Eric E Schadt

List of Publications by Citations

297 papers	47,034 citations	90 h-index	216 g-index
326 ext. papers	58,814 ext. citations	14.4 avg, IF	6.89 L-index

#	Paper	IF	Citations
297	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature*, **2012**, 491, 119-24	50.4	3239
296	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
295	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
294	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
293	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
292	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
291	Genetics of gene expression surveyed in maize, mouse and man. *Nature*, **2003**, 422, 297-302	50.4	1244
290	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
289	Geroscience: linking aging to chronic disease. *Cell*, **2014**, 159, 709-13	56.2	1068
288	Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. *Cell*, **2013**, 153, 707-20	56.2	1058
287	Genetics of gene expression and its effect on disease. *Nature*, **2008**, 452, 423-8	50.4	1058
286	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
285	An inflammatory cytokine signature predicts COVID-19 severity and survival. *Nature Medicine*, **2020**, 26, 1636-1643	50.5	895
284	Bayesian test for colocalisation between pairs of genetic association studies using summary statistics. *PLoS Genetics*, **2014**, 10, e1004383	6	868
283	From noncoding variant to phenotype via SORT1 at the 1p13 cholesterol locus. *Nature*, **2010**, 466, 714-9	50.4	820
282	An integrative genomics approach to infer causal associations between gene expression and disease. *Nature Genetics*, **2005**, 37, 710-7	36.3	820
281	Mapping the genetic architecture of gene expression in human liver. *PLoS Biology*, **2008**, 6, e107	9.7	768

280	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, 949-60	36.3	724
279	Variations in DNA elucidate molecular networks that cause disease. *Nature*, **2008**, 452, 429-35	50.4	723
278	Origins of the E. coli strain causing an outbreak of hemolytic-uremic syndrome in Germany. *New England Journal of Medicine*, **2011**, 365, 709-17	59.2	658
277	A window into third-generation sequencing. *Human Molecular Genetics*, **2010**, 19, R227-40	5.6	628
276	Tissue-specific expression and regulation of sexually dimorphic genes in mice. *Genome Research*, **2006**, 16, 995-1004	9.7	628
275	Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nature Neuroscience*, **2016**, 19, 1442-1453	25.5	622
274	Molecular networks as sensors and drivers of common human diseases. *Nature*, **2009**, 461, 218-23	50.4	589
273	The origin of the Haitian cholera outbreak strain. *New England Journal of Medicine*, **2011**, 364, 33-42	59.2	559
272	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. *Science*, **2018**, 359, 693-697	33.3	547
271	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
270	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
269	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. *Nature Genetics*, **2008**, 40, 854-61	36.3	430
268	Assembly and diploid architecture of an individual human genome via single-molecule technologies. *Nature Methods*, **2015**, 12, 780-6	21.6	383
267	Experimental annotation of the human genome using microarray technology. *Nature*, **2001**, 409, 922-7	50.4	373
266	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
265	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. *Neuron*, **2018**, 99, 64-82.e7	13.9	357
264	Extensive sequencing of seven human genomes to characterize benchmark reference materials. *Scientific Data*, **2016**, 3, 160025	8.2	345
263	Genome-wide mapping of methylated adenine residues in pathogenic Escherichia coli using single-molecule real-time sequencing. *Nature Biotechnology*, **2012**, 30, 1232-9	44.5	256

262	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. *Nature Medicine*, **2020**, 26, 769-780	50.5	226
261	AKI in Hospitalized Patients with COVID-19. *Journal of the American Society of Nephrology: JASN*, **2021**, 32, 151-160	12.7	225
260	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. *Nature Genetics*, **2009**, 41, 415-23	36.3	224
259	Single-Cell Analysis of Crohn's Disease Lesions Identifies a Pathogenic Cellular Module Associated with Resistance to Anti-TNF Therapy. *Cell*, **2019**, 178, 1493-1508.e20	56.2	219
258	A network view of disease and compound screening. *Nature Reviews Drug Discovery*, **2009**, 8, 286-95	64.1	219
257	Cis-acting expression quantitative trait loci in mice. *Genome Research*, **2005**, 15, 681-91	9.7	216
256	Integrating pathway analysis and genetics of gene expression for genome-wide association studies. *American Journal of Human Genetics*, **2010**, 86, 581-91	11	202
255	variancePartition: interpreting drivers of variation in complex gene expression studies. *BMC Bioinformatics*, **2016**, 17, 483	3.6	201
254	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. *Nature Genetics*, **2012**, 44, 841-7	36.3	198
253	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. *Nature Biotechnology*, **2016**, 34, 531-8	44.5	196
252	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. *Genome Research*, **2010**, 20, 1020-36	9.7	193
251	Massive parallel sequencing uncovers actionable FGFR2-PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. *Nature Communications*, **2015**, 6, 6087	17.4	183
250	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
249	An integrative genomics approach to the reconstruction of gene networks in segregating populations. *Cytogenetic and Genome Research*, **2004**, 105, 363-74	1.9	178
248	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. *Stem Cell Reports*, **2017**, 8, 1516-1524	8	176
247	A role for noncoding variation in schizophrenia. *Cell Reports*, **2014**, 9, 1417-29	10.6	174
246	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. *Cell*, **2019**, 179, 964-983.e31	56.2	173
245	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. *Science*, **2016**, 353, 827-30	33.3	166

