

# Hai Fang

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

5,915  
citations

186265

28  
h-index

133252

59  
g-index

68  
all docs

68  
docs citations

68  
times ranked

12315  
citing authors

#	ARTICLE	IF	CITATIONS
1	Priority index: database of genetic targets in immune-mediated disease. <i>Nucleic Acids Research</i> , 2022, 50, D1358-D1367.	14.5	16
2	Hepatitis B virus-associated follicular lymphoma presents T <sub>H</sub> 1 cell inflamed phenotype and response to lenalidomide. <i>Cancer Communications</i> , 2022, 42, 170-174.	9.2	3
3	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. <i>Cell</i> , 2022, 185, 916-938.e58.	28.9	164
4	Genomic Evidence Supports the Recognition of Endometriosis as an Inflammatory Systemic Disease and Reveals Disease-Specific Therapeutic Potentials of Targeting Neutrophil Degranulation. <i>Frontiers in Immunology</i> , 2022, 13, 758440.	4.8	10
5	Oncogenic Mutations and Tumor Microenvironment Alterations of Older Patients With Diffuse Large B-Cell Lymphoma. <i>Frontiers in Immunology</i> , 2022, 13, 842439.	4.8	5
6	Transcriptome-wide subtyping of pediatric and adult T cell acute lymphoblastic leukemia in an international study of 707 cases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2120787119.	7.1	18
7	PiER: web-based facilities tailored for genetic target prioritisation harnessing human disease genetics, functional genomics and protein interactions. <i>Nucleic Acids Research</i> , 2022, 50, W583-W592.	14.5	5
8	Epigenomic analysis reveals a dynamic and context-specific macrophage enhancer landscape associated with innate immune activation and tolerance. <i>Genome Biology</i> , 2022, 23, .	8.8	9
9	A PML/RAR $\alpha$ direct target atlas redefines transcriptional deregulation in acute promyelocytic leukemia. <i>Blood</i> , 2021, 137, 1503-1516.	1.4	47
10	Transcriptomic Analysis of Inflammatory Cardiomyopathy Identifies Molecular Signatures of Disease and Informs in silico Prediction of a Network-Based Rationale for Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 640837.	4.8	3
11	Integration of Genomic and Transcriptomic Markers Improves the Prognosis Prediction of Acute Promyelocytic Leukemia. <i>Clinical Cancer Research</i> , 2021, 27, 3683-3694.	7.0	16
12	Integrating longitudinal clinical laboratory tests with targeted proteomic and transcriptomic analyses reveal the landscape of host responses in COVID-19. <i>Cell Discovery</i> , 2021, 7, 42.	6.7	23
13	Genetic Prioritization, Therapeutic Repositioning and Cross-Disease Comparisons Reveal Inflammatory Targets Tractable for Kidney Stone Disease. <i>Frontiers in Immunology</i> , 2021, 12, 687291.	4.8	6
14	Genomic Insights into Myasthenia Gravis Identify Distinct Immunological Mechanisms in Early and Late Onset Disease. <i>Annals of Neurology</i> , 2021, 90, 455-463.	5.3	8
15	Genetic Interaction Network Interpretation: A Tidy Data Science Perspective. <i>Methods in Molecular Biology</i> , 2021, 2212, 347-376.	0.9	0
16	Distinct immune signatures discriminate between asymptomatic and presymptomatic SARS-CoV-2pos subjects. <i>Cell Research</i> , 2021, 31, 1148-1162.	12.0	12
17	Identification of copy number variation-driven molecular subtypes informative for prognosis and treatment in pancreatic adenocarcinoma of a Chinese cohort. <i>EBioMedicine</i> , 2021, 74, 103716.	6.1	14
18	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. <i>Lancet Rheumatology</i> , The, 2020, 2, e50-e62.	3.9	17

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19	Identifying collagen VI as a target of fibrotic diseases regulated by CREBBP/EP300. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20753-20763.	7.1	45
20	Peripheral CD8+ T cell characteristics associated with durable responses to immune checkpoint blockade in patients with metastatic melanoma. Nature Medicine, 2020, 26, 193-199.	30.7	211
21	A genetics-led approach defines the drug target landscape of 30 immune-related traits. Nature Genetics, 2019, 51, 1082-1091.	21.4	157
22	The association between endometriosis and autoimmune diseases: a systematic review and meta-analysis. Human Reproduction Update, 2019, 25, 486-503.	10.8	179
23	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
24	I3: A Self-organising Learning Workflow for Intuitive Integrative Interpretation of Complex Genetic Data. Genomics, Proteomics and Bioinformatics, 2019, 17, 503-510.	6.9	2
25	Regulatory Genomic Data Cubism. IScience, 2018, 3, 217-225.	4.1	2
26	Genome-wide studies identify a novel interplay between AML1 and AML1/ETO in t(8;21) acute myeloid leukemia. Blood, 2016, 127, 233-242.	1.4	44
27	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
28	Evolution of the Calcium-Based Intracellular Signaling System. Genome Biology and Evolution, 2016, 8, 2118-2132.	2.5	35
29	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. Genome Medicine, 2016, 8, 129.	8.2	137
30	A predictive computational framework for direct reprogramming between human cell types. Nature Genetics, 2016, 48, 331-335.	21.4	263
31	Function-selective domain architecture plasticity potentials in eukaryotic genome evolution. Biochimie, 2015, 119, 269-277.	2.6	5
32	The SUPERFAMILY 1.75 database in 2014: a doubling of data. Nucleic Acids Research, 2015, 43, D227-D233.	14.5	74
33	A proteome quality index. Environmental Microbiology, 2015, 17, 4-9.	3.8	6
34	A Derived Network-Based Interferon-Related Signature of Human Macrophages Responding to Mycobacterium tuberculosis. BioMed Research International, 2014, 2014, 1-16.	1.9	3
35	dcGOR: An R Package for Analysing Ontologies and Protein Domain Annotations. PLoS Computational Biology, 2014, 10, e1003929.	3.2	18
36	The Evolution of Human Cells in Terms of Protein Innovation. Molecular Biology and Evolution, 2014, 31, 1364-1374.	8.9	13

