Eric E Schadt

List of Publications by Year
in descending order

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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	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	0.6	37
2	Integrative Analysis of the Inflammatory Bowel Disease Serum Metabolome Improves Our Understanding of Genetic Etiology and Points to Novel Putative Therapeutic Targets. Gastroenterology, 2022, 162, 828-843.e11.	0.6	26
3	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
4	Targeted Next-Generation Sequencing Reveals Exceptionally High Rates of Molecular Driver Mutations in Never-Smokers With Lung Adenocarcinoma. Oncologist, 2022, 27, 476-486.	1.9	15
5	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. Nature Communications, 2022, 13, 1592.	5.8	16
6	Whole genome sequencingâ€“based copy number variations reveal novel pathways and targets in Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 1846-1867.	0.4	13
7	Traversing industry and academia in biomedicine: the best of both worlds?. Nature Reviews Genetics, 2022, 23, 461-466.	7.7	2
8	QOPI Clinical Informatics: A digital platform to enable real-time quality reporting, clinical decision support, and rapid learning.. Journal of Clinical Oncology, 2022, 40, e13545-e13545.	0.8	0
9	Health outcomes modelling of RNA-based versus DNA-based detection of driver gene rearrangements in non-small cell lung cancer.. Journal of Clinical Oncology, 2022, 40, e18837-e18837.	0.8	0
10	Landscape of tumor genetic testing and targeted therapies over an eight-year span in a rural population.. Journal of Clinical Oncology, 2022, 40, e15036-e15036.	0.8	0
11	Implementation of the Avera/Sema4 oncology and analytics protocol (ASAP).. Journal of Clinical Oncology, 2022, 40, TPS6605-TPS6605.	0.8	0
12	Incident Cancer Risk and Signatures Among Older MUTYH Carriers: Analysis of Population-Based and Genomic Cohorts. Cancer Prevention Research, 2022, 15, 509-519.	0.7	1
13	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
14	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
15	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 372-387.	1.8	12
16	Network study of nasal transcriptome profiles reveals master regulator genes of asthma. Journal of Allergy and Clinical Immunology, 2021, 147, 879-893.	1.5	22
17	AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160.	3.0	500
18	Molecular subtyping of Alzheimerâ€™s disease using RNA sequencing data reveals novel mechanisms and targets. Science Advances, 2021, 7, .	4.7	137

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19	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	5.8	35
20	Polygenic risk score for alcohol drinking behavior improves prediction of inflammatory bowel disease risk. Human Molecular Genetics, 2021, 30, 514-523.	1.4	2
21	A Drosophila platform identifies a novel, personalized therapy for a patient with adenoid cystic carcinoma. IScience, 2021, 24, 102212.	1.9	23
22	Rare Germline Pathogenic Variants Identified by Multigene Panel Testing and the Risk of Aggressive Prostate Cancer. Cancers, 2021, 13, 1495.	1.7	12
23	Bayesian Model Infers Drug Repurposing Candidates for Treatment of COVID-19. Applied Sciences (Switzerland), 2021, 11, 2466.	1.3	2
24	Haploinsufficiency of POU4F1 causes an ataxia syndrome with hypotonia and intention tremor. Human Mutation, 2021, 42, 685-693.	1.1	0
25	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18
26	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
27	A composite biomarker of neutrophil-lymphocyte ratio and hemoglobin level correlates with clinical response to PD-1 and PD-L1 inhibitors in advanced non-small cell lung cancers. BMC Cancer, 2021, 21, 441.	1.1	25
28	Phenotyping of clinical trial eligibility text from cancer studies into computable criteria in electronic health records.. Journal of Clinical Oncology, 2021, 39, 6592-6592.	0.8	0
29	Detecting and phasing minor single-nucleotide variants from long-read sequencing data. Nature Communications, 2021, 12, 3032.	5.8	15
30	Extracting longitudinal anticancer treatments at scale using deep natural language processing and temporal reasoning.. Journal of Clinical Oncology, 2021, 39, e18747-e18747.	0.8	0
31	Analyzing treatment patterns and time to the next treatment in chronic lymphocytic leukemia real-world data using automated temporal phenotyping.. Journal of Clinical Oncology, 2021, 39, e19512-e19512.	0.8	1
32	Continuous genomic monitoring of multiple myeloma patients to identify patients of high risk for poor prognosis.. Journal of Clinical Oncology, 2021, 39, e20035-e20035.	0.8	0
33	Effect of APOE and a polygenic risk score on incident dementia and cognitive decline in a healthy older population. Aging Cell, 2021, 20, e13384.	3.0	16
34	Genetic variants associated with inherited cardiovascular disorders among 13,131 asymptomatic older adults of European descent. Npj Genomic Medicine, 2021, 6, 51.	1.7	11
35	Genomic Risk Prediction for Breast Cancer in Older Women. Cancers, 2021, 13, 3533.	1.7	6
36	Protective lipid-lowering variants in healthy older individuals without coronary heart disease. Open Heart, 2021, 8, e001710.	0.9	1

