Katerina J Kechris

List of Publications by Year
in descending order

120 papers	3,872 citations	147801 31 h-index	149698 56 g-index
129 all docs	129 docs citations	129 times ranked	7427 citing authors

#	Article	IF	Citations
1	The multiMiR R package and database: integration of microRNA–target interactions along with their disease and drug associations. Nucleic Acids Research, 2014, 42, e133-e133.	14.5	409
2	Comb-p: software for combining, analyzing, grouping and correcting spatially correlated P-values. Bioinformatics, 2012, 28, 2986-2988.	4.1	331
3	Genetical genomic determinants of alcohol consumption in rats and humans. BMC Biology, 2009, 7, 70.	3.8	148
4	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
5	Plasma Sphingolipids Associated with Chronic Obstructive Pulmonary Disease Phenotypes. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 275-284.	5.6	137
6	Structural and functional characterization of endothelial microparticles released by cigarette smoke. Scientific Reports, 2016, 6, 31596.	3.3	112
7	Peripheral Blood Mononuclear Cell Gene Expression in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2013, 49, 316-323.	2.9	110
8	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	1.9	105
9	Multiple biomarkers predict disease severity, progression and mortality in COPD. Respiratory Research, 2017, 18, 117.	3.6	103
10	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.	6.0	102
11	Biomarkers Predictive of Exacerbations in the SPIROMICS and COPDGene Cohorts. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 473-481.	5.6	101
12	Common Genetic Polymorphisms Influence Blood Biomarker Measurements in COPD. PLoS Genetics, 2016, 12, e1006011.	3.5	88
13	Narrow Band Ultraviolet B Treatment for Human Vitiligo Is Associated with Proliferation, Migration, and Differentiation of Melanocyte Precursors. Journal of Investigative Dermatology, 2015, 135, 2068-2076.	0.7	86
14	The value of blood cytokines and chemokines in assessing COPD. Respiratory Research, 2017, 18, 180.	3.6	83
15	Transcriptional Adaptation of Drug-tolerant *Mycobacterium tuberculosis* During Treatment of Human Tuberculosis. Journal of Infectious Diseases, 2015, 212, 990-998.	4.0	82
16	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383.	2.7	73
17	Metabolomics and transcriptomics pathway approach reveals outcome-specific perturbations in COPD. Scientific Reports, 2018, 8, 17132.	3.3	62
18	The association of plasma biomarkers with computed tomography-assessed emphysema phenotypes. Respiratory Research, 2014, 15, 127.	3.6	61

#	Article	IF	Citations
19	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.	6.5	57
20	Blood Transcriptional Biomarkers for Active Tuberculosis among Patients in the United States: a Case-Control Study with Systematic Cross-Classifier Evaluation. Journal of Clinical Microbiology, 2016, 54, 274-282.	3.9	55
21	Exposure to Maternal Diabetes in Utero and DNA Methylation Patterns in the Offspring. Immunometabolism, 2013, 1, 1-9.	6.0	54
22	A systems genetic analysis of alcohol drinking by mice, rats and men: Influence of brain GABAergic transmission. Neuropharmacology, 2011, 60, 1269-1280.	4.1	50
23	Prenatal Exposure to Per- and Polyfluoroalkyl Substances, Umbilical Cord Blood DNA Methylation, and Cardio-Metabolic Indicators in Newborns: The Healthy Start Study. Environmental Health Perspectives, 2020, 128, 127014.	6.0	49
24	The Association of Adiponectin with Computed Tomography Phenotypes in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 561-566.	5.6	48
25	MSPrepâ€"Summarization, normalization and diagnostics for processing of mass spectrometryâ€"based metabolomic data. Bioinformatics, 2014, 30, 133-134.	4.1	48
26	Prenatal exposure to per- and polyfluoroalkyl substances and infant growth and adiposity: the Healthy Start Study. Environment International, 2019, 131, 104983.	10.0	48
27	Gene Expression Changes in <scp>C</scp>57<scp>BL</scp>/6<scp>J</scp> and <scp>DBA</scp>/2<scp>J</scp> Mice Following Prenatal Alcohol Exposure. Alcoholism: Clinical and Experimental Research, 2012, 36, 1519-1529.	2.4	47
28	High-Risk Human Papillomavirus E7 Alters Host DNA Methylome and Represses HLA-E Expression in Human Keratinocytes. Scientific Reports, 2017, 7, 3633.	3.3	45
29	Joint MiRNA/mRNA Expression Profiling Reveals Changes Consistent with Development of Dysfunctional Corpus Luteum after Weight Gain. PLoS ONE, 2015, 10, e0135163.	2.5	42
30	Longitudinal DNA methylation differences precede type 1 diabetes. Scientific Reports, 2020, 10, 3721.	3.3	37
31	Generalizing Moving Averages for Tiling Arrays Using Combined P-Value Statistics. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article29.	0.6	36
32	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.	2.5	35
33	Metabolite-related dietary patterns and the development of islet autoimmunity. Scientific Reports, 2019, 9, 14819.	3.3	34
34	Bronchoalveolar Lavage Fluid from COPD Patients Reveals More Compounds Associated with Disease than Matched Plasma. Metabolites, 2019, 9, 157.	2.9	32
35	Predictive Modeling for Metabolomics Data. Methods in Molecular Biology, 2020, 2104, 313-336.	0.9	32
36	Integrative Omics Approach Identifies Interleukin-16 as a Biomarker of Emphysema. OMICS A Journal of Integrative Biology, 2013, 17, 619-626.	2.0	31

