

# Cheng-Jian Xu

## List of Publications by Year in descending order

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Version: 2024-02-01

102  
papers

6,301  
citations

101384

36  
h-index

79541

73  
g-index

120  
all docs

120  
docs citations

120  
times ranked

12574  
citing authors

#	ARTICLE	IF	CITATIONS
1	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020, 182, 1419-1440.e23.	13.5	1,162
2	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016, 98, 680-696.	2.6	717
3	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015, 47, 1449-1456.	9.4	529
4	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
5	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017, 26, 4067-4085.	1.4	211
6	Epigenome-Wide Meta-Analysis of Methylation in Children Related to Prenatal NO <sub>2</sub> Air Pollution Exposure. <i>Environmental Health Perspectives</i> , 2017, 125, 104-110.	2.8	176
7	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. <i>Lancet Respiratory Medicine</i> , 2018, 6, 379-388.	5.2	170
8	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2062-2074.	1.5	147
9	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. <i>Lancet Respiratory Medicine</i> , 2019, 7, 336-346.	5.2	147
10	Mechanisms of the Development of Allergy (MeDALL): Introducing novel concepts in allergy phenotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 388-399.	1.5	145
11	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, 1893.	5.8	140
12	Pretreatments of chromatographic fingerprints for quality control of herbal medicines. <i>Journal of Chromatography A</i> , 2006, 1134, 253-259.	1.8	111
13	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. <i>Environmental Health Perspectives</i> , 2019, 127, 57012.	2.8	111
14	Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood Asthma with Functional Follow-up. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 1373-1383.	2.5	107
15	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	0.9	105
16	Induction of trained immunity by influenza vaccination - impact on COVID-19. <i>PLoS Pathogens</i> , 2021, 17, e1009928.	2.1	93
17	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020, 12, 25.	3.6	81
18	Paving the way of systems biology and precision medicine in allergic diseases: the MeDALL success story. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2016, 71, 1513-1525.	2.7	77

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19	Genome-wide DNA methylation and long-term ambient air pollution exposure in Korean adults. <i>Clinical Epigenetics</i> , 2019, 11, 37.	1.8	76
20	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019, 11, 1487-1500.	1.0	64
21	Analyzing of the volatile chemical constituents in <i>Artemisia capillaris</i> herba by GC-MS and correlative chemometric resolution methods. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2004, 35, 469-478.	1.4	61
22	Association of season of birth with DNA methylation and allergic disease. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2016, 71, 1314-1324.	2.7	61
23	Recipe for Uncovering the Bioactive Components in Herbal Medicine. <i>Analytical Chemistry</i> , 2009, 81, 7217-7225.	3.2	56
24	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1655-1663.	1.5	56
25	Chemometric treatment of vanillin fingerprint chromatograms. <i>Journal of Chromatography A</i> , 2006, 1120, 291-298.	1.8	55
26	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 3248-3260.	2.7	55
27	Determination of the volatile chemical constituents of <i>Notopterygium incium</i> by gas chromatography-mass spectrometry and iterative or non-iterative chemometrics resolution methods. <i>Journal of Chromatography A</i> , 2003, 1016, 99-110.	1.8	54
28	Sequential uniform designs for fingerprints development of <i>Ginkgo biloba</i> extracts by capillary electrophoresis. <i>Journal of Chromatography A</i> , 2006, 1128, 273-281.	1.8	53
29	Multivariate modeling of complications with data driven variable selection: Guarding against overfitting and effects of data set size. <i>Radiotherapy and Oncology</i> , 2012, 105, 115-121.	0.3	53
30	The emerging landscape of dynamic DNA methylation in early childhood. <i>BMC Genomics</i> , 2017, 18, 25.	1.2	49
31	Evolving window orthogonal projections method for two-way data resolution. <i>Analyst</i> , 1999, 124, 1471-1476.	1.7	48
32	Impact of Statistical Learning Methods on the Predictive Power of Multivariate Normal Tissue Complication Probability Models. <i>International Journal of Radiation Oncology Biology Physics</i> , 2012, 82, e677-e684.	0.4	46
33	Spectral correlative chromatography and its application to analysis of chromatographic fingerprints of herbal medicines. <i>Journal of Separation Science</i> , 2004, 27, 581-588.	1.3	42
34	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020, 12, 105.	3.6	41
35	Epigenome-wide association study of DNA methylation and adult asthma in the Agricultural Lung Health Study. <i>European Respiratory Journal</i> , 2020, 56, 2000217.	3.1	40
36	The role of epigenetics in the development of childhood asthma. <i>Expert Review of Clinical Immunology</i> , 2019, 15, 1287-1302.	1.3	39

