Shaoqi Rao

List of Publications by Year
in descending order

78 papers	2,896 citations	236833 25 h-index	168321 53 g-index
80 all docs	80 docs citations	80 times ranked	3919 citing authors

#	Article	IF	Citations
1	Identification of an angiogenic factor that when mutated causes susceptibility to Klippelâ€“Trenaunay syndrome. Nature, 2004, 427, 640-645.	13.7	289
2	Premature Myocardial Infarction Novel Susceptibility Locus on Chromosome 1P34-36 Identified by Genomewide Linkage Analysis. American Journal of Human Genetics, 2004, 74, 262-271.	2.6	195
3	Genomewide Linkage Scan Identifies a Novel Susceptibility Locus for Restless Legs Syndrome on Chromosome 9p. American Journal of Human Genetics, 2004, 74, 876-885.	2.6	186
4	Four SNPs on Chromosome 9p21 in a South Korean Population Implicate a Genetic Locus That Confers High Cross-Race Risk for Development of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 360-365.	1.1	183
5	Short-term Outcomes of Induction Therapy With Tacrolimus Versus Cyclophosphamide for Active Lupus Nephritis: A Multicenter Randomized Clinical Trial. American Journal of Kidney Diseases, 2011, 57, 235-244.	2.1	169
6	Towards precise classification of cancers based on robust gene functional expression profiles. BMC Bioinformatics, 2005, 6, 58.	1.2	146
7	Edge-based scoring and searching method for identifying condition-responsive protein protein interaction sub-network. Bioinformatics, 2007, 23, 2121-2128.	1.8	139
8	Genome-Wide Linkage Scan Identifies a Novel Genetic Locus on Chromosome 5p13 for Neonatal Atrial Fibrillation Associated With Sudden Death and Variable Cardiomyopathy. Circulation, 2004, 110, 3753-3759.	1.6	114
9	A robust hybrid between genetic algorithm and support vector machine for extracting an optimal feature gene subset. Genomics, 2005, 85, 16-23.	1.3	112
10	Association between four SNPs on chromosome 9p21 and myocardial infarction is replicated in an Italian population. Journal of Human Genetics, 2008, 53, 144-150.	1.1	112
11	DOSim: An R package for similarity between diseases based on Disease Ontology. BMC Bioinformatics, 2011, 12, 266.	1.2	88
12	Gene mining: a novel and powerful ensemble decision approach to hunting for disease genes using microarray expression profiling. Nucleic Acids Research, 2004, 32, 2685-2694.	6.5	85
13	An LRP8 Variant Is Associated with Familial and Premature Coronary Artery Disease and Myocardial Infarction. American Journal of Human Genetics, 2007, 81, 780-791.	2.6	77
14	Behavioural development of school-aged children who live around a multi-metal sulphide mine in Guangdong province, China: a cross-sectional study. BMC Public Health, 2009, 9, 217.	1.2	69
15	Psychometric properties of the Chinese version of the Pediatric Quality of Life Inventoryâ„¢ 4.0 generic core scales. Quality of Life Research, 2010, 19, 1229-1233.	1.5	68
16	Constructing disease-specific gene networks using pair-wise relevance metric: Application to colon cancer identifies interleukin 8, desmin and enolase 1 as the central elements. BMC Systems Biology, 2008, 2, 72.	3.0	64
17	Discovery of Time-Delayed Gene Regulatory Networks based on temporal gene expression profiling. BMC Bioinformatics, 2006, 7, 26.	1.2	60
18	Mapping quantitative trait loci for ordered categorical traits in four-way crosses. Heredity, 1998, 81, 214-224.	1.2	58

