Eric E Schadt

List of Publications by Year
in descending order

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Version: 2024-02-01

304 papers	66,407 citations	2311 98 h-index	959 238 g-index
326 all docs	326 docs citations	326 times ranked	82686 citing authors

#	Article	IF	Citations
1	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
5	Bayesian Test for Colocalisation between Pairs of Genetic Association Studies Using Summary Statistics. PLoS Genetics, 2014, 10, e1004383.	1.5	2,012
6	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
7	An inflammatory cytokine signature predicts COVID-19 severity and survival. Nature Medicine, 2020, 26, 1636-1643.	15.2	1,860
8	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
9	Geroscience: Linking Aging to Chronic Disease. Cell, 2014, 159, 709-713.	13.5	1,709
10	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimerâ€™s Disease. Cell, 2013, 153, 707-720.	13.5	1,505
11	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
12	Genetics of gene expression surveyed in maize, mouse and man. Nature, 2003, 422, 297-302.	13.7	1,401
13	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
14	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	13.7	1,209
15	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
16	From noncoding variant to phenotype via SORT1 at the 1p13 cholesterol locus. Nature, 2010, 466, 714-719.	13.7	1,018
17	An integrative genomics approach to infer causal associations between gene expression and disease. Nature Genetics, 2005, 37, 710-717.	9.4	967
18	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952

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19	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	2.6	872
20	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
21	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	13.7	840
22	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
23	Tissue-specific expression and regulation of sexually dimorphic genes in mice. Genome Research, 2006, 16, 995-1004.	2.4	785
24	Origins of theE. coliStrain Causing an Outbreak of Hemolyticâ€“Uremic Syndrome in Germany. New England Journal of Medicine, 2011, 365, 709-717.	13.9	778
25	A window into third-generation sequencing. Human Molecular Genetics, 2010, 19, R227-R240.	1.4	761
26	Molecular networks as sensors and drivers of common human diseases. Nature, 2009, 461, 218-223.	13.7	700
27	The Origin of the Haitian Cholera Outbreak Strain. New England Journal of Medicine, 2011, 364, 33-42.	13.9	676
28	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
29	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	2.4	575
30	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
31	Multiscale Analysis of Independent Alzheimerâ€™s Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. Neuron, 2018, 99, 64-82.e7.	3.8	558
32	Large-scale proteomic analysis of Alzheimerâ€™s disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. Nature Medicine, 2020, 26, 769-780.	15.2	547
33	Single-Cell Analysis of Crohnâ€™s Disease Lesions Identifies a Pathogenic Cellular Module Associated with Resistance to Anti-TNF Therapy. Cell, 2019, 178, 1493-1508.e20.	13.5	519
34	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. Nature Genetics, 2008, 40, 854-861.	9.4	515
35	AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160.	3.0	500
36	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	9.0	465

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37	variancePartition: interpreting drivers of variation in complex gene expression studies. BMC Bioinformatics, 2016, 17, 483.	1.2	441
38	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
39	Experimental annotation of the human genome using microarray technology. Nature, 2001, 409, 922-927.	13.7	427
40	Genome-wide mapping of methylated adenine residues in pathogenic Escherichia coli using single-molecule real-time sequencing. Nature Biotechnology, 2012, 30, 1232-1239.	9.4	365
41	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
42	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimerâ€™s disease susceptibility. Nature Genetics, 2018, 50, 1584-1592.	9.4	307
43	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	9.4	273
44	Functional variants in the LRRK2 gene confer shared effects on risk for Crohnâ€™s disease and Parkinsonâ€™s disease. Science Translational Medicine, 2018, 10, .	5.8	273
45	A network view of disease and compound screening. Nature Reviews Drug Discovery, 2009, 8, 286-295.	21.5	269
46	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. Stem Cell Reports, 2017, 8, 1516-1524.	2.3	260
47	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. Nature Genetics, 2009, 41, 415-423.	9.4	257
48	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. Nature Genetics, 2012, 44, 841-847.	9.4	252
49	Cis-acting expression quantitative trait loci in mice. Genome Research, 2005, 15, 681-691.	2.4	246
50	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	3.9	246
51	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
52	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	2.9	241
53	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	6.0	241
54	Massive parallel sequencing uncovers actionable FGFR2â€“PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. Nature Communications, 2015, 6, 6087.	5.8	240