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37	Profiling of healthy and asthmatic airway smooth muscle cells following interleukin-1 $\beta$ treatment: a novel role for CCL20 in chronic mucus hypersecretion. <i>European Respiratory Journal</i> , 2018, 52, 1800310.	3.1	38
38	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. <i>BMC Bioinformatics</i> , 2020, 21, 243.	1.2	38
39	Single-cell RNA sequencing reveals induction of distinct trained-immunity programs in human monocytes. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	36
40	Statistical Validation of Normal Tissue Complication Probability Models. <i>International Journal of Radiation Oncology Biology Physics</i> , 2012, 84, e123-e129.	0.4	35
41	Identification of essential components of by gas chromatography/mass spectrometry and the integrated chemometric approach. <i>Talanta</i> , 2005, 68, 108-115.	2.9	32
42	Preparing graphene oxideâ€“copper composite material from spent lithium ion batteries and catalytic performance analysis. <i>Research on Chemical Intermediates</i> , 2018, 44, 5075-5089.	1.3	32
43	Differential DNA methylation in bronchial biopsies between persistent asthma and asthma in remission. <i>European Respiratory Journal</i> , 2020, 55, 1901280.	3.1	29
44	Phenotypic and functional translation of IL33 genetics in asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 144-157.	1.5	29
45	Genetic and epigenetic regulation of YKL-40 in childhood. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1105-1114.	1.5	27
46	The Early Growth Genetics (EGG) and EARly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. <i>European Journal of Epidemiology</i> , 2019, 34, 279-300.	2.5	26
47	Integration of metabolomics, genomics, and immune phenotypes reveals the causal roles of metabolites in disease. <i>Genome Biology</i> , 2021, 22, 198.	3.8	26
48	Improving the classification accuracy in chemistry via boosting technique. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2004, 70, 39-46.	1.8	24
49	Genetic regulation of <i>IL1RL1</i> methylation and <i>IL1RL1</i> -a protein levels in asthma. <i>European Respiratory Journal</i> , 2018, 51, 1701377.	3.1	24
50	Shared DNA methylation signatures in childhood allergy: The MeDALL study. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1031-1040.	1.5	24
51	Analytical comparison of different parts of <i>Radix Angelicae Sinensis</i> by gas chromatography coupled with mass spectrometry. <i>Journal of Chromatography A</i> , 2008, 1187, 232-238.	1.8	22
52	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. <i>Pediatric Pulmonology</i> , 2021, 56, 1896-1905.	1.0	22
53	Multi-omics examination of Q fever fatigue syndrome identifies similarities with chronic fatigue syndrome. <i>Journal of Translational Medicine</i> , 2020, 18, 448.	1.8	21
54	Epigenome-Wide DNA Methylation and Pesticide Use in the Agricultural Lung Health Study. <i>Environmental Health Perspectives</i> , 2021, 129, 97008.	2.8	20

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55	Resolution of the essential constituents of <i>Ramulus cinnamomi</i> by an evolving chemometric approach. <i>Fresenius' Journal of Analytical Chemistry</i> , 2001, 371, 331-336.	1.5	18
56	Orthogonalization of Block Variables by Subspace-Projection for Quantitative Structure Property Relationship (QSPR) Research. <i>Journal of Chemical Information and Computer Sciences</i> , 2002, 42, 993-1003.	2.8	17
57	Comparing chemical fingerprints of herbal medicines using modified window target-testing factor analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2005, 381, 913-924.	1.9	16
58	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. <i>European Respiratory Journal</i> , 2021, 57, 2002693.	3.1	15
59	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.	2.3	15
60	Evolution of cytokine production capacity in ancient and modern European populations. <i>ELife</i> , 2021, 10, .	2.8	15
61	Determinants of expression of SARS-CoV-2 entry-related genes in upper and lower airways. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 690-694.	2.7	15
62	Chemical rank estimation by noise perturbation in functional principal component analysis. <i>Analyst</i> , 2003, 128, 75-81.	1.7	14
63	Integrated Allergy and Asthma Prevention and Care: Report of the MeDALL/AIRWAYS ICPs Meeting at the Ministry of Health and Care Services, Oslo, Norway. <i>International Archives of Allergy and Immunology</i> , 2015, 167, 57-64.	0.9	14
64	Soluble immune markers in the different phases of chronic hepatitis B virus infection. <i>Scientific Reports</i> , 2019, 9, 14118.	1.6	14
65	Robust linear discriminant analysis for chemical pattern recognition. <i>Journal of Chemometrics</i> , 1999, 13, 3-13.	0.7	13
66	A new method based on counterpropagation network algorithm for chemical pattern recognition. <i>Analytica Chimica Acta</i> , 1999, 388, 161-170.	2.6	12
67	Development of Normal Tissue Complication Probability Model for Trismus in Head and Neck Cancer Patients Treated With Radiotherapy: The Role of Dosimetric and Clinical Factors. <i>Anticancer Research</i> , 2019, 39, 6787-6798.	0.5	12
68	Epigenome-wide association study identifies DNA methylation markers for asthma remission in whole blood and nasal epithelium. <i>Clinical and Translational Allergy</i> , 2020, 10, 60.	1.4	12
69	Resolution and identification of the acidic fraction of a petroleum ether extract of <i>Radix Rehmanniae Preparata</i> by an evolving chemometric approach. <i>Chromatographia</i> , 2003, 57, 235-243.	0.7	11
70	Sectional moving window factor analysis for diagnosing elution chromatographic patterns. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2003, 69, 89-101.	1.8	10
71	Local factor analysis of rank-deficient reaction systems. <i>Analytica Chimica Acta</i> , 2006, 575, 1-8.	2.6	10
72	Using orthogonal projection approach (OPA) for rank-deficient reaction processes. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2006, 81, 3-12.	1.8	10

