

# Juan Sandoval

## List of Publications by Year in descending order

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Version: 2024-02-01

71  
papers

5,853  
citations

109321

35  
h-index

85541

71  
g-index

72  
all docs

72  
docs citations

72  
times ranked

11595  
citing authors

#	ARTICLE	IF	CITATIONS
1	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , 2011, 6, 692-702.	2.7	908
2	Cancer epigenomics: beyond genomics. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 50-55.	3.3	421
3	Age-dependent epigenetic control of differentiation inhibitors is critical for remyelination efficiency. <i>Nature Neuroscience</i> , 2008, 11, 1024-1034.	14.8	411
4	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013, 23, 1363-1372.	5.5	353
5	A Prognostic DNA Methylation Signature for Stage I Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 4140-4147.	1.6	250
6	The Transcription Factor Yin Yang 1 Is Essential for Oligodendrocyte Progenitor Differentiation. <i>Neuron</i> , 2007, 55, 217-230.	8.1	235
7	A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , 2015, 9, 555-568.	4.6	156
8	Epigenetic inactivation of the p53-induced long noncoding RNA TP53 target 1 in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7535-E7544.	7.1	140
9	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014, 512, 87-90.	27.8	136
10	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013, 34, 102-108.	2.8	135
11	Epigenetics and Oxidative Stress in Aging. <i>Oxidative Medicine and Cellular Longevity</i> , 2017, 2017, 1-8.	4.0	129
12	Interaction Between Cytokines and Oxidative Stress in Acute Pancreatitis. <i>Current Medicinal Chemistry</i> , 2006, 13, 2775-2787.	2.4	123
13	RNAPol-ChIP: a novel application of chromatin immunoprecipitation to the analysis of real-time gene transcription. <i>Nucleic Acids Research</i> , 2004, 32, e88-e88.	14.5	122
14	A Novel Epigenetic Signature for Early Diagnosis in Lung Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 3361-3371.	7.0	113
15	Intergenic transcripts originating from a subclass of ribosomal DNA repeats silence ribosomal RNA genes in <i>trans</i> . <i>EMBO Reports</i> , 2010, 11, 52-58.	4.5	106
16	A DERL3-associated defect in the degradation of SLC2A1 mediates the Warburg effect. <i>Nature Communications</i> , 2014, 5, 3608.	12.8	94
17	Epigenetic Disruption of the PIWI Pathway in Human Spermatogenic Disorders. <i>PLoS ONE</i> , 2012, 7, e47892.	2.5	94
18	MicroRNA Expression Profiling and DNA Methylation Signature for Deregulated MicroRNA in Cutaneous T-Cell Lymphoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1128-1137.	0.7	87

