Cheng-Jian Xu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7940602/publications.pdf

Version: 2024-02-01

102 6,301 36 73
papers citations h-index g-index

120 120 120 120 12574

times ranked

citing authors

docs citations

all docs

#	Article	IF	CITATIONS
1	Determinants of expression of SARSâ€CoVâ€2 entryâ€related genes in upper and lower airways. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 690-694.	2.7	15
2	Reverse Inflammaging: Biological age is accelerated in chronic HCV patients and decelerates after HCV cure. Zeitschrift Fur Gastroenterologie, 2022, 60, .	0.2	O
3	Single-cell RNA sequencing reveals induction of distinct trained-immunity programs in human monocytes. Journal of Clinical Investigation, 2022, 132, .	3.9	36
4	Evolutionary Trajectories of Complex Traits in European Populations of Modern Humans. Frontiers in Genetics, 2022, 13, 833190.	1.1	2
5	Multi-Omics Integration Reveals Only Minor Long-Term Molecular and Functional Sequelae in Immune Cells of Individuals Recovered From COVID-19. Frontiers in Immunology, 2022, 13, 838132.	2.2	10
6	The Genetic Risk for COVID-19 Severity Is Associated With Defective Immune Responses. Frontiers in Immunology, 2022, 13, .	2.2	4
7	Cellâ€type <scp>eQTL</scp> deconvolution of bronchial epithelium through integration of singleâ€cell and bulk <scp>RNA</scp> â€seq. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 3663-3666.	2.7	O
8	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. European Respiratory Journal, 2021, 57, 2002693.	3.1	15
9	Shared DNA methylation signatures in childhood allergy: The MeDALL study. Journal of Allergy and Clinical Immunology, 2021, 147, 1031-1040.	1.5	24
10	Identification of Novel Population-Specific Cell Subsets in Chinese Ulcerative Colitis Patients Using Single-Cell RNA Sequencing. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 99-117.	2.3	15
11	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. Pediatric Pulmonology, 2021, 56, 1896-1905.	1.0	22
12	Integration of metabolomics, genomics, and immune phenotypes reveals the causal roles of metabolites in disease. Genome Biology, 2021, 22, 198.	3.8	26
13	Residential PM2.5 exposure and the nasal methylome in children. Environment International, 2021, 153, 106505.	4.8	10
14	Infant RSV immunoprophylaxis changes nasal epithelial DNA methylation at 6 years of age. Pediatric Pulmonology, 2021, 56, 3822-3831.	1.0	8
15	Evolution of cytokine production capacity in ancient and modern European populations. ELife, 2021, 10 ,	2.8	15
16	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
17	Epigenome-Wide DNA Methylation and Pesticide Use in the Agricultural Lung Health Study. Environmental Health Perspectives, 2021, 129, 97008.	2.8	20
18	Phenotypic and functional translation of IL33 genetics in asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 144-157.	1.5	29

#	Article	IF	Citations
19	Induction of trained immunity by influenza vaccination - impact on COVID-19. PLoS Pathogens, 2021, 17, e1009928.	2.1	93
20	Cell type eQTL deconvolution of bronchial epithelium through integration of single cell and bulk RNA-seq. , 2021, , .		0
21	Predicting childhood allergy using machine learning methods on multi-omics data. , 2021, , .		O
22	IRF7 and RNH1 are modifying factors of HIV-1 reservoirs: a genome-wide association analysis. BMC Medicine, 2021, 19, 282.	2.3	8
23	Differential DNA methylation in bronchial biopsies between persistent asthma and asthma in remission. European Respiratory Journal, 2020, 55, 1901280.	3.1	29
24	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. Genome Medicine, 2020, 12, 105.	3.6	41
25	Multi-omics examination of Q fever fatigue syndrome identifies similarities with chronic fatigue syndrome. Journal of Translational Medicine, 2020, 18, 448.	1.8	21
26	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. Cell, 2020, 182, 1419-1440.e23.	13.5	1,162
27	Epigenome-wide association study identifies DNA methylation markers for asthma remission in whole blood and nasal epithelium. Clinical and Translational Allergy, 2020, 10, 60.	1.4	12
28	Epigenome-wide association study of DNA methylation and adult asthma in the Agricultural Lung Health Study. European Respiratory Journal, 2020, 56, 2000217.	3.1	40
29	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	1.2	38
30	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. Genome Medicine, 2020, 12, 25.	3.6	81
31	Nasal DNA methylation profiling of asthma and rhinitis. Journal of Allergy and Clinical Immunology, 2020, 145, 1655-1663.	1.5	56
32	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 3248-3260.	2.7	55
33	RNA sequencing in bronchial biopsies of wheezing infants developing asthma at school age reveals epithelial dysfunction., 2020,,.		0
34	The role of epigenetics in the development of childhood asthma. Expert Review of Clinical Immunology, 2019, 15, 1287-1302.	1.3	39
35	Soluble immune markers in the different phases of chronic hepatitis B virus infection. Scientific Reports, 2019, 9, 14118.	1.6	14
36	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	1.0	64

