

Damien J Downes

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,281
citations

567144

15
h-index

454834

30
g-index

49
all docs

49
docs citations

49
times ranked

1894
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly efficient CRISPR-Cas9-mediated editing identifies novel mechanosensitive microRNA-140 targets in primary human articular chondrocytes. <i>Osteoarthritis and Cartilage</i> , 2022, , .	0.6	6
2	Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. <i>Nature Protocols</i> , 2022, 17, 445-475.	5.5	24
3	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. <i>Nature Communications</i> , 2022, 13, 773.	5.8	10
4	Natural and Experimental Rewiring of Gene Regulatory Regions. <i>Annual Review of Genomics and Human Genetics</i> , 2022, 23, .	2.5	1
5	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. <i>Nature Communications</i> , 2022, 13, .	5.8	20
6	Genetic and functional insights into CDA-I prevalence and pathogenesis. <i>Journal of Medical Genetics</i> , 2021, 58, 185-195.	1.5	9
7	A remarkable case of HbH disease illustrates the relative contributions of the $\hat{1}\pm$ -globin enhancers to gene expression. <i>Blood</i> , 2021, 137, 572-575.	0.6	6
8	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. <i>Nature Communications</i> , 2021, 12, 531.	5.8	32
9	Fra-1 regulates its target genes via binding to remote enhancers without exerting major control on chromatin architecture in triple negative breast cancers. <i>Nucleic Acids Research</i> , 2021, 49, 2488-2508.	6.5	15
10	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. <i>Molecular Cell</i> , 2021, 81, 983-997.e7.	4.5	27
11	Multi Locus View: an extensible web-based tool for the analysis of genomic data.. <i>Communications Biology</i> , 2021, 4, 623.	2.0	4
12	Defining genome architecture at base-pair resolution. <i>Nature</i> , 2021, 595, 125-129.	13.7	107
13	Duplication and Functional Divergence of Branched-Chain Amino Acid Biosynthesis Genes in <i>Aspergillus nidulans</i> . <i>MBio</i> , 2021, 12, e0076821.	1.8	8
14	A gain-of-function single nucleotide variant creates a new promoter which acts as an orientation-dependent enhancer-blocker. <i>Nature Communications</i> , 2021, 12, 3806.	5.8	18
15	Reactivation of a developmentally silenced embryonic globin gene. <i>Nature Communications</i> , 2021, 12, 4439.	5.8	19
16	Recapitulation of erythropoiesis in congenital dyserythropoietic anemia type I (CDA-I) identifies defects in differentiation and nucleolar abnormalities. <i>Haematologica</i> , 2021, 106, 2960-2970.	1.7	10
17	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. <i>Nature Genetics</i> , 2021, 53, 1606-1615.	9.4	93
18	Hypoxia Induces Transcriptional and Translational Downregulation of the Type I IFN Pathway in Multiple Cancer Cell Types. <i>Cancer Research</i> , 2020, 80, 5245-5256.	0.4	46

#	ARTICLE	IF	CITATIONS
19	Comparing the two leading erythroid lines BEL-A and HUDEP-2. <i>Haematologica</i> , 2020, 105, e389-e394.	1.7	27
20	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	4.5	83
21	DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. <i>Nature Communications</i> , 2019, 10, 2803.	5.8	99
22	High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. <i>Methods and Protocols</i> , 2018, 1, 29.	0.9	6
23	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. <i>Nature Genetics</i> , 2018, 50, 1744-1751.	9.4	150
24	Impaired DNA demethylation of C/EBP sites causes premature aging. <i>Genes and Development</i> , 2018, 32, 742-762.	2.7	30
25	Functional characterisation of cis-regulatory elements governing dynamic <i>Eomes</i> expression in the early mouse embryo. <i>Development (Cambridge)</i> , 2017, 144, 1249-1260.	1.2	32
26	Tissue-specific CTCF-cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. <i>Nature Cell Biology</i> , 2017, 19, 952-961.	4.6	179
27	Robust detection of chromosomal interactions from small numbers of cells using low-input Capture-C. <i>Nucleic Acids Research</i> , 2017, 45, e184-e184.	6.5	27
28	Low-input Capture-C: A Chromosome Conformation Capture Assay to Analyze Chromatin Architecture in Small Numbers of Cells. <i>Bio-protocol</i> , 2017, 7, .	0.2	15
29	Spatial differentiation of gene expression in <i>Aspergillus niger</i> colony grown for sugar beet pulp utilization. <i>Scientific Reports</i> , 2015, 5, 13592.	1.6	15
30	Characterization of the Mutagenic Spectrum of 4-Nitroquinoline 1-Oxide (4-NQO) in <i>Aspergillus nidulans</i> by Whole Genome Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2483-2492.	0.8	38
31	Dual DNA binding and coactivator functions of <i>Aspergillus nidulans</i> TamA, a Zn(II)2Cys6 transcription factor. <i>Molecular Microbiology</i> , 2014, 92, 1198-1211.	1.2	16
32	Regulation of the NADP-glutamate dehydrogenase gene <i>gdhA</i> in <i>Aspergillus nidulans</i> by the Zn(II)2Cys6 transcription factor <i>LeuB</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 2467-2480.	0.7	27