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19	Cross-Talk between Oxidative Stress and Pro-Inflammatory Cytokines in Acute Pancreatitis: A Key Role for Protein Phosphatases. <i>Current Pharmaceutical Design</i> , 2009, 15, 3027-3042.	1.9	85
20	Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. <i>Cell Reports</i> , 2017, 19, 1268-1280.	6.4	79
21	Dysregulation of the long non-coding RNA transcriptome in a Rett syndrome mouse model. <i>RNA Biology</i> , 2013, 10, 1197-1203.	3.1	77
22	Primary cutaneous marginal zone B-cell lymphoma: Response to treatment and disease-free survival in a series of 137 patients. <i>Journal of the American Academy of Dermatology</i> , 2013, 69, 357-365.	1.2	76
23	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , 2012, 7, 542-550.	2.7	68
24	Non-CpG island promoter hypomethylation and miR-149 regulate the expression of <i>SRPX2</i> in colorectal cancer. <i>International Journal of Cancer</i> , 2013, 132, 2303-2315.	5.1	68
25	Novel Insights into DNA Methylation Features in Spermatozoa: Stability and Peculiarities. <i>PLoS ONE</i> , 2012, 7, e44479.	2.5	68
26	Epigenetic biomarkers in laboratory diagnostics: emerging approaches and opportunities. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 457-471.	3.1	54
27	Identification of a gene-pathway associated with non-alcoholic steatohepatitis. <i>Journal of Hepatology</i> , 2007, 46, 708-718.	3.7	52
28	MiR-204 silencing in intraepithelial to invasive cutaneous squamous cell carcinoma progression. <i>Molecular Cancer</i> , 2016, 15, 53.	19.2	48
29	Inhibition of p53 Transcriptional Activity: A Potential Target for Future Development of Therapeutic Strategies for Primary Demyelination. <i>Journal of Neuroscience</i> , 2008, 28, 6118-6127.	3.6	47
30	Identification of an epigenetic signature of human colorectal cancer associated with obesity by genome-wide DNA methylation analysis. <i>International Journal of Obesity</i> , 2019, 43, 176-188.	3.4	42
31	Oxidative Stress in the Pathogenesis of Crohn's Disease and the Interconnection with Immunological Response, Microbiota, External Environmental Factors, and Epigenetics. <i>Antioxidants</i> , 2021, 10, 64.	5.1	41
32	Events at the transition between cell cycle exit and oligodendrocyte progenitor differentiation: the role of HDAC and YY1. <i>Neuron Glia Biology</i> , 2007, 3, 221-231.	1.6	40
33	Translating cancer epigenomics into the clinic: focus on lung cancer. <i>Translational Research</i> , 2017, 189, 76-92.	5.0	40
34	A two-gene epigenetic signature for the prediction of response to neoadjuvant chemotherapy in triple-negative breast cancer patients. <i>Clinical Epigenetics</i> , 2019, 11, 33.	4.1	39
35	Oxidative and nitrosative stress in acute pancreatitis. Modulation by pentoxifylline and oxypurinol. <i>Biochemical Pharmacology</i> , 2012, 83, 122-130.	4.4	38
36	Cancer Epigenetic Biomarkers in Liquid Biopsy for High Incidence Malignancies. <i>Cancers</i> , 2021, 13, 3016.	3.7	38

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37	Epigenetic Regulation of microRNAs in Cancer: Shortening the Distance from Bench to Bedside. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7350.	4.1	38
38	Id2 leaves the chromatin of the E2F4/p130-controlled c-myc promoter during hepatocyte priming for liver regeneration. <i>Biochemical Journal</i> , 2006, 398, 431-437.	3.7	37
39	Methods for analysis of specific DNA methylation status. <i>Methods</i> , 2021, 187, 3-12.	3.8	36
40	Analysis of copy number alterations reveals the lncRNA ALAL-1 as a regulator of lung cancer immune evasion. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	36
41	Obesity and menopause modify the epigenomic profile of breast cancer. <i>Endocrine-Related Cancer</i> , 2017, 24, 351-363.	3.1	35
42	CD137 (4-1BB) Costimulation Modifies DNA Methylation in CD8+ T Cell-Relevant Genes. <i>Cancer Immunology Research</i> , 2018, 6, 69-78.	3.4	34
43	Label-free DNA-methylation detection by direct ds-DNA fragment screening using poly-purine hairpins. <i>Biosensors and Bioelectronics</i> , 2018, 120, 47-54.	10.1	34
44	Vitamin E deficiency induces liver nuclear factor- $\kappa$ B DNA-binding activity and changes in related genes. <i>Free Radical Research</i> , 2005, 39, 1127-1138.	3.3	33
45	Genome-wide DNA methylation profiling predicts relapse in childhood B-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2013, 160, 406-409.	2.5	33
46	Genome wide DNA methylation profiling identifies specific epigenetic features in high-risk cutaneous squamous cell carcinoma. <i>PLoS ONE</i> , 2019, 14, e0223341.	2.5	32
47	Notch1 Pathway Activation Results from the Epigenetic Abrogation of Notch-Related MicroRNAs in Mycosis Fungoides. <i>Journal of Investigative Dermatology</i> , 2015, 135, 3144-3152.	0.7	31
48	Epigenetic alterations leading to TMRSS4 promoter hypomethylation and protein overexpression predict poor prognosis in squamous lung cancer patients. <i>Oncotarget</i> , 2016, 7, 22752-22769.	1.8	29
49	Epigenetic Regulation of Vitamin D Metabolism in Human Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2014, 9, 473-482.	1.1	28
50	Epigenetic Regulation of Early- and Late-Response Genes in Acute Pancreatitis. <i>Journal of Immunology</i> , 2016, 197, 4137-4150.	0.8	28
51	Pentoxifylline Prevents Loss of PP2A Phosphatase Activity and Recruitment of Histone Acetyltransferases to Proinflammatory Genes in Acute Pancreatitis. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2009, 331, 609-617.	2.5	27
52	Epigenetic Modifiers Are Necessary but Not Sufficient for Reprogramming Non-Myelinating Cells into Myelin Gene-Expressing Cells. <i>PLoS ONE</i> , 2010, 5, e13023.	2.5	27
53	An Epigenetic Signature in Adipose Tissue Is Linked to Nicotinamide N-methyltransferase Gene Expression. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1700933.	3.3	26
54	Transcription of the MAT2A gene, coding for methionine adenosyltransferase, is up-regulated by E2F and Sp1 at a chromatin level during proliferation of liver cells. <i>International Journal of Biochemistry and Cell Biology</i> , 2007, 39, 842-850.	2.8	23