244	iPSC-derived dopamine neurons reveal differences between monozygotic twins discordant for Parkinson's disease. *Cell Reports*, **2014**, 9, 1173-82	10.6	166
243	Functional variants in the gene confer shared effects on risk for Crohn's disease and Parkinson's disease. *Science Translational Medicine*, **2018**, 10,	17.5	165
242	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	18	164
241	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. *Cell Systems* , **2015**, 1, 72-87	10.6	164
240	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	6	163
239	Disentangling molecular relationships with a causal inference test. *BMC Genetics*, **2009**, 10, 23	2.6	163
238	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	11.6	162
237	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. *Nature Genetics*, **2018**, 50, 1584-1592	36.3	162
236	Genome-wide identification of microRNAs regulating cholesterol and triglyceride homeostasis. *Nature Medicine*, **2015**, 21, 1290-7	50.5	160
235	A hybrid approach for the automated finishing of bacterial genomes. *Nature Biotechnology*, **2012**, 30, 701-707	44.5	157
234	Causal effects of body mass index on cardiometabolic traits and events: a Mendelian randomization analysis. *American Journal of Human Genetics*, **2014**, 94, 198-208	11	156
233	Increasing the power to detect causal associations by combining genotypic and expression data in segregating populations. *PLoS Computational Biology*, **2007**, 3, e69	5	156
232	Moving toward a system genetics view of disease. *Mammalian Genome*, **2007**, 18, 389-401	3.2	148
231	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
230	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. *Scientific Data*, **2018**, 5, 180185	8.2	144
229	Stitching together multiple data dimensions reveals interacting metabolomic and transcriptomic networks that modulate cell regulation. *PLoS Biology*, **2012**, 10, e1001301	9.7	142
228	A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. *Genome Research*, **2011**, 21, 1008-16	9.7	141
227	Human Pancreatic Cell lncRNAs Control Cell-Specific Regulatory Networks. *Cell Metabolism*, **2017**, 25, 400-411	24.6	139

226	Liver and adipose expression associated SNPs are enriched for association to type 2 diabetes. *PLoS Genetics*, **2010**, 6, e1000932	6	139
225	Mutations in tetratricopeptide repeat domain 7A result in a severe form of very early onset inflammatory bowel disease. *Gastroenterology*, **2014**, 146, 1028-39	13.3	138
224	Integrative network analysis of nineteen brain regions identifies molecular signatures and networks underlying selective regional vulnerability to Alzheimer's disease. *Genome Medicine*, **2016**, 8, 104	14.4	135
223	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
222	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. *Nature Communications*, **2017**, 8, 59	17.4	130
221	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. *Scientific Reports*, **2015**, 5, 15145	4.9	128
220	Multi-tissue coexpression networks reveal unexpected subnetworks associated with disease. *Genome Biology*, **2009**, 10, R55	18.3	121
219	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. *Nature Biotechnology*, **2017**, 35, 354-362	44.5	118
218	Genome-wide significant loci: how important are they? Systems genetics to understand heritability of coronary artery disease and other common complex disorders. *Journal of the American College of Cardiology*, **2015**, 65, 830-845	15.1	108
217	Bayesian method to predict individual SNP genotypes from gene expression data. *Nature Genetics*, **2012**, 44, 603-8	36.3	108
216	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. *Nature Genetics*, **2017**, 49, 1437-1449	36.3	107
215	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
214	Intratumoral heterogeneity and clonal evolution in liver cancer. *Nature Communications*, **2020**, 11, 291	17.4	102
213	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. *Molecular Systems Biology*, **2014**, 10, 743	12.2	101
212	Personalized Circulating Tumor DNA Biomarkers Dynamically Predict Treatment Response and Survival In Gynecologic Cancers. *PLoS ONE*, **2015**, 10, e0145754	3.7	97
211	NEW: network-enabled wisdom in biology, medicine, and health care. *Science Translational Medicine*, **2012**, 4, 115rv1	17.5	97
210	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. *Molecular Systems Biology*, **2012**, 8, 594	12.2	95
209	Systems biology of asthma and allergic diseases: a multiscale approach. *Journal of Allergy and Clinical Immunology*, **2015**, 135, 31-42	11.5	91

