Tim Kacprowski

List of Publications by Year
in descending order

79	4,765	109264 35	118793 62
papers	citations	h-index	g-index

96	96	96	11122
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Robust disease module mining via enumeration of diverse prize-collecting Steiner trees. Bioinformatics, 2022, 38, 1600-1606.	1.8	10
2	Small RNA Sequencing in the Tg4â€“42 Mouse Model Suggests the Involvement of snoRNAs in the Etiology of Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2022, 87, 1671-1681.	1.2	2
3	A framework for modeling epistatic interaction. Bioinformatics, 2021, 37, 1708-1716.	1.8	5
4	Multi-Omics Analysis in a Network Context. , 2021, , 224-233.		1
5	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. Gut, 2021, 70, 522-530.	6.1	96
6	DIGGER: exploring the functional role of alternative splicing in protein interactions. Nucleic Acids Research, 2021, 49, D309-D318.	6.5	30
7	CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes. Scientific Reports, 2021, 11, 4132.	1.6	10
8	Enabling single-cell trajectory network enrichment. Nature Computational Science, 2021, 1, 153-163.	3.8	5
9	ASimulatoR: splice-aware RNA-Seq data simulation. Bioinformatics, 2021, 37, 3008-3010.	1.8	7
10	Carrying asymptomatic gallstones is not associated with changes in intestinal microbiota composition and diversity but cholecystectomy with significant dysbiosis. Scientific Reports, 2021, 11, 6677.	1.6	19
11	The AIMe registry for artificial intelligence in biomedical research. Nature Methods, 2021, 18, 1128-1131.	9.0	38
12	Network analysis methods for studying microbial communities: A mini review. Computational and Structural Biotechnology Journal, 2021, 19, 2687-2698.	1.9	130
13	BiCoN: network-constrained biclustering of patients and omics data. Bioinformatics, 2021, 37, 2398-2404.	1.8	15
14	Network medicine for disease module identification and drug repurposing with the NeDRex platform. Nature Communications, 2021, 12, 6848.	5.8	39
15	Functional enrichment of alternative splicing events with NEASE reveals insights into tissue identity and diseases. Genome Biology, 2021, 22, 327.	3.8	12
16	Importance of considering the growth response after partial harvesting and economic risk of discounted net revenues when optimizing uneven-aged forest management. Canadian Journal of Forest Research, 2020, 50, 487-499.	0.8	13
17	Association of proteome and metabolome signatures with severity in patients with community-acquired pneumonia. Journal of Proteomics, 2020, 214, 103627.	1.2	6
18	miRNA Alterations Elicit Pathways Involved in Memory Decline and Synaptic Function in the Hippocampus of Aged Tg4-42 Mice. Frontiers in Neuroscience, 2020, 14, 580524.	1.4	5

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19	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
20	Exploring the SARS-CoV-2 virus-host-drug interactome for drug repurposing. Nature Communications, 2020, 11, 3518.	5.8	144
21	Multiple Sclerosis Atlas: A Molecular Map of Brain Lesion Stages in Progressive Multiple Sclerosis. Network and Systems Medicine, 2020, 3, 122-129.	2.7	12
22	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
23	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
24	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. PLoS Computational Biology, 2020, 16, e1007616.	1.5	54
25	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. Nature Genetics, 2020, 52, 167-176.	9.4	101
26	EpiGEN: an epistasis simulation pipeline. Bioinformatics, 2020, 36, 4957-4959.	1.8	6
27	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype. PLoS Biology, 2020, 18, e3000885.	2.6	23
28	The Gut Microbiome in Patients With Chronic Pancreatitis Is Characterized by Significant Dysbiosis and Overgrowth by Opportunistic Pathogens. Clinical and Translational Gastroenterology, 2020, 11, e00232.	1.3	49
29	Title is missing!. , 2020, 18, e3000885.		0
30	Title is missing!. , 2020, 18, e3000885.		0
31	Title is missing!. , 2020, 18, e3000885.		0
32	Title is missing!. , 2020, 18, e3000885.		0
33	Title is missing!. , 2020, 18, e3000885.		0
34	Title is missing!. , 2020, 18, e3000885.		0
35	Title is missing!. , 2020, 18, e3000885.		0
36	Functional abdominal pain and discomfort (IBS) is not associated with faecal microbiota composition in the general population. Gut, 2019, 68, 1131.1-1133.	6.1	13