#	Article	IF	Citations
37	The discordant method: a novel approach for differential correlation. Bioinformatics, 2016, 32, 690-696.	4.1	30
38	Unsupervised discovery of phenotype-specific multi-omics networks. Bioinformatics, 2019, 35, 4336-4343.	4.1	30
39	A Practical Guide to Metabolomics Software Development. Analytical Chemistry, 2021, 93, 1912-1923.	6.5	30
40	Biphasic pro-melanogenic and pro-apoptotic effects of all-trans-retinoic acid (ATRA) on human melanocytes: Time-course study. Journal of Dermatological Science, 2013, 72, 168-176.	1.9	26
41	Soluble receptor for advanced glycation end products (sRAGE) as a biomarker of COPD. Respiratory Research, 2021, 22, 127.	3.6	26
42	Identifying Protein–metabolite Networks Associated with COPD Phenotypes. Metabolites, 2020, 10, 124.	2.9	25
43	Differential correlation for sequencing data. BMC Research Notes, 2017, 10, 54.	1.4	24
44	Multiple Amino Acid Sequence Alignment Nitrogenase Component 1: Insights into Phylogenetics and Structure-Function Relationships. PLoS ONE, 2013, 8, e72751.	2.5	23
45	Plasma Metabolomic Signatures of Chronic Obstructive Pulmonary Disease and the Impact of Genetic Variants on Phenotype-Driven Modules. Network and Systems Medicine, 2020, 3, 159-181.	2.5	22
46	Qualitative Differences Between the IFNα subtypes and IFNβ Influence Chronic Mucosal HIV-1 Pathogenesis. PLoS Pathogens, 2020, 16, e1008986.	4.7	22
47	Adaptation of Mycobacterium tuberculosis to Impaired Host Immunity in HIV-Infected Patients. Journal of Infectious Diseases, 2016, 214, 1205-1211.	4.0	19
48	Metabolomic similarities between bronchoalveolar lavage fluid and plasma in humans and mice. Scientific Reports, 2017, 7, 5108.	3.3	19
49	Gene and metabolite time-course response to cigarette smoking in mouse lung and plasma. PLoS ONE, 2017, 12, e0178281.	2.5	19
50	Metabolomic Profiling Reveals Sex Specific Associations with Chronic Obstructive Pulmonary Disease and Emphysema. Metabolites, 2021, 11, 161.	2.9	19
51	Multi-omics subtyping pipeline for chronic obstructive pulmonary disease. PLoS ONE, 2021, 16, e0255337.	2.5	19
52	Aptardi predicts polyadenylation sites in sample-specific transcriptomes using high-throughput RNA sequencing and DNA sequence. Nature Communications, 2021, 12, 1652.	12.8	18
53	Meta-analysis of peripheral blood gene expression modules for COPD phenotypes. PLoS ONE, 2017, 12, e0185682.	2.5	17
54	Condition-adaptive fused graphical lasso (CFGL): An adaptive procedure for inferring condition-specific gene co-expression network. PLoS Computational Biology, 2018, 14, e1006436.	3.2	17