208	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
207	Analytical validation of whole exome and whole genome sequencing for clinical applications. *BMC Medical Genomics*, **2014**, 7, 20	3.7	82
206	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	7.6	82
205	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. *Cell Systems*, **2016**, 2, 196-208	10.6	81
204	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 Suppl 1, 50-62	6	78
203	Comprehensive methylome characterization of Mycoplasma genitalium and Mycoplasma pneumoniae at single-base resolution. *PLoS Genetics*, **2013**, 9, e1003191	6	75
202	Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation. *Nature Biotechnology*, **2018**, 36, 61-69	44.5	74
201	CRISPR/Cas9-Correctable mutation-related molecular and physiological phenotypes in iPSC-derived Alzheimer's PSEN2 neurons. *Acta Neuropathologica Communications*, **2017**, 5, 77	7.3	73
200	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. *Nature Communications*, **2016**, 7, 12092	17.4	70
199	Variants in TRIM22 That Affect NOD2 Signaling Are Associated With Very-Early-Onset Inflammatory Bowel Disease. *Gastroenterology*, **2016**, 150, 1196-1207	13.3	69
198	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. *Cell Reports*, **2020**, 32, 107908	10.6	68
197	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	10.2	67
196	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	5.3	64
195	Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. *Nature Communications*, **2015**, 6, 7438	17.4	64
194	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 2207-17	9.4	64
193	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
192	Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases. *Genome Research*, **2013**, 23, 129-41	9.7	63
191	Ppargamma2 is a key driver of longevity in the mouse. *PLoS Genetics*, **2009**, 5, e1000752	6	62

190	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. *Molecular Neurodegeneration*, **2017**, 12, 82	19	61
189	Deciphering bacterial epigenomes using modern sequencing technologies. *Nature Reviews Genetics* , **2019**, 20, 157-172	30.1	61
188	Genomic and network patterns of schizophrenia genetic variation in human evolutionary accelerated regions. *Molecular Biology and Evolution*, **2015**, 32, 1148-60	8.3	60
187	Biallelic Mutations in MRPS34 Lead to Instability of the Small Mitoribosomal Subunit and Leigh Syndrome. *American Journal of Human Genetics*, **2017**, 101, 239-254	11	59
186	Development and clinical application of an integrative genomic approach to personalized cancer therapy. *Genome Medicine*, **2016**, 8, 62	14.4	58
185	Deficiency of TYROBP, an adapter protein for TREM2 and CR3 receptors, is neuroprotective in a mouse model of early Alzheimer's pathology. *Acta Neuropathologica*, **2017**, 134, 769-788	14.3	55
184	A Next Generation Multiscale View of Inborn Errors of Metabolism. *Cell Metabolism*, **2016**, 23, 13-26	24.6	55
183	A Bayesian partition method for detecting pleiotropic and epistatic eQTL modules. *PLoS Computational Biology*, **2010**, 6, e1000642	5	55
182	Integrative analysis of DNA methylation and gene expression data identifies EPAS1 as a key regulator of COPD. *PLoS Genetics*, **2015**, 11, e1004898	6	54
181	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	3.7	51
180	Meditation and vacation effects have an impact on disease-associated molecular phenotypes. *Translational Psychiatry*, **2016**, 6, e880	8.6	50
179	Characterizing dynamic changes in the human blood transcriptional network. *PLoS Computational Biology*, **2010**, 6, e1000671	5	50
178	Genomic profiling reveals mutational landscape in parathyroid carcinomas. *JCI Insight*, **2017**, 2, e92061	9.9	50
177	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2-related Disease. *Gastroenterology*, **2021**, 160, 287-301.e20	13.3	50
176	Integrative analysis of a cross-loci regulation network identifies App as a gene regulating insulin secretion from pancreatic islets. *PLoS Genetics*, **2012**, 8, e1003107	6	49
175	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. *American Journal of Human Genetics*, **2017**, 100, 885-894	11	48
174	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. *Genome Research*, **2018**, 28, 1067-1078	9.7	48
173	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. *Nature Communications*, **2017**, 8, 767	17.4	47

