

Roderick C Sliker

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54
papers

2,513
citations

23
h-index

50
g-index

60
ext. papers

3,498
ext. citations

10.8
avg, IF

4.56
L-index

#	Paper	IF	Citations
54	Functional genomics analysis identifies T and NK cell activation as a driver of epigenetic clock progression.. <i>Genome Biology</i> , 2022 , 23, 24	18.3	6
53	Response to Comment on Dawed et al. Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. <i>Diabetes Care</i> 2021;44:2673-2682.. <i>Diabetes Care</i> , 2022 , 45, e82-e83	14.6	
52	OVOL1 inhibits breast cancer cell invasion by enhancing the degradation of TGF- β type I receptor.. <i>Signal Transduction and Targeted Therapy</i> , 2022 , 7, 126	21	0
51	Diabetes risk loci-associated pathways are shared across metabolic tissues.. <i>BMC Genomics</i> , 2022 , 23, 368	4.5	
50	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
49	Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. <i>Diabetes Care</i> , 2021 , 44, 2673-2682	14.6	5
48	Breast cancer dormancy is associated with a 4NG1 state and not senescence. <i>Npj Breast Cancer</i> , 2021 , 7, 140	7.8	3
47	Prognostic models for predicting the risk of foot ulcer or amputation in people with type 2 diabetes: a systematic review and external validation study. <i>Diabetologia</i> , 2021 , 64, 1550-1562	10.3	3
46	Replication and cross-validation of type 2 diabetes subtypes based on clinical variables: an IMI-RHAPSODY study. <i>Diabetologia</i> , 2021 , 64, 1982-1989	10.3	11
45	Serum Magnesium Is Inversely Associated With Heart Failure, Atrial Fibrillation, and Microvascular Complications in Type 2 Diabetes. <i>Diabetes Care</i> , 2021 , 44, 1757-1765	14.6	2
44	Long RNA Sequencing and Ribosome Profiling of Inflamed β Cells Reveal an Extensive Translatome Landscape. <i>Diabetes</i> , 2021 , 70, 2299-2312	0.9	2
43	The tissue-specific aspect of genome-wide DNA methylation in newborn and placental tissues: implications for epigenetic epidemiologic studies. <i>Journal of Developmental Origins of Health and Disease</i> , 2021 , 12, 113-123	2.4	4
42	Transgenerational modification of dopaminergic dysfunctions induced by maternal immune activation. <i>Neuropsychopharmacology</i> , 2021 , 46, 404-412	8.7	9
41	Prediction of mortality and major cardiovascular complications in type 2 diabetes: External validation of UK Prospective Diabetes Study outcomes model version 2 in two European observational cohorts. <i>Diabetes, Obesity and Metabolism</i> , 2021 , 23, 1084-1091	6.7	2
40	Distinct Molecular Signatures of Clinical Clusters in People With Type 2 Diabetes: An IMI-RHAPSODY Study. <i>Diabetes</i> , 2021 , 70, 2683-2693	0.9	4
39	Performance of prediction models for nephropathy in people with type 2 diabetes: systematic review and external validation study. <i>BMJ, The</i> , 2021 , 374, n2134	5.9	2
38	NACHO: an R package for quality control of NanoString nCounter data. <i>Bioinformatics</i> , 2020 , 36, 970-971	7.2	4

