

Yang Li

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

110
papers

8,258
citations

34
h-index

90
g-index

131
ext. papers

11,211
ext. citations

13.6
avg, IF

5.26
L-index

#	Paper	IF	Citations
110	Single-cell RNA sequencing reveals induction of distinct trained immunity programs in human monocytes.. <i>Journal of Clinical Investigation</i> , 2022 ,	15.9	2
109	Type 2 Diabetes-Related Variants Influence the Risk of Developing Prostate Cancer: A Population-Based Case-Control Study and Meta-Analysis. <i>Cancers</i> , 2022 , 14, 2376	6.6	1
108	IRF7 and RNH1 are modifying factors of HIV-1 reservoirs: a genome-wide association analysis. <i>BMC Medicine</i> , 2021 , 19, 282	11.4	2
107	An integrative genomics approach identifies KDM4 as a modulator of trained immunity. <i>European Journal of Immunology</i> , 2021 ,	6.1	1
106	Induction of trained immunity by influenza vaccination - impact on COVID-19. <i>PLoS Pathogens</i> , 2021 , 17, e1009928	7.6	12
105	Validation of GWAS-Identified Variants for Anti-TNF Drug Response in Rheumatoid Arthritis: A Meta-Analysis of Two Large Cohorts. <i>Frontiers in Immunology</i> , 2021 , 12, 672255	8.4	1
104	Impact of HBsAg and HBcAg levels on phenotype and function of HBV-specific T cells in patients with chronic hepatitis B virus infection. <i>Gut</i> , 2021 ,	19.2	3
103	Prosaposin mediates inflammation in atherosclerosis. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	7
102	Resolving trained immunity with systems biology. <i>European Journal of Immunology</i> , 2021 , 51, 773-784	6.1	6
101	Potential impact of celiac disease genetic risk factors on T cell receptor signaling in gluten-specific CD4+ T cells. <i>Scientific Reports</i> , 2021 , 11, 9252	4.9	3
100	Data of common and species-specific transcriptional host responses to pathogenic fungi. <i>Data in Brief</i> , 2021 , 35, 106928	1.2	2
99	A fetal wave of human type 3 effector T cells with restricted TCR diversity persists into adulthood. <i>Science Immunology</i> , 2021 , 6,	28	8
98	Immune memory in individuals with COVID-19. <i>Nature Cell Biology</i> , 2021 , 23, 582-584	23.4	4
97	Multi-Omics Approaches in Immunological Research. <i>Frontiers in Immunology</i> , 2021 , 12, 668045	8.4	2
96	Common gene variants within 3' untranslated regions as modulators of multiple myeloma risk and survival. <i>International Journal of Cancer</i> , 2021 , 148, 1887-1894	7.5	1
95	Shared DNA methylation signatures in childhood allergy: The MeDALL study. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 1031-1040	11.5	5
94	Identification of Novel Population-Specific Cell Subsets in Chinese Ulcerative Colitis Patients Using Single-Cell RNA Sequencing. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021 , 12, 99-117	7.9	4