172	Inferring causal genomic alterations in breast cancer using gene expression data. *BMC Systems Biology*, **2011**, 5, 121	3.5	46
171	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. *BMC Medical Genomics*, **2014**, 7, 48	3.7	45
170	Integrating siRNA and protein-protein interaction data to identify an expanded insulin signaling network. *Genome Research*, **2009**, 19, 1057-67	9.7	45
169	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. *Cell*, **2020**, 183, 1962-1985.e31	56.2	45
168	Detecting DNA modifications from SMRT sequencing data by modeling sequence context dependence of polymerase kinetic. *PLoS Computational Biology*, **2013**, 9, e1002935	5	44
167	Psychological and behavioural impact of returning personal results from whole-genome sequencing: the HealthSeq project. *European Journal of Human Genetics*, **2017**, 25, 280-292	5.3	42
166	Deciphering H3K4me3 broad domains associated with gene-regulatory networks and conserved epigenomic landscapes in the human brain. *Translational Psychiatry*, **2015**, 5, e679	8.6	42
165	Integrative transcriptomic analysis reveals key drivers of acute peanut allergic reactions. *Nature Communications*, **2017**, 8, 1943	17.4	42
164	Dissection of immune gene networks in primary melanoma tumors critical for antitumor surveillance of patients with stage II-III resectable disease. *Journal of Investigative Dermatology*, **2014**, 134, 2202-2211	4.3	42
163	Downregulation of carnitine acyl-carnitine translocase by miRNAs 132 and 212 amplifies glucose-stimulated insulin secretion. *Diabetes*, **2014**, 63, 3805-14	0.9	40
162	Personalized ovarian cancer disease surveillance and detection of candidate therapeutic drug target in circulating tumor DNA. *Neoplasia*, **2014**, 16, 97-103	6.4	40
161	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	4.5	40
160	Family-Based Approaches to Cardiovascular Health Promotion. *Journal of the American College of Cardiology*, **2016**, 67, 1725-37	15.1	40
159	The effect of food intake on gene expression in human peripheral blood. *Human Molecular Genetics* , **2010**, 19, 159-69	5.6	39
158	Molecular subtyping of Alzheimer's disease using RNA sequencing data reveals novel mechanisms and targets. *Science Advances*, **2021**, 7,	14.3	39
157	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. *Nature Communications*, **2018**, 9, 4412	17.4	39
156	The role of macromolecular damage in aging and age-related disease. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2014**, 69 Suppl 1, S28-32	6.4	38
155	GJA1 (connexin43) is a key regulator of Alzheimer's disease pathogenesis. *Acta Neuropathologica Communications*, **2018**, 6, 144	7.3	37

154	exposures to environmental organic pollutants disrupt epigenetic marks linked to fetoplacental development. *Environmental Epigenetics*, **2016**, 2,	2.4	36
153	Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. *Nature Microbiology*, **2020**, 5, 166-180	26.6	36
152	From smartphone to EHR: a case report on integrating patient-generated health data. *Npj Digital Medicine*, **2018**, 1, 23	15.7	36
151	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. *Science Advances*, **2019**, 5, eaav6528	14.3	35
150	Genomic analyses implicate noncoding de novo variants in congenital heart disease. *Nature Genetics*, **2020**, 52, 769-777	36.3	33
149	A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. *Scientific Reports*, **2018**, 8, 8826	4.9	33
148	Translational genomics. Clues from the resilient. *Science*, **2014**, 344, 970-2	33.3	33
147	Altering Sphingolipid Metabolism Attenuates Cell Death and Inflammatory Response After Myocardial Infarction. *Circulation*, **2020**, 141, 916-930	16.7	32
146	Genome Plasticity of -Defective Staphylococcus aureus during Clinical Infection. *Infection and Immunity*, **2018**, 86,	3.7	32
145	Autotransporters but not pAA are critical for rabbit colonization by Shiga toxin-producing Escherichia coli O104:H4. *Nature Communications*, **2014**, 5, 3080	17.4	32
144	Evolving toward a human-cell based and multiscale approach to drug discovery for CNS disorders. *Frontiers in Pharmacology*, **2014**, 5, 252	5.6	31
143	Integrative approach to sporadic Alzheimer's disease: deficiency of TYROBP in cerebral A amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing A burden. *Molecular Psychiatry*, **2019**, 24, 431-446	15.1	31
142	Melanocortin 4 Receptor Pathway Dysfunction in Obesity: Patient Stratification Aimed at MC4R Agonist Treatment. *Journal of Clinical Endocrinology and Metabolism*, **2018**, 103, 2601-2612	5.6	31
141	Transcriptional dissection of melanoma identifies a high-risk subtype underlying TP53 family genes and epigenome deregulation. *JCI Insight*, **2017**, 2,	9.9	30
140	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. *PLoS Genetics*, **2017**, 13, e1006565	6	30
139	TGF receptor 1: an immune susceptibility gene in HPV-associated cancer. *Cancer Research*, **2014**, 74, 6833-44	10.1	29
138	Transformative Network Modeling of Multi-omics Data Reveals Detailed Circuits, Key Regulators, and Potential Therapeutics for Alzheimer's Disease. *Neuron*, **2021**, 109, 257-272.e14	13.9	29
137	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. *Nature Communications*, **2019**, 10, 3834	17.4	28

