Tim Becker

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5541198/publications.pdf

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55	2,827	236925	175258
papers	citations	25 h-index	52 g-index

56	56	56	5572
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339.	12.8	294
2	Genetic Variation in the Human Androgen Receptor Gene Is the Major Determinant of Common Early-Onset Androgenetic Alopecia. American Journal of Human Genetics, 2005, 77, 140-148.	6.2	198
3	Maximumâ€likelihood estimation of haplotype frequencies in nuclear families. Genetic Epidemiology, 2004, 27, 21-32.	1.3	191
4	The DTNBP1 (Dysbindin) Gene Contributes to Schizophrenia, Depending on Family History of the Disease. American Journal of Human Genetics, 2003, 73, 1438-1443.	6.2	180
5	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
6	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
7	A Powerful Strategy to Account for Multiple Testing in the Context of Haplotype Analysis. American Journal of Human Genetics, 2004, 75, 561-570.	6.2	153
8	INTERSNP: genome-wide interaction analysis guided by a priori information. Bioinformatics, 2009, 25, 3275-3281.	4.1	129
9	Susceptibility variants for male-pattern baldness on chromosome 20p11. Nature Genetics, 2008, 40, 1279-1281.	21.4	119
10	Follow-Up Study of the First Genome-Wide Association Scan in Alopecia Areata: IL13 and KIAA0350 as Susceptibility Loci Supported with Genome-Wide Significance. Journal of Investigative Dermatology, 2012, 132, 2192-2197.	0.7	107
11	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	3.5	92
12	Androgenetic Alopecia: Identification of Four Genetic Risk Loci and Evidence for the Contribution of WNT Signaling to Its Etiology. Journal of Investigative Dermatology, 2013, 133, 1489-1496.	0.7	83
13	Genes that determine immunology and inflammation modify the basic defect of impaired ion conductance in cystic fibrosis epithelia. Journal of Medical Genetics, 2011, 48, 24-31.	3.2	62
14	PLD3 in non-familial Alzheimer's disease. Nature, 2015, 520, E3-E5.	27.8	58
15	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. Nature Communications, 2017, 8, 14694.	12.8	58
16	Family-Based Association Analysis with Tightly Linked Markers. Human Heredity, 2003, 56, 2-9.	0.8	55
17	Low-levelAPCmutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases. Journal of Medical Genetics, 2016, 53, 172-179.	3.2	51
18	Alzheimer's disease risk variants modulate endophenotypes in mild cognitive impairment. Alzheimer's and Dementia, 2016, 12, 872-881.	0.8	50

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19	SUCLG2 identified as both a determinator of CSF AÎ²1â€“42 levels and an attenuator of cognitive decline in Alzheimer's disease. Human Molecular Genetics, 2014, 23, 6644-6658.	2.9	45
20	Haplotype interaction analysis of unlinked regions. Genetic Epidemiology, 2005, 29, 313-322.	1.3	43
21	The TNFÎ± receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in cystic fibrosis. Human Genetics, 2006, 119, 331-343.	3.8	43
22	Genetic Variants in CTLA4 Are Strongly Associated with Alopecia Areata. Journal of Investigative Dermatology, 2011, 131, 1169-1172.	0.7	43
23	Investigation of the role of rare TREM2 variants in frontotemporal dementia subtypes. Neurobiology of Aging, 2014, 35, 2657.e13-2657.e19.	3.1	34
24	Impact of Genotyping Errors on Type I Error Rate of the Haplotype-Sharing Transmission/Disequilibrium Test (HS-TDT). American Journal of Human Genetics, 2004, 74, 589-591.	6.2	33
25	Efficiency of Haplotype Frequency Estimation when Nuclear Familiy Information Is Included. Human Heredity, 2002, 54, 45-53.	0.8	29
26	The influence of genetic variants in SORL1 gene on the manifestation of Alzheimer's disease. Neurobiology of Aging, 2015, 36, 1605.e13-1605.e20.	3.1	27
27	The CF-modifying gene EHF promotes p.Phe508del-CFTR residual function by altering protein glycosylation and trafficking in epithelial cells. European Journal of Human Genetics, 2014, 22, 660-666.	2.8	26
28	Significance Levels in Genome-Wide Interaction Analysis (GWIA). Annals of Human Genetics, 2011, 75, 29-35.	0.8	21
29	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. Human Molecular Genetics, 2014, 23, 5536-5544.	2.9	19
30	METAINTER: meta-analysis of multiple regression models in genome-wide association studies. Bioinformatics, 2015, 31, 151-157.	4.1	18
31	Joint analysis of tightly linked SNPs in screening step of genome-wide association studies leads to increased power. European Journal of Human Genetics, 2009, 17, 1043-1049.	2.8	17
32	TREM2 rare variant p.R47H is not associated with Parkinson's disease. Parkinsonism and Related Disorders, 2016, 23, 109-111.	2.2	17
33	Single nucleotide polymorphisms in the angiogenic and lymphangiogenic pathways are associated with lymphedema caused by Wuchereria bancrofti. Human Genomics, 2017, 11, 26.	2.9	17
34	Identification of probable genotyping errors by consideration of haplotypes. European Journal of Human Genetics, 2006, 14, 450-458.	2.8	15
35	Detection of Parent-of-Origin Effects in Nuclear Families Using Haplotype Analysis. Human Heredity, 2006, 62, 64-76.	0.8	15
36	Transmission ratio distortion and maternal effects confound the analysis of modulators of cystic fibrosis disease severity on 19q13. European Journal of Human Genetics, 2007, 15, 774-778.	2.8	15