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19	Molecular Basis of Gene-Gene Interaction: Cyclic Cross-Regulation of Gene Expression and Post-GWAS Gene-Gene Interaction Involved in Atrial Fibrillation. PLoS Genetics, 2015, 11, e1005393.	1.5	47
20	Genomic Scan Reveals Loci under Altitude Adaptation in Tibetan and Dahe Pigs. PLoS ONE, 2014, 9, e110520.	1.1	42
21	Effects of replacing the unreliable cDNA microarray measurements on the disease classification based on gene expression profiles and functional modules. Bioinformatics, 2006, 22, 2883-2889.	1.8	36
22	Longitudinal data analysis in pedigree studies. Genetic Epidemiology, 2003, 25, S18-S28.	0.6	32
23	Genome-Wide Association and Functional Studies Identify SCML4 and THSD7A as Novel Susceptibility Genes for Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 964-975.	1.1	32
24	Adaptation of the Audit of Diabetes-Dependent Quality of Life questionnaire to people with diabetes in China. Diabetes Research and Clinical Practice, 2011, 94, 45-52.	1.1	31
25	Atorvastatin Treatment of Rats with Ischemia-Reperfusion Injury Improves Adipose-Derived Mesenchymal Stem Cell Migration and Survival via the SDF-1Î±/CXCR-4 Axis. PLoS ONE, 2013, 8, e79100.	1.1	27
26	Efficacy of Atorvastatin combined with adipose-derived mesenchymal stem cell transplantation on cardiac function in rats with acute myocardial infarction. Acta Biochimica Et Biophysica Sinica, 2011, 43, 857-866.	0.9	26
27	SDF-1Î± upregulation by atorvastatin in rats with acute myocardial infarction via nitric oxide production confers anti-inflammatory and anti-apoptotic effects. Journal of Biomedical Science, 2012, 19, 99.	2.6	24
28	Association of DRD3, COMT, and SLC6A4 Gene Polymorphisms with Type 2 Diabetes in Southern Chinese: A Hospital-Based Caseâ€“Control Study. Diabetes Technology and Therapeutics, 2015, 17, 580-586.	2.4	24
29	Joint Effects of Genetic Variants in Multiple Loci on the Risk of Coronary Artery Disease in Chinese Han Subjects. Circulation Journal, 2012, 76, 1987-1992.	0.7	21
30	A Novel Molecular Diagnostic Marker for Familial and Early-Onset Coronary Artery Disease and Myocardial Infarction in the LRP8 Gene. Circulation: Cardiovascular Genetics, 2014, 7, 514-520.	5.1	21
31	Strategies for genetic mapping of categorical traits. Genetica, 2000, 109, 183-197.	0.5	20
32	Ala499Val (C > T) and Lys939Gln (A > C) polymorphisms of the XPC gene: their correlation with the risk of primary gallbladder adenocarcinoma--a case-control study in China. Carcinogenesis, 2011, 32, 496-501.	1.3	18
33	Plasma oxidized low-density lipoprotein is an independent risk factor in young patients with coronary artery disease. Disease Markers, 2011, 31, 295-301.	0.6	17
34	Linkage of chromosome 1 markers to alcoholismâ€related phenotypes by sib pair linkage analysis of principal components. Genetic Epidemiology, 1999, 17, S271-6.	0.6	16
35	Lack of association between four SNPs in the SLC22A3-LPAL2-LPA gene cluster and coronary artery disease in a Chinese Han population: a case control study. Lipids in Health and Disease, 2012, 11, 128.	1.2	15
36	Knowledge-based analysis of genetic associations of rheumatoid arthritis to inform studies searching for pleiotropic genes: a literature review and network analysis. Arthritis Research and Therapy, 2015, 17, 202.	1.6	14

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37	Plasma Oxidized Low-Density Lipoprotein Is an Independent Risk Factor in Young Patients with Coronary Artery Disease. Disease Markers, 2011, 31, 295-301.	0.6	14
38	Miscues on the "lack of MEF2A mutations" in coronary artery disease. Journal of Clinical Investigation, 2005, 115, 1399-1400.	3.9	14
39	A systematic method for mapping multiple loci: An application to construct a genetic network for rheumatoid arthritis. Gene, 2008, 408, 104-111.	1.0	13
40	A genome-wide linkage scan identifies multiple quantitative trait loci for HDL-cholesterol levels in families with premature CAD and MI. Journal of Lipid Research, 2010, 51, 1442-1451.	2.0	11
41	Brief communication: Yâ€chromosome haplogroup analysis indicates that Chinese Tuvans share distinctive affinity with Siberian Tuvans. American Journal of Physical Anthropology, 2011, 144, 492-497.	2.1	11
42	Identifying functional modules for coronary artery disease by a prior knowledge-based approach. Gene, 2014, 537, 260-268.	1.0	11
43	Locating the Genes Underlying a Simulated Complex Disease by Discriminant Analysis. Genetic Epidemiology, 2001, 21, S516-S521.	0.6	10
44	Widely predicting specific protein functions based on protein-protein interaction data and gene expression profile. Science in China Series C: Life Sciences, 2007, 50, 125-134.	1.3	10
45	Phenotypeâ€“Genotype Correlation in 295 Chinese Deaf Subjects with Biallelic Causative Mutations in the GJB2 Gene. Genetic Testing and Molecular Biomarkers, 2011, 15, 619-625.	0.3	10
46	Functional Homogeneity in microRNA Target Heterogeneityâ€”a New Sight into Human microRNomics. OMICS A Journal of Integrative Biology, 2011, 15, 25-35.	1.0	10
47	Disease embryo development network reveals the relationship between disease genes and embryo development genes. Journal of Theoretical Biology, 2011, 287, 100-108.	0.8	9
48	Genome-Wide Linkage Scan Identifies Two Novel Genetic Loci for Coronary Artery Disease: In GeneQuest Families. PLoS ONE, 2014, 9, e113935.	1.1	8
49	Unravelling the hidden heterogeneities of diffuse large B-cell lymphoma based on coupled two-way clustering. BMC Genomics, 2007, 8, 332.	1.2	7
50	Stratified meta-analysis by ethnicity revealed that ADRB3 Trp64Arg polymorphism was associated with coronary artery disease in Asians, but not in Caucasians. Medicine (United States), 2020, 99, e18914.	0.4	7
51	Multivariate sib-pair linkage analysis of longitudinal phenotypes by three step-wise analysis approaches. BMC Genetics, 2003, 4, S68.	2.7	6
52	Reply to Ray and Weeks: Linkage for Restless Legs Syndrome on Chromosome 9p Is Significant. American Journal of Human Genetics, 2005, 76, 707-710.	2.6	6
53	Pathway-based Analysis of the Hidden Genetic Heterogeneities in Cancers. Genomics, Proteomics and Bioinformatics, 2014, 12, 31-38.	3.0	6
54	Association Between Apolipoprotein B XbaI Polymorphism and Coronary Heart Disease in Han Chinese Population: A Meta-Analysis. Genetic Testing and Molecular Biomarkers, 2016, 20, 304-311.	0.3	6