93	Comparative host transcriptome in response to pathogenic fungi identifies common and species-specific transcriptional antifungal host response pathways. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 647-663	6.8	4
92	Thyrotrophin and thyroxine support immune homeostasis in humans. <i>Immunology</i> , 2021 , 163, 155-168	7.8	5
91	COVID-19 immune signatures reveal stable antiviral T cell function despite declining humoral responses. <i>Immunity</i> , 2021 , 54, 340-354.e6	32.3	87
90	Integration of metabolomics, genomics, and immune phenotypes reveals the causal roles of metabolites in disease. <i>Genome Biology</i> , 2021 , 22, 198	18.3	6
89	Inflammatory Protein Profiles in Plasma of Candidaemia Patients and the Contribution of Host Genetics to Their Variability. <i>Frontiers in Immunology</i> , 2021 , 12, 662171	8.4	2
88	Evolution of cytokine production capacity in ancient and modern European populations. <i>ELife</i> , 2021 , 10,	8.9	7
87	Circulating miRNAs as Potential Biomarkers for Celiac Disease Development.. <i>Frontiers in Immunology</i> , 2021 , 12, 734763	8.4	2
86	CRELD1 modulates homeostasis of the immune system in mice and humans. <i>Nature Immunology</i> , 2020 , 21, 1517-1527	19.1	3
85	Sex-Specific Regulation of Inflammation and Metabolic Syndrome in Obesity. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020 , 40, 1787-1800	9.4	29
84	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. <i>BMC Bioinformatics</i> , 2020 , 21, 243	3.6	15
83	BCG Vaccination in Humans Elicits Trained Immunity via the Hematopoietic Progenitor Compartment. <i>Cell Host and Microbe</i> , 2020 , 28, 322-334.e5	23.4	119
82	Platelet Integrin α IIb β 3 Activation is Associated with 25-Hydroxyvitamin D Concentrations in Healthy Adults. <i>Thrombosis and Haemostasis</i> , 2020 , 120, 768-775	7	1
81	NFKB2 polymorphisms associate with the risk of developing rheumatoid arthritis and response to TNF inhibitors: Results from the REPAIR consortium. <i>Scientific Reports</i> , 2020 , 10, 4316	4.9	7
80	Tissue alarmins and adaptive cytokine induce dynamic and distinct transcriptional responses in tissue-resident intraepithelial cytotoxic T lymphocytes. <i>Journal of Autoimmunity</i> , 2020 , 108, 102422	15.5	7
79	Rewiring of glucose metabolism defines trained immunity induced by oxidized low-density lipoprotein. <i>Journal of Molecular Medicine</i> , 2020 , 98, 819-831	5.5	29
78	Polymorphisms within the and Loci Influence the Risk of Developing Invasive Aspergillosis: A Two-Stage Case Control Study in the Context of the aspBIOmics Consortium. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020 , 7,	5.6	1
77	Reprogramming of bone marrow myeloid progenitor cells in patients with severe coronary artery disease. <i>ELife</i> , 2020 , 9,	8.9	5
76	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. <i>Nature Communications</i> , 2020 , 11, 4930	17.4	8

75	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020 , 53, 1296-1314.e9	32.3	109
74	Multi-omics examination of Q fever fatigue syndrome identifies similarities with chronic fatigue syndrome. <i>Journal of Translational Medicine</i> , 2020 , 18, 448	8.5	9
73	Host immune genetic variations influence the risk of developing acute myeloid leukaemia: results from the NuCLEAR consortium. <i>Blood Cancer Journal</i> , 2020 , 10, 75	7	1
72	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020 , 182, 1419-1440.e236.2	36.2	558
71	The Set7 Lysine Methyltransferase Regulates Plasticity in Oxidative Phosphorylation Necessary for Trained Immunity Induced by β -Glucan. <i>Cell Reports</i> , 2020 , 31, 107548	10.6	34
70	Systematic Prioritization of Candidate Genes in Disease Loci Identifies a Master Regulator of IFN β Signaling in Celiac Disease. <i>Frontiers in Genetics</i> , 2020 , 11, 562434	4.5	9
69	Soluble immune markers in the different phases of chronic hepatitis B virus infection. <i>Scientific Reports</i> , 2019 , 9, 14118	4.9	5
68	A Genome-Wide Functional Genomics Approach Identifies Susceptibility Pathways to Fungal Bloodstream Infection in Humans. <i>Journal of Infectious Diseases</i> , 2019 , 220, 862-872	7	13
67	Steroid hormone-related polymorphisms associate with the development of bone erosions in rheumatoid arthritis and help to predict disease progression: Results from the REPAIR consortium. <i>Scientific Reports</i> , 2019 , 9, 14812	4.9	4
66	Leukocyte-Released Mediators in Response to Both Bacterial and Fungal Infections Trigger IFN Pathways, Independent of IL-1 and TNF- α in Endothelial Cells. <i>Frontiers in Immunology</i> , 2019 , 10, 2508	8.4	5
65	Role of Glutamine Metabolism in Host Defense Against Mycobacterium tuberculosis Infection. <i>Journal of Infectious Diseases</i> , 2019 , 219, 1662-1670	7	16
64	The Itaconate Pathway Is a Central Regulatory Node Linking Innate Immune Tolerance and Trained Immunity. <i>Cell Metabolism</i> , 2019 , 29, 211-220.e5	24.6	141
63	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. <i>Lancet Respiratory Medicine</i> , 2018 , 6, 379-388	35.1	119
62	Tissue Metabolic Changes Drive Cytokine Responses to Mycobacterium tuberculosis. <i>Journal of Infectious Diseases</i> , 2018 , 218, 165-170	7	11
61	Cerebral tryptophan metabolism and outcome of tuberculous meningitis: an observational cohort study. <i>Lancet Infectious Diseases</i> , 2018 , 18, 526-535	25.5	46
60	Metabolic Induction of Trained Immunity through the Mevalonate Pathway. <i>Cell</i> , 2018 , 172, 135-146.e9	56.2	314
59	Western Diet Triggers NLRP3-Dependent Innate Immune Reprogramming. <i>Cell</i> , 2018 , 172, 162-175.e14	56.2	435
58	TNF-Induced protein 3 (TNFAIP3)/A20 acts as a master switch in TNF-blockade-driven IL-17A expression. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 142, 517-529	11.5	22

