Dirk S Paul

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6333800/publications.pdf

Version: 2024-02-01

45 papers	8,725 citations	126708 33 h-index	223531 46 g-index
66 all docs	66 docs citations	66 times ranked	19660 citing authors

#	Article	IF	Citations
1	Genomic atlas of the human plasma proteome. Nature, 2018, 558, 73-79.	13.7	1,180
2	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	13.5	1,052
3	PhenoScanner: a database of human genotypeâ€“phenotype associations. Bioinformatics, 2016, 32, 3207-3209.	1.8	983
4	Risk thresholds for alcohol consumption: combined analysis of individual-participant data for 599â€˜912 current drinkers in 83 prospective studies. Lancet, The, 2018, 391, 1513-1523.	6.3	858
5	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
6	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
7	Compound inheritance of a low-frequency regulatory SNP and a rare null mutation in exon-junction complex subunit RBM8A causes TAR syndrome. Nature Genetics, 2012, 44, 435-439.	9.4	355
8	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
9	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	9.4	270
10	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
11	Rare variant contribution to human disease in 281,104 UK Biobank exomes. Nature, 2021, 597, 527-532.	13.7	224
12	Correlation of an epigenetic mitotic clock with cancer risk. Genome Biology, 2016, 17, 205.	3.8	197
13	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. Nature Medicine, 2019, 25, 517-525.	15.2	178
14	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
15	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
16	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
17	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	3.8	97
18	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91

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19	ProGeM: a framework for the prioritization of candidate causal genes at molecular quantitative trait loci. Nucleic Acids Research, 2019, 47, e3-e3.	6.5	90
20	UroMarkâ€"a urinary biomarker assay for the detection of bladder cancer. Clinical Epigenetics, 2017, 9, 8.	1.8	81
21	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.3	77
22	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
23	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
24	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. BioEssays, 2018, 40, 1700148.	1.2	71
25	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. Genome Medicine, 2018, 10, 64.	3.6	71
26	Advances in epigenome-wide association studies for common diseases. Trends in Molecular Medicine, 2014, 20, 541-543.	3.5	58
27	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. Genome Research, 2018, 28, 1779-1790.	2.4	56
28	An Unbiased Lipid Phenotyping Approach To Study the Genetic Determinants of Lipids and Their Association with Coronary Heart Disease Risk Factors. Journal of Proteome Research, 2019, 18, 2397-2410.	1.8	55
29	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
30	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. ELife, 2019, 8, .	2.8	53
31	Functional interpretation of nonâ€coding sequence variation: Concepts and challenges. BioEssays, 2014, 36, 191-199.	1.2	47
32	Interleukin-6 Receptor Signaling and Abdominal Aortic Aneurysm Growth Rates. Circulation Genomic and Precision Medicine, 2019, 12, e002413.	1.6	46
33	A GWAS sequence variant for platelet volume marks an alternative DNM3 promoter in megakaryocytes near a MEIS1 binding site. Blood, 2012, 120, 4859-4868.	0.6	44
34	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. Aging, 2018, 10, 3541-3557.	1.4	42
35	Maps of Open Chromatin Guide the Functional Follow-Up of Genome-Wide Association Signals: Application to Hematological Traits. PLoS Genetics, 2011, 7, e1002139.	1.5	38
36	Assessing the Role of Rare Genetic Variation in Patients With Heart Failure. JAMA Cardiology, 2021, 6, 379.	3.0	37

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37	Neutrophil-mediated IL-6 receptor trans-signaling and the risk of chronic obstructive pulmonary disease and asthma. Human Molecular Genetics, 2017, 26, 1584-1596.	1.4	36
38	Maps of open chromatin highlight cell typeâ€“restricted patterns of regulatory sequence variation at hematological trait loci. Genome Research, 2013, 23, 1130-1141.	2.4	34
39	Assessment of RainDrop BS-seq as a method for large-scale, targeted bisulfite sequencing. Epigenetics, 2014, 9, 678-684.	1.3	28
40	Genome-wide analysis of blood lipid metabolites in over 5000 South Asians reveals biological insights at cardiometabolic disease loci. BMC Medicine, 2021, 19, 232.	2.3	25
41	Assessment of patient-derived tumour xenografts (PDXs) as a discovery tool for cancer epigenomics. Genome Medicine, 2014, 6, 116.	3.6	22
42	Tensorial blind source separation for improved analysis of multi-omic data. Genome Biology, 2018, 19, 76.	3.8	20
43	A donor-specific epigenetic classifier for acute graft-versus-host disease severity in hematopoietic stem cell transplantation. Genome Medicine, 2015, 7, 128.	3.6	7
44	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5
45	Pharmacogenomic study of heart failure and candesartan response from the CHARM programme. ESC Heart Failure, 2022, 9, 2997-3008.	1.4	3