

Roderick C Sliker

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,344
citations

201385

27
h-index

168136

53
g-index

60
all docs

60
docs citations

60
times ranked

8705
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014, 5, 5592.	5.8	494
2	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017, 49, 131-138.	9.4	390
3	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
4	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.	5.2	337
5	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	13.7	230
6	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.	4.7	219
7	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013, 6, 26.	1.8	192
8	Zebrafish as potential model for developmental neurotoxicity testing. <i>Neurotoxicology and Teratology</i> , 2012, 34, 545-553.	1.2	163
9	MethylAid: visual and interactive quality control of large Illumina 450k datasets. <i>Bioinformatics</i> , 2014, 30, 3435-3437.	1.8	154
10	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016, 17, 138.	3.8	154
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, 1211-1223.	0.9	139
12	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. <i>Epigenetics and Chromatin</i> , 2018, 11, 25.	1.8	130
13	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016, 17, 191.	3.8	120
14	Alternative Routes to Induce Na ⁺ ve Pluripotency in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2015, 33, 2686-2698.	1.4	118
15	Locomotor activity assay in zebrafish larvae: Influence of age, strain and ethanol. <i>Neurotoxicology and Teratology</i> , 2012, 34, 425-433.	1.2	105
16	DNA Methylation Landscapes of Human Fetal Development. <i>PLoS Genetics</i> , 2015, 11, e1005583.	1.5	73
17	Design, measurement and processing of region-specific DNA methylation assays: the mass spectrometry-based method EpiTYPER. <i>Frontiers in Genetics</i> , 2015, 6, 287.	1.1	66
18	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.	1.7	66

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19	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drugâ€™ metabolite atlas. <i>Nature Medicine</i> , 2020, 26, 110-117.	15.2	54
20	DNA methylation and transcriptional trajectories during human development and reprogramming of isogenic pluripotent stem cells. <i>Nature Communications</i> , 2017, 8, 908.	5.8	53
21	Early- and late-onset preeclampsia and the tissue-specific epigenome of the placenta and newborn. <i>Placenta</i> , 2017, 58, 122-132.	0.7	52
22	Epigenetic Variation in Monozygotic Twins: A Genome-Wide Analysis of DNA Methylation in Buccal Cells. <i>Genes</i> , 2014, 5, 347-365.	1.0	49
23	A SNP panel for identification of DNA and RNA specimens. <i>BMC Genomics</i> , 2018, 19, 90.	1.2	47
24	Epigenomic Analysis of SÃ©zary Syndrome Defines Patterns of Aberrant DNA Methylation and Identifies DiagnosticÂ Markers. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1876-1884.	0.3	46
25	Replication and cross-validation of type 2 diabetes subtypes based on clinical variables: an IMI-RHAPSODY study. <i>Diabetologia</i> , 2021, 64, 1982-1989.	2.9	44
26	Prolonged high-fat diet induces gradual and fat depot-specific DNA methylation changes in adult mice. <i>Scientific Reports</i> , 2017, 7, 43261.	1.6	38
27	A Type 1 Diabetes Genetic Risk Score Can Identify Patients With GAD65 Autoantibodyâ€™ Positive Type 2 Diabetes Who Rapidly Progress to Insulin Therapy. <i>Diabetes Care</i> , 2019, 42, 208-214.	4.3	35
28	SMCHD1 regulates a limited set of gene clusters on autosomal chromosomes. <i>Skeletal Muscle</i> , 2017, 7, 12.	1.9	32
29	Functional genomics analysis identifies T and NK cell activation as a driver of epigenetic clock progression. <i>Genome Biology</i> , 2022, 23, 24.	3.8	30
30	Transgenerational modification of dopaminergic dysfunctions induced by maternal immune activation. <i>Neuropsychopharmacology</i> , 2021, 46, 404-412.	2.8	28
31	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.	2.9	27
32	Distinct Molecular Signatures of Clinical Clusters in People With Type 2 Diabetes: An IMI-RHAPSODY Study. <i>Diabetes</i> , 2021, 70, 2683-2693.	0.3	26
33	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.	1.8	25
34	Re-exposure and environmental enrichment reveal NPY-Y1 as a possible target for post-traumatic stress disorder. <i>Neuropharmacology</i> , 2012, 63, 733-742.	2.0	24
35	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.	3.0	24
36	Visit-to-visit variability of glycemia and vascular complications: the Hoorn Diabetes Care System cohort. <i>Cardiovascular Diabetology</i> , 2019, 18, 170.	2.7	23

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37	Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. <i>Diabetes Care</i> , 2021, 44, 2673-2682.	4.3	23
38	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.	4.3	21
39	OVOL1 inhibits breast cancer cell invasion by enhancing the degradation of TGF- β 2 type I receptor. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 126.	7.1	15
40	Plasma protein N-glycosylation is associated with cardiovascular disease, nephropathy, and retinopathy in type 2 diabetes. <i>BMJ Open Diabetes Research and Care</i> , 2021, 9, e002345.	1.2	14
41	NACHO: an R package for quality control of NanoString nCounter data. <i>Bioinformatics</i> , 2020, 36, 970-971.	1.8	13
42	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.	0.7	13
43	HbA1c is associated with altered expression in blood of cell cycle- and immune response-related genes. <i>Diabetologia</i> , 2018, 61, 138-146.	2.9	10
44	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.	2.9	10
45	Long RNA Sequencing and Ribosome Profiling of Inflamed β 2-Cells Reveal an Extensive Translatome Landscape. <i>Diabetes</i> , 2021, 70, 2299-2312.	0.3	10
46	Breast cancer dormancy is associated with a 4NG1 state and not senescence. <i>Npj Breast Cancer</i> , 2021, 7, 140.	2.3	9
47	Serum Matrix Metalloproteinases and Left Atrial Remodeling—The Hoorn Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4944.	1.8	8
48	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , 2020, 12, 109.	3.6	8
49	Metformin and statin use associate with plasma protein N-glycosylation in people with type 2 diabetes. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001230.	1.2	8
50	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.	2.2	8
51	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.	1.1	7
52	CONQUER: an interactive toolbox to understand functional consequences of GWAS hits. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa085.	1.5	3
53	Repeat UVA exposure of human skin fibroblasts induces both a transitional and recovery DNA methylation response. <i>Epigenomics</i> , 2020, 12, 563-573.	1.0	2
54	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.	4.3	0

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55	Diabetes risk loci-associated pathways are shared across metabolic tissues. BMC Genomics, 2022, 23, 368.	1.2	0