Johannes Waage

List of Publications by Year
in descending order

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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	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
2	Distinct immune phenotypes in infants developing asthma during childhood. Science Translational Medicine, 2020, 12, .	12.4	19
3	Infant airway microbiota and topical immune perturbations in the origins of childhood asthma. Nature Communications, 2019, 10, 5001.	12.8	92
4	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
5	Genetic, Clinical, and Environmental Factors Associated With Persistent Atopic Dermatitis in Childhood. JAMA Dermatology, 2019, 155, 50.	4.1	50
6	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
7	Maturation of the gut microbiome and risk of asthma in childhood. Nature Communications, 2018, 9, 141.	12.8	380
8	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
9	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
10	Consortium-based genome-wide meta-analysis for childhood dental caries traits. Human Molecular Genetics, 2018, 27, 3113-3127.	2.9	32
11	NKG2D gene variation and susceptibility to viral bronchiolitis in childhood. Pediatric Research, 2018, 84, 451-457.	2.3	3
12	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
13	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	2.9	63
14	CDHR3 gene variation and childhood bronchiolitis. Journal of Allergy and Clinical Immunology, 2017, 140, 1469-1471.e7.	2.9	11
15	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	3.5	126
16	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
17	Incidence and Determinants of Ventilation Tubes in Denmark. PLoS ONE, 2016, 11, e0165657.	2.5	10
18	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

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19	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
20	The developing hypopharyngeal microbiota in early life. Microbiome, 2016, 4, 70.	11.1	46
21	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
22	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
23	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
24	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
25	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
26	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
27	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
28	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
29	Genetics of allergy and allergic sensitization: common variants, rare mutations. Current Opinion in Immunology, 2015, 36, 115-126.	5.5	56
30	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
31	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
32	Human nonsense-mediated RNA decay initiates widely by endonucleolysis and targets snoRNA host genes. Genes and Development, 2014, 28, 2498-2517.	5.9	163
33	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
34	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
35	microRNA-9 targets the long non-coding RNA MALAT1 for degradation in the nucleus. Scientific Reports, 2013, 3, 2535.	3.3	231
36	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

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37	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. Genome Biology, 2012, 13, R35.	9.6	113
38	UPF2 Is a Critical Regulator of Liver Development, Function and Regeneration. PLoS ONE, 2010, 5, e11650.	2.5	80