

Katerina J Kechris

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

3,872
citations

168829

31
h-index

169272

56
g-index

129
all docs

129
docs citations

129
times ranked

8123
citing authors

#	ARTICLE	IF	CITATIONS
1	Longitudinal analysis of SARS-CoV-2 spike and RNA-dependent RNA polymerase protein sequences reveals the emergence and geographic distribution of diverse mutations. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105153.	1.0	16
2	Chronic Marijuana Use Is Associated with Gene Expression Changes in BAL. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2022, 66, 238-239.	1.4	0
3	Metabolomic Profiles in Childhood and Adolescence Are Associated with Fetal Overnutrition. <i>Metabolites</i> , 2022, 12, 265.	1.3	5
4	Granzyme B ⁺ CD4 T cells accumulate in the colon during chronic HIV-1 infection. <i>Gut Microbes</i> , 2022, 14, 2045852.	4.3	3
5	A Metabolomic Severity Score for Airflow Obstruction and Emphysema. <i>Metabolites</i> , 2022, 12, 368.	1.3	8
6	Sex-Specific Differences in MicroRNA Expression During Human Fetal Lung Development. <i>Frontiers in Genetics</i> , 2022, 13, 762834.	1.1	4
7	Mechanism-aware imputation: a two-step approach in handling missing values in metabolomics. <i>BMC Bioinformatics</i> , 2022, 23, 179.	1.2	7
8	Changes in the Coexpression of Innate Immunity Genes During Persistent Islet Autoimmunity Are Associated With Progression of Islet Autoimmunity: Diabetes Autoimmunity Study in the Young (DAISY). <i>Diabetes</i> , 2022, 71, 2048-2057.	0.3	3
9	Ambient air pollution during pregnancy and DNA methylation in umbilical cord blood, with potential mediation of associations with infant adiposity: The Healthy Start study. <i>Environmental Research</i> , 2022, 214, 113881.	3.7	4
10	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (<i>Schistosoma japonicum</i>). <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009020.	1.3	8
11	A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021, 93, 1912-1923.	3.2	30
12	Placental Insulin/IGF-1 Signaling, PGC-1 α , and Inflammatory Pathways Are Associated With Metabolic Outcomes at 4-6 Years of Age: The ECHO Healthy Start Cohort. <i>Diabetes</i> , 2021, 70, 745-751.	0.3	11
13	tidyMicro: a pipeline for microbiome data analysis and visualization using the tidyverse in R. <i>BMC Bioinformatics</i> , 2021, 22, 41.	1.2	12
14	Aptardi predicts polyadenylation sites in sample-specific transcriptomes using high-throughput RNA sequencing and DNA sequence. <i>Nature Communications</i> , 2021, 12, 1652.	5.8	18
15	Metabolomic Profiling Reveals Sex Specific Associations with Chronic Obstructive Pulmonary Disease and Emphysema. <i>Metabolites</i> , 2021, 11, 161.	1.3	19
16	The oxylipin profile is associated with development of type 1 diabetes: the Diabetes Autoimmunity Study in the Young (DAISY). <i>Diabetologia</i> , 2021, 64, 1785-1794.	2.9	15
17	Soluble receptor for advanced glycation end products (sRAGE) as a biomarker of COPD. <i>Respiratory Research</i> , 2021, 22, 127.	1.4	26
18	Phospholipid Levels at Seroconversion Are Associated With Resolution of Persistent Islet Autoimmunity: The Diabetes Autoimmunity Study in the Young. <i>Diabetes</i> , 2021, 70, 1592-1601.	0.3	5

