

Maureen A Sartor

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.

77
papers

3,363
citations

27
h-index

57
g-index

80
ext. papers

4,370
ext. citations

7.2
avg, IF

5.3
L-index

#	Paper	IF	Citations
77	ATRX loss in glioma results in dysregulation of cell-cycle phase transition and ATM inhibitor radio-sensitization.. <i>Cell Reports</i> , 2022 , 38, 110216	10.6	2
76	Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data.. <i>Genome Biology</i> , 2022 , 23, 105	18.3	0
75	Characterization of the immune response in patients with cancer of the oral cavity after neoadjuvant immunotherapy with the IRX-2 regimen. <i>Oral Oncology</i> , 2021 , 123, 105587	4.4	0
74	Tissue and sex-specific programming of DNA methylation by perinatal lead exposure: implications for environmental epigenetics studies. <i>Epigenetics</i> , 2021 , 16, 1102-1122	5.7	4
73	Molecular Tumor Subtypes of HPV-Positive Head and Neck Cancers: Biological Characteristics and Implications for Clinical Outcomes. <i>Cancers</i> , 2021 , 13,	6.6	2
72	Machine learning approaches and databases for prediction of drug-target interaction: a survey paper. <i>Briefings in Bioinformatics</i> , 2021 , 22, 247-269	13.4	66
71	Effect of concentration and duration of particulate matter exposure on the transcriptome and DNA methylome of bronchial epithelial cells. <i>Environmental Epigenetics</i> , 2021 , 7, dvaa022	2.4	5
70	Perinatal DEHP exposure induces sex- and tissue-specific DNA methylation changes in both juvenile and adult mice. <i>Environmental Epigenetics</i> , 2021 , 7, dvab004	2.4	1
69	Sex-Specific Alterations in Cardiac DNA Methylation in Adult Mice by Perinatal Lead Exposure. <i>International Journal of Environmental Research and Public Health</i> , 2021 , 18,	4.6	2
68	Novel role of ASH1L histone methyltransferase in anaplastic thyroid carcinoma. <i>Journal of Biological Chemistry</i> , 2020 , 295, 8834-8845	5.4	12
67	Significant association between host transcriptome-derived HPV oncogene E6* influence score and carcinogenic pathways, tumor size, and survival in head and neck cancer. <i>Head and Neck</i> , 2020 , 42, 2375-2389	4.2	6
66	The role of the histone H3 variant CENPA in prostate cancer. <i>Journal of Biological Chemistry</i> , 2020 , 295, 8537-8549	5.4	23
65	Testing Proximity of Genomic Regions to Transcription Start Sites and Enhancers Complements Gene Set Enrichment Testing. <i>Frontiers in Genetics</i> , 2020 , 11, 199	4.5	2
64	Poly-Enrich: count-based methods for gene set enrichment testing with genomic regions. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa006	3.7	5
63	CBIO-03. ATRX LOSS IN GLIOMA RESULTS IN EPIGENETIC DYSREGULATION OF CELL CYCLE PHASE TRANSITION. <i>Neuro-Oncology</i> , 2020 , 22, ii16-ii16	1	
62	Universal concept signature analysis: genome-wide quantification of new biological and pathological functions of genes and pathways. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1717-1732	13.4	3
61	Interleukin 22 Signaling Regulates Acinar Cell Plasticity to Promote Pancreatic Tumor Development in Mice. <i>Gastroenterology</i> , 2020 , 158, 1417-1432.e11	13.3	22

