

Sergi Sayols

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

6,130
citations

159358

30
h-index

288905

40
g-index

40
all docs

40
docs citations

40
times ranked

12907
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Methylation Profiling of Human Hepatocarcinogenesis. <i>Hepatology</i> , 2021, 74, 183-199.	3.6	42
2	E3 ubiquitin ligase Atrogin-1 mediates adaptive resistance to KIT-targeted inhibition in gastrointestinal stromal tumor. <i>Oncogene</i> , 2021, 40, 6614-6626.	2.6	7
3	Signalling codes for the maintenance and lineage commitment of embryonic gastric epithelial progenitors. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	12
4	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. <i>Nature Protocols</i> , 2020, 15, 3894-3941.	5.5	19
5	The RNA fold interactome of evolutionary conserved RNA structures in <i>S. cerevisiae</i> . <i>Nature Communications</i> , 2020, 11, 2789.	5.8	11
6	Spatial Chromosome Folding and Active Transcription Drive DNA Fragility and Formation of Oncogenic MLL Translocations. <i>Molecular Cell</i> , 2019, 75, 267-283.e12.	4.5	104
7	Liver X Receptorâ€“Binding DNA Motif Associated With Atherosclerosisâ€“Specific DNA Methylation Profiles of <i>Alu</i> Elements and Neighboring CpG Islands. <i>Journal of the American Heart Association</i> , 2018, 7, .	1.6	9
8	PM20D1 is a quantitative trait locus associated with Alzheimerâ€™s disease. <i>Nature Medicine</i> , 2018, 24, 598-603.	15.2	73
9	Role for the transcriptional activator ZRF1 in early metastatic events in breast cancer progression and endocrine resistance. <i>Oncotarget</i> , 2018, 9, 28666-28690.	0.8	7
10	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , 2017, 71, e21959.	0.6	13
11	Id2 controls specification of Lgr5 ⁺ intestinal stem cell progenitors during gut development. <i>EMBO Journal</i> , 2017, 36, 869-885.	3.5	45
12	ZBTB48 is both a vertebrate telomere-binding protein and a transcriptional activator. <i>EMBO Reports</i> , 2017, 18, 929-946.	2.0	50
13	A DNA methylation map of human cancer at single base-pair resolution. <i>Oncogene</i> , 2017, 36, 5648-5657.	2.6	75
14	Dynamic changes in chromatin states during specification and differentiation of adult intestinal stem cells. <i>Nucleic Acids Research</i> , 2017, 45, 5770-5784.	6.5	71
15	The developmental proteome of <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2017, 27, 1273-1285.	2.4	135
16	Distinct populations of embryonic epithelial progenitors generate Lgr5 ⁺ intestinal stem cells. <i>Developmental Biology</i> , 2017, 432, 258-264.	0.9	3
17	DNA Methylomes Reveal Biological Networks Involved in Human Eye Development, Functions and Associated Disorders. <i>Scientific Reports</i> , 2017, 7, 11762.	1.6	44
18	dupRadar: a Bioconductor package for the assessment of PCR artifacts in RNA-Seq data. <i>BMC Bioinformatics</i> , 2016, 17, 428.	1.2	99

#	ARTICLE	IF	CITATIONS
19	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	13.5	1,518
20	Dual role of Med12 in PRC1-dependent gene repression and ncRNA-mediated transcriptional activation. <i>Cell Cycle</i> , 2016, 15, 1479-1493.	1.3	28
21	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1386-1395.	5.1	357
22	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016, 6, e718-e718.	2.4	137
23	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016, 17, 11.	3.8	184
24	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	1.1	34
25	DNA methylation-based prognosis and epidrivers in hepatocellular carcinoma. <i>Hepatology</i> , 2015, 61, 1945-1956.	3.6	367
26	Unique Genomic Profile of Fibrolamellar Hepatocellular Carcinoma. <i>Gastroenterology</i> , 2015, 148, 806-818.e10.	0.6	109
27	The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. <i>BMC Medical Genomics</i> , 2015, 8, 7.	0.7	85
28	Head-to-head antisense transcription and R-loop formation promotes transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5785-5790.	3.3	194
29	A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , 2015, 9, 555-568.	2.1	156
30	A Comprehensive DNA Methylation Profile of Epithelial-to-Mesenchymal Transition. <i>Cancer Research</i> , 2014, 74, 5608-5619.	0.4	69
31	DNA Methylation Map of Human Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 692-700.	5.1	207
32	Linkage of DNA Methylation Quantitative Trait Loci to Human Cancer Risk. <i>Cell Reports</i> , 2014, 7, 331-338.	2.9	76
33	Gene amplification of the histone methyltransferase SETDB1 contributes to human lung tumorigenesis. <i>Oncogene</i> , 2014, 33, 2807-2813.	2.6	126
34	A Prognostic DNA Methylation Signature for Stage I Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 4140-4147.	0.8	250
35	Dysregulation of the long non-coding RNA transcriptome in a Rett syndrome mouse model. <i>RNA Biology</i> , 2013, 10, 1197-1203.	1.5	77
36	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013, 23, 1363-1372.	2.4	353

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37	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013, 34, 102-108.	1.3	135
38	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , 2012, 7, 542-550.	1.3	68
39	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527.	3.3	687
40	Epigenetic Disruption of the PIWI Pathway in Human Spermatogenic Disorders. <i>PLoS ONE</i> , 2012, 7, e47892.	1.1	94