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55	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. Genome Research, 2010, 20, 1020-1036.	2.4	231
56	Analysis of Transcriptional Variability in a Large Human iPSC Library Reveals Genetic and Non-genetic Determinants of Heterogeneity. Cell Stem Cell, 2017, 20, 518-532.e9.	5.2	230
57	Intratumoral heterogeneity and clonal evolution in liver cancer. Nature Communications, 2020, 11, 291.	5.8	230
58	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
59	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	5.8	225
60	Integrating Pathway Analysis and Genetics of Gene Expression for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 581-591.	2.6	224
61	Integrative network analysis of nineteen brain regions identifies molecular signatures and networks underlying selective regional vulnerability to Alzheimerâ€™s disease. Genome Medicine, 2016, 8, 104.	3.6	224
62	Genome-wide identification of microRNAs regulating cholesterol and triglyceride homeostasis. Nature Medicine, 2015, 21, 1290-1297.	15.2	214
63	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
64	An integrative genomics approach to the reconstruction of gene networks in segregating populations. Cytogenetic and Genome Research, 2004, 105, 363-374.	0.6	204
65	iPSC-Derived Dopamine Neurons Reveal Differences between Monozygotic Twins Discordant for Parkinsonâ€™s Disease. Cell Reports, 2014, 9, 1173-1182.	2.9	202
66	Disentangling molecular relationships with a causal inference test. BMC Genetics, 2009, 10, 23.	2.7	199
67	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. American Journal of Human Genetics, 2014, 94, 198-208.	2.6	199
68	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	9.4	199
69	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	2.9	199
70	Human Pancreatic Î² Cell lncRNAs Control Cell-Specific Regulatory Networks. Cell Metabolism, 2017, 25, 400-411.	7.2	195
71	An Integration of Genome-Wide Association Study and Gene Expression Profiling to Prioritize the Discovery of Novel Susceptibility Loci for Osteoporosis-Related Traits. PLoS Genetics, 2010, 6, e1000977.	1.5	191
72	Increasing the Power to Detect Causal Associations by Combining Genotypic and Expression Data in Segregating Populations. PLoS Computational Biology, 2007, 3, e69.	1.5	188

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73	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. Nature Biotechnology, 2017, 35, 354-362.	9.4	185
74	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	3.2	182
75	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	1.6	180
76	A hybrid approach for the automated finishing of bacterial genomes. Nature Biotechnology, 2012, 30, 701-707.	9.4	178
77	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
78	Mutations in Tetratricopeptide Repeat Domain 7A Result in a Severe Form of Very Early Onset Inflammatory Bowel Disease. Gastroenterology, 2014, 146, 1028-1039.	0.6	175
79	Machine Learning to Predict Mortality and Critical Events in a Cohort of Patients With COVID-19 in New York City: Model Development and Validation. Journal of Medical Internet Research, 2020, 22, e24018.	2.1	174
80	Stitching together Multiple Data Dimensions Reveals Interacting Metabolomic and Transcriptomic Networks That Modulate Cell Regulation. PLoS Biology, 2012, 10, e1001301.	2.6	173
81	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
82	Moving toward a system genetics view of disease. Mammalian Genome, 2007, 18, 389-401.	1.0	165
83	Liver and Adipose Expression Associated SNPs Are Enriched for Association to Type 2 Diabetes. PLoS Genetics, 2010, 6, e1000932.	1.5	161
84	A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. Genome Research, 2011, 21, 1008-1016.	2.4	161
85	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
86	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
87	Deciphering bacterial epigenomes using modern sequencing technologies. Nature Reviews Genetics, 2019, 20, 157-172.	7.7	143
88	Multi-tissue coexpression networks reveal unexpected subnetworks associated with disease. Genome Biology, 2009, 10, R55.	13.9	137
89	Molecular subtyping of Alzheimerâ€™s disease using RNA sequencing data reveals novel mechanisms and targets. Science Advances, 2021, 7, .	4.7	137
90	Bayesian method to predict individual SNP genotypes from gene expression data. Nature Genetics, 2012, 44, 603-608.	9.4	136

