and susceptibility to viral bronchiolitis in childhood. Pediatric Research, 2018, 84, 451-457.	2.3	3