

Owen J L Rackham

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

8,877
citations

185998

28
h-index

174990

52
g-index

68
all docs

68
docs citations

68
times ranked

18415
citing authors

#	ARTICLE	IF	CITATIONS
1	Cardiomyocyte BRAF and type 1 RAF inhibitors promote cardiomyocyte and cardiac hypertrophy in mice <i>in vivo</i> . <i>Biochