

Xiang-Yang Lou

List of Publications by Year in descending order

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27
papers

1,435
citations

535685

17
h-index

620720

26
g-index

27
all docs

27
docs citations

27
times ranked

1989
citing authors

#	ARTICLE	IF	CITATIONS
1	A Generalized Combinatorial Approach for Detecting Gene-by-Gene and Gene-by-Environment Interactions with Application to Nicotine Dependence. <i>American Journal of Human Genetics</i> , 2007, 80, 1125-1137.	2.6	533
2	Ethnic- and gender-specific association of the nicotinic acetylcholine receptor $\alpha 4$ subunit gene (CHRNA4) with nicotine dependence. <i>Human Molecular Genetics</i> , 2005, 14, 1211-1219.	1.4	182
3	A Combinatorial Approach to Detecting Gene-Gene and Gene-Environment Interactions in Family Studies. <i>American Journal of Human Genetics</i> , 2008, 83, 457-467.	2.6	90
4	A Genomewide Search Finds Major Susceptibility Loci for Nicotine Dependence on Chromosome 10 in African Americans. <i>American Journal of Human Genetics</i> , 2006, 79, 745-751.	2.6	68
5	Gene-Gene Interactions Among CHRNA4, CHRN2, BDNF, and NTRK2 in Nicotine Dependence. <i>Biological Psychiatry</i> , 2008, 64, 951-957.	0.7	60
6	Association and interaction analysis of variants in <i>CHRNA5/CHRNA3/CHRN4</i> gene cluster with nicotine dependence in African and European Americans. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 745-756.	1.1	53
7	Practical and Theoretical Considerations in Study Design for Detecting Gene-Gene Interactions Using MDR and GMDR Approaches. <i>PLoS ONE</i> , 2011, 6, e16981.	1.1	45
8	Association of Specific Haplotypes of Neurotrophic Tyrosine Kinase Receptor 2 Gene (NTRK2) with Vulnerability to Nicotine Dependence in African-Americans and European-Americans. <i>Biological Psychiatry</i> , 2007, 61, 48-55.	0.7	44
9	GMDR: Versatile Software for Detecting Gene-Gene and Gene-Environment Interactions Underlying Complex Traits. <i>Current Genomics</i> , 2016, 17, 396-402.	0.7	44
10	Gene-based analysis suggests association of the nicotinic acetylcholine receptor $\alpha 1$ subunit (CHRN1) and M1 muscarinic acetylcholine receptor (CHRM1) with vulnerability for nicotine dependence. <i>Human Genetics</i> , 2006, 120, 381-389.	1.8	43
11	Association and Interaction Analyses of GABBR1 and GABBR2 with Nicotine Dependence in European- and African-American Populations. <i>PLoS ONE</i> , 2009, 4, e7055.	1.1	40
12	A Haplotype-Based Algorithm for Multilocus Linkage Disequilibrium Mapping of Quantitative Trait Loci With Epistasis. <i>Genetics</i> , 2003, 163, 1533-1548.	1.2	40
13	Fine mapping of a linkage region on chromosome 17p13 reveals that GABARAP and DLG4 are associated with vulnerability to nicotine dependence in European-Americans. <i>Human Molecular Genetics</i> , 2007, 16, 142-153.	1.4	32
14	A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. <i>Human Genetics</i> , 2014, 133, 139-150.	1.8	23
15	A General Statistical Framework for Unifying Interval and Linkage Disequilibrium Mapping. <i>Journal of the American Statistical Association</i> , 2005, 100, 158-171.	1.8	20
16	Association analysis of the protein phosphatase 1 regulatory subunit 1B (PPP1R1B) gene with nicotine dependence in European- and African-American smokers. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007, 144B, 285-290.	1.1	19
17	The extent and distribution of linkage disequilibrium in a multi-hierarchic outbred canine pedigree. <i>Mammalian Genome</i> , 2003, 14, 555-564.	1.0	18
18	Multivariate Dimensionality Reduction Approaches to Identify Gene-Gene and Gene-Environment Interactions Underlying Multiple Complex Traits. <i>PLoS ONE</i> , 2014, 9, e108103.	1.1	18

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19	Association of amyloid precursor protein-binding protein, family B, member 1 with nicotine dependence in African and European American smokers. <i>Human Genetics</i> , 2008, 124, 393-398.	1.8	11
20	Generalized multifactor dimensionality reduction approaches to identification of genetic interactions underlying ordinal traits. <i>Genetic Epidemiology</i> , 2019, 43, 24-36.	0.6	11
21	A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. <i>Statistics and Its Interface</i> , 2011, 4, 295-304.	0.2	11
22	Analysis of genetic effects of major genes and polygenes on quantitative traits. II. Genetic models for seed traits of crops. <i>Theoretical and Applied Genetics</i> , 2002, 105, 964-971.	1.8	10
23	Improvement of Mapping Accuracy by Unifying Linkage and Association Analysis. <i>Genetics</i> , 2006, 172, 647-661.	1.2	8
24	A new mapping method for quantitative trait loci of silkworm. <i>BMC Genetics</i> , 2011, 12, 19.	2.7	7
25	Estimating effects of a single gene and polygenes on quantitative traits from a diallel design. <i>Genetica</i> , 2006, 128, 471-484.	0.5	3
26	Conditional and unconditional genome-wide association study reveal complicate genetic architecture of human body weight and impacts of smoking. <i>Scientific Reports</i> , 2020, 10, 12136.	1.6	2
27	Gene-Gene and Gene-Environment Interactions Underlying Complex Traits and their Detection. <i>Biometrics & Biostatistics International Journal</i> , 2014, 1, .	0.2	0