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37	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
38	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	5.8	42
39	Prognostic value of polygenic risk scores for adults with psychosis. Nature Medicine, 2021, 27, 1576-1581.	15.2	31
40	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. Gastroenterology, 2021, 161, 1953-1968.e15.	0.6	14
41	Deep Analysis of the Peripheral Immune System in IBD Reveals New Insight in Disease Subtyping and Response to Monotherapy or Combination Therapy. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 599-632.	2.3	17
42	Population-based estimates of breast cancer risk for carriers of pathogenic variants identified by gene-panel testing. Npj Breast Cancer, 2021, 7, 153.	2.3	10
43	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. GeroScience, 2020, 42, 353-372.	2.1	50
44	Lessons learned from expanded reproductive carrier screening in selfâ€reported Ashkenazi, Sephardi, and Mizrahi Jewish patients. Molecular Genetics & Genomic Medicine, 2020, 8, e1053.	0.6	16
45	A New Liver Expression Quantitative Trait Locus Map From 1,183 Individuals Provides Evidence for Novel Expression Quantitative Trait Loci of Drug Response, Metabolic, and Sexâ€Biased Phenotypes. Clinical Pharmacology and Therapeutics, 2020, 107, 1383-1393.	2.3	20
46	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
47	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
48	Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. Nature Microbiology, 2020, 5, 166-180.	5.9	75
49	Sex differences in human adipose tissue gene expression and genetic regulation involve adipogenesis. Genome Research, 2020, 30, 1379-1392.	2.4	35
50	Aberrant methylation underlies insulin gene expression in human insulinoma. Nature Communications, 2020, 11, 5210.	5.8	9
51	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
52	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	2.9	199
53	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
54	Multiscale causal networks identify VGF as a key regulator of Alzheimerâ€™s disease. Nature Communications, 2020, 11, 3942.	5.8	94