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55	An ensemble method for gene discovery based on DNA mi-croarray data. Science in China Series C: Life Sciences, 2004, 47, 396.	1.3	6
56	A Seven-Long Non-coding RNA Signature Improves Prognosis Prediction of Lung Adenocarcinoma: An Integrated Competing Endogenous RNA Network Analysis. Frontiers in Genetics, 2020, 11, 625977.	1.1	5
57	Genetic linkage analysis of longitudinal hypertension phenotypes using three summary measures. BMC Genetics, 2003, 4, S24.	2.7	4
58	On the Significance of Linkage Studies of Complex Traits: Reply to Newton-Cheh et al.. American Journal of Human Genetics, 2004, 75, 152-154.	2.6	4
59	Identifying disease feature genes based on cellular localized gene functional modules and regulation networks. Science Bulletin, 2006, 51, 1848-1856.	1.7	3
60	Cell cycle-dependent gene networks relevant to cancer. Progress in Natural Science: Materials International, 2008, 18, 945-952.	1.8	3
61	Association between rs10118757(A/G) in methylthioadenosine phosphorylase gene and coronary artery disease in Chinese Hans. Gene, 2013, 526, 344-346.	1.0	3
62	To Control False Positives in Gene-Gene Interaction Analysis: Two Novel Conditional Entropy-Based Approaches. PLoS ONE, 2013, 8, e81984.	1.1	3
63	SAGE Programs. Methods in Molecular Medicine, 2006, , 61-89.	0.8	3
64	A novel model-free approach for reconstruction of time-delayed gene regulatory networks. Science in China Series C: Life Sciences, 2006, 49, 190-200.	1.3	2
65	Association between apolipoprotein B EcoRI polyï»¿morï»¿phisms and coronary heart disease. Wiener Klinische Wochenschrift, 2016, 128, 890-897.	1.0	2
66	SAGE Programs: Model-Free Linkage Analysis for Complex Cardiovascular Phenotypes. , 2006, 128, 61-90.		2
67	Data mining of RNA expression and DNA genotype data: Presentation Group 5 contributions to Genetic Analysis Workshop 15. Genetic Epidemiology, 2007, 31, S43-S50.	0.6	1
68	A feature ensemble technology to identify molecular mechanisms for distinction between multiple subtypes of lymphoma. Progress in Natural Science: Materials International, 2008, 18, 1491-1500.	1.8	1
69	Mapping and characterization of two relevance networks from SNP and gene levels. Progress in Natural Science: Materials International, 2009, 19, 653-657.	1.8	1
70	Effects of cutoff thresholds for minor allele frequencies on HapMap resolution: A real dataset-based evaluation of the Chinese Han and Tibetan populations. Science Bulletin, 2009, 54, 2069-2075.	4.3	1
71	Complex Segregation Analysis Provides Evidence for Autosomal Dominant Transmission in the Chinese Han Families with Ankylosing Spondylitis. BioMed Research International, 2017, 2017, 1-6.	0.9	1
72	A Novel Evolution-Based Method for Detecting Gene-Gene Interactions. PLoS ONE, 2011, 6, e26435.	1.1	1

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73	Analysis of Sib-Pair IBD Profiles and Genomic Context for Identification of the Relevant Molecular Signatures for Alcoholism. Lecture Notes in Computer Science, 2005, , 845-851.	1.0	1
74	Large-Scale Ensemble Decision Analysis of Sib-Pair IBD Profiles for Identification of the Relevant Molecular Signatures for Alcoholism. Lecture Notes in Computer Science, 2005, , 1184-1189.	1.0	1
75	A Novel Ensemble Decision Tree Approach for Mining Genes Coding Ion Channels for Cardiopathy Subtype. Lecture Notes in Computer Science, 2005, , 852-860.	1.0	1
76	A Novel Feature Ensemble Technology to Improve Prediction Performance of Multiple Heterogeneous Phenotypes Based on Microarray Data. Lecture Notes in Computer Science, 2005, , 869-879.	1.0	0
77	Analysis of Sib-Pair IBD Profiles Using Ensemble Decision Tree Approach: Application to Alcoholism. Lecture Notes in Computer Science, 2006, , 774-779.	1.0	0
78	Association Research on Potassium Channel Subtypes and Functional Sites. Lecture Notes in Computer Science, 2006, , 780-785.	1.0	0