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91	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. Molecular Systems Biology, 2012, 8, 594.	3.2	134
92	The changing privacy landscape in the era of big data. Molecular Systems Biology, 2012, 8, 612.	3.2	131
93	Personalized Circulating Tumor DNA Biomarkers Dynamically Predict Treatment Response and Survival In Gynecologic Cancers. PLoS ONE, 2015, 10, e0145754.	1.1	129
94	Genome-Wide Significant Loci: HowÂImportant Are They?. Journal of the American College of Cardiology, 2015, 65, 830-845.	1.2	129
95	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. Nature Communications, 2016, 7, 12092.	5.8	123
96	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
97	Systems biology of asthma and allergic diseases: AÂmultiscale approach. Journal of Allergy and Clinical Immunology, 2015, 135, 31-42.	1.5	121
98	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. Cell Systems, 2016, 2, 196-208.	2.9	120
99	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
100	Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation. Nature Biotechnology, 2018, 36, 61-69.	9.4	116
101	NEW: Network-Enabled Wisdom in Biology, Medicine, and Health Care. Science Translational Medicine, 2012, 4, 115rv1.	5.8	115
102	Comprehensive Methylome Characterization of Mycoplasma genitalium and Mycoplasma pneumoniae at Single-Base Resolution. PLoS Genetics, 2013, 9, e1003191.	1.5	109
103	Transformative Network Modeling of Multi-omics Data Reveals Detailed Circuits, Key Regulators, and Potential Therapeutics for Alzheimerâ€™s Disease. Neuron, 2021, 109, 257-272.e14.	3.8	108
104	CRISPR/Cas9-Correctable mutation-related molecular and physiological phenotypes in iPSC-derived Alzheimerâ€™s PSEN2 N141I neurons. Acta Neuropathologica Communications, 2017, 5, 77.	2.4	102
105	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	1.1	101
106	Analytical validation of whole exome and whole genome sequencing for clinical applications. BMC Medical Genomics, 2014, 7, 20.	0.7	100
107	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimerâ€™s disease. Molecular Neurodegeneration, 2017, 12, 82.	4.4	100
108	Very Early Onset Inflammatory Bowel Disease: A Clinical Approach With a Focus on the Role of Genetics and Underlying Immune Deficiencies. Inflammatory Bowel Diseases, 2020, 26, 820-842.	0.9	100

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109	Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases. Genome Research, 2013, 23, 129-141.	2.4	99
110	Phase 2 Trial of Gemcitabine, Cisplatin, plus Ipilimumab in Patients with Metastatic Urothelial Cancer and Impact of DNA Damage Response Gene Mutations on Outcomes. European Urology, 2018, 73, 751-759.	0.9	99
111	Genomic and Network Patterns of Schizophrenia Genetic Variation in Human Evolutionary Accelerated Regions. Molecular Biology and Evolution, 2015, 32, 1148-1160.	3.5	98
112	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2â€“related Disease. Gastroenterology, 2021, 160, 287-301.e20.	0.6	98
113	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	9.4	97
114	Motivations, concerns and preferences of personal genome sequencing research participants: Baseline findings from the HealthSeq project. European Journal of Human Genetics, 2016, 24, 14-20.	1.4	94
115	Multiscale causal networks identify VGF as a key regulator of Alzheimerâ€™s disease. Nature Communications, 2020, 11, 3942.	5.8	94
116	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
117	Elucidating the murine brain transcriptional network in a segregating mouse population to identify core functional modules for obesity and diabetes. Journal of Neurochemistry, 2006, 97, 50-62.	2.1	89
118	Variants in TRIM22 That Affect NOD2 Signaling Are Associated With Very-Early-Onset Inflammatory Bowel Disease. Gastroenterology, 2016, 150, 1196-1207.	0.6	88
119	Deficiency of TYROBP, an adapter protein for TREM2 and CR3 receptors, is neuroprotective in a mouse model of early Alzheimerâ€™s pathology. Acta Neuropathologica, 2017, 134, 769-788.	3.9	85
120	Altering Sphingolipid Metabolism Attenuates Cell Death and Inflammatory Response After Myocardial Infarction. Circulation, 2020, 141, 916-930.	1.6	84
121	Genomic profiling reveals mutational landscape in parathyroid carcinomas. JCI Insight, 2017, 2, e92061.	2.3	84
122	Biallelic Mutations in MRPS34 Lead to Instability of the Small Mitoribosomal Subunit and Leigh Syndrome. American Journal of Human Genetics, 2017, 101, 239-254.	2.6	83
123	Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. Nature Communications, 2015, 6, 7438.	5.8	82
124	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	1.5	82
125	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. Genome Research, 2018, 28, 1067-1078.	2.4	80
126	A Next Generation Multiscale View of Inborn Errors of Metabolism. Cell Metabolism, 2016, 23, 13-26.	7.2	79