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55	Sampling the host response to SARS-CoV-2 in hospitals under siege. Nature Medicine, 2020, 26, 1157-1158.	15.2	27
56	An inflammatory cytokine signature predicts COVID-19 severity and survival. Nature Medicine, 2020, 26, 1636-1643.	15.2	1,860
57	A consensus proteomic analysis of Alzheimerâ€™s disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. Alzheimer's and Dementia, 2020, 16, e039504.	0.4	0
58	Familial Hypercholesterolemia in a Healthy Elderly Population. Circulation Genomic and Precision Medicine, 2020, 13, e002938.	1.6	8
59	A reference profile-free deconvolution method to infer cancer cell-intrinsic subtypes and tumor-type-specific stromal profiles. Genome Medicine, 2020, 12, 24.	3.6	34
60	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	9.4	97
61	Medically actionable pathogenic variants in a population of 13,131 healthy elderly individuals. Genetics in Medicine, 2020, 22, 1883-1886.	1.1	20
62	Systems modeling of white matter microstructural abnormalities in Alzheimer's disease. NeuroImage: Clinical, 2020, 26, 102203.	1.4	12
63	Intratumoral heterogeneity and clonal evolution in liver cancer. Nature Communications, 2020, 11, 291.	5.8	230
64	Altering Sphingolipid Metabolism Attenuates Cell Death and Inflammatory Response After Myocardial Infarction. Circulation, 2020, 141, 916-930.	1.6	84
65	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
66	Comparison of brain connectomes by MRI and genomics and its implication in Alzheimerâ€™s disease. BMC Medicine, 2020, 18, 23.	2.3	6
67	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
68	Prevalence and disease predisposition of p.A91V perforin in an aged population of European ancestry. Blood, 2020, 135, 582-584.	0.6	6
69	Integrative study of the upper and lower airway microbiome and transcriptome in asthma. JCI Insight, 2020, 5, .	2.3	44
70	Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for insulin responsiveness. PLoS Computational Biology, 2020, 16, e1008491.	1.5	14
71	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
72	289â€…PGV-001: a phase 1 trial of a personalized neoantigen peptide vaccine for the treatment of malignancies in the adjuvant setting. , 2020, , .		0

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73	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
74	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. BMC Medical Genomics, 2019, 12, 108.	0.7	8
75	Structural variation at the CYP2C locus: Characterization of deletion and duplication alleles. Human Mutation, 2019, 40, e37-e51.	1.1	15
76	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
77	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	5.8	68
78	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
79	Discovering genetic interactions bridging pathways in genome-wide association studies. Nature Communications, 2019, 10, 4274.	5.8	52
80	A Network Analysis of Multiple Myeloma Related Gene Signatures. Cancers, 2019, 11, 1452.	1.7	23
81	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
82	Biology and Bias in Cell Type-Specific RNAseq of Nucleus Accumbens Medium Spiny Neurons. Scientific Reports, 2019, 9, 8350.	1.6	27
83	Contribution of Gene Regulatory Networks to Heritability of CoronaryÂArtery Disease. Journal of the American College of Cardiology, 2019, 73, 2946-2957.	1.2	45
84	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. Science Advances, 2019, 5, eaav6528.	4.7	74
85	ORE identifies extreme expression effects enriched for rare variants. Bioinformatics, 2019, 35, 3906-3912.	1.8	8
86	Predispositional genome sequencing in healthy adults: design, participant characteristics, and early outcomes of the PeopleSeq Consortium. Genome Medicine, 2019, 11, 10.	3.6	41
87	A Complete Genome Screening Program of Clinical Methicillin-Resistant Staphylococcus aureus Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. Journal of Clinical Microbiology, 2019, 57, .	1.8	16
88	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2019, 13, 462-471.	0.6	18
89	CDT2â€controlled cell cycle reentry regulates the pathogenesis of Alzheimer's disease. Alzheimer's and Dementia, 2019, 15, 217-231.	0.4	28
90	Deciphering bacterial epigenomes using modern sequencing technologies. Nature Reviews Genetics, 2019, 20, 157-172.	7.7	143

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91	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
92	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
93	Investigating racial differences in treatment responses through analysis of real-world data (RWD).. Journal of Clinical Oncology, 2019, 37, e18141-e18141.	0.8	0
94	Analysis of real-world data (RWD) on treatment (tx) sequencing in patients with advanced non-small cell lung cancer (aNSCLC).. Journal of Clinical Oncology, 2019, 37, e20642-e20642.	0.8	0
95	Inching towards precision medicine for multiple myeloma with causal network models.. Journal of Clinical Oncology, 2019, 37, e19526-e19526.	0.8	0
96	A phase I study of the safety and immunogenicity of a multi-peptide personalized genomic vaccine in the adjuvant treatment of solid tumors and hematological malignancies.. Journal of Clinical Oncology, 2019, 37, e14307-e14307.	0.8	2
97	STAR Chimeric Post for rapid detection of circular RNA and fusion transcripts. Bioinformatics, 2018, 34, 2364-2370.	1.8	20
98	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
99	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
100	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
101	Integrated biology approach reveals molecular and pathological interactions among Alzheimerâ€™s AÎ²42, Tau, TREM2, and TYROBP in Drosophila models. Genome Medicine, 2018, 10, 26.	3.6	23
102	Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation. Nature Biotechnology, 2018, 36, 61-69.	9.4	116
103	GJA1 (connexin43) is a key regulator of Alzheimerâ€™s disease pathogenesis. Acta Neuropathologica Communications, 2018, 6, 144.	2.4	59
104	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
105	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. PLoS Genetics, 2018, 14, e1007755.	1.5	30
106	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
107	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimerâ€™s disease susceptibility. Nature Genetics, 2018, 50, 1584-1592.	9.4	307
108	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. Nature Communications, 2018, 9, 3980.	5.8	5

