

# Tim Becker

## List of Publications by Year in descending order

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Version: 2024-02-01

55  
papers

2,827  
citations

236925

25  
h-index

175258

52  
g-index

56  
all docs

56  
docs citations

56  
times ranked

5572  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessment of significance of conditionally independent GWAS signals. <i>Bioinformatics</i> , 2021, 37, 3521-3529.	4.1	1
2	Consistent Assignment of Risk and Benign Allele at rs2303153 in the CF Modifier Gene SCNN1B in Three Independent F508del-CFTR Homozygous Patient Populations. <i>Genes</i> , 2021, 12, 1554.	2.4	2
3	Prior fluid and electrolyte imbalance is associated with COVID-19 mortality. <i>Communications Medicine</i> , 2021, 1, .	4.2	12
4	The exhaustive genomic scan approach, with an application to rare-variant association analysis. <i>European Journal of Human Genetics</i> , 2020, 28, 1283-1291.	2.8	3
5	Genetic information from discordant sibling pairs points to ESRP2 as a candidate trans-acting regulator of the CF modifier gene SCNN1B. <i>Scientific Reports</i> , 2020, 10, 22447.	3.3	4
6	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. <i>Nature Communications</i> , 2017, 8, 14694.	12.8	58
7	Single nucleotide polymorphisms in the angiogenic and lymphangiogenic pathways are associated with lymphedema caused by <i>Wuchereria bancrofti</i> . <i>Human Genomics</i> , 2017, 11, 26.	2.9	17
8	Low-level <i>APC</i> mutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases. <i>Journal of Medical Genetics</i> , 2016, 53, 172-179.	3.2	51
9	Haplotype synthesis analysis reveals functional variants underlying known genome-wide associated susceptibility loci. <i>Bioinformatics</i> , 2016, 32, 2136-2142.	4.1	2
10	TREM2 rare variant p.R47H is not associated with Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2016, 23, 109-111.	2.2	17
11	Alzheimer's disease risk variants modulate endophenotypes in mild cognitive impairment. <i>Alzheimer's and Dementia</i> , 2016, 12, 872-881.	0.8	50
12	Association of age-of-onset groups with GWAS significant schizophrenia and bipolar disorder loci in Romanian bipolar I patients. <i>Psychiatry Research</i> , 2015, 230, 964-967.	3.3	11
13	The influence of genetic variants in SORL1 gene on the manifestation of Alzheimer's disease. <i>Neurobiology of Aging</i> , 2015, 36, 1605.e13-1605.e20.	3.1	27
14	Novel genetic matching methods for handling population stratification in genome-wide association studies. <i>BMC Bioinformatics</i> , 2015, 16, 84.	2.6	8
15	PLD3 in non-familial Alzheimer's disease. <i>Nature</i> , 2015, 520, E3-E5.	27.8	58
16	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.	0.8	173
17	ImmunoChip-Based Analysis: High-Density Genotyping of Immune-Related Loci Sheds Further Light on the Autoimmune Genetic Architecture of Alopecia Areata. <i>Journal of Investigative Dermatology</i> , 2015, 135, 919-921.	0.7	7
18	METAINTER: meta-analysis of multiple regression models in genome-wide association studies. <i>Bioinformatics</i> , 2015, 31, 151-157.	4.1	18

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19	SUCLG2 identified as both a determinant of CSF A $\beta$ 1-42 levels and an attenuator of cognitive decline in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2014, 23, 6644-6658.	2.9	45
20	The CF-modifying gene EHF promotes p.Phe508del-CFTR residual function by altering protein glycosylation and trafficking in epithelial cells. <i>European Journal of Human Genetics</i> , 2014, 22, 660-666.	2.8	26
21	Genome-wide association study reveals two new risk loci for bipolar disorder. <i>Nature Communications</i> , 2014, 5, 3339.	12.8	294
22	Genome-wide association study and mouse expression data identify a highly conserved 32 kb intergenic region between WNT3 and WNT9b as possible susceptibility locus for isolated classic exstrophy of the bladder. <i>Human Molecular Genetics</i> , 2014, 23, 5536-5544.	2.9	19
23	Investigation of the role of rare TREM2 variants in frontotemporal dementia subtypes. <i>Neurobiology of Aging</i> , 2014, 35, 2657.e13-2657.e19.	3.1	34
24	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e94661.	2.5	155
25	Androgenetic Alopecia: Identification of Four Genetic Risk Loci and Evidence for the Contribution of WNT Signaling to Its Etiology. <i>Journal of Investigative Dermatology</i> , 2013, 133, 1489-1496.	0.7	83
26	CLCA4 variants determine the manifestation of the cystic fibrosis basic defect in the intestine. <i>European Journal of Human Genetics</i> , 2013, 21, 691-694.	2.8	11
27	A One-Degree-of-Freedom Test for Supra-Multiplicativity of SNP Effects. <i>PLoS ONE</i> , 2013, 8, e78038.	2.5	2
28	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. <i>PLoS Genetics</i> , 2012, 8, e1002746.	3.5	92
29	Integrated Genome-Wide Pathway Association Analysis with INTERSNP. <i>Human Heredity</i> , 2012, 73, 63-72.	0.8	11
30	Quick, $\epsilon$ -Imputation-free meta-analysis with proxy-SNPs. <i>BMC Bioinformatics</i> , 2012, 13, 231.	2.6	7
31	Follow-Up Study of the First Genome-Wide Association Scan in Alopecia Areata: IL13 and KIAA0350 as Susceptibility Loci Supported with Genome-Wide Significance. <i>Journal of Investigative Dermatology</i> , 2012, 132, 2192-2197.	0.7	107
32	Significance Levels in Genome-Wide Interaction Analysis (GWIA). <i>Annals of Human Genetics</i> , 2011, 75, 29-35.	0.8	21
33	Genetic Variants in CTLA4 Are Strongly Associated with Alopecia Areata. <i>Journal of Investigative Dermatology</i> , 2011, 131, 1169-1172.	0.7	43
34	An association study on contrasting cystic fibrosis endophenotypes recognizes KRT8 but not KRT18 as a modifier of cystic fibrosis disease severity and CFTR mediated residual chloride secretion. <i>BMC Medical Genetics</i> , 2011, 12, 62.	2.1	15
35	Genes that determine immunology and inflammation modify the basic defect of impaired ion conductance in cystic fibrosis epithelia. <i>Journal of Medical Genetics</i> , 2011, 48, 24-31.	3.2	62
36	Initial interrogation, confirmation and fine mapping of modifying genes: STAT3, IL1B and IFNGR1 determine cystic fibrosis disease manifestation. <i>European Journal of Human Genetics</i> , 2011, 19, 1281-1288.	2.8	15

