

Ayellet V SegrÃ

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

22,481
citations

109311

35
h-index

265191

42
g-index

49
all docs

49
docs citations

49
times ranked

39827
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
3	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
4	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748
5	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	21.4	1,631
6	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	12.6	1,127
7	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
8	The Lin28/let-7 Axis Regulates Glucose Metabolism. <i>Cell</i> , 2011, 147, 81-94.	28.9	812
9	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. <i>Biopreservation and Biobanking</i> , 2015, 13, 311-319.	1.0	674
10	Colocalization of GWAS and eQTL Signals Detects Target Genes. <i>American Journal of Human Genetics</i> , 2016, 99, 1245-1260.	6.2	569
11	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	21.4	445
12	Common Inherited Variation in Mitochondrial Genes Is Not Enriched for Associations with Type 2 Diabetes or Related Glycemic Traits. <i>PLoS Genetics</i> , 2010, 6, e1001058.	3.5	429
13	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	21.4	428
14	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
15	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
16	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018, 50, 956-967.	21.4	389
17	RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. <i>Science</i> , 2019, 364, .	12.6	369
18	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	329

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19	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	21.4	282
20	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252
21	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	210
22	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. <i>Nature Communications</i> , 2021, 12, 1258.	12.8	196
23	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	3.5	192
24	Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1392-1397.	21.4	190
25	Meta-analysis of 542,934 subjects of European ancestry identifies new genes and mechanisms predisposing to refractive error and myopia. <i>Nature Genetics</i> , 2020, 52, 401-407.	21.4	180
26	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. <i>Science</i> , 2022, 376, eabl4290.	12.6	180
27	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, 49.	8.8	150
28	Genetic and environmental risk factors in congenital heart disease functionally converge in protein networks driving heart development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14035-14040.	7.1	117
29	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. <i>PLoS Genetics</i> , 2010, 6, e1001183.	3.5	85
30	Widespread Allelic Heterogeneity in Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 789-802.	6.2	74
31	High-Resolution Mutation Mapping Reveals Parallel Experimental Evolution in Yeast. <i>PLoS Biology</i> , 2006, 4, e256.	5.6	73
32	Systems Genetics Analysis of Genome-Wide Association Study Reveals Novel Associations Between Key Biological Processes and Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1712-1722.	2.4	72
33	Deep Learning of the Retina Enables Phenome- and Genome-Wide Analyses of the Microvasculature. <i>Circulation</i> , 2022, 145, 134-150.	1.6	57
34	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. <i>Diabetes</i> , 2019, 68, 441-456.	0.6	54
35	Heterothallism in <i>Saccharomyces cerevisiae</i> isolates from nature: effect of <i>HO</i> locus on the mode of reproduction. <i>Molecular Ecology</i> , 2010, 19, 121-131.	3.9	46
36	Pathways Targeted by Antidiabetes Drugs Are Enriched for Multiple Genes Associated With Type 2 Diabetes Risk. <i>Diabetes</i> , 2015, 64, 1470-1483.	0.6	31

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37	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1793-1798.	1.8	30
38	Characteristics of p.Gln368Ter Myocilin Variant and Influence of Polygenic Risk on Glaucoma Penetrance in the UK Biobank. <i>Ophthalmology</i> , 2021, 128, 1300-1311.	5.2	27
39	Identification of Novel Type 2 Diabetes Candidate Genes Involved in the Crosstalk between the Mitochondrial and the Insulin Signaling Systems. <i>PLoS Genetics</i> , 2012, 8, e1003046.	3.5	23
40	Photoreceptor Layer Thinning Is an Early Biomarker for Age-Related Macular Degeneration. <i>Ophthalmology</i> , 2022, 129, 694-707.	5.2	21
41	Gene Set Enrichment Analyses Identify Pathways Involved in Genetic Risk for Diabetic Retinopathy. <i>American Journal of Ophthalmology</i> , 2022, 233, 111-123.	3.3	7
42	Background polygenic risk modulates the association between glaucoma and cardiopulmonary diseases and measures: an analysis from the UK Biobank. <i>British Journal of Ophthalmology</i> , 2023, 107, 1112-1118.	3.9	4