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109	Detection of endometrial precancer by a targeted gynecologic cancer liquid biopsy. Journal of Physical Education and Sports Management, 2018, 4, a003269.	0.5	11
110	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. Nature Communications, 2018, 9, 4412.	5.8	63
111	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. Genome Research, 2018, 28, 1067-1078.	2.4	80
112	The asthma mobile health study, smartphone data collected using ResearchKit. Scientific Data, 2018, 5, 180096.	2.4	43
113	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
114	From smartphone to EHR: a case report on integrating patient-generated health data. Npj Digital Medicine, 2018, 1, 23.	5.7	52
115	Genome Plasticity of agr -Defective Staphylococcus aureus during Clinical Infection. Infection and Immunity, 2018, 86, .	1.0	50
116	iPSC-derived familial Alzheimerâ€™s PSEN2 N141I cholinergic neurons exhibit mutation-dependent molecular pathology corrected by insulin signaling. Molecular Neurodegeneration, 2018, 13, 33.	4.4	35
117	B Cell Defects Observed in Nod2 Knockout Mice Are a Consequence of a Dock2 Mutation Frequently Found in Inbred Strains. Journal of Immunology, 2018, 201, 1442-1451.	0.4	13
118	Impacts of incorporating personal genome sequencing into graduate genomics education: a longitudinal study over three course years. BMC Medical Genomics, 2018, 11, 5.	0.7	17
119	The human brainome: network analysis identifies HSPA2 as a novel Alzheimerâ€™s disease target. Brain, 2018, 141, 2721-2739.	3.7	31
120	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
121	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
122	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
123	Global analysis of A-to-I RNA editing reveals association with common disease variants. PeerJ, 2018, 6, e4466.	0.9	21
124	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
125	Heterozygous Pathogenic Variant inDACT1Causes an Autosomal-Dominant Syndrome with Features Overlapping Townes-Brocks Syndrome. Human Mutation, 2017, 38, 373-377.	1.1	17
126	Rationale and Design of F amily-Based A pproach in a M inority Community I ntegrating Systemsâ€“Bio l ogy for Promot i on of He a lth (FAMILIA). American Heart Journal, 2017, 187, 170-181.	1.2	19

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127	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
128	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
129	Identification of a novel RASD1 somatic mutation in a USP8-mutated corticotroph adenoma. Journal of Physical Education and Sports Management, 2017, 3, a001602.	0.5	8
130	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. Stem Cell Reports, 2017, 8, 1516-1524.	2.3	260
131	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
132	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. Nature Biotechnology, 2017, 35, 354-362.	9.4	185
133	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
134	Human Pancreatic Î² Cell lncRNAs Control Cell-Specific Regulatory Networks. Cell Metabolism, 2017, 25, 400-411.	7.2	195
135	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. Nature Communications, 2017, 8, 767.	5.8	67
136	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386.	0.6	20
137	Germline deletion of KrÃ¼ppel-like factor 14 does not increase risk of diet induced metabolic syndrome in male C57BL/6 mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 3277-3285.	1.8	15
138	Carbonyl reductase 1 catalyzes 20Î²-reduction of glucocorticoids, modulating receptor activation and metabolic complications of obesity. Scientific Reports, 2017, 7, 10633.	1.6	15
139	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	9.4	199
140	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
141	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
142	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
143	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. Npj Systems Biology and Applications, 2017, 3, 35.	1.4	11
144	Integrative transcriptomic analysis reveals key drivers of acute peanut allergic reactions. Nature Communications, 2017, 8, 1943.	5.8	64