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37	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. BMC Medical Genetics, 2011, 12, 62.	2.1	15
38	Initial interrogation, confirmation and fine mapping of modifying genes: STAT3, IL1B and IFNGR1 determine cystic fibrosis disease manifestation. European Journal of Human Genetics, 2011, 19, 1281-1288.	2.8	15
39	Hierarchical fine mapping of the cystic fibrosis modifier locus on 19q13 identifies an association with two elements near the genes CEACAM3 and CEACAM6. Human Genetics, 2010, 127, 383-394.	3.8	12
40	Prior fluid and electrolyte imbalance is associated with COVID-19 mortality. Communications Medicine, 2021, 1, .	4.2	12
41	Integrated Genome-Wide Pathway Association Analysis with INTERSNP. Human Heredity, 2012, 73, 63-72.	0.8	11
42	CLCA4 variants determine the manifestation of the cystic fibrosis basic defect in the intestine. European Journal of Human Genetics, 2013, 21, 691-694.	2.8	11
43	Association of age-of-onset groups with GWAS significant schizophrenia and bipolar disorder loci in Romanian bipolar I patients. Psychiatry Research, 2015, 230, 964-967.	3.3	11
44	Association study between genetic variants at the VAMP2 and VAMP3 loci and bipolar affective disorder. Psychiatric Genetics, 2008, 18, 199-203.	1.1	10
45	Novel genetic matching methods for handling population stratification in genome-wide association studies. BMC Bioinformatics, 2015, 16, 84.	2.6	8
46	Quick, â€œImputation-freeâ€•meta-analysis with proxy-SNPs. BMC Bioinformatics, 2012, 13, 231.	2.6	7
47	Immunochip-Based Analysis: High-Density Genotyping of Immune-Related Loci Sheds Further Light on the Autoimmune Genetic Architecture of Alopecia Areata. Journal of Investigative Dermatology, 2015, 135, 919-921.	0.7	7
48	Impact of Missing Genotype Data on Monte-Carlo Simulation Based Haplotype Analysis. Human Heredity, 2005, 59, 185-189.	0.8	6
49	Genetic information from discordant sibling pairs points to ESRP2 as a candidate trans-acting regulator of the CF modifier gene SCNN1B. Scientific Reports, 2020, 10, 22447.	3.3	4
50	Evaluation of Potential Power Gain with Imputed Genotypes in Genome-Wide Association Studies. Human Heredity, 2009, 68, 23-34.	0.8	3
51	The exhaustive genomic scan approach, with an application to rare-variant association analysis. European Journal of Human Genetics, 2020, 28, 1283-1291.	2.8	3
52	A One-Degree-of-Freedom Test for Supra-Multiplicativity of SNP Effects. PLoS ONE, 2013, 8, e78038.	2.5	2
53	Haplotype synthesis analysis reveals functional variants underlying known genome-wide associated susceptibility loci. Bioinformatics, 2016, 32, 2136-2142.	4.1	2
54	Consistent Assignment of Risk and Benign Allele at rs2303153 in the CF Modifier Gene SCNN1B in Three Independent F508del-CFTR Homozygous Patient Populations. Genes, 2021, 12, 1554.	2.4	2

#	Article	IF	Citations
55	Assessment of significance of conditionally independent GWAS signals. Bioinformatics, 2021, 37, 3521-3529.	4.1	1