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127	PparÎ³2 Is a Key Driver of Longevity in the Mouse. PLoS Genetics, 2009, 5, e1000752.	1.5	78
128	Integrative Analysis of a Cross-Loci Regulation Network Identifies App as a Gene Regulating Insulin Secretion from Pancreatic Islets. PLoS Genetics, 2012, 8, e1003107.	1.5	76
129	Meditation and vacation effects have an impact on disease-associated molecular phenotypes. Translational Psychiatry, 2016, 6, e880-e880.	2.4	76
130	Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. Nature Microbiology, 2020, 5, 166-180.	5.9	75
131	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
132	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. Science Advances, 2019, 5, eaav6528.	4.7	74
133	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	3.6	71
134	Predictive Genes in Adjacent Normal Tissue Are Preferentially Altered by sCNV during Tumorigenesis in Liver Cancer and May Rate Limiting. PLoS ONE, 2011, 6, e20090.	1.1	68
135	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	5.8	68
136	Detecting DNA Modifications from SMRT Sequencing Data by Modeling Sequence Context Dependence of Polymerase Kinetic. PLoS Computational Biology, 2013, 9, e1002935.	1.5	67
137	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. Nature Communications, 2017, 8, 767.	5.8	67
138	Integrative approach to sporadic Alzheimerâ€™s disease:Âdeficiency of TYROBPÂin cerebral AÎ² amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing AÎ² burden. Molecular Psychiatry, 2019, 24, 431-446.	4.1	67
139	Inferring causal genomic alterations in breast cancer using gene expression data. BMC Systems Biology, 2011, 5, 121.	3.0	64
140	Integrative transcriptomic analysis reveals key drivers of acute peanut allergic reactions. Nature Communications, 2017, 8, 1943.	5.8	64
141	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. BMC Medical Genomics, 2014, 7, 48.	0.7	63
142	Family-Based Approaches to Cardiovascular Health Promotion. Journal of the American College of Cardiology, 2016, 67, 1725-1737.	1.2	63
143	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. Nature Communications, 2018, 9, 4412.	5.8	63
144	A Bayesian Partition Method for Detecting Pleiotropic and Epistatic eQTL Modules. PLoS Computational Biology, 2010, 6, e1000642.	1.5	61

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145	GJA1 (connexin43) is a key regulator of Alzheimerâ€™s disease pathogenesis. Acta Neuropathologica Communications, 2018, 6, 144.	2.4	59
146	The Role of Macromolecular Damage in Aging and Age-related Disease. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2014, 69, S28-S32.	1.7	57
147	Deciphering H3K4me3 broad domains associated with gene-regulatory networks and conserved epigenomic landscapes in the human brain. Translational Psychiatry, 2015, 5, e679-e679.	2.4	57
148	Characterizing Dynamic Changes in the Human Blood Transcriptional Network. PLoS Computational Biology, 2010, 6, e1000671.	1.5	54
149	Psychological and behavioural impact of returning personal results from whole-genome sequencing: the HealthSeq project. European Journal of Human Genetics, 2017, 25, 280-292.	1.4	54
150	Integrating siRNA and proteinâ€“protein interaction data to identify an expanded insulin signaling network. Genome Research, 2009, 19, 1057-1067.	2.4	53
151	From smartphone to EHR: a case report on integrating patient-generated health data. Npj Digital Medicine, 2018, 1, 23.	5.7	52
152	Discovering genetic interactions bridging pathways in genome-wide association studies. Nature Communications, 2019, 10, 4274.	5.8	52
153	VGF-derived peptide TLQP-21 modulates microglial function through C3aR1 signaling pathways and reduces neuropathology in 5xFAD mice. Molecular Neurodegeneration, 2020, 15, 4.	4.4	52
154	Dissection of Immune Gene Networks in Primary Melanoma Tumors Critical for Antitumor Surveillance of Patients with Stage IIâ€“III Resectable Disease. Journal of Investigative Dermatology, 2014, 134, 2202-2211.	0.3	51
155	A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. Scientific Reports, 2018, 8, 8826.	1.6	51
156	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
157	Melanocortin 4 Receptor Pathway Dysfunction in Obesity: Patient Stratification Aimed at MC4R Agonist Treatment. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 2601-2612.	1.8	50
158	Genome Plasticity of agr -Defective Staphylococcus aureus during Clinical Infection. Infection and Immunity, 2018, 86, .	1.0	50
159	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. GeroScience, 2020, 42, 353-372.	2.1	50
160	Transcriptional dissection of melanoma identifies a high-risk subtype underlying TP53 family genes and epigenome deregulation. JCI Insight, 2017, 2, .	2.3	48
161	Integrative approach to sporadic Alzheimerâ€™s disease: deficiency of TYROBP in a tauopathy mouse model reduces C1q and normalizes clinical phenotype while increasing spread and state of phosphorylation of tau. Molecular Psychiatry, 2019, 24, 1383-1397.	4.1	46
162	Downregulation of Carnitine Acyl-Carnitine Translocase by miRNAs 132 and 212 Amplifies Glucose-Stimulated Insulin Secretion. Diabetes, 2014, 63, 3805-3814.	0.3	45

