

Maureen A Sartor

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

5,040
citations

147801

31
h-index

98798

67
g-index

80
all docs

80
docs citations

80
times ranked

9882
citing authors

#	ARTICLE	IF	CITATIONS
1	ATRX loss in glioma results in dysregulation of cell-cycle phase transition and ATM inhibitor radio-sensitization. <i>Cell Reports</i> , 2022, 38, 110216.	6.4	32
2	Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data. <i>Genome Biology</i> , 2022, 23, 105.	8.8	6
3	Identification of occupations susceptible to high exposure and risk associated with multiple toxicants in an observational study: National Health and Nutrition Examination Survey 1999–2014. <i>Exposome</i> , 2022, 2, .	2.8	6
4	Tissue and sex-specific programming of DNA methylation by perinatal lead exposure: implications for environmental epigenetics studies. <i>Epigenetics</i> , 2021, 16, 1102-1122.	2.7	15
5	Machine learning approaches and databases for prediction of drug–target interaction: a survey paper. <i>Briefings in Bioinformatics</i> , 2021, 22, 247-269.	6.5	217
6	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.	1.8	14
7	Perinatal DEHP exposure induces sex- and tissue-specific DNA methylation changes in both juvenile and adult mice. <i>Environmental Epigenetics</i> , 2021, 7, dvab004.	1.8	10
8	Molecular Tumor Subtypes of HPV-Positive Head and Neck Cancers: Biological Characteristics and Implications for Clinical Outcomes. <i>Cancers</i> , 2021, 13, 2721.	3.7	10
9	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, 577.	2.6	12
10	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.	1.5	2
11	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.	6.5	9
12	Interleukin 22 Signaling Regulates Acinar Cell Plasticity to Promote Pancreatic Tumor Development in Mice. <i>Gastroenterology</i> , 2020, 158, 1417-1432.e11.	1.3	48
13	5-Hydroxymethylation highlights the heterogeneity in keratinization and cell junctions in head and neck cancers. <i>Clinical Epigenetics</i> , 2020, 12, 175.	4.1	8
14	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.	1.5	9
15	Sex-Specific Programming of Cardiac DNA Methylation by Developmental Phthalate Exposure. <i>Epigenetics Insights</i> , 2020, 13, 251686572093997.	2.0	15
16	Tissue- and Sex-Specific DNA Methylation Changes in Mice Perinatally Exposed to Lead (Pb). <i>Frontiers in Genetics</i> , 2020, 11, 840.	2.3	16
17	Novel role of ASH1L histone methyltransferase in anaplastic thyroid carcinoma. <i>Journal of Biological Chemistry</i> , 2020, 295, 8834-8845.	3.4	21
18	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.	2.0	9

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19	The role of the histone H3 variant CENPA in prostate cancer. <i>Journal of Biological Chemistry</i> , 2020, 295, 8537-8549.	3.4	43
20	Testing Proximity of Genomic Regions to Transcription Start Sites and Enhancers Complements Gene Set Enrichment Testing. <i>Frontiers in Genetics</i> , 2020, 11, 199.	2.3	4
21	Poly-Enrich: count-based methods for gene set enrichment testing with genomic regions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa006.	3.2	13
22	CBIO-03. ATRX LOSS IN GLIOMA RESULTS IN EPIGENETIC DYSREGULATION OF CELL CYCLE PHASE TRANSITION. <i>Neuro-Oncology</i> , 2020, 22, ii16-ii16.	1.2	0
23	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.	2.0	7
24	Somatic expression of piRNA and associated machinery in the mouse identifies short, tissue-specific piRNA. <i>Epigenetics</i> , 2019, 14, 504-521.	2.7	59
25	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, .	12.4	169
26	Novel Bioinformatics Methods for Toxicoeugenetics. , 2019, , 265-288.		11
27	Secreted nuclear protein DEK regulates hematopoiesis through CXCR2 signaling. <i>Journal of Clinical Investigation</i> , 2019, 129, 2555-2570.	8.2	28
28	Integrated Genomic-Transcriptomic Study Highlights Accumulation of Genetic Variants and Activation of Inflammatory Pathways. <i>Blood</i> , 2019, 134, 4212-4212.	1.4	0
29	The NIEHS TaRGET II Consortium and environmental epigenomics. <i>Nature Biotechnology</i> , 2018, 36, 225-227.	17.5	79
30	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.	2.7	15
31	Heterogeneity of Human Breast Stem and Progenitor Cells as Revealed by Transcriptional Profiling. <i>Stem Cell Reports</i> , 2018, 10, 1596-1609.	4.8	112
32	HPV Integration in HNSCC Correlates with Survival Outcomes, Immune Response Signatures, and Candidate Drivers. <i>Molecular Cancer Research</i> , 2018, 16, 90-102.	3.4	151
33	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.	6.0	42
34	Expressed HNSCC variants by HPV-status in a well-characterized Michigan cohort. <i>Scientific Reports</i> , 2018, 8, 11458.	3.3	18
35	Age-related epigenome-wide DNA methylation and hydroxymethylation in longitudinal mouse blood. <i>Epigenetics</i> , 2018, 13, 779-792.	2.7	25
36	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.	3.1	20

