

Chuan-Xing Li

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,006
citations

777949

13
h-index

591227

27
g-index

38
all docs

38
docs citations

38
times ranked

1923
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiomics integration-based molecular characterizations of COVID-19. Briefings in Bioinformatics, 2022, 23, .	3.2	24
2	Impact on physical and mental health among medical personnel in Wuhan during COVID-19 outbreak: a cluster analysis. International Journal of Medical Sciences, 2021, 18, 1185-1188.	1.1	4
3	MicroRNA miR-24-3p reduces DNA damage responses, apoptosis, and susceptibility to chronic obstructive pulmonary disease. JCI Insight, 2021, 6, .	2.3	16
4	Baseline characteristics and survival of patients of idiopathic pulmonary fibrosis: a longitudinal analysis of the Swedish IPF Registry. Respiratory Research, 2021, 22, 40.	1.4	36
5	Editorial: Omics Data Integration Towards Mining of Phenotype Specific Biomarkers in Cancers and Diseases. Frontiers in Cell and Developmental Biology, 2021, 9, 763447.	1.8	1
6	Smoking-associated increase in mucins 1 and 4 in human airways. Respiratory Research, 2020, 21, 239.	1.4	11
7	<p>Sputum Vitamin D Binding Protein (VDBP) GC1S/1S Genotype Predicts Airway Obstruction: A Prospective Study in Smokers with COPD</p>. International Journal of COPD, 2020, Volume 15, 1049-1059.	0.9	9
8	The unsynchronized changes of CT image and nucleic acid detection in COVID-19: reports the two cases from Gansu, China. Respiratory Research, 2020, 21, 96.	1.4	10
9	Sputum Vitamin D binding protein (VDBP) GC1S/1S genotype predicts airway obstruction: a prospective study in smokers with COPD. , 2020, , .		0
10	Baseline characteristics and survival of patients with idiopathic pulmonary fibrosis (IPF): analysis from the Swedish IPF registry. , 2020, , .		1
11	Profiling of airway epithelial proteome reveals sex differences in early stage COPD linked to xenobiotic metabolism and ER stress. , 2020, , .		1
12	MiRNA-mRNA-protein network integration reveals dysregulation of oxidative stress and apoptosis in smoking-induced COPD in women. , 2020, , .		0
13	Integration of multi-omics datasets enables molecular classification of COPD. European Respiratory Journal, 2018, 51, 1701930.	3.1	83
14	U-BIOPRED accessible handprint: combining omics platforms to identify stable asthma subphenotypes. , 2018, , .		2
15	Integration at the network- and pathway level of multi-omics data from multiple anatomical locations facilitate COPD sub-phenotyping in small cohorts. , 2017, , .		0
16	LSC Abstract “ Prediction of COPD- and smoking status by network-based multi-'omics data fusion analysis. , 2016, , .		0
17	Correlation between gene expression and mutator phenotype predicts homologous recombination deficiency and outcome in ovarian cancer. Journal of Molecular Medicine, 2014, 92, 1159-1168.	1.7	31
18	Systematic large-scale study of the inheritance mode of Mendelian disorders provides new insight into human disease. European Journal of Human Genetics, 2014, 22, 1260-1267.	1.4	4

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19	Global gene expression distribution in non-cancerous complex diseases. <i>Molecular BioSystems</i> , 2014, 10, 728-731.	2.9	5
20	Network-based analysis of genotype-phenotype correlations between different inheritance modes. <i>Bioinformatics</i> , 2014, 30, 3223-3231.	1.8	5
21	Dissection of the potential characteristic of miRNA-miRNA functional synergistic regulations. <i>Molecular BioSystems</i> , 2013, 9, 217-224.	2.9	23
22	Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. <i>FEBS Letters</i> , 2013, 587, 976-982.	1.3	16
23	Revisiting the variation of clustering coefficient of biological networks suggests new modular structure. <i>BMC Systems Biology</i> , 2012, 6, 34.	3.0	33
24	Characterization and Evolution of microRNA Genes Derived from Repetitive Elements and Duplication Events in Plants. <i>PLoS ONE</i> , 2012, 7, e34092.	1.1	41
25	MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. <i>Nucleic Acids Research</i> , 2011, 39, 825-836.	6.5	245
26	Disease-driven detection of differential inherited SNP modules from SNP network. <i>Gene</i> , 2011, 489, 119-129.	1.0	8
27	The Dichotomy in Degree Correlation of Biological Networks. <i>PLoS ONE</i> , 2011, 6, e28322.	1.1	35
28	Prioritizing Candidate Disease miRNAs by Topological Features in the miRNA Target-Dysregulated Network: Case Study of Prostate Cancer. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 1857-1866.	1.9	216
29	Novel strategies to mine alcoholism-related haplotypes and genes by combining existing knowledge framework. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 163-172.	1.3	3
30	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. <i>BMC Systems Biology</i> , 2008, 2, 72.	3.0	64
31	A feature ensemble technology to identify molecular mechanisms for distinction between multiple subtypes of lymphoma. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 1491-1500.	1.8	1
32	A systematic method for mapping multiple loci: An application to construct a genetic network for rheumatoid arthritis. <i>Gene</i> , 2008, 408, 104-111.	1.0	13
33	Single-nucleotide polymorphism-gene intermixed networking reveals co-linkers connected to multiple gene expression phenotypes. <i>BMC Proceedings</i> , 2007, 1, S45.	1.8	2
34	A novel model-free approach for reconstruction of time-delayed gene regulatory networks. <i>Science in China Series C: Life Sciences</i> , 2006, 49, 190-200.	1.3	2
35	Discovery of Time-Delayed Gene Regulatory Networks based on temporal gene expression profiling. <i>BMC Bioinformatics</i> , 2006, 7, 26.	1.2	60
36	Novel strategies to identify relevant molecular signatures for complex human diseases based on data of identical-by-decent profiles and genomic context. <i>Beijing Da Xue Xue Bao</i> , 2006, 38, 74-7.	0.2	0