

Matthias Wielscher

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,800
citations

293460

24
h-index

299063

42
g-index

57
all docs

57
docs citations

57
times ranked

5627
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	9.4	60
2	Single-cell transcriptomics defines keratinocyte differentiation in avian scutate scales. <i>Scientific Reports</i> , 2022, 12, 126.	1.6	4
3	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. <i>Nature Communications</i> , 2022, 13, 2408.	5.8	26
4	Single-Cell RNA Sequencing Reveals Tissue Compartment-Specific Plasticity of Mycosis Fungoides Tumor Cells. <i>Frontiers in Immunology</i> , 2021, 12, 666935.	2.2	27
5	Genetic variation in cervical preinvasive and invasive disease: a genome-wide association study. <i>Lancet Oncology</i> , The, 2021, 22, 548-557.	5.1	46
6	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. <i>Nature Communications</i> , 2021, 12, 2579.	5.8	51
7	Genetic correlation and causal relationships between cardio-metabolic traits and lung function impairment. <i>Genome Medicine</i> , 2021, 13, 104.	3.6	11
8	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. <i>Scientific Reports</i> , 2021, 11, 19365.	1.6	2
9	100,000 Genomes Pilot on Rare-Disease Diagnosis in Health Care – Preliminary Report. <i>New England Journal of Medicine</i> , 2021, 385, 1868-1880.	13.9	352
10	Rare variant analysis in eczema identifies exonic variants in DUSP1, NOTCH4 and SLC9A4. <i>Nature Communications</i> , 2021, 12, 6618.	5.8	17
11	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
12	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
13	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. <i>International Journal of Epidemiology</i> , 2020, 49, 233-243.	0.9	18
14	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , the, 2020, 8, 696-708.	5.2	69
15	Determinants of accelerated metabolomic and epigenetic aging in a UK cohort. <i>Aging Cell</i> , 2020, 19, e13149.	3.0	95
16	Role of DNA methylation in the association of lung function with body mass index: a two-step epigenetic Mendelian randomisation study. <i>BMC Pulmonary Medicine</i> , 2020, 20, 171.	0.8	3
17	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020, 12, 25.	3.6	81
18	Association of adult lung function with accelerated biological aging. <i>Aging</i> , 2020, 12, 518-542.	1.4	23

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19	Early life origins of lung ageing: A study of lung function decline the ECRHS and NFBC1966 cohorts. , 2020, , .		0
20	DNA methylation links prenatal smoking exposure to later life health outcomes in offspring. <i>Clinical Epigenetics</i> , 2019, 11, 97.	1.8	88
21	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 2019, 54, 1900457.	3.1	49
22	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. <i>Nature Communications</i> , 2019, 10, 3927.	5.8	49
23	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2062-2074.	1.5	147
24	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, 1893.	5.8	140
25	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	9.4	350
26	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , 2018, 27, 1664-1674.	1.4	30
27	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor \pm . <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33
28	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , 2018, 38, 206-216.	2.7	43
29	SERPINA1 methylation and lung function in tobacco-smoke exposed European children and adults: a meta-analysis of ALEC population-based cohorts. <i>Respiratory Research</i> , 2018, 19, 156.	1.4	11
30	Increased Obesity Is Causal for Increased Inflammationâ€™A Mendelian Randomisation Study. <i>Diabetes</i> , 2018, 67, .	0.3	4
31	Body mass index and lung function: A two-step epigenetic Mendelian randomization study. , 2018, , .		0
32	DNA-methylation and autoantibodies based cancer diagnosis from body fluids. <i>European Journal of Molecular and Clinical Medicine</i> , 2017, 2, 64.	0.5	0
33	Middle age enhances expression of innate immunity genes in a female mouse model of pulmonary fibrosis. <i>Biogerontology</i> , 2017, 18, 253-262.	2.0	6
34	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	9.4	257
35	Age at menarche and lung function: a Mendelian randomization study. <i>European Journal of Epidemiology</i> , 2017, 32, 701-710.	2.5	37
36	Systematic review of lung function and COPD with peripheral blood DNA methylation in population based studies. <i>BMC Pulmonary Medicine</i> , 2017, 17, 54.	0.8	28

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37	Diagnostic Performance of Plasma DNA Methylation Profiles in Lung Cancer, Pulmonary Fibrosis and COPD. <i>EBioMedicine</i> , 2015, 2, 929-936.	2.7	83
38	Increased Antioxidant Defense Mechanism in Human Adventitia-Derived Progenitor Cells Is Associated with Therapeutic Benefit in Ischemia. <i>Antioxidants and Redox Signaling</i> , 2014, 21, 1591-1604.	2.5	29
39	Strategies for validation and testing of DNA methylation biomarkers. <i>Epigenomics</i> , 2014, 6, 603-622.	1.0	28
40	Cytosine 5-Hydroxymethylation of the LZTS1 Gene Is Reduced in Breast Cancer. <i>Translational Oncology</i> , 2013, 6, 715-727.	1.7	26
41	Age influence on hypersensitivity pneumonitis induced in mice by exposure to <i>Pantoea agglomerans</i> . <i>Inhalation Toxicology</i> , 2013, 25, 640-650.	0.8	10
42	The stem cell signature of CHH/CHG methylation is not present in 271 cancer associated 5'UTR gene regions. <i>Biochimie</i> , 2012, 94, 2345-2352.	1.3	17
43	DNA methylation testing and marker validation using PCR: diagnostic applications. <i>Expert Review of Molecular Diagnostics</i> , 2012, 12, 75-92.	1.5	24
44	Methyl-binding domain protein-based DNA isolation from human blood serum combines DNA analyses and serum-autoantibody testing. <i>BMC Clinical Pathology</i> , 2011, 11, 11.	1.8	7
45	Coordinated ARP2/3 and Glycolytic Activities Regulate the Morphological Fitness of Human Effector T Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0