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163	Personalized Ovarian Cancer Disease Surveillance and Detection of Candidate Therapeutic Drug Target in Circulating Tumor DNA. Neoplasia, 2014, 16, 97-W29.	2.3	45
164	Contribution of Gene Regulatory Networks to Heritability of CoronaryÂArtery Disease. Journal of the American College of Cardiology, 2019, 73, 2946-2957.	1.2	45
165	The effect of food intake on gene expression in human peripheral blood. Human Molecular Genetics, 2010, 19, 159-169.	1.4	44
166	Clues from the resilient. Science, 2014, 344, 970-972.	6.0	44
167	In uteroexposures to environmental organic pollutants disrupt epigenetic marks linked to fetoplacental development. Environmental Epigenetics, 2016, 2, dvv013.	0.9	44
168	Dual transcriptomic and epigenomic study of reaction severity in peanut-allergic children. Journal of Allergy and Clinical Immunology, 2020, 145, 1219-1230.	1.5	44
169	Integrative study of the upper and lower airway microbiome and transcriptome in asthma. JCI Insight, 2020, 5, .	2.3	44
170	The asthma mobile health study, smartphone data collected using ResearchKit. Scientific Data, 2018, 5, 180096.	2.4	43
171	TGFÎ² Receptor 1: An Immune Susceptibility Gene in HPV-Associated Cancer. Cancer Research, 2014, 74, 6833-6844.	0.4	42
172	Myeloid Cellâ€“associated Resistance to PD-1/PD-L1 Blockade in Urothelial Cancer Revealed Through Bulk and Single-cell RNA Sequencing. Clinical Cancer Research, 2021, 27, 4287-4300.	3.2	42
173	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	5.8	42
174	Predispositional genome sequencing in healthy adults: design, participant characteristics, and early outcomes of the PeopleSeq Consortium. Genome Medicine, 2019, 11, 10.	3.6	41
175	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. PLoS Genetics, 2017, 13, e1006565.	1.5	41
176	Discover the network mechanisms underlying the connections between aging and age-related diseases. Scientific Reports, 2016, 6, 32566.	1.6	40
177	Blood and Intestine eQTLs from an Anti-TNF-Resistant Crohn's Disease Cohort Inform IBD Genetic Association Loci. Clinical and Translational Gastroenterology, 2016, 7, e177.	1.3	40
178	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	4.1	40
179	Autotransporters but not pAA are critical for rabbit colonization by Shiga toxin-producing Escherichia coli O104:H4. Nature Communications, 2014, 5, 3080.	5.8	39
180	Cancer gene profiling in non-small cell lung cancers reveals activating mutations in JAK2 and JAK3 with therapeutic implications. Genome Medicine, 2017, 9, 89.	3.6	39

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181	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.	6.5	39
182	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	0.6	37
183	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	1.5	35
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