60	5-Hydroxymethylation highlights the heterogeneity in keratinization and cell junctions in head and neck cancers. <i>Clinical Epigenetics</i> , 2020 , 12, 175	7.7	3
59	Tumor infiltrating lymphocytes after neoadjuvant IRX-2 immunotherapy in oral squamous cell carcinoma: Interim findings from the INSPIRE trial. <i>Oral Oncology</i> , 2020 , 111, 104928	4.4	5
58	Sex-Specific Programming of Cardiac DNA Methylation by Developmental Phthalate Exposure. <i>Epigenetics Insights</i> , 2020 , 13, 2516865720939971	3	5
57	Tissue- and Sex-Specific DNA Methylation Changes in Mice Perinatally Exposed to Lead (Pb). <i>Frontiers in Genetics</i> , 2020 , 11, 840	4.5	4
56	Soy Isoflavone Supplementation Increases Long Interspersed Nucleotide Element-1 (LINE-1) Methylation in Head and Neck Squamous Cell Carcinoma. <i>Nutrition and Cancer</i> , 2019 , 71, 772-780	2.8	4
55	Somatic expression of piRNA and associated machinery in the mouse identifies short, tissue-specific piRNA. <i>Epigenetics</i> , 2019 , 14, 504-521	5.7	31
54	Secreted nuclear protein DEK regulates hematopoiesis through CXCR2 signaling. <i>Journal of Clinical Investigation</i> , 2019 , 129, 2555-2570	15.9	14
53	Integrated Genomic-Transcriptomic Study Highlights Accumulation of Genetic Variants and Activation of Inflammatory Pathways. <i>Blood</i> , 2019 , 134, 4212-4212	2.2	
52	IDH1-R132H acts as a tumor suppressor in glioma via epigenetic up-regulation of the DNA damage response. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	98
51	Novel Bioinformatics Methods for Toxicoeigenetics 2019 , 265-288		1
50	The NIEHS TaRGET II Consortium and environmental epigenomics. <i>Nature Biotechnology</i> , 2018 , 36, 225-247.5	44.5	44
49	Group B streptococcus activates transcriptomic pathways related to premature birth in human extraplacental membranes in vitro. <i>Biology of Reproduction</i> , 2018 , 98, 396-407	3.9	6
48	Heterogeneity of Human Breast Stem and Progenitor Cells as Revealed by Transcriptional Profiling. <i>Stem Cell Reports</i> , 2018 , 10, 1596-1609	8	72
47	HPV Integration in HNSCC Correlates with Survival Outcomes, Immune Response Signatures, and Candidate Drivers. <i>Molecular Cancer Research</i> , 2018 , 16, 90-102	6.6	91
46	Expressed HNSCC variants by HPV-status in a well-characterized Michigan cohort. <i>Scientific Reports</i> , 2018 , 8, 11458	4.9	12
45	Age-related epigenome-wide DNA methylation and hydroxymethylation in longitudinal mouse blood. <i>Epigenetics</i> , 2018 , 13, 779-792	5.7	18
44	Cadmium Exposure Inhibits Branching Morphogenesis and Causes Alterations Consistent With HIF-1 α Inhibition in Human Primary Breast Organoids. <i>Toxicological Sciences</i> , 2018 , 164, 592-602	4.4	12
43	Longitudinal Effects of Developmental Bisphenol A Exposure on Epigenome-Wide DNA Hydroxymethylation at Imprinted Loci in Mouse Blood. <i>Environmental Health Perspectives</i> , 2018 , 126, 077006	8.4	19

42	annotatr: genomic regions in context. <i>Bioinformatics</i> , 2017 , 33, 2381-2383	7.2	127
41	Integrating DNA Methylation and Hydroxymethylation Data with the Mint Pipeline. <i>Cancer Research</i> , 2017 , 77, e27-e30	10.1	9
40	Genomic binding of PAX8-PPARG fusion protein regulates cancer-related pathways and alters the immune landscape of thyroid cancer. <i>Oncotarget</i> , 2017 , 8, 5761-5773	3.3	11
39	Adipogenic Differentiation of Thyroid Cancer Cells Through the Pax8-PPAR γ Fusion Protein Is Regulated by Thyroid Transcription Factor 1 (TTF-1). <i>Journal of Biological Chemistry</i> , 2016 , 291, 19274-86	5.4	9
38	Detection of differential DNA methylation in repetitive DNA of mice and humans perinatally exposed to bisphenol A. <i>Epigenetics</i> , 2016 , 11, 489-500	5.7	37
37	Transcriptomic profiling of curcumin-treated human breast stem cells identifies a role for stearoyl-coa desaturase in breast cancer prevention. <i>Breast Cancer Research and Treatment</i> , 2016 , 158, 29-41	4.4	42
36	A Mouse Model of X-linked Intellectual Disability Associated with Impaired Removal of Histone Methylation. <i>Cell Reports</i> , 2016 , 14, 1000-1009	10.6	68
35	Mono-2-ethylhexyl phthalate disrupts neurulation and modifies the embryonic redox environment and gene expression. <i>Reproductive Toxicology</i> , 2016 , 63, 32-48	3.4	22
34	Stability of methylation markers in head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2016 , 38 Suppl 1, E1325-31	4.2	7
33	ConceptMetab: exploring relationships among metabolite sets to identify links among biomedical concepts. <i>Bioinformatics</i> , 2016 , 32, 1536-43	7.2	9
32	Ultra-Deep Sequencing of Bisulfite-Modified DNA 2016 , 47-72		
31	RNA-Enrich: a cut-off free functional enrichment testing method for RNA-seq with improved detection power. <i>Bioinformatics</i> , 2016 , 32, 1100-2	7.2	32
30	Subtypes of HPV-Positive Head and Neck Cancers Are Associated with HPV Characteristics, Copy Number Alterations, PIK3CA Mutation, and Pathway Signatures. <i>Clinical Cancer Research</i> , 2016 , 22, 4735-45	12.9	72
29	Sequencing of first-strand cDNA library reveals full-length transcriptomes. <i>Nature Communications</i> , 2015 , 6, 6002	17.4	13
28	Bisphenol A-associated alterations in genome-wide DNA methylation and gene expression patterns reveal sequence-dependent and non-monotonic effects in human fetal liver. <i>Environmental Epigenetics</i> , 2015 , 1,	2.4	45
27	NDN and CD1A are novel prognostic methylation markers in patients with head and neck squamous carcinomas. <i>BMC Cancer</i> , 2015 , 15, 825	4.8	16
26	Genomic binding and regulation of gene expression by the thyroid carcinoma-associated PAX8-PPARG fusion protein. <i>Oncotarget</i> , 2015 , 6, 40418-32	3.3	16
25	MethylSig: a whole genome DNA methylation analysis pipeline. <i>Bioinformatics</i> , 2014 , 30, 2414-22	7.2	141

