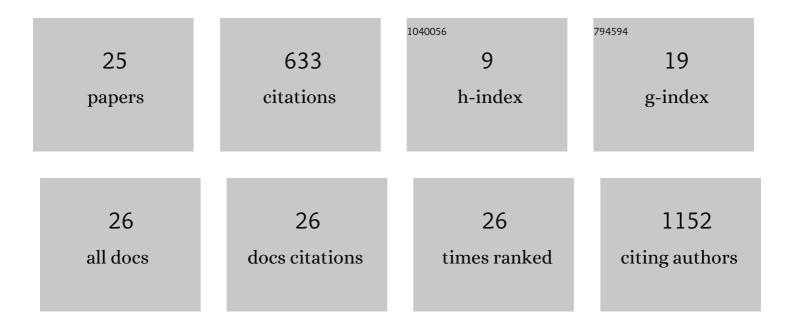
Guangjian Liu

List of Publications by Year in descending order

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GUANCHAN LUI

#	Article	IF	CITATIONS
1	A proposed artificial intelligence workflow to address application challenges leveraged on algorithm uncertainty. IScience, 2022, 25, 103961.	4.1	3
2	Identifying the Key Residues Regulating the Binding between Antibody Avelumab and PD-L1 VIA Molecular Dynamics Simulation. , 2021, , .		1
3	Molecular Dynamics Simulation to Investigate the Blockade Mechanism of Anti-PD-1 Antibody Toripalimab. , 2021, , .		0
4	Unsupervised Hierarchical Clustering Identifies Immune Gene Subtypes in Gastric Cancer. Frontiers in Pharmacology, 2021, 12, 692454.	3.5	11
5	Unsupervised Clustering Reveals Distinct Subtypes of Biliary Atresia Based on Immune Cell Types and Gene Expression. Frontiers in Immunology, 2021, 12, 720841.	4.8	10
6	Characterization of the interactions of ADAMTS13 CUB1 domain to WT- and GOF-Spacer domain by molecular dynamics simulation. Journal of Molecular Graphics and Modelling, 2021, 109, 108029.	2.4	2
7	Machine learning identifies girls with central precocious puberty based on multisource data. JAMIA Open, 2021, 3, 567-575.	2.0	5
8	in Silico Analysis to Map Epitope to Paratope Residues of Anti-PD-L1 Antibody BMS-936559. , 2021, , .		0
9	Residues R1075, D1090, R1095, and C1130 Are Critical in ADAMTS13 TSP8-Spacer Interaction Predicted by Molecular Dynamics Simulation. Molecules, 2021, 26, 7525.	3.8	0
10	Network analysis of autistic disease comorbidities in Chinese children based on ICD-10 codes. BMC Medical Informatics and Decision Making, 2020, 20, 268.	3.0	6
11	Machine Learning Algorithms Identify Pathogen-Specific Biomarkers of Clinical and Metabolomic Characteristics in Septic Patients with Bacterial Infections. BioMed Research International, 2020, 2020, 1-11.	1.9	9
12	Investigating the Role of the N-Terminal Loop of PD-1 in Binding Process Between PD-1 and Nivolumab via Molecular Dynamics Simulation. Frontiers in Molecular Biosciences, 2020, 7, 574759.	3.5	6
13	In-hospital Mortality Prediction for ICU Patients on Large Healthcare MIMIC Datasets Using Class Imbalance Learning. , 2020, , .		4
14	Insights into pathological mutations in insulin-like growth factor I through in silico screening and molecular dynamics simulation. Journal of Molecular Modeling, 2019, 25, 276.	1.8	1
15	Middle-term bowel function and quality of life in low-type anorectal malformation. Italian Journal of Pediatrics, 2019, 45, 98.	2.6	9
16	Accuracy Comparison Between Age-Adapted SOFA and SIRS in Predicting in-Hospital Mortality of Infected Children at China's PICU. Shock, 2019, 52, 347-352.	2.1	12
17	Evaluation and accurate diagnoses of pediatric diseases using artificial intelligence. Nature Medicine, 2019, 25, 433-438.	30.7	386
18	Development of Prediction Models Using Machine Learning Algorithms for Girls with Suspected Central Precocious Puberty: Retrospective Study. JMIR Medical Informatics, 2019, 7, e11728.	2.6	27

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#	Article	IF	CITATIONS
19	Establishment of an induced pluripotent stem cell model of Hirschsrpung disease, a congenital condition of the enteric nervous system, from a patient carrying a novel RET mutation. NeuroReport, 2018, 29, 975-980.	1.2	1
20	Phenotype Prediction of Pathogenic Nonsynonymous Single Nucleotide Polymorphisms in Insulin with Bioinformatics Tools. , 2018, , .		0
21	Bioinformatics analysis of <i>CYP1B1</i> mutation hotspots in Chinese primary congenital glaucoma patients. Bioscience Reports, 2018, 38, .	2.4	9
22	Molecular dynamics simulations elucidate conformational selection and induced fit mechanisms in the binding of PD-1 and PD-L1. Molecular BioSystems, 2017, 13, 892-900.	2.9	35
23	Machine learning applications for prediction of relapse in childhood acute lymphoblastic leukemia. Scientific Reports, 2017, 7, 7402.	3.3	68
24	Developing a Machine Learning System for Identification of Severe Hand, Foot, and Mouth Disease from Electronic Medical Record Data. Scientific Reports, 2017, 7, 16341.	3.3	17
25	Mapping Paratope on Antithrombotic Antibody 6B4 to Epitope on Platelet Glycoprotein Ibalpha via Molecular Dynamic Simulations. PLoS ONE, 2012, 7, e42263.	2.5	11