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19	Comparing Statistical Tests for Differential Network Analysis of Gene Modules. <i>Frontiers in Genetics</i> , 2021, 12, 630215.	1.1	4
20	Semi-Supervised Learning Using Hierarchical Mixture Models: Gene Essentiality Case Study. <i>Mathematical and Computational Applications</i> , 2021, 26, 40.	0.7	1
21	Inverse probability weighting is an effective method to address selection bias during the analysis of high dimensional data. <i>Genetic Epidemiology</i> , 2021, 45, 593-603.	0.6	6
22	A Mediation Approach to Discovering Causal Relationships between the Metabolome and DNA Methylation in Type 1 Diabetes. <i>Metabolites</i> , 2021, 11, 542.	1.3	1
23	Multi-omics subtyping pipeline for chronic obstructive pulmonary disease. <i>PLoS ONE</i> , 2021, 16, e0255337.	1.1	19
24	Reproducibility of mass spectrometry based metabolomics data. <i>BMC Bioinformatics</i> , 2021, 22, 423.	1.2	13
25	An effective processing pipeline for harmonizing DNA methylation data from Illumina's 450K and EPIC platforms for epidemiological studies. <i>BMC Research Notes</i> , 2021, 14, 352.	0.6	11
26	MSCAT: A Machine Learning Assisted Catalog of Metabolomics Software Tools. <i>Metabolites</i> , 2021, 11, 678.	1.3	10
27	Identifying miRNA-mRNA Networks Associated With COPD Phenotypes. <i>Frontiers in Genetics</i> , 2021, 12, 748356.	1.1	12
28	PaIRKAT: A pathway integrated regression-based kernel association test with applications to metabolomics and COPD phenotypes. <i>PLoS Computational Biology</i> , 2021, 17, e1008986.	1.5	4
29	Epigenome-Wide Association Study of Infant Feeding and DNA Methylation in Infancy and Childhood in a Population at Increased Risk for Type 1 Diabetes. <i>Nutrients</i> , 2021, 13, 4057.	1.7	4
30	An Augmented High-Dimensional Graphical Lasso Method to Incorporate Prior Biological Knowledge for Global Network Learning. <i>Frontiers in Genetics</i> , 2021, 12, 760299.	1.1	3
31	Bayesian inference of networks across multiple sample groups and data types. <i>Biostatistics</i> , 2020, 21, 561-576.	0.9	10
32	Metabolomics-related nutrient patterns at seroconversion and risk of progression to type 1 diabetes. <i>Pediatric Diabetes</i> , 2020, 21, 1202-1209.	1.2	12
33	MCMSeq: Bayesian hierarchical modeling of clustered and repeated measures RNA sequencing experiments. <i>BMC Bioinformatics</i> , 2020, 21, 375.	1.2	9
34	Associations between the activity of placental nutrient-sensing pathways and neonatal and postnatal metabolic health: the ECHO Healthy Start cohort. <i>International Journal of Obesity</i> , 2020, 44, 2203-2212.	1.6	6
35	Alcohol Use Disorders Are Associated With a Unique Impact on Airway Epithelial Cell Gene Expression. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 1571-1584.	1.4	2
36	DNA methylation near the <i>INS</i> gene is associated with <i>INS</i> genetic variation (rs689) and type 1 diabetes in the Diabetes Autoimmunity Study in the Young. <i>Pediatric Diabetes</i> , 2020, 21, 597-605.	1.2	6

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37	Longitudinal DNA methylation differences precede type 1 diabetes. <i>Scientific Reports</i> , 2020, 10, 3721.	1.6	37
38	Predictive Modeling for Metabolomics Data. <i>Methods in Molecular Biology</i> , 2020, 2104, 313-336.	0.4	32
39	Identifying Protein-metabolite Networks Associated with COPD Phenotypes. <i>Metabolites</i> , 2020, 10, 124.	1.3	25
40	Plasma Metabolomic Signatures of Chronic Obstructive Pulmonary Disease and the Impact of Genetic Variants on Phenotype-Driven Modules. <i>Network and Systems Medicine</i> , 2020, 3, 159-181.	2.7	22
41	Prenatal Exposure to Per- and Polyfluoroalkyl Substances, Umbilical Cord Blood DNA Methylation, and Cardio-Metabolic Indicators in Newborns: The Healthy Start Study. <i>Environmental Health Perspectives</i> , 2020, 128, 127014.	2.8	49
42	Qualitative Differences Between the IFN α subtypes and IFN α Influence Chronic Mucosal HIV-1 Pathogenesis. <i>PLoS Pathogens</i> , 2020, 16, e1008986.	2.1	22
43	Development of a tissue augmented Bayesian model for expression quantitative trait loci analysis. <i>Mathematical Biosciences and Engineering</i> , 2020, 17, 122-143.	1.0	1
44	Biomarkers Predictive of Exacerbations in the SPIROMICS and COPD Gene Cohorts. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 473-481.	2.5	1
45	Systems genetics analysis of the LXS recombinant inbred mouse strains: Genetic and molecular insights into acute ethanol tolerance. <i>PLoS ONE</i> , 2020, 15, e0240253.	1.1	1
46	Title is missing!. , 2020, 15, e0240253.		0
47	Title is missing!. , 2020, 15, e0240253.		0
48	Title is missing!. , 2020, 15, e0240253.		0
49	Title is missing!. , 2020, 15, e0240253.		0
50	Title is missing!. , 2020, 16, e1008986.		0
51	Title is missing!. , 2020, 16, e1008986.		0
52	Title is missing!. , 2020, 16, e1008986.		0
53	Title is missing!. , 2020, 16, e1008986.		0
54	Title is missing!. , 2020, 16, e1008986.		0

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55	Title is missing!. , 2020, 16, e1008986.		0
56	Prenatal exposure to per- and polyfluoroalkyl substances and infant growth and adiposity: the Healthy Start Study. Environment International, 2019, 131, 104983.	4.8	48
57	Bronchoalveolar Lavage Fluid from COPD Patients Reveals More Compounds Associated with Disease than Matched Plasma. Metabolites, 2019, 9, 157.	1.3	32
58	Metabolite-related dietary patterns and the development of islet autoimmunity. Scientific Reports, 2019, 9, 14819.	1.6	34
59	Pre-analytic Considerations for Mass Spectrometry-Based Untargeted Metabolomics Data. Methods in Molecular Biology, 2019, 1978, 323-340.	0.4	8
60	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383.	1.3	73
61	A2ML1 and otitis media: novel variants, differential expression, and relevant pathways. Human Mutation, 2019, 40, 1156-1171.	1.1	10
62	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
63	Unsupervised discovery of phenotype-specific multi-omics networks. Bioinformatics, 2019, 35, 4336-4343.	1.8	30
64	Insight into genetic regulation of miRNA in mouse brain. BMC Genomics, 2019, 20, 849.	1.2	4
65	Using a spatial point process framework to characterize lung computed tomography scans. Spatial Statistics, 2019, 29, 243-267.	0.9	2
66	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
67	A Bayesian Approach for Learning Gene Networks Underlying Disease Severity in COPD. Statistics in Biosciences, 2018, 10, 59-85.	0.6	9
68	Metabolomics and transcriptomics pathway approach reveals outcome-specific perturbations in COPD. Scientific Reports, 2018, 8, 17132.	1.6	62
69	Condition-adaptive fused graphical lasso (CFGL): An adaptive procedure for inferring condition-specific gene co-expression network. PLoS Computational Biology, 2018, 14, e1006436.	1.5	17
70	Predictive modeling of miRNA-mediated predisposition to alcohol-related phenotypes in mouse. BMC Genomics, 2018, 19, 639.	1.2	6
71	miR-MaGiC improves quantification accuracy for small RNA-seq. BMC Research Notes, 2018, 11, 296.	0.6	9
72	Post-GWAS Prioritization Through Data Integration Provides Novel Insights on Chronic Obstructive Pulmonary Disease. Statistics in Biosciences, 2017, 9, 605-621.	0.6	2

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73	Model based heritability scores for high-throughput sequencing data. BMC Bioinformatics, 2017, 18, 143.	1.2	11
74	High-Risk Human Papillomavirus E7 Alters Host DNA Methylome and Represses HLA-E Expression in Human Keratinocytes. Scientific Reports, 2017, 7, 3633.	1.6	45
75	Metabolomic similarities between bronchoalveolar lavage fluid and plasma in humans and mice. Scientific Reports, 2017, 7, 5108.	1.6	19
76	Maternal obesity alters fatty acid oxidation, AMPK activity, and associated DNA methylation in mesenchymal stem cells from human infants. Molecular Metabolism, 2017, 6, 1503-1516.	3.0	57
77	Multiple biomarkers predict disease severity, progression and mortality in COPD. Respiratory Research, 2017, 18, 117.	1.4	103
78	Differential correlation for sequencing data. BMC Research Notes, 2017, 10, 54.	0.6	24
79	Biomarkers Predictive of Exacerbations in the SPIROMICS and COPD Gene Cohorts. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 473-481.	2.5	101
80	Gene and metabolite time-course response to cigarette smoking in mouse lung and plasma. PLoS ONE, 2017, 12, e0178281.	1.1	19
81	Meta-analysis of peripheral blood gene expression modules for COPD phenotypes. PLoS ONE, 2017, 12, e0185682.	1.1	17
82	The value of blood cytokines and chemokines in assessing COPD. Respiratory Research, 2017, 18, 180.	1.4	83
83	Perfluoroalkyl Substances during Pregnancy and Offspring Weight and Adiposity at Birth: Examining Mediation by Maternal Fasting Glucose in the Healthy Start Study. Environmental Health Perspectives, 2017, 125, 067016.	2.8	102
84	Adaptation of Mycobacterium tuberculosis to Impaired Host Immunity in HIV-Infected Patients. Journal of Infectious Diseases, 2016, 214, 1205-1211.	1.9	19
85	Structural and functional characterization of endothelial microparticles released by cigarette smoke. Scientific Reports, 2016, 6, 31596.	1.6	112
86	Blood Transcriptional Biomarkers for Active Tuberculosis among Patients in the United States: a Case-Control Study with Systematic Cross-Classifer Evaluation. Journal of Clinical Microbiology, 2016, 54, 274-282.	1.8	55
87	The discordant method: a novel approach for differential correlation. Bioinformatics, 2016, 32, 690-696.	1.8	30
88	Common Genetic Polymorphisms Influence Blood Biomarker Measurements in COPD. PLoS Genetics, 2016, 12, e1006011.	1.5	88
89	Transcriptional Adaptation of Drug-tolerant <i>Mycobacterium tuberculosis</i> During Treatment of Human Tuberculosis. Journal of Infectious Diseases, 2015, 212, 990-998.	1.9	82
90	Genetic analysis of a murine QTL for diet restriction on chromosome 15. Age, 2015, 37, 9740.	3.0	3

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91	Narrow Band Ultraviolet B Treatment for Human Vitiligo Is Associated with Proliferation, Migration, and Differentiation of Melanocyte Precursors. <i>Journal of Investigative Dermatology</i> , 2015, 135, 2068-2076.	0.3	86
92	Plasma Sphingolipids Associated with Chronic Obstructive Pulmonary Disease Phenotypes. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 191, 275-284.	2.5	137
93	Joint MiRNA/mRNA Expression Profiling Reveals Changes Consistent with Development of Dysfunctional Corpus Luteum after Weight Gain. <i>PLoS ONE</i> , 2015, 10, e0135163.	1.1	42
94	MSPrep—Summarization, normalization and diagnostics for processing of mass spectrometry—based metabolomic data. <i>Bioinformatics</i> , 2014, 30, 133-134.	1.8	48
95	The association of plasma biomarkers with computed tomography-assessed emphysema phenotypes. <i>Respiratory Research</i> , 2014, 15, 127.	1.4	61
96	The multiMiR R package and database: integration of microRNA—target interactions along with their disease and drug associations. <i>Nucleic Acids Research</i> , 2014, 42, e133-e133.	6.5	409
97	Integrative Omics Approach Identifies Interleukin-16 as a Biomarker of Emphysema. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 619-626.	1.0	31
98	Biphasic pro-melanogenic and pro-apoptotic effects of all-trans-retinoic acid (ATRA) on human melanocytes: Time-course study. <i>Journal of Dermatological Science</i> , 2013, 72, 168-176.	1.0	26
99	Modeling considerations for using expression data from multiple species. <i>Statistics in Medicine</i> , 2013, 32, 4057-4070.	0.8	0
100	Hands-on Workshops as An Effective Means of Learning Advanced Technologies Including Genomics, Proteomics and Bioinformatics. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 368-377.	3.0	12
101	Peripheral Blood Mononuclear Cell Gene Expression in Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2013, 49, 316-323.	1.4	110
102	The Association of Adiponectin with Computed Tomography Phenotypes in Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 188, 561-566.	2.5	48
103	Exposure to Maternal Diabetes in Utero and DNA Methylation Patterns in the Offspring. <i>Immunometabolism</i> , 2013, 1, 1-9.	6.0	54
104	A graphical model method for integrating multiple sources of genome-scale data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 469-87.	0.2	5
105	Multiple Amino Acid Sequence Alignment Nitrogenase Component 1: Insights into Phylogenetics and Structure-Function Relationships. <i>PLoS ONE</i> , 2013, 8, e72751.	1.1	23
106	Comb-p: software for combining, analyzing, grouping and correcting spatially correlated <i>P</i>-values. <i>Bioinformatics</i> , 2012, 28, 2986-2988.	1.8	331
107	Gene Expression Changes in <sc>C</sc>57<sc>BL</sc>/6<sc>J</sc> and <sc>DBA</sc>/2<sc>J</sc> Mice Following Prenatal Alcohol Exposure. <i>Alcoholism: Clinical and Experimental Research</i> , 2012, 36, 1519-1529.	1.4	47
108	A systems genetic analysis of alcohol drinking by mice, rats and men: Influence of brain GABAergic transmission. <i>Neuropharmacology</i> , 2011, 60, 1269-1280.	2.0	50

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109	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. PLoS ONE, 2011, 6, e26105.	1.1	2
110	Interleukin-16 Expression Is Down Regulated In Peripheral Blood Mononuclear Cells From Patients With COPD. , 2011, , .		0
111	Using the Phenogen website for "in silico"™ analysis of morphine-induced analgesia: identifying candidate genes. Addiction Biology, 2011, 16, 393-404.	1.4	12
112	Genetical Genomic Analysis of Complex Phenotypes Using the PhenoGen Website. Behavior Genetics, 2011, 41, 625-628.	1.4	9
113	Generalizing Moving Averages for Tiling Arrays Using Combined P-Value Statistics. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article29.	0.2	36
114	Hedgehog targets in the <i>Drosophila</i> embryo and the mechanisms that generate tissue-specific outputs of Hedgehog signaling. Development (Cambridge), 2010, 137, 3887-3898.	1.2	35
115	Conserved Amino Acid Sequence Features in the Î± Subunits of MoFe, VFe, and FeFe Nitrogenases. PLoS ONE, 2009, 4, e6136.	1.1	11
116	Prediction of Motifs Based on a Repeated-Measures Model for Integrating Cross-Species Sequence and Expression Data. Statistical Applications in Genetics and Molecular Biology, 2009, 8, 1-34.	0.2	3
117	Genetical genomic determinants of alcohol consumption in rats and humans. BMC Biology, 2009, 7, 70.	1.7	148
118	c-REDUCE: Incorporating sequence conservation to detect motifs that correlate with expression. BMC Bioinformatics, 2008, 9, 506.	1.2	2
119	Prediction of alternatively skipped exons and splicing enhancers from exon junction arrays. BMC Genomics, 2008, 9, 551.	1.2	9
120	Significant Subgraph Detection in Multi-omics Networks for Disease Pathway Identification. Frontiers in Big Data, 0, 5, .	1.8	1