136	Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. *Journal of the American College of Cardiology*, **2019**, 73, 2946-2957	15.1	28
135	Discover the network underlying the connections between aging and age-related diseases. *Scientific Reports*, **2016**, 6, 32566	4.9	28
134	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. *Nature Communications*, **2020**, 11, 3942	17.4	28
133	The asthma mobile health study, smartphone data collected using ResearchKit. *Scientific Data*, **2018**, 5, 180096	8.2	28
132	VGF-derived peptide TLQP-21 modulates microglial function through C3aR1 signaling pathways and reduces neuropathology in 5xFAD mice. *Molecular Neurodegeneration*, **2020**, 15, 4	19	27
131	Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. *BMC Genomics*, **2010**, 11, 473	4.5	27
130	Discovering genetic interactions bridging pathways in genome-wide association studies. *Nature Communications*, **2019**, 10, 4274	17.4	26
129	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. *Scientific Data*, **2020**, 7, 340	8.2	26
128	Integrative approach to sporadic Alzheimer'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	15.1	26
127	iPSC-derived familial Alzheimer's PSEN2 cholinergic neurons exhibit mutation-dependent molecular pathology corrected by insulin signaling. *Molecular Neurodegeneration*, **2018**, 13, 33	19	25
126	How do students react to analyzing their own genomes in a whole-genome sequencing course?: outcomes of a longitudinal cohort study. *Genetics in Medicine*, **2015**, 17, 866-74	8.1	25
125	MODMatcher: multi-omics data matcher for integrative genomic analysis. *PLoS Computational Biology*, **2014**, 10, e1003790	5	25
124	Informed decision-making among students analyzing their personal genomes on a whole genome sequencing course: a longitudinal cohort study. *Genome Medicine*, **2013**, 5, 113	14.4	25
123	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. *GeroScience*, **2020**, 42, 353-372	8.9	24
122	Cancer gene profiling in non-small cell lung cancers reveals activating mutations in JAK2 and JAK3 with therapeutic implications. *Genome Medicine*, **2017**, 9, 89	14.4	23
121	Predispositional genome sequencing in healthy adults: design, participant characteristics, and early outcomes of the PeopleSeq Consortium. *Genome Medicine*, **2019**, 11, 10	14.4	22
120	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. *Bioinformatics*, **2016**, 32, 96-105	7.2	21
119	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	4.2	21

118	Novel, compound heterozygous, single-nucleotide variants in MARS2 associated with developmental delay, poor growth, and sensorineural hearing loss. *Human Mutation*, **2015**, 36, 587-92	4.7	21
117	Dual transcriptomic and epigenomic study of reaction severity in peanut-allergic children. *Journal of Allergy and Clinical Immunology*, **2020**, 145, 1219-1230	11.5	21
116	Identification of Altered Metabolomic Profiles Following a Panchakarma-based Ayurvedic Intervention in Healthy Subjects: The Self-Directed Biological Transformation Initiative (SBTI). *Scientific Reports*, **2016**, 6, 32609	4.9	20
115	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. *Molecular Psychiatry*, **2019**, 24, 1685-1695	15.1	20
114	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer’s disease target. *Brain*, **2018**, 141, 2721-2739	11.2	19
113	Integrative study of the upper and lower airway microbiome and transcriptome in asthma. *JCI Insight*, **2020**, 5,	9.9	19
112	CR1 and the "vanishing amyloid" hypothesis of Alzheimer's disease. *Biological Psychiatry*, **2013**, 73, 393-5	7.9	18
111	Biomarkers for combat-related PTSD: focus on molecular networks from high-dimensional data. *Högre Utbildning*, **2014**, 5,	5	17
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