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145	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	5.8	225
146	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. BMC Genomics, 2017, 18, 987.	1.2	19
147	EXPLORING THE REPRODUCIBILITY OF PROBABILISTIC CAUSAL MOLECULAR NETWORK MODELS. , 2017, 22, 120-131.		14
148	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
149	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimerâ€™s disease. Molecular Neurodegeneration, 2017, 12, 82.	4.4	100
150	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
151	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
152	Genomic profiling reveals mutational landscape in parathyroid carcinomas. JCI Insight, 2017, 2, e92061.	2.3	84
153	Transcriptional dissection of melanoma identifies a high-risk subtype underlying TP53 family genes and epigenome deregulation. JCI Insight, 2017, 2, .	2.3	48
154	A phase I study of the safety and immunogenicity of a multipeptide personalized genomic vaccine in the adjuvant treatment of solid cancers.. Journal of Clinical Oncology, 2017, 35, TPS3114-TPS3114.	0.8	4
155	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
156	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. Bioinformatics, 2016, 32, 96-105.	1.8	31
157	Continuous Surveillance by Whole-Genome Sequencing to Identify and Manage Methicillin-Resistant Staphylococcus aureus Outbreaks. Open Forum Infectious Diseases, 2016, 3, .	0.4	2
158	Genetic Variation and Altered Virulence Associated With Loss of Agr Quorum-Sensing Functionality in Patients With Staphylococcus aureus Bacteremia. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
159	Epigenomic Landscape of Clostridium difficile: Largely Neglected Complexity and Opportunity Learned from 45 Hospital Isolates. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
160	Comparative Genomics and Assessment of Strain Diversity, Pathogenicity and Transmission of Clostridium difficile Isolates From a Hospital Setting. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
161	S4â€02â€03: Accelerating Medicines Partnership: Coâ€Expression Networks. Alzheimer's and Dementia, 2016, 12, P322.	0.4	0
162	P4â€027: Combing Evidence Across Multiple Cohorts for Systemsâ€Based Target Discovery: the AMPâ€AD Knowledge Portal. Alzheimer's and Dementia, 2016, 12, P1025.	0.4	0

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163	P4â€031: Integrative Network Analysis of Multiple Alzheimer's Disease Rnaseq Studies From the Accelerating Medicine Partnershipâ€Alzheimer's Disease Consortium. Alzheimer's and Dementia, 2016, 12, P1026.	0.4	1
164	P4â€278: Characterization of Basal Forebrain Cholinergic Neurons From Induced Pluripotent Stem Cells Harboring Familial Alzheimerâ€™S MUTATION PSEN2^{N141I}. Alzheimer's and Dementia, 2016, 12, P1139.	0.4	0
165	Family-Based Approaches to Cardiovascular Health Promotion. Journal of the American College of Cardiology, 2016, 67, 1725-1737.	1.2	63
166	A new molecular signature method for prediction of driver cancer pathways from transcriptional data. Nucleic Acids Research, 2016, 44, e110-e110.	6.5	15
167	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	9.4	273
168	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
169	Decision-Making in the Age of Whole Genome Sequencing. , 2016, , 357-373.		0
170	Meditation and vacation effects have an impact on disease-associated molecular phenotypes. Translational Psychiatry, 2016, 6, e880-e880.	2.4	76
171	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	6.0	241
172	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. Nature Communications, 2016, 7, 12092.	5.8	123
173	Reconstructing Causal Network Models of Human Disease. , 2016, , 141-160.		2
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