#	Article	IF	Citations
37	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	1.5	147
38	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. Environmental Health Perspectives, 2019, 127, 57012.	2.8	111
39	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	5.8	140
40	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. European Journal of Epidemiology, 2019, 34, 279-300.	2.5	26
41	Genome-wide DNA methylation and long-term ambient air pollution exposure in Korean adults. Clinical Epigenetics, 2019, 11, 37.	1.8	76
42	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. Anticancer Research, 2019, 39, 6787-6798.	0.5	12
43	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. Lancet Respiratory Medicine, the, 2019, 7, 336-346.	5.2	147
44	Infant RSV infection changes nasal epithelial DNA methylation at 6 years of age., 2019,,.		1
45	IL33 receptor activation is IL33 isoform and receptor genotype specific. , 2019, , .		1
46	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. Lancet Respiratory Medicine, the, 2018, 6, 379-388.	5 . 2	170
47	Preparing graphene oxide–copper composite material from spent lithium ion batteries and catalytic performance analysis. Research on Chemical Intermediates, 2018, 44, 5075-5089.	1.3	32
48	Genetic regulation of <i>IL1RL1</i> methylation and IL1RL1-a protein levels in asthma. European Respiratory Journal, 2018, 51, 1701377.	3.1	24
49	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
50	Genetic and epigenetic regulation of YKL-40 in childhood. Journal of Allergy and Clinical Immunology, 2018, 141, 1105-1114.	1.5	27
51	Profiling of healthy and asthmatic airway smooth muscle cells following interleukin- $\hat{\Pi}^2$ treatment: a novel role for CCL20 in chronic mucus hypersecretion. European Respiratory Journal, 2018, 52, 1800310.	3.1	38
52	Mechanisms of the Development of Allergy (MeDALL): Introducing novel concepts in allergy phenotypes. Journal of Allergy and Clinical Immunology, 2017, 139, 388-399.	1.5	145
53	Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood Asthma with Functional Follow-up. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 1373-1383.	2,5	107
54	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. Human Molecular Genetics, 2017, 26, 4067-4085.	1.4	211

#	Article	ΙF	Citations
55	The emerging landscape of dynamic DNA methylation in early childhood. BMC Genomics, 2017, 18, 25.	1.2	49
56	Epigenome-Wide Meta-Analysis of Methylation in Children Related to Prenatal NO ₂ Air Pollution Exposure. Environmental Health Perspectives, 2017, 125, 104-110.	2.8	176
57	Gene expression in bronchial biopsies from subjects with persistent asthma and asthma in remission. , 2017, , .		O
58	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
59	Paving the way of systems biology and precision medicine in allergic diseases: the Me <scp>DALL</scp> success story. Allergy: European Journal of Allergy and Clinical Immunology, 2016, 71, 1513-1525.	2.7	77
60	Association of season of birth with <scp>DNA</scp> methylation and allergic disease. Allergy: European Journal of Allergy and Clinical Immunology, 2016, 71, 1314-1324.	2.7	61
61	meQTL analysis of asthma GWAS loci and DNA methylation. , 2016, , .		0
62	Differentially methylated genes related to gestational age are also expressed during fetal lung development. , $2016, , .$		0
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. International Archives of Allergy and Immunology, 2015, 167, 57-64.	0.9	14
64	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	9.4	529
65	An integrative genomics approach identifies new asthma pathways related to air pollution exposure. , 2015, , .		1
66	Epigenome-Wide Pooled Analysis Of Methylation In Children Related To Air Pollution Exposure At Birth: The Medall Study. ISEE Conference Abstracts, 2015, 2015, 690.	0.0	0
67	Impact of Statistical Learning Methods on the Predictive Power of Multivariate Normal Tissue Complication Probability Models. International Journal of Radiation Oncology Biology Physics, 2012, 82, e677-e684.	0.4	46
68	Statistical Validation of Normal Tissue Complication Probability Models. International Journal of Radiation Oncology Biology Physics, 2012, 84, e123-e129.	0.4	35
69	Multivariate modeling of complications with data driven variable selection: Guarding against overfitting and effects of data set size. Radiotherapy and Oncology, 2012, 105, 115-121.	0.3	53
70	To aggregate or not to aggregate high-dimensional classifiers. BMC Bioinformatics, 2011, 12, 153.	1.2	9
71	WE-G-BRA-04: Bootstrapping Guards against Overfitting in Multivariate NTCP Modeling with Automated Variable Selection. Medical Physics, 2011, 38, 3826-3827.	1.6	0
72	Computational modeling of the human serum proteome response to colon resection surgery. Analytica Chimica Acta, 2010, 661, 20-27.	2.6	1

