

Gary K Chen

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

3,451
citations

257101

24
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288905

40
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all docs

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docs citations

41
times ranked

7764
citing authors

#	ARTICLE	IF	CITATIONS
1	Determining reaction pathways at low temperatures by isotopic substitution: the case of $\text{BeD} + \text{H}_2\text{O}$. <i>New Journal of Physics</i> , 2021, 23, 115004.	1.2	4
2	Isomer-specific kinetics of the $\text{C} + \text{H}_2\text{O}$ reaction at the temperature of interstellar clouds. <i>Science Advances</i> , 2021, 7, .	4.7	16
3	Isotope-selective chemistry in the $\text{Be}(\text{S}) + \text{HOD}$ reaction. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 14005-14011.	1.3	14
4	Optical Control of Reactions between Water and Laser-Cooled Be^+ Ions. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 3555-3560.	2.1	37
5	Iterative hard thresholding for model selection in genome-wide association studies. <i>Genetic Epidemiology</i> , 2017, 41, 756-768.	0.6	6
6	Mapping adipose and muscle tissue expression quantitative trait loci in African Americans to identify genes for type 2 diabetes and obesity. <i>Human Genetics</i> , 2016, 135, 869-880.	1.8	44
7	cit: hypothesis testing software for mediation analysis in genomic applications. <i>Bioinformatics</i> , 2016, 32, 2364-2365.	1.8	42
8	Methodological Considerations in Estimation of Phenotype Heritability Using Genome-Wide SNP Data, Illustrated by an Analysis of the Heritability of Height in a Large Sample of African Ancestry Adults. <i>PLoS ONE</i> , 2015, 10, e0131106.	1.1	2
9	al3c: high-performance software for parameter inference using Approximate Bayesian Computation: Table 1.. <i>Bioinformatics</i> , 2015, 31, 3549-3551.	1.8	2
10	Convex Clustering: An Attractive Alternative to Hierarchical Clustering. <i>PLoS Computational Biology</i> , 2015, 11, e1004228.	1.5	34
11	A comprehensive examination of breast cancer risk loci in African American women. <i>Human Molecular Genetics</i> , 2014, 23, 5518-5526.	1.4	42
12	A genome-wide association study of breast cancer in women of African ancestry. <i>Human Genetics</i> , 2013, 132, 39-48.	1.8	70
13	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
14	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013, 45, 690-696.	9.4	232
15	Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation. <i>Bioinformatics</i> , 2013, 29, 1407-1415.	1.8	38
16	Precise inference of copy number alterations in tumor samples from SNP arrays. <i>Bioinformatics</i> , 2013, 29, 2964-2970.	1.8	12
17	A Genome-Wide Scan for Breast Cancer Risk Haplotypes among African American Women. <i>PLoS ONE</i> , 2013, 8, e57298.	1.1	20
18	Discovering epistasis in large scale genetic association studies by exploiting graphics cards. <i>Frontiers in Genetics</i> , 2013, 4, 266.	1.1	5

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19	Admixture mapping identifies a locus on 6q25 associated with breast cancer risk in US Latinas. <i>Human Molecular Genetics</i> , 2012, 21, 1907-1917.	1.4	60
20	A scalable and portable framework for massively parallel variable selection in genetic association studies. <i>Bioinformatics</i> , 2012, 28, 719-720.	1.8	8
21	Mendel-GPU: haplotyping and genotype imputation on graphics processing units. <i>Bioinformatics</i> , 2012, 28, 2979-2980.	1.8	11
22	Evaluating Genetic Risk for Prostate Cancer among Japanese and Latinos. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 2048-2058.	1.1	51
23	Common variants at 11q12, 10q26 and 3p11.2 are associated with prostate cancer susceptibility in Japanese. <i>Nature Genetics</i> , 2012, 44, 426-429.	9.4	98
24	Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , 2012, 44, 307-311.	9.4	372
25	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
26	Reproducibility, Performance, and Clinical Utility of a Genetic Risk Prediction Model for Prostate Cancer in Japanese. <i>PLoS ONE</i> , 2012, 7, e46454.	1.1	30
27	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor- α negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	9.4	279
28	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. <i>Nature Genetics</i> , 2011, 43, 570-573.	9.4	198
29	Enhancing the discovery of rare disease variants through hierarchical modeling. <i>BMC Proceedings</i> , 2011, 5, S16.	1.8	2
30	Incorporating biological information into association studies of sequencing data. <i>Genetic Epidemiology</i> , 2011, 35, S29-34.	0.6	4
31	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	13.7	319
32	Fine-mapping of breast cancer susceptibility loci characterizes genetic risk in African Americans. <i>Human Molecular Genetics</i> , 2011, 20, 4491-4503.	1.4	61
33	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARE and a Breast Cancer Consortium. <i>PLoS Genetics</i> , 2011, 7, e1001371.	1.5	110
34	Characterizing Genetic Risk at Known Prostate Cancer Susceptibility Loci in African Americans. <i>PLoS Genetics</i> , 2011, 7, e1001387.	1.5	117
35	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. <i>PLoS Genetics</i> , 2011, 7, e1002298.	1.5	93
36	Using biological knowledge to discover higher order interactions in genetic association studies. <i>Genetic Epidemiology</i> , 2010, 34, 863-878.	0.6	20

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37	The Potential for Enhancing the Power of Genetic Association Studies in African Americans through the Reuse of Existing Genotype Data. PLoS Genetics, 2010, 6, e1001096.	1.5	8
38	Fast and flexible simulation of DNA sequence data. Genome Research, 2009, 19, 136-142.	2.4	358
39	Enriching the Analysis of Genomewide Association Studies with Hierarchical Modeling. American Journal of Human Genetics, 2007, 81, 397-404.	2.6	82
40	Genome-wide association analyses of expression phenotypes. Genetic Epidemiology, 2007, 31, S7-S11.	0.6	0
41	Accommodating Chromosome Inversions in Linkage Analysis. American Journal of Human Genetics, 2006, 79, 238-251.	2.6	8