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37	Hierarchical fine mapping of the cystic fibrosis modifier locus on 19q13 identifies an association with two elements near the genes CEACAM3 and CEACAM6. <i>Human Genetics</i> , 2010, 127, 383-394.	3.8	12
38	Evaluation of Potential Power Gain with Imputed Genotypes in Genome-Wide Association Studies. <i>Human Heredity</i> , 2009, 68, 23-34.	0.8	3
39	INTERSNP: genome-wide interaction analysis guided by a priori information. <i>Bioinformatics</i> , 2009, 25, 3275-3281.	4.1	129
40	Joint analysis of tightly linked SNPs in screening step of genome-wide association studies leads to increased power. <i>European Journal of Human Genetics</i> , 2009, 17, 1043-1049.	2.8	17
41	Susceptibility variants for male-pattern baldness on chromosome 20p11. <i>Nature Genetics</i> , 2008, 40, 1279-1281.	21.4	119
42	Association study between genetic variants at the VAMP2 and VAMP3 loci and bipolar affective disorder. <i>Psychiatric Genetics</i> , 2008, 18, 199-203.	1.1	10
43	Transmission ratio distortion and maternal effects confound the analysis of modulators of cystic fibrosis disease severity on 19q13. <i>European Journal of Human Genetics</i> , 2007, 15, 774-778.	2.8	15
44	Identification of probable genotyping errors by consideration of haplotypes. <i>European Journal of Human Genetics</i> , 2006, 14, 450-458.	2.8	15
45	The TNF $\alpha$ receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in cystic fibrosis. <i>Human Genetics</i> , 2006, 119, 331-343.	3.8	43
46	Detection of Parent-of-Origin Effects in Nuclear Families Using Haplotype Analysis. <i>Human Heredity</i> , 2006, 62, 64-76.	0.8	15
47	Haplotype interaction analysis of unlinked regions. <i>Genetic Epidemiology</i> , 2005, 29, 313-322.	1.3	43
48	Impact of Missing Genotype Data on Monte-Carlo Simulation Based Haplotype Analysis. <i>Human Heredity</i> , 2005, 59, 185-189.	0.8	6
49	Genetic Variation in the Human Androgen Receptor Gene Is the Major Determinant of Common Early-Onset Androgenetic Alopecia. <i>American Journal of Human Genetics</i> , 2005, 77, 140-148.	6.2	198
50	Maximum-likelihood estimation of haplotype frequencies in nuclear families. <i>Genetic Epidemiology</i> , 2004, 27, 21-32.	1.3	191
51	Impact of Genotyping Errors on Type I Error Rate of the Haplotype-Sharing Transmission/Disequilibrium Test (HS-TDT). <i>American Journal of Human Genetics</i> , 2004, 74, 589-591.	6.2	33
52	A Powerful Strategy to Account for Multiple Testing in the Context of Haplotype Analysis. <i>American Journal of Human Genetics</i> , 2004, 75, 561-570.	6.2	153
53	The DTNBP1 (Dysbindin) Gene Contributes to Schizophrenia, Depending on Family History of the Disease. <i>American Journal of Human Genetics</i> , 2003, 73, 1438-1443.	6.2	180
54	Family-Based Association Analysis with Tightly Linked Markers. <i>Human Heredity</i> , 2003, 56, 2-9.	0.8	55

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55	Efficiency of Haplotype Frequency Estimation when Nuclear Family Information Is Included. Human Heredity, 2002, 54, 45-53.	0.8	29