24	Regulation of the human endogenous retrovirus K (HML-2) transcriptome by the HIV-1 Tat protein. <i>Journal of Virology</i> , 2014 , 88, 8924-35	6.6	46
23	Epigenetics: relevance and implications for public health. <i>Annual Review of Public Health</i> , 2014 , 35, 105-220.6	20.6	66
22	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014 , 23, 4528-42	5.6	36
21	Broad-Enrich: functional interpretation of large sets of broad genomic regions. <i>Bioinformatics</i> , 2014 , 30, i393-400	7.2	11
20	Novel bioinformatics method for identification of genome-wide non-canonical spliced regions using RNA-Seq data. <i>PLoS ONE</i> , 2014 , 9, e100864	3.7	10
19	PePr: a peak-calling prioritization pipeline to identify consistent or differential peaks from replicated ChIP-Seq data. <i>Bioinformatics</i> , 2014 , 30, 2568-75	7.2	73
18	ChIP-Enrich: gene set enrichment testing for ChIP-seq data. <i>Nucleic Acids Research</i> , 2014 , 42, e105	20.1	80
17	ER-stress-induced transcriptional regulation increases protein synthesis leading to cell death. <i>Nature Cell Biology</i> , 2013 , 15, 481-90	23.4	976
16	Comprehensive analysis of DNA methylation in head and neck squamous cell carcinoma indicates differences by survival and clinicopathologic characteristics. <i>PLoS ONE</i> , 2013 , 8, e54742	3.7	41
15	LRpath analysis reveals common pathways dysregulated via DNA methylation across cancer types. <i>BMC Genomics</i> , 2012 , 13, 526	4.5	50
14	Bioinformatics for High-Throughput Toxico-Epigenomics Studies 2012 , 569-588		1
13	Metab2MeSH: annotating compounds with medical subject headings. <i>Bioinformatics</i> , 2012 , 28, 1408-10	7.2	27
12	Pretreatment dietary intake is associated with tumor suppressor DNA methylation in head and neck squamous cell carcinomas. <i>Epigenetics</i> , 2012 , 7, 883-91	5.7	31
11	Genome-wide methylation and expression differences in HPV(+) and HPV(-) squamous cell carcinoma cell lines are consistent with divergent mechanisms of carcinogenesis. <i>Epigenetics</i> , 2011 , 6, 777-87	5.7	118
10	Identification of maternally regulated fetal gene networks in the placenta with a novel embryo transfer system in mice. <i>Physiological Genomics</i> , 2011 , 43, 317-24	3.6	3
9	ConceptGen: a gene set enrichment and gene set relation mapping tool. <i>Bioinformatics</i> , 2010 , 26, 456-637.2	7.2	120
8	Genome-wide binding of the orphan nuclear receptor TR4 suggests its general role in fundamental biological processes. <i>BMC Genomics</i> , 2010 , 11, 689	4.5	25
7	A genetic network model of cellular responses to lithium treatment and cocaine abuse in bipolar disorder. <i>BMC Systems Biology</i> , 2010 , 4, 158	3.5	18

6	Modeling complex genetic and environmental influences on comorbid bipolar disorder with tobacco use disorder. <i>BMC Medical Genetics</i> , 2010 , 11, 14	2.1	21
5	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. <i>Bioinformatics</i> , 2009 , 25, 211-7	7.2	138
4	Intensity-based hierarchical Bayes method improves testing for differentially expressed genes in microarray experiments. <i>BMC Bioinformatics</i> , 2006 , 7, 538	3.6	195
3	Poly-Enrich: Count-based Methods for Gene Set Enrichment Testing with Genomic Regions		1
2	annotatr: Genomic regions in context		3
1	Heterogeneity of normal human breast stem and progenitor cells as revealed by transcriptional profiling		3