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37	annotatr: genomic regions in context. <i>Bioinformatics</i> , 2017, 33, 2381-2383.	4.1	297
38	Integrating DNA Methylation and Hydroxymethylation Data with the Mint Pipeline. <i>Cancer Research</i> , 2017, 77, e27-e30.	0.9	12
39	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.	1.8	14
40	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, 4735-4745.	7.0	107
41	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, 19274-19286.	3.4	14
42	Detection of differential DNA methylation in repetitive DNA of mice and humans perinatally exposed to bisphenol A. <i>Epigenetics</i> , 2016, 11, 489-500.	2.7	48
43	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.	2.5	56
44	A Mouse Model of X-linked Intellectual Disability Associated with Impaired Removal of Histone Methylation. <i>Cell Reports</i> , 2016, 14, 1000-1009.	6.4	112
45	Mono-2-ethylhexyl phthalate disrupts neurulation and modifies the embryonic redox environment and gene expression. <i>Reproductive Toxicology</i> , 2016, 63, 32-48.	2.9	28
46	Stability of methylation markers in head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2016, 38, E1325-31.	2.0	9
47	ConceptMetab: exploring relationships among metabolite sets to identify links among biomedical concepts. <i>Bioinformatics</i> , 2016, 32, 1536-1543.	4.1	10
48	Ultra-Deep Sequencing of Bisulfite-Modified DNA. , 2016, , 47-72.		0
49	RNA-Enrich: a cut-off free functional enrichment testing method for RNA-seq with improved detection power. <i>Bioinformatics</i> , 2016, 32, 1100-1102.	4.1	48
50	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, dvv006.	1.8	62
51	NDN and CD1A are novel prognostic methylation markers in patients with head and neck squamous carcinomas. <i>BMC Cancer</i> , 2015, 15, 825.	2.6	18
52	Sequencing of first-strand cDNA library reveals full-length transcriptomes. <i>Nature Communications</i> , 2015, 6, 6002.	12.8	24
53	Genomic binding and regulation of gene expression by the thyroid carcinoma-associated PAX8-PPARG fusion protein. <i>Oncotarget</i> , 2015, 6, 40418-40432.	1.8	19
54	Novel Bioinformatics Method for Identification of Genome-Wide Non-Canonical Spliced Regions Using RNA-Seq Data. <i>PLoS ONE</i> , 2014, 9, e100864.	2.5	10

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55	PePr: a peak-calling prioritization pipeline to identify consistent or differential peaks from replicated ChIP-Seq data. <i>Bioinformatics</i> , 2014, 30, 2568-2575.	4.1	114
56	ChIP-Enrich: gene set enrichment testing for ChIP-seq data. <i>Nucleic Acids Research</i> , 2014, 42, e105-e105.	14.5	136
57	MethylSig: a whole genome DNA methylation analysis pipeline. <i>Bioinformatics</i> , 2014, 30, 2414-2422.	4.1	186
58	Regulation of the Human Endogenous Retrovirus K (HML-2) Transcriptome by the HIV-1 Tat Protein. <i>Journal of Virology</i> , 2014, 88, 8924-8935.	3.4	56
59	Epigenetics: Relevance and Implications for Public Health. <i>Annual Review of Public Health</i> , 2014, 35, 105-122.	17.4	90
60	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014, 23, 4528-4542.	2.9	45
61	Broad-Enrich: functional interpretation of large sets of broad genomic regions. <i>Bioinformatics</i> , 2014, 30, i393-i400.	4.1	21
62	ER-stress-induced transcriptional regulation increases protein synthesis leading to cell death. <i>Nature Cell Biology</i> , 2013, 15, 481-490.	10.3	1,315
63	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.	2.5	46
64	Metab2MeSH: annotating compounds with medical subject headings. <i>Bioinformatics</i> , 2012, 28, 1408-1410.	4.1	33
65	Pretreatment dietary intake is associated with tumor suppressor DNA methylation in head and neck squamous cell carcinomas. <i>Epigenetics</i> , 2012, 7, 883-891.	2.7	34
66	LRpath analysis reveals common pathways dysregulated via DNA methylation across cancer types. <i>BMC Genomics</i> , 2012, 13, 526.	2.8	65
67	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, 777-787.	2.7	145
68	Identification of maternally regulated fetal gene networks in the placenta with a novel embryo transfer system in mice. <i>Physiological Genomics</i> , 2011, 43, 317-324.	2.3	3
69	Genome-wide binding of the orphan nuclear receptor TR4 suggests its general role in fundamental biological processes. <i>BMC Genomics</i> , 2010, 11, 689.	2.8	34
70	A genetic network model of cellular responses to lithium treatment and cocaine abuse in bipolar disorder. <i>BMC Systems Biology</i> , 2010, 4, 158.	3.0	19
71	Modeling complex genetic and environmental influences on comorbid bipolar disorder with tobacco use disorder. <i>BMC Medical Genetics</i> , 2010, 11, 14.	2.1	26
72	ConceptGen: a gene set enrichment and gene set relation mapping tool. <i>Bioinformatics</i> , 2010, 26, 456-463.	4.1	134

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73	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. <i>Bioinformatics</i> , 2009, 25, 211-217.	4.1	163
74	Intensity-based hierarchical Bayes method improves testing for differentially expressed genes in microarray experiments. <i>BMC Bioinformatics</i> , 2006, 7, 538.	2.6	219