#	Article	IF	CITATIONS
73	Recipe for Uncovering the Bioactive Components in Herbal Medicine. Analytical Chemistry, 2009, 81, 7217-7225.	3.2	56
74	Analytical comparison of different parts of Radix Angelicae Sinensis by gas chromatography coupled with mass spectrometry. Journal of Chromatography A, 2008, 1187, 232-238.	1.8	22
75	Local factor analysis of rank-deficient reaction systems. Analytica Chimica Acta, 2006, 575, 1-8.	2.6	10
76	Using orthogonal projection approach (OPA) for rank-deficient reaction processes. Chemometrics and Intelligent Laboratory Systems, 2006, 81, 3-12.	1.8	10
77	Chemometric treatment of vanillin fingerprint chromatograms. Journal of Chromatography A, 2006, 1120, 291-298.	1.8	55
78	Sequential uniform designs for fingerprints development of Ginkgo biloba extracts by capillary electrophoresis. Journal of Chromatography A, 2006, 1128, 273-281.	1.8	53
79	Pretreatments of chromatographic fingerprints for quality control of herbal medicines. Journal of Chromatography A, 2006, 1134, 253-259.	1.8	111
80	Comparing chemical fingerprints of herbal medicines using modified window target-testing factor analysis. Analytical and Bioanalytical Chemistry, 2005, 381, 913-924.	1.9	16
81	Identification of essential components of by gas chromatography/mass spectrometry and the integrated chemometric approach. Talanta, 2005, 68, 108-115.	2.9	32
82	Spectral correlative chromatography and its application to analysis of chromatographic fingerprints of herbal medicines. Journal of Separation Science, 2004, 27, 581-588.	1.3	42
83	Analyzing of the volatile chemical constituents in Artemisia capillaris herba by GC–MS and correlative chemometric resolution methods. Journal of Pharmaceutical and Biomedical Analysis, 2004, 35, 469-478.	1.4	61
84	Improving the classification accuracy in chemistry via boosting technique. Chemometrics and Intelligent Laboratory Systems, 2004, 70, 39-46.	1.8	24
85	Comparison of the volatile constituents of Artemisia capillaris from different locations by gas chromatography-mass spectrometry and projection method. Journal of Chromatography A, 2004, 1054, 73-9.	1.8	8
86	Resolution and identification of the acidic fraction of a petroleum ether extract of Radix Rehmanniae Preparata by an evolving chemometric approach. Chromatographia, 2003, 57, 235-243.	0.7	11
87	Determination of the volatile chemical constituents of Notoptergium incium by gas chromatography–mass spectrometry and iterative or non-iterative chemometrics resolution methods. Journal of Chromatography A, 2003, 1016, 99-110.	1.8	54
88	Sectional moving window factor analysis for diagnosing elution chromatographic patterns. Chemometrics and Intelligent Laboratory Systems, 2003, 69, 89-101.	1.8	10
89	External Factor Variable Connectivity Index. Journal of Chemical Information and Computer Sciences, 2003, 43, 773-778.	2.8	6
90	Chemical rank estimation by noise perturbation in functional principal component analysis. Analyst, The, 2003, 128, 75-81.	1.7	14

#	Article	IF	CITATION
91	Building an Honest Tree for Mass Spectra Classification Based on Prior Logarithm Normal Distribution. Journal of Data Science, 2003, 1, 497-509.	0.5	3
92	The Classification Tree Combined with SIR and Its Applications to Classification of Mass Spectra. Journal of Data Science, 2003, 1, 425-445.	0.5	4
93	Orthogonalization of Block Variables by Subspace-Projection for Quantitative Structure Property Relationship (QSPR) Research. Journal of Chemical Information and Computer Sciences, 2002, 42, 993-1003.	2.8	17
94	Resolution of the essential constituents of Ramulus cinnamomi by an evolving chemometric approach. Fresenius' Journal of Analytical Chemistry, 2001, 371, 331-336.	1.5	18
95	Incorporating the prior information of spectra into identification of elution region in hyphenated chromatography. Analytica Chimica Acta, 2001, 428, 235-244.	2.6	8
96	Resolution of the Embedded Chromatographic Peaks by Modified Orthogonal Projection Resolution and Entropy Maximization Method. Analytical Letters, 2000, 33, 2105-2128.	1.0	7
97	A new method based on counterpropagation network algorithm for chemical pattern recognition. Analytica Chimica Acta, 1999, 388, 161-170.	2.6	12
98	Robust linear discriminant analysis for chemical pattern recognition. Journal of Chemometrics, 1999, 13, 3-13.	0.7	13
99	Evolving window orthogonal projections method for two-way data resolution. Analyst, The, 1999, 124, 1471-1476.	1.7	48
100	Mimicking the olfactory system by a thickness-shear-mode acoustic sensor array. Analytica Chimica Acta, 1996, 335, 117-125.	2.6	7
101	A Genome-wide Study of DNA Methylation in Nasal Epithelium and Atopy and Atopic Asthma in Children. SSRN Electronic Journal, 0, , .	0.4	0
102	A genome-wide functional genomics approach uncovers genetic determinants of immune phenotypes in type 1 diabetes. ELife, $0,11,.$	2.8	1