

Tim Kacprowski

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4977779/publications.pdf>

Version: 2024-02-01

79
papers

4,765
citations

109321

35
h-index

118850

62
g-index

96
all docs

96
docs citations

96
times ranked

11122
citing authors

#	ARTICLE	IF	CITATIONS
1	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
2	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
3	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.2	326
4	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. <i>Cell Host and Microbe</i> , 2019, 26, 252-264.e10.	11.0	274
5	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016, 13, 310-318.	19.0	209
6	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
7	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018, 9, 2397.	12.8	147
8	Exploring the SARS-CoV-2 virus-host-drug interactome for drug repurposing. <i>Nature Communications</i> , 2020, 11, 3518.	12.8	144
9	Associations of circulating plasma microRNAs with age, body mass index and sex in a population-based study. <i>BMC Medical Genomics</i> , 2015, 8, 61.	1.5	133
10	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016, 2, e1501678.	10.3	133
11	Network analysis methods for studying microbial communities: A mini review. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2687-2698.	4.1	130
12	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017, 49, 125-130.	21.4	116
13	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	11.1	109
14	Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior. <i>Human Molecular Genetics</i> , 2016, 25, dww334.	2.9	107
15	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	21.4	101
16	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. <i>Gut</i> , 2021, 70, 522-530.	12.1	96
17	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
18	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. <i>PLoS Genetics</i> , 2015, 11, e1005487.	3.5	83

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19	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82
20	A structured weight loss program increases gut microbiota phylogenetic diversity and reduces levels of <i>Collinsella</i> in obese type 2 diabetics: A pilot study. <i>PLoS ONE</i> , 2019, 14, e0219489.	2.5	82
21	Deciphering the Molecular Profile of Plaques, Memory Decline and Neuron Loss in Two Mouse Models for Alzheimer's Disease by Deep Sequencing. <i>Frontiers in Aging Neuroscience</i> , 2014, 6, 75.	3.4	78
22	Profiling and validation of circulating microRNAs for cardiovascular events in patients presenting with ST-segment elevation myocardial infarction. <i>European Heart Journal</i> , 2017, 38, ehw563.	2.2	77
23	Impaired Exocrine Pancreatic Function Associates With Changes in Intestinal Microbiota Composition and Diversity. <i>Gastroenterology</i> , 2019, 156, 1010-1015.	1.3	74
24	Multi-omic signature of body weight change: results from a population-based cohort study. <i>BMC Medicine</i> , 2015, 13, 48.	5.5	69
25	Molecular signature of different lesion types in the brain white matter of patients with progressive multiple sclerosis. <i>Acta Neuropathologica Communications</i> , 2019, 7, 205.	5.2	61
26	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60
27	Recent approaches to the prioritization of candidate disease genes. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 429-442.	6.6	59
28	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	1.4	55
29	Characterization of the EGFR interactome reveals associated protein complex networks and intracellular receptor dynamics. <i>Proteomics</i> , 2013, 13, 3131-3144.	2.2	54
30	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. <i>PLoS Computational Biology</i> , 2020, 16, e1007616.	3.2	54
31	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. <i>Scientific Reports</i> , 2017, 7, 14111.	3.3	51
32	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016, 99, 22-39.	6.2	50
33	<i>Helicobacter pylori</i> infection associates with fecal microbiota composition and diversity. <i>Scientific Reports</i> , 2019, 9, 20100.	3.3	49
34	The Gut Microbiome in Patients With Chronic Pancreatitis Is Characterized by Significant Dysbiosis and Overgrowth by Opportunistic Pathogens. <i>Clinical and Translational Gastroenterology</i> , 2020, 11, e00232.	2.5	49
35	Cohort profile: Greifswald approach to individualized medicine (GANI_MED). <i>Journal of Translational Medicine</i> , 2014, 12, 144.	4.4	43
36	Network medicine for disease module identification and drug repurposing with the NeDRex platform. <i>Nature Communications</i> , 2021, 12, 6848.	12.8	39

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37	The AIME registry for artificial intelligence in biomedical research. <i>Nature Methods</i> , 2021, 18, 1128-1131.	19.0	38
38	NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. <i>Bioinformatics</i> , 2013, 29, 1471-1473.	4.1	35
39	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. <i>Hypertension</i> , 2017, 70, 743-750.	2.7	34
40	A GWAS meta-analysis from 5 population-based cohorts implicates ion channel genes in the pathogenesis of irritable bowel syndrome. <i>Neurogastroenterology and Motility</i> , 2018, 30, e13358.	3.0	34
41	Plasma proteome and metabolome characterization of an experimental human thyrotoxicosis model. <i>BMC Medicine</i> , 2017, 15, 6.	5.5	30
42	DIGGER: exploring the functional role of alternative splicing in protein interactions. <i>Nucleic Acids Research</i> , 2021, 49, D309-D318.	14.5	30
43	MicroRNA analysis of gastroenteropancreatic neuroendocrine tumors and metastases. <i>Oncotarget</i> , 2018, 9, 28379-28390.	1.8	27
44	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.6	26
45	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and therapeutic target of an age-related hypertension endotype. <i>PLoS Biology</i> , 2020, 18, e3000885.	5.6	23
46	Carrying asymptomatic gallstones is not associated with changes in intestinal microbiota composition and diversity but cholecystectomy with significant dysbiosis. <i>Scientific Reports</i> , 2021, 11, 6677.	3.3	19
47	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw090.	6.5	17
48	Empowering thyroid hormone research in human subjects using OMICs technologies. <i>Journal of Endocrinology</i> , 2018, 238, R13-R29.	2.6	17
49	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019, 14, e0216222.	2.5	17
50	Measuring and analyzing tissue specificity of human genes and protein complexes. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2011, 2011, 5.	1.4	16
51	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016, 6, 35371.	3.3	15
52	BiCoN: network-constrained biclustering of patients and omics data. <i>Bioinformatics</i> , 2021, 37, 2398-2404.	4.1	15
53	Functional abdominal pain and discomfort (IBS) is not associated with faecal microbiota composition in the general population. <i>Gut</i> , 2019, 68, 1131.1-1133.	12.1	13
54	Importance of considering the growth response after partial harvesting and economic risk of discounted net revenues when optimizing uneven-aged forest management. <i>Canadian Journal of Forest Research</i> , 2020, 50, 487-499.	1.7	13

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73	Title is missing!. , 2020, 18, e3000885.		0
74	Title is missing!. , 2020, 18, e3000885.		0
75	Title is missing!. , 2020, 18, e3000885.		0
76	Title is missing!. , 2020, 18, e3000885.		0
77	Title is missing!. , 2020, 18, e3000885.		0
78	Title is missing!. , 2020, 18, e3000885.		0
79	Title is missing!. , 2020, 18, e3000885.		0