

Ian M Sudbery

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

4,210
citations

471061

17
h-index

676716

22
g-index

30
all docs

30
docs citations

30
times ranked

9381
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromatin-based, in cis and in trans regulatory rewiring underpins distinct oncogenic transcriptomes in multiple myeloma. <i>Nature Communications</i> , 2021, 12, 5450.	5.8	19
2	Tribbles-1 Expression and Its Function to Control Inflammatory Cytokines, Including Interleukin-8 Levels are Regulated by miRNAs in Macrophages and Prostate Cancer Cells. <i>Frontiers in Immunology</i> , 2020, 11, 574046.	2.2	18
3	Macrophage polarisation associated with atherosclerosis differentially affects their capacity to handle lipids. <i>Atherosclerosis</i> , 2020, 305, 10-18.	0.4	19
4	Co-transcriptional Loading of RNA Export Factors Shapes the Human Transcriptome. <i>Molecular Cell</i> , 2019, 75, 310-323.e8.	4.5	75
5	Proteins that physically interact with the phosphatase Cdc14 in <i>Candida albicans</i> have diverse roles in the cell cycle. <i>Scientific Reports</i> , 2019, 9, 6258.	1.6	18
6	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. <i>Genome Biology</i> , 2019, 20, 65.	3.8	195
7	BS25â€¦Investigating the MIR-101-3P/TRIB1 axis in macrophage immunometabolism. , 2019, , .		1
8	Oncogenic MAF in Co-Operation with IRF4 Confers Extensive Chromatin Re-Arrangement in Plasma Cells and Generates 'Neo-Enhancers' That Regulate Genes Critical for Myeloma Biology. <i>Blood</i> , 2019, 134, 3783-3783.	0.6	1
9	The m6A-methylase complex recruits TREX and regulates mRNA export. <i>Scientific Reports</i> , 2018, 8, 13827.	1.6	89
10	UCLH3 Regulates Topoisomerase-Induced Chromosomal Break Repair by Controlling TDP1 Proteostasis. <i>Cell Reports</i> , 2018, 23, 3352-3365.	2.9	40
11	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. <i>Genome Research</i> , 2017, 27, 491-499.	2.4	1,316
12	201â€¦Human oxidised phospholipid macrophages have high lipoprotein handling capabilities without readily forming unwanted foam cells. <i>Heart</i> , 2017, 103, A136.1-A136.	1.2	0
13	Cell Cycle-Independent Phospho-Regulation of Fkh2 during Hyphal Growth Regulates <i>Candida albicans</i> Pathogenesis. <i>PLoS Pathogens</i> , 2015, 11, e1004630.	2.1	26
14	Phosphoregulation of Nap1 Plays a Role in Septin Ring Dynamics and Morphogenesis in <i>Candida albicans</i> . <i>MBio</i> , 2014, 5, e00915-13.	1.8	19
15	CGAT: computational genomics analysis toolkit. <i>Bioinformatics</i> , 2014, 30, 1290-1291.	1.8	65
16	Identification of a candidate prognostic gene signature by transcriptome analysis of matched pre- and post-treatment prostatic biopsies from patients with advanced prostate cancer. <i>BMC Cancer</i> , 2014, 14, 977.	1.1	49
17	Sequencing depth and coverage: key considerations in genomic analyses. <i>Nature Reviews Genetics</i> , 2014, 15, 121-132.	7.7	1,116
18	Next-generation Sequencing of Advanced Prostate Cancer Treated with Androgen-deprivation Therapy. <i>European Urology</i> , 2014, 66, 32-39.	0.9	139

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19	KDM2B links the Polycomb Repressive Complex 1 (PRC1) to recognition of CpG islands. <i>ELife</i> , 2012, 1, e00205.	2.8	414
20	Systematic analysis of off-target effects in an RNAi screen reveals microRNAs affecting sensitivity to TRAIL-induced apoptosis. <i>BMC Genomics</i> , 2010, 11, 175.	1.2	41
21	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010, 11, 25.	2.7	64
22	Next-generation sequencing of vertebrate experimental organisms. <i>Mammalian Genome</i> , 2009, 20, 327-338.	1.0	34
23	Deep short-read sequencing of chromosome 17 from the mouse strains A/J and CAST/Ei identifies significant germline variation and candidate genes that regulate liver triglyceride levels. <i>Genome Biology</i> , 2009, 10, R112.	13.9	36
24	Apoptosis induced by environmental stresses and amphotericin B in <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14327-14332.	3.3	357
25	CGAT-core: a python framework for building scalable, reproducible computational biology workflows. <i>F1000Research</i> , 0, 8, 377.	0.8	11
26	CGAT-core: a python framework for building scalable, reproducible computational biology workflows. <i>F1000Research</i> , 0, 8, 377.	0.8	20