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37	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
38	The $\delta$ net <sup>TM</sup> approach promotes emerging research on cancer patient survival. <i>Genome Medicine</i> , 2014, 6, 64.	8.2	52
39	Sequential transcriptional changes dictate safe and effective antigen-specific immunotherapy. <i>Nature Communications</i> , 2014, 5, 4741.	12.8	147
40	supraHex: An R/Bioconductor package for tabular omics data analysis using a supra-hexagonal map. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 285-289.	2.1	37
41	The $\delta$ net <sup>v2</sup> approach promotes emerging research on cancer patient survival. <i>Genome Medicine</i> , 2014, 6, 64.	8.2	25
42	Reactive oxygen species in eradicating acute myeloid leukemic stem cells. <i>Stem Cell Investigation</i> , 2014, 1, 13.	3.0	20
43	A domain-centric solution to functional genomics via dcGO Predictor. <i>BMC Bioinformatics</i> , 2013, 14, S9.	2.6	42
44	A disease-drug-phenotype matrix inferred by walking on a functional domain network. <i>Molecular BioSystems</i> , 2013, 9, 1686.	2.9	10
45	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
46	A daily-updated tree of (sequenced) life as a reference for genome research. <i>Scientific Reports</i> , 2013, 3, 2015.	3.3	47
47	Endoplasmic reticulum stress-mediated apoptosis in imatinib-resistant leukemic K562-r cells triggered by AMN107 combined with arsenic trioxide. <i>Experimental Biology and Medicine</i> , 2013, 238, 932-942.	2.4	13
48	Preferential eradication of acute myelogenous leukemia stem cells by fenretinide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5606-5611.	7.1	49
49	dcGO: database of domain-centric ontologies on functions, phenotypes, diseases and more. <i>Nucleic Acids Research</i> , 2013, 41, D536-D544.	14.5	98
50	An Interferon-Related Signature in the Transcriptional Core Response of Human Macrophages to <i>Mycobacterium tuberculosis</i> Infection. <i>PLoS ONE</i> , 2012, 7, e38367.	2.5	29
51	An organogenesis network-based comparative transcriptome analysis for understanding early human development in vivo and in vitro. <i>BMC Systems Biology</i> , 2011, 5, 108.	3.0	2
52	A Topology-Preserving Selection and Clustering Approach to Multidimensional Biological Data. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 483-494.	2.0	6
53	SUPERFAMILY 1.75 including a domain-centric gene ontology method. <i>Nucleic Acids Research</i> , 2011, 39, D427-D434.	14.5	147
54	p21-Activated kinase 3 is overexpressed in thymic neuroendocrine tumors (carcinoids) with ectopic ACTH syndrome and participates in cell migration. <i>Endocrine</i> , 2010, 38, 38-47.	2.3	33

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55	PML/RAR $\alpha$ Targets Promoter Regions Containing PU.1 Consensus and RARE Half Sites in Acute Promyelocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 186-197.	16.8	143
56	Transcriptome Analysis of Early Organogenesis in Human Embryos. <i>Developmental Cell</i> , 2010, 19, 174-184.	7.0	69
57	Converting Redox Signaling to Apoptotic Activities by Stress-Responsive Regulators HSF1 and NRF2 in Fenretinide Treated Cancer Cells. <i>PLoS ONE</i> , 2009, 4, e7538.	2.5	34
58	Connecting Biological Themes Using a Single Human Network of Gene Associations. , 2009, , .		0
59	Gene expression profiles of thymic neuroendocrine tumors (carcinoids) with ectopic ACTH syndrome reveal novel molecular mechanism. <i>Endocrine-Related Cancer</i> , 2009, 16, 1273-1282.	3.1	22
60	Transcriptome and Proteome Analyses of Drug Interactions with Natural Products. <i>Current Drug Metabolism</i> , 2008, 9, 1038-1048.	1.2	18
61	Coordination of Fenretinide-Induced Apoptosis by Stress-Responsive Regulators in Leukemia Cells. <i>Blood</i> , 2008, 112, 4730-4730.	1.4	0
62	A Probabilistic Integrated Gene Network Model of Multiple Hematopoietic Lineage Specification. <i>Blood</i> , 2008, 112, 4767-4767.	1.4	0
63	Coordination of intrinsic, extrinsic, and endoplasmic reticulum-mediated apoptosis by imatinib mesylate combined with arsenic trioxide in chronic myeloid leukemia. <i>Blood</i> , 2006, 107, 1582-1590.	1.4	91
64	Coordination of Intrinsic, Extrinsic and Endoplasmic Reticulum-Mediated Apoptosis by Imatinib Mesylate Combined with Arsenic Trioxide in Chronic Myeloid Leukemia.. <i>Blood</i> , 2005, 106, 4841-4841.	1.4	0
65	Using Self-Organizing Maps to Visualize, Filter and Cluster Multidimensional Bio-Omics Data. , 0, , .		4
66	Identification of Copy Number Variation-Driven Molecular Subtypes in Pancreatic Adenocarcinoma of Chinese Cohort. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0