

Peng Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5329256/publications.pdf>

Version: 2024-02-01

43
papers

6,907
citations

236833

25
h-index

265120

42
g-index

47
all docs

47
docs citations

47
times ranked

12092
citing authors

#	ARTICLE	IF	CITATIONS
1	Autoantibodies against type I IFNs in patients with life-threatening COVID-19. <i>Science</i> , 2020, 370, .	6.0	1,983
2	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. <i>Science</i> , 2020, 370, .	6.0	1,749
3	Therapeutic target database update 2018: enriched resource for facilitating bench-to-clinic research of targeted therapeutics. <i>Nucleic Acids Research</i> , 2018, 46, D1121-D1127.	6.5	462
4	Therapeutic target database update 2012: a resource for facilitating target-oriented drug discovery. <i>Nucleic Acids Research</i> , 2012, 40, D1128-D1136.	6.5	459
5	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. <i>Science Immunology</i> , 2021, 6, .	5.6	267
6	Human genetic and immunological determinants of critical COVID-19 pneumonia. <i>Nature</i> , 2022, 603, 587-598.	13.7	216
7	NPASS: natural product activity and species source database for natural product research, discovery and tool development. <i>Nucleic Acids Research</i> , 2018, 46, D1217-D1222.	6.5	177
8	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. <i>Science Translational Medicine</i> , 2021, 13, eabh2624.	5.8	155
9	Therapeutic target database update 2014: a resource for targeted therapeutics. <i>Nucleic Acids Research</i> , 2014, 42, D1118-D1123.	6.5	116
10	The risk of COVID-19 death is much greater and age dependent with type I IFN autoantibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2200413119.	3.3	110
11	SARS-CoV-2-related MIS-C: A key to the viral and genetic causes of Kawasaki disease?. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	100
12	SVM-Prot 2016: A Web-Server for Machine Learning Prediction of Protein Functional Families from Sequence Irrespective of Similarity. <i>PLoS ONE</i> , 2016, 11, e0155290.	1.1	98
13	Human T-bet Governs Innate and Innate-like Adaptive IFN- γ Immunity against Mycobacteria. <i>Cell</i> , 2020, 183, 1826-1847.e31.	13.5	83
14	Human SNORA31 variations impair cortical neuron-intrinsic immunity to HSV-1 and underlie herpes simplex encephalitis. <i>Nature Medicine</i> , 2019, 25, 1873-1884.	15.2	76
15	Recent progresses in the exploration of machine learning methods as in-silico ADME prediction tools. <i>Advanced Drug Delivery Reviews</i> , 2015, 86, 83-100.	6.6	69
16	CMAUP: a database of collective molecular activities of useful plants. <i>Nucleic Acids Research</i> , 2019, 47, D1118-D1127.	6.5	68
17	Inherited PD-1 deficiency underlies tuberculosis and autoimmunity in a child. <i>Nature Medicine</i> , 2021, 27, 1646-1654.	15.2	65
18	Herpes simplex encephalitis in a patient with a distinctive form of inherited IFNAR1 deficiency. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	64

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19	TLR3 controls constitutive IFN- $\hat{2}$ antiviral immunity in human fibroblasts and cortical neurons. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	64
20	PopViz: a webserver for visualizing minor allele frequencies and damage prediction scores of human genetic variations. <i>Bioinformatics</i> , 2018, 34, 4307-4309.	1.8	55
21	Inherited IFNAR1 Deficiency in a Child with Both Critical COVID-19 Pneumonia and Multisystem Inflammatory Syndrome. <i>Journal of Clinical Immunology</i> , 2022, 42, 471-483.	2.0	44
22	De novo variants in exomes of congenital heart disease patients identify risk genes and pathways. <i>Genome Medicine</i> , 2020, 12, 9.	3.6	43
23	PROFEAT Update: A Protein Features Web Server with Added Facility to Compute Network Descriptors for Studying Omics-Derived Networks. <i>Journal of Molecular Biology</i> , 2017, 429, 416-425.	2.0	36
24	A protein network descriptor server and its use in studying protein, disease, metabolic and drug targeted networks. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw071.	3.2	34
25	Biochemically deleterious human <i>NFKB1</i> variants underlie an autosomal dominant form of common variable immunodeficiency. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	32
26	Biological Network Approaches and Applications in Rare Disease Studies. <i>Genes</i> , 2019, 10, 797.	1.0	30
27	Human <i>STAT3</i> variants underlie autosomal dominant hyper-IgE syndrome by negative dominance. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	30
28	Multibatch Cytometry Data Integration for Optimal Immunophenotyping. <i>Journal of Immunology</i> , 2021, 206, 206-213.	0.4	25
29	Human OTULIN haploinsufficiency impairs cell-intrinsic immunity to staphylococcal $\hat{1}\pm$ -toxin. <i>Science</i> , 2022, 376, eabm6380.	6.0	25
30	Monoclonal antibody-mediated neutralization of SARS-CoV-2 in an IRF9-deficient child. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
31	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	21
32	Clustered Distribution of Natural Product Leads of Drugs in the Chemical Space as Influenced by the Privileged Target-Sites. <i>Scientific Reports</i> , 2015, 5, 9325.	1.6	20
33	Database and Bioinformatics Studies of Probiotics. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 7599-7606.	2.4	18
34	The Assessment of the Readiness of Molecular Biomarker-Based Mobile Health Technologies for Healthcare Applications. <i>Scientific Reports</i> , 2015, 5, 17854.	1.6	15
35	SeqTailor: a user-friendly webserver for the extraction of DNA or protein sequences from next-generation sequencing data. <i>Nucleic Acids Research</i> , 2019, 47, W623-W631.	6.5	15
36	Discovery of novel dual VEGFR2 and Src inhibitors using a multistep virtual screening approach. <i>Future Medicinal Chemistry</i> , 2017, 9, 7-24.	1.1	11

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37	CFam: a chemical families database based on iterative selection of functional seeds and seed-directed compound clustering. <i>Nucleic Acids Research</i> , 2015, 43, D558-D565.	6.5	6
38	A computational approach for detecting physiological homogeneity in the midst of genetic heterogeneity. <i>American Journal of Human Genetics</i> , 2021, 108, 1012-1025.	2.6	6
39	Towards cheminformatics-based estimation of drug therapeutic index: Predicting the protective index of anticonvulsants using a new quantitative structure-index relationship approach. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 67, 102-110.	1.3	3
40	Protein music of enhanced musicality by music style guided exploration of diverse amino acid properties. <i>Heliyon</i> , 2021, 7, e07933.	1.4	3
41	HEROD: a human ethnic and regional specific omics database. <i>Bioinformatics</i> , 2017, 33, 3276-3282.	1.8	3
42	Pharmacological relationships and ligand discovery of G protein-coupled receptors revealed by simultaneous ligand and receptor clustering. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 76, 136-142.	1.3	1
43	A Resource for Facilitating the Development of Tools in the Education and Implementation of Genomics-Informed Personalized Medicine. <i>Clinical Pharmacology and Therapeutics</i> , 2014, 95, 590-591.	2.3	0