37	Prediction models for development of retinopathy in people with type 2 diabetes: systematic review and external validation in a Dutch primary care setting. <i>Diabetologia</i> , 2020 , 63, 1110-1119	10.3	10
36	Human-iPSC-Derived Cardiac Stromal Cells Enhance Maturation in 3D Cardiac Microtissues and Reveal Non-cardiomyocyte Contributions to Heart Disease. <i>Cell Stem Cell</i> , 2020 , 26, 862-879.e11	18	148
35	Repeat UVA exposure of human skin fibroblasts induces both a transitional and recovery DNA methylation response. <i>Epigenomics</i> , 2020 , 12, 563-573	4.4	1
34	Metformin and statin use associate with plasma protein -glycosylation in people with type 2 diabetes. <i>BMJ Open Diabetes Research and Care</i> , 2020 , 8,	4.5	2
33	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug-metabolite atlas. <i>Nature Medicine</i> , 2020 , 26, 110-117	50.5	19
32	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. <i>PLoS ONE</i> , 2020 , 15, e0242360	3.7	2
31	Serum Matrix Metalloproteinases and Left Atrial Remodeling-The Hoorn Study. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	4
30	CONQUER: an interactive toolbox to understand functional consequences of GWAS hits. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa085	3.7	1
29	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , 2020 , 12, 109	14.4	3
28	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020 , 588, 135-140.	50.4	75
27	Visit-to-visit variability of glycemia and vascular complications: the Hoorn Diabetes Care System cohort. <i>Cardiovascular Diabetology</i> , 2019 , 18, 170	8.7	11
26	A Type 1 Diabetes Genetic Risk Score Can Identify Patients With GAD65 Autoantibody-Positive Type 2 Diabetes Who Rapidly Progress to Insulin Therapy. <i>Diabetes Care</i> , 2019 , 42, 208-214	14.6	20
25	DNA methylation as a mediator of the association between prenatal adversity and risk factors for metabolic disease in adulthood. <i>Science Advances</i> , 2018 , 4, eaao4364	14.3	143
24	A SNP panel for identification of DNA and RNA specimens. <i>BMC Genomics</i> , 2018 , 19, 90	4.5	17
23	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. <i>Epigenetics and Chromatin</i> , 2018 , 11, 25	5.8	76
22	HbA is associated with altered expression in blood of cell cycle- and immune response-related genes. <i>Diabetologia</i> , 2018 , 61, 138-146	10.3	7
21	Blood Metabolomic Measures Associate With Present and Future Glycemic Control in Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 4569-4579	5.6	18
20	Prolonged high-fat diet induces gradual and fat depot-specific DNA methylation changes in adult mice. <i>Scientific Reports</i> , 2017 , 7, 43261	4.9	31

19	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017 , 49, 131-138	36.3	252
18	Early- and late-onset preeclampsia and the tissue-specific epigenome of the placenta and newborn. <i>Placenta</i> , 2017 , 58, 122-132	3.4	37
17	DNA methylation and transcriptional trajectories during human development and reprogramming of isogenic pluripotent stem cells. <i>Nature Communications</i> , 2017 , 8, 908	17.4	37
16	SMCHD1 regulates a limited set of gene clusters on autosomal chromosomes. <i>Skeletal Muscle</i> , 2017 , 7, 12	5.1	18
15	Systemic Age-Associated DNA Hypermethylation of ELOVL2 Gene: In Vivo and In Vitro Evidences of a Cell Replication Process. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017 , 72, 1015-1023	6.4	50
14	Epigenomic Analysis of Scleroderma Syndrome Defines Patterns of Aberrant DNA Methylation and Identifies Diagnostic Markers. <i>Journal of Investigative Dermatology</i> , 2016 , 136, 1876-1884	4.3	31
13	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016 , 17, 191	18.3	80
12	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016 , 17, 138	18.3	118
11	Early gestation as the critical time-window for changes in the prenatal environment to affect the adult human blood methylome. <i>International Journal of Epidemiology</i> , 2015 , 44, 1211-23	7.8	107
10	Alternative Routes to Induce Naïve Pluripotency in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2015 , 33, 2686-98	5.8	91
9	Design, measurement and processing of region-specific DNA methylation assays: the mass spectrometry-based method EpiTYPER. <i>Frontiers in Genetics</i> , 2015 , 6, 287	4.5	51
8	DNA Methylation Landscapes of Human Fetal Development. <i>PLoS Genetics</i> , 2015 , 11, e1005583	6	54
7	MethylAid: visual and interactive quality control of large Illumina 450k datasets. <i>Bioinformatics</i> , 2014 , 30, 3435-7	7.2	95
6	Epigenetic variation in monozygotic twins: a genome-wide analysis of DNA methylation in buccal cells. <i>Genes</i> , 2014 , 5, 347-65	4.2	43
5	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014 , 5, 5592	17.4	368
4	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013 , 6, 26	5.8	168
3	Locomotor activity assay in zebrafish larvae: influence of age, strain and ethanol. <i>Neurotoxicology and Teratology</i> , 2012 , 34, 425-33	3.9	88
2	Re-exposure and environmental enrichment reveal NPY-Y1 as a possible target for post-traumatic stress disorder. <i>Neuropharmacology</i> , 2012 , 63, 733-42	5.5	22

- 1 Zebrafish as potential model for developmental neurotoxicity testing: a mini review. *Neurotoxicology and Teratology*, **2012**, 34, 545-53 3.9 134