57	BCG Vaccination Protects against Experimental Viral Infection in Humans through the Induction of Cytokines Associated with Trained Immunity. <i>Cell Host and Microbe</i> , 2018 , 23, 89-100.e5	23.4	537
56	The effects of signal transducer and activator of transcription three mutations on human platelets. <i>Platelets</i> , 2018 , 29, 602-609	3.6	1
55	Identification of Discriminating Metabolic Pathways and Metabolites in Human PBMCs Stimulated by Various Pathogenic Agents. <i>Frontiers in Physiology</i> , 2018 , 9, 139	4.6	2
54	Running-wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a post-transcriptional mechanism. <i>Aging Cell</i> , 2018 , 17, e12700	9.9	22
53	The Inter-Relationship of Platelets with Interleukin-1EMediated Inflammation in Humans. <i>Thrombosis and Haemostasis</i> , 2018 , 118, 2112-2125	7	19
52	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. <i>Nature Immunology</i> , 2018 , 19, 776-786	19.1	63
51	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. <i>Science Immunology</i> , 2017 , 2,	28	28
50	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017 , 49, 131-138	36.3	252
49	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240
48	The emerging landscape of dynamic DNA methylation in early childhood. <i>BMC Genomics</i> , 2017 , 18, 25	4.5	32
47	reGenotyper: Detecting mislabeled samples in genetic data. <i>PLoS ONE</i> , 2017 , 12, e0171324	3.7	13
46	An integrative genomics approach identifies novel pathways that influence candidaemia susceptibility. <i>PLoS ONE</i> , 2017 , 12, e0180824	3.7	17
45	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. <i>Cell Reports</i> , 2016 , 17, 2474-2487	10.6	100
44	Functional and Genomic Architecture of <i>Borrelia burgdorferi</i> -Induced Cytokine Responses in Humans. <i>Cell Host and Microbe</i> , 2016 , 20, 822-833	23.4	27
43	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. <i>Cell</i> , 2016 , 167, 1099-1110.e14	56.2	163
42	Host and Environmental Factors Influencing Individual Human Cytokine Responses. <i>Cell</i> , 2016 , 167, 1111-1124.e13	56.2	163
41	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016 , 68, 62-74	15.5	44
40	Understanding Celiac Disease by Genomics. <i>Trends in Genetics</i> , 2016 , 32, 295-308	8.5	50

