Dirk S Paul

List of Publications by Year
in descending order

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

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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	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5
2	Pharmacogenomic study of heart failure and candesartan response from the CHARM programme. ESC Heart Failure, 2022, 9, 2997-3008.	1.4	3
3	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
4	Assessing the Role of Rare Genetic Variation in Patients With Heart Failure. JAMA Cardiology, 2021, 6, 379.	3.0	37
5	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
6	Rare variant contribution to human disease in 281,104 UK Biobank exomes. Nature, 2021, 597, 527-532.	13.7	224
7	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
8	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
9	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. Nature Medicine, 2019, 25, 517-525.	15.2	178
10	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
11	Interleukin-6 Receptor Signaling and Abdominal Aortic Aneurysm Growth Rates. Circulation Genomic and Precision Medicine, 2019, 12, e002413.	1.6	46
12	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.3	77
13	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
14	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. ELife, 2019, 8, .	2.8	53
15	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
16	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
17	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. BioEssays, 2018, 40, 1700148.	1.2	71
18	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. Genome Research, 2018, 28, 1779-1790.	2.4	56

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19	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. Genome Medicine, 2018, 10, 64.	3.6	71
20	Tensorial blind source separation for improved analysis of multi-omic data. Genome Biology, 2018, 19, 76.	3.8	20
21	Genomic atlas of the human plasma proteome. Nature, 2018, 558, 73-79.	13.7	1,180
22	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. Aging, 2018, 10, 3541-3557.	1.4	42
23	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	3.8	97
24	UroMarkâ€"a urinary biomarker assay for the detection of bladder cancer. Clinical Epigenetics, 2017, 9, 8.	1.8	81
25	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
26	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
27	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
28	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
29	Correlation of an epigenetic mitotic clock with cancer risk. Genome Biology, 2016, 17, 205.	3.8	197
30	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
31	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
32	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
33	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
34	PhenoScanner: a database of human genotypeâ€"phenotype associations. Bioinformatics, 2016, 32, 3207-3209.	1.8	983
35	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	9.4	270
36	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

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37	Assessment of patient-derived tumour xenografts (PDXs) as a discovery tool for cancer epigenomics. Genome Medicine, 2014, 6, 116.	3.6	22
38	Assessment of RainDrop BS-seq as a method for large-scale, targeted bisulfite sequencing. Epigenetics, 2014, 9, 678-684.	1.3	28
39	Functional interpretation of nonâ€coding sequence variation: Concepts and challenges. BioEssays, 2014, 36, 191-199.	1.2	47
40	Advances in epigenome-wide association studies for common diseases. Trends in Molecular Medicine, 2014, 20, 541-543.	3.5	58
41	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
42	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
43	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
44	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
45	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