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37	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. Cell Host and Microbe, 2019, 26, 252-264.e10.	5.1	274
38	A structured weight loss program increases gut microbiota phylogenetic diversity and reduces levels of Collinsella in obese type 2 diabetics: A pilot study. PLoS ONE, 2019, 14, e0219489.	1.1	82
39	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
40	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	1.1	17
41	Impaired Exocrine Pancreatic Function Associates With Changes in Intestinal Microbiota Composition and Diversity. Gastroenterology, 2019, 156, 1010-1015.	0.6	74
42	Helicobacter pylori infection associates with fecal microbiota composition and diversity. Scientific Reports, 2019, 9, 20100.	1.6	49
43	Molecular signature of different lesion types in the brain white matter of patients with progressive multiple sclerosis. Acta Neuropathologica Communications, 2019, 7, 205.	2.4	61
44	Notions of similarity for systems biology models. Briefings in Bioinformatics, 2018, 19, bbw090.	3.2	17
45	A <scp>GWAS</scp> metaâ€analysis from 5 populationâ€based cohorts implicates ion channel genes in the pathogenesis of irritable bowel syndrome. Neurogastroenterology and Motility, 2018, 30, e13358.	1.6	34
46	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
47	Empowering thyroid hormone research in human subjects using OMICs technologies. Journal of Endocrinology, 2018, 238, R13-R29.	1.2	17
48	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. Microbiome, 2018, 6, 101.	4.9	109
49	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. Nature Communications, 2018, 9, 2397.	5.8	147
50	MicroRNA analysis of gastroenteropancreatic neuroendocrine tumors and metastases. Oncotarget, 2018, 9, 28379-28390.	0.8	27
51	Profiling and validation of circulating microRNAs for cardiovascular events in patients presenting with ST-segment elevation myocardial infarction. European Heart Journal, 2017, 38, ehw563.	1.0	77
52	Plasma proteome and metabolome characterization of an experimental human thyrotoxicosis model. BMC Medicine, 2017, 15, 6.	2.3	30
53	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	9.4	116
54	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. Scientific Reports, 2017, 7, 14111.	1.6	51

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55	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. Hypertension, 2017, 70, 743-750.	1.3	34
56	Exome Variant Analysis of Chronic Periodontitis in 2 Large Cohort Studies. Journal of Dental Research, 2017, 96, 73-80.	2.5	6
57	Gene Expression Profiling in the APP/PS1KI Mouse Model of Familial Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2016, 50, 397-409.	1.2	12
58	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
59	Gene transcripts associated with muscle strength: a CHARGE meta-analysis of 7,781 persons. Physiological Genomics, 2016, 48, 1-11.	1.0	11
60	Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior. Human Molecular Genetics, 2016, 25, ddw334.	1.4	107
61	Gene-gene Interaction Analyses for Atrial Fibrillation. Scientific Reports, 2016, 6, 35371.	1.6	15
62	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. Science Advances, 2016, 2, e1501678.	4.7	133
63	Transcriptome Alterations In X-Irradiated Human Gingiva Fibroblasts. Health Physics, 2016, 111, 75-84.	0.3	7
64	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
65	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	2.6	50
66	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	9.0	209
67	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55
68	Associations of circulating plasma microRNAs with age, body mass index and sex in a population-based study. BMC Medical Genomics, 2015, 8, 61.	0.7	133
69	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. PLoS Genetics, 2015, 11, e1005487.	1.5	83
70	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
71	Multi-omic signature of body weight change: results from a population-based cohort study. BMC Medicine, 2015, 13, 48.	2.3	69
72	Deciphering the Molecular Profile of Plaques, Memory Decline and Neuron Loss in Two Mouse Models for AlzheimerÃ¢â‚¬â„¢s Disease by Deep Sequencing. Frontiers in Aging Neuroscience, 2014, 6, 75.	1.7	78

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73	Cohort profile: Greifswald approach to individualized medicine (GANI_MED). Journal of Translational Medicine, 2014, 12, 144.	1.8	43
74	Characterization of the EGFR interactome reveals associated protein complex networks and intracellular receptor dynamics. Proteomics, 2013, 13, 3131-3144.	1.3	54
75	NetworkPrioritizer: a versatile tool for network-based prioritization of candidate disease genes or other molecules. Bioinformatics, 2013, 29, 1471-1473.	1.8	35
76	Recent approaches to the prioritization of candidate disease genes. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 429-442.	6.6	59
77	Measuring and analyzing tissue specificity of human genes and protein complexes. Eurasip Journal on Bioinformatics and Systems Biology, 2011, 2011, 5.	1.4	16
78	Molecular fingerprint of experimental thyrotoxicosis on human metabolism: combined metabolome and proteome study. Endocrine Abstracts, 0, , .	0.0	0
79	Coding Variant In <i>LEP</i> Associated with Lower Leptin Concentrations Implicates Leptin in the Regulation of Early Adiposity. SSRN Electronic Journal, 0, , .	0.4	0