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55	Identification of <sc>HERC</sc>5 and its potential role in <sc>NSCLC</sc> progression. International Journal of Cancer, 2015, 136, 2264-2272.	5.1	23
56	The Oxygen Load Supplied during Delivery Room Stabilization of Preterm Infants Modifies the DNA Methylation Profile. Journal of Pediatrics, 2018, 202, 70-76.e2.	1.8	23
57	An integrated approach to design novel therapeutic interventions for demyelinating disorders. European Journal of Neuroscience, 2012, 35, 1879-1886.	2.6	22
58	Identification of Epigenetic Methylation Signatures With Clinical Value in Crohn's Disease. Clinical and Translational Gastroenterology, 2019, 10, e00083.	2.5	22
59	Epigenomic signature of adrenoleukodystrophy predicts compromised oligodendrocyte differentiation. Brain Pathology, 2018, 28, 902-919.	4.1	21
60	Generation and Characterization of Rat and Mouse Monoclonal Antibodies Specific for MeCP2 and Their Use in X-Inactivation Studies. PLoS ONE, 2011, 6, e26499.	2.5	20
61	Disruption of NIPBL/Sccl in Cornelia de Lange Syndrome provokes cohesin genome-wide redistribution with an impact in the transcriptome. Nature Communications, 2021, 12, 4551.	12.8	20
62	Glutamate cysteine ligase up-regulation fails in necrotizing pancreatitis. Free Radical Biology and Medicine, 2008, 44, 1599-1609.	2.9	18
63	In vivo GSH depletion induces c-myc expression by modulation of chromatin protein complexes. Free Radical Biology and Medicine, 2009, 46, 1534-1542.	2.9	18
64	Thyroid hormone biosynthesis machinery is altered in the ischemic myocardium: An epigenomic study. International Journal of Cardiology, 2017, 243, 27-33.	1.7	17
65	ZNF577 Methylation Levels in Leukocytes From Women With Breast Cancer Is Modulated by Adiposity, Menopausal State, and the Mediterranean Diet. Frontiers in Endocrinology, 2020, 11, 245.	3.5	14
66	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. Synapse, 2017, 71, e21959.	1.2	13
67	<i>ASB1</i> differential methylation in ischaemic cardiomyopathy: relationship with left ventricular performance in end-stage heart failure patients. ESC Heart Failure, 2018, 5, 732-737.	3.1	13
68	Identification of a novel synthetic lethal vulnerability in non-small cell lung cancer by co-targeting TMRSS4 and DDR1. Scientific Reports, 2019, 9, 15400.	3.3	13
69	Epigenetic Silencing of Tumor Suppressor miR-124 Directly Supports STAT3 Activation in Cutaneous T-Cell Lymphoma. Cells, 2020, 9, 2692.	4.1	5
70	MethCORR modelling of methylomes from formalin-fixed paraffin-embedded tissue enables characterization and prognostication of colorectal cancer. Nature Communications, 2020, 11, 2025.	12.8	5
71	Molecular mechanisms of Id2 down-regulation in rat liver after acetaminophen overdose. Protection by N-acetyl-L-cysteine. Free Radical Research, 2010, 44, 1044-1053.	3.3	4