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73	Residential PM2.5 exposure and the nasal methylome in children. <i>Environment International</i> , 2021, 153, 106505.	4.8	10
74	Multi-Omics Integration Reveals Only Minor Long-Term Molecular and Functional Sequelae in Immune Cells of Individuals Recovered From COVID-19. <i>Frontiers in Immunology</i> , 2022, 13, 838132.	2.2	10
75	To aggregate or not to aggregate high-dimensional classifiers. <i>BMC Bioinformatics</i> , 2011, 12, 153.	1.2	9
76	Incorporating the prior information of spectra into identification of elution region in hyphenated chromatography. <i>Analytica Chimica Acta</i> , 2001, 428, 235-244.	2.6	8
77	Infant RSV immunoprophylaxis changes nasal epithelial DNA methylation at 6 years of age. <i>Pediatric Pulmonology</i> , 2021, 56, 3822-3831.	1.0	8
78	IRF7 and RNH1 are modifying factors of HIV-1 reservoirs: a genome-wide association analysis. <i>BMC Medicine</i> , 2021, 19, 282.	2.3	8
79	Comparison of the volatile constituents of <i>Artemisia capillaris</i> from different locations by gas chromatography-mass spectrometry and projection method. <i>Journal of Chromatography A</i> , 2004, 1054, 73-9.	1.8	8
80	Mimicking the olfactory system by a thickness-shear-mode acoustic sensor array. <i>Analytica Chimica Acta</i> , 1996, 335, 117-125.	2.6	7
81	Resolution of the Embedded Chromatographic Peaks by Modified Orthogonal Projection Resolution and Entropy Maximization Method. <i>Analytical Letters</i> , 2000, 33, 2105-2128.	1.0	7
82	External Factor Variable Connectivity Index. <i>Journal of Chemical Information and Computer Sciences</i> , 2003, 43, 773-778.	2.8	6
83	The Classification Tree Combined with SIR and Its Applications to Classification of Mass Spectra. <i>Journal of Data Science</i> , 2003, 1, 425-445.	0.5	4
84	The Genetic Risk for COVID-19 Severity Is Associated With Defective Immune Responses. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	4
85	Building an Honest Tree for Mass Spectra Classification Based on Prior Logarithm Normal Distribution. <i>Journal of Data Science</i> , 2003, 1, 497-509.	0.5	3
86	Evolutionary Trajectories of Complex Traits in European Populations of Modern Humans. <i>Frontiers in Genetics</i> , 2022, 13, 833190.	1.1	2
87	Computational modeling of the human serum proteome response to colon resection surgery. <i>Analytica Chimica Acta</i> , 2010, 661, 20-27.	2.6	1
88	An integrative genomics approach identifies new asthma pathways related to air pollution exposure. , 2015, , .		1
89	Infant RSV infection changes nasal epithelial DNA methylation at 6 years of age. , 2019, , .		1
90	IL33 receptor activation is IL33 isoform and receptor genotype specific. , 2019, , .		1

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91	A genome-wide functional genomics approach uncovers genetic determinants of immune phenotypes in type 1 diabetes. <i>ELife</i> , 0, 11, .	2.8	1
92	WE-G-BRA-04: Bootstrapping Guards against Overfitting in Multivariate NTCF Modeling with Automated Variable Selection. <i>Medical Physics</i> , 2011, 38, 3826-3827.	1.6	0
93	Epigenome-Wide Pooled Analysis Of Methylation In Children Related To Air Pollution Exposure At Birth: The Medall Study. <i>ISEE Conference Abstracts</i> , 2015, 2015, 690.	0.0	0
94	meQTL analysis of asthma GWAS loci and DNA methylation. , 2016, , .		0
95	Differentially methylated genes related to gestational age are also expressed during fetal lung development. , 2016, , .		0
96	Gene expression in bronchial biopsies from subjects with persistent asthma and asthma in remission. , 2017, , .		0
97	A Genome-wide Study of DNA Methylation in Nasal Epithelium and Atopy and Atopic Asthma in Children. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
98	Cell type eQTL deconvolution of bronchial epithelium through integration of single cell and bulk RNA-seq. , 2021, , .		0
99	Predicting childhood allergy using machine learning methods on multi-omics data. , 2021, , .		0
100	RNA sequencing in bronchial biopsies of wheezing infants developing asthma at school age reveals epithelial dysfunction. , 2020, , .		0
101	Reverse Inflammaging: Biological age is accelerated in chronic HCV patients and decelerates after HCV cure. <i>Zeitschrift Fur Gastroenterologie</i> , 2022, 60, .	0.2	0
102	Cell type eQTL deconvolution of bronchial epithelium through integration of single cell and bulk RNA-seq. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 3663-3666.	2.7	0