39	Correlation Trait Loci (CTL) mapping: phenotype network inference subject to genotype. <i>Journal of Open Source Software</i> , 2016 , 1, 87	5.2	3
38	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. <i>Nature Medicine</i> , 2016 , 22, 952-60	50.5	106
37	Autophagy suppresses host adaptive immune responses toward <i>Borrelia burgdorferi</i> . <i>Journal of Leukocyte Biology</i> , 2016 , 100, 589-98	6.5	6
36	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016 , 48, 1407-1412	36.3	434
35	Understanding human immune function using the resources from the Human Functional Genomics Project. <i>Nature Medicine</i> , 2016 , 22, 831-3	50.5	43
34	Pheno2Geno - High-throughput generation of genetic markers and maps from molecular phenotypes for crosses between inbred strains. <i>BMC Bioinformatics</i> , 2015 , 16, 51	3.6	6
33	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
32	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. <i>Human Molecular Genetics</i> , 2015 , 24, 397-409	5.6	43
31	mTOR- and HIF-1 β -mediated aerobic glycolysis as metabolic basis for trained immunity. <i>Science</i> , 2014 , 345, 1250684	33.3	1020
30	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. <i>Genome Medicine</i> , 2014 , 6, 88	14.4	79
29	WormQTLHD--a web database for linking human disease to natural variation data in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2014 , 42, D794-801	20.1	18
28	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013 , 45, 1238-1243	36.3	1244
27	Identifying genotype-by-environment interactions in the metabolism of germinating arabidopsis seeds using generalized genetical genomics. <i>Plant Physiology</i> , 2013 , 162, 553-66	6.6	37
26	WormQTL--public archive and analysis web portal for natural variation data in <i>Caenorhabditis</i> spp. <i>Nucleic Acids Research</i> , 2013 , 41, D738-43	20.1	27
25	Global genetic robustness of the alternative splicing machinery in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2010 , 186, 405-10	4	43
24	Critical reasoning on causal inference in genome-wide linkage and association studies. <i>Trends in Genetics</i> , 2010 , 26, 493-8	8.5	47
23	Expression quantitative trait loci are highly sensitive to cellular differentiation state. <i>PLoS Genetics</i> , 2009 , 5, e1000692	6	74
22	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. <i>BMC Bioinformatics</i> , 2009 , 10, 188	3.6	6

21	Generalizing genetical genomics: getting added value from environmental perturbation. <i>Trends in Genetics</i> , 2008 , 24, 518-24	8.5	33
20	Genetical genomics: spotlight on QTL hotspots. <i>PLoS Genetics</i> , 2008 , 4, e1000232	6	146
19	Quantitative trait loci affecting phenotypic variation in the vacuolated lens mouse mutant, a multigenic mouse model of neural tube defects. <i>Physiological Genomics</i> , 2008 , 35, 296-304	3.6	14
18	Sequence polymorphisms cause many false cis eQTLs. <i>PLoS ONE</i> , 2007 , 2, e622	3.7	105
17	Analysis of Tiling Microarray Data by Learning Vector Quantization and Relevance Learning 2007 , 880-889		6
16	Mapping determinants of gene expression plasticity by genetical genomics in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2006 , 2, e222	6	210
15	Chemical rank estimation by noise perturbation in functional principal component analysis. <i>Analyst, The</i> , 2003 , 128, 75-81	5	13
14	Pseudo alternating least squares algorithm for trilinear decomposition. <i>Journal of Chemometrics</i> , 2001 , 15, 149-167	1.6	24
13	Alternating coupled matrices resolution method for three-way arrays analysis. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2000 , 52, 33-43	3.8	21
12	A novel trilinear decomposition algorithm for second-order linear calibration. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2000 , 52, 75-86	3.8	160
11	Novel constrained PARAFAC algorithm for second-order linear calibration. <i>Analytica Chimica Acta</i> , 2000 , 423, 187-196	6.6	14
10	Fuzzy linear discriminant analysis for chemical data sets. <i>Chemometrics and Intelligent Laboratory Systems</i> , 1999 , 45, 295-302	3.8	22
9	Nonlinear mapping using real-valued genetic algorithm. <i>Chemometrics and Intelligent Laboratory Systems</i> , 1999 , 45, 409-418	3.8	9
8	Smoothed window factor analysis. <i>Analytica Chimica Acta</i> , 1999 , 381, 233-246	6.6	12
7	A new method based on counterpropagation network algorithm for chemical pattern recognition. <i>Analytica Chimica Acta</i> , 1999 , 388, 161-170	6.6	9
6	The genetic risk for COVID-19 severity is associated with defective innate immune responses		1
5	Covid-19 Immune Signatures Reveal Stable Antiviral T-Cell Function Despite Declining Humoral Responses. <i>SSRN Electronic Journal</i> ,	1	2
4	A novel Mendelian randomization method identifies causal relationships between gene expression and low-density lipoprotein cholesterol levels		1

3	Suppressive myeloid cells are a hallmark of severe COVID-19	10
2	Deconvolution of bulk blood eQTL effects into immune cell subpopulations	3
1	The BNT162b2 mRNA vaccine against SARS-CoV-2 reprograms both adaptive and innate immune responses	7