#	Article	IF	Citations
55	Longitudinal analysis of SARS-CoV-2 spike and RNA-dependent RNA polymerase protein sequences reveals the emergence and geographic distribution of diverse mutations. Infection, Genetics and Evolution, 2022, 97, 105153.	2.3	16
56	The oxylipin profile is associated with development of type 1 diabetes: the Diabetes Autoimmunity Study in the Young (DAISY). Diabetologia, 2021, 64, 1785-1794.	6.3	15
57	Reproducibility of mass spectrometry based metabolomics data. BMC Bioinformatics, 2021, 22, 423.	2.6	13
58	Using the Phenogen website for 'in silico' analysis of morphine-induced analgesia: identifying candidate genes. Addiction Biology, 2011, 16, 393-404.	2.6	12
59	Hands-on Workshops as An Effective Means of Learning Advanced Technologies Including Genomics, Proteomics and Bioinformatics. Genomics, Proteomics and Bioinformatics, 2013, 11, 368-377.	6.9	12
60	Metabolomics-related nutrient patterns at seroconversion and risk of progression to type 1 diabetes. Pediatric Diabetes, 2020, 21, 1202-1209.	2.9	12
61	tidyMicro: a pipeline for microbiome data analysis and visualization using the tidyverse in R. BMC Bioinformatics, 2021, 22, 41.	2.6	12
62	Identifying miRNA-mRNA Networks Associated With COPD Phenotypes. Frontiers in Genetics, 2021, 12, 748356.	2.3	12
63	Conserved Amino Acid Sequence Features in the α Subunits of MoFe, VFe, and FeFe Nitrogenases. PLoS ONE, 2009, 4, e6136.	2.5	11
64	Model based heritability scores for high-throughput sequencing data. BMC Bioinformatics, 2017, 18, 143.	2.6	11
65	Placental Insulin/IGF-1 Signaling, PGC-1α, and Inflammatory Pathways Are Associated With Metabolic Outcomes at 4–6 Years of Age: The ECHO Healthy Start Cohort. Diabetes, 2021, 70, 745-751.	0.6	11
66	An effective processing pipeline for harmonizing DNA methylation data from Illumina's 450K and EPIC platforms for epidemiological studies. BMC Research Notes, 2021, 14, 352.	1.4	11
67	A2ML1and otitis media: novel variants, differential expression, and relevant pathways. Human Mutation, 2019, 40, 1156-1171.	2.5	10
68	Bayesian inference of networks across multiple sample groups and data types. Biostatistics, 2020, 21, 561-576.	1.5	10
69	MSCAT: A Machine Learning Assisted Catalog of Metabolomics Software Tools. Metabolites, 2021, 11, 678.	2.9	10
70	Prediction of alternatively skipped exons and splicing enhancers from exon junction arrays. BMC Genomics, 2008, 9, 551.	2.8	9
71	Genetical Genomic Analysis of Complex Phenotypes Using the PhenoGen Website. Behavior Genetics, 2011, 41, 625-628.	2.1	9
72	A Bayesian Approach for Learning Gene Networks Underlying Disease Severity in COPD. Statistics in Biosciences, 2018, 10, 59-85.	1.2	9

#	Article	IF	Citations
73	miR-MaGiC improves quantification accuracy for small RNA-seq. BMC Research Notes, 2018, 11, 296.	1.4	9
74	MCMSeq: Bayesian hierarchical modeling of clustered and repeated measures RNA sequencing experiments. BMC Bioinformatics, 2020, 21, 375.	2.6	9
75	Pre-analytic Considerations for Mass Spectrometry-Based Untargeted Metabolomics Data. Methods in Molecular Biology, 2019, 1978, 323-340.	0.9	8
76	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (Schistosoma japonicum). PLoS Neglected Tropical Diseases, 2021, 15, e0009020.	3.0	8
77	A Metabolomic Severity Score for Airflow Obstruction and Emphysema. Metabolites, 2022, 12, 368.	2.9	8
78	Mechanism-aware imputation: a two-step approach in handling missing values in metabolomics. BMC Bioinformatics, 2022, 23, 179.	2.6	7
79	Predictive modeling of miRNA-mediated predisposition to alcohol-related phenotypes in mouse. BMC Genomics, 2018, 19, 639.	2.8	6
80	Associations between the activity of placental nutrient-sensing pathways and neonatal and postnatal metabolic health: the ECHO Healthy Start cohort. International Journal of Obesity, 2020, 44, 2203-2212.	3.4	6
81	DNA methylation near the INS gene is associated with INS genetic variation (rs689) and type 1 diabetes in the Diabetes Autoimmunity Study in the Young. Pediatric Diabetes, 2020, 21, 597-605.	2.9	6
82	Inverse probability weighting is an effective method to address selection bias during the analysis of high dimensional data. Genetic Epidemiology, 2021, 45, 593-603.	1.3	6
83	A graphical model method for integrating multiple sources of genome-scale data. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 469-87.	0.6	5
84	Phospholipid Levels at Seroconversion Are Associated With Resolution of Persistent Islet Autoimmunity: The Diabetes Autoimmunity Study in the Young. Diabetes, 2021, 70, 1592-1601.	0.6	5
85	Metabolomic Profiles in Childhood and Adolescence Are Associated with Fetal Overnutrition. Metabolites, 2022, 12, 265.	2.9	5
86	Insight into genetic regulation of miRNA in mouse brain. BMC Genomics, 2019, 20, 849.	2.8	4
87	Comparing Statistical Tests for Differential Network Analysis of Gene Modules. Frontiers in Genetics, 2021, 12, 630215.	2.3	4
88	PaIRKAT: A pathway integrated regression-based kernel association test with applications to metabolomics and COPD phenotypes. PLoS Computational Biology, 2021, 17, e1008986.	3.2	4
89	Epigenome-Wide Association Study of Infant Feeding and DNA Methylation in Infancy and Childhood in a Population at Increased Risk for Type 1 Diabetes. Nutrients, 2021, 13, 4057.	4.1	4
90	Sex-Specific Differences in MicroRNA Expression During Human Fetal Lung Development. Frontiers in Genetics, 2022, 13, 762834.	2.3	4

#	Article	IF	Citations
91	Ambient air pollution during pregnancy and DNA methylation in umbilical cord blood, with potential mediation of associations with infant adiposity: The Healthy Start study. Environmental Research, 2022, 214, 113881.	7.5	4
92	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.	0.6	3
93	Genetic analysis of a murine QTL for diet restriction on chromosome 15. Age, 2015, 37, 9740.	3.0	3
94	An Augmented High-Dimensional Graphical Lasso Method to Incorporate Prior Biological Knowledge for Global Network Learning. Frontiers in Genetics, 2021, 12, 760299.	2.3	3
95	Granzyme B $^+$ CD4 T cells accumulate in the colon during chronic HIV-1 infection. Gut Microbes, 2022, 14, 2045852.	9.8	3
96	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). Diabetes, 2022, 71, 2048-2057.	0.6	3
97	c-REDUCE: Incorporating sequence conservation to detect motifs that correlate with expression. BMC Bioinformatics, 2008, 9, 506.	2.6	2
98	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. PLoS ONE, 2011, 6, e26105.	2.5	2
99	Post-GWAS Prioritization Through Data Integration Provides Novel Insights on Chronic Obstructive Pulmonary Disease. Statistics in Biosciences, 2017, 9, 605-621.	1.2	2
100	Using a spatial point process framework to characterize lung computed tomography scans. Spatial Statistics, 2019, 29, 243-267.	1.9	2
101	Alcohol Use Disorders Are Associated With a Unique Impact on Airway Epithelial Cell Gene Expression. Alcoholism: Clinical and Experimental Research, 2020, 44, 1571-1584.	2.4	2
102	Semi-Supervised Learning Using Hierarchical Mixture Models: Gene Essentiality Case Study. Mathematical and Computational Applications, 2021, 26, 40.	1.3	1
103	A Mediation Approach to Discovering Causal Relationships between the Metabolome and DNA Methylation in Type 1 Diabetes. Metabolites, 2021, 11, 542.	2.9	1
104	Development of a tissue augmented Bayesian model for expression quantitative trait loci analysis. Mathematical Biosciences and Engineering, 2020, 17, 122-143.	1.9	1
105	Biomarkers Predictive of Exacerbations in the SPIROMICS and COPDGene Cohorts. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 473-481.	5.6	1
106	Systems genetics analysis of the LXS recombinant inbred mouse strains:Genetic and molecular insights into acute ethanol tolerance. PLoS ONE, 2020, 15, e0240253.	2.5	1
107	Significant Subgraph Detection in Multi-omics Networks for Disease Pathway Identification. Frontiers in Big Data, 0, 5, .	2.9	1
108	Interleukin-16 Expression Is Down Regulated In Peripheral Blood Mononuclear Cells From Patients With COPD. , 2011, , .		0

#	Article	IF	Citations
109	Modeling considerations for using expression data from multiple species. Statistics in Medicine, 2013, 32, 4057-4070.	1.6	0
110	Chronic Marijuana Use Is Associated with Gene Expression Changes in BAL. American Journal of Respiratory Cell and Molecular Biology, 2022, 66, 238-239.	2.9	0
111	Title is missing!. , 2020, 15, e0240253.		0
112	Title is missing!. , 2020, 15, e0240253.		0
113	Title is missing!. , 2020, 15, e0240253.		0
114	Title is missing!. , 2020, 15, e0240253.		0
115	Title is missing!. , 2020, 16, e1008986.		0
116	Title is missing!. , 2020, 16, e1008986.		0
117	Title is missing!. , 2020, 16, e1008986.		0
118	Title is missing!. , 2020, 16, e1008986.		0
119	Title is missing!. , 2020, 16, e1008986.		0
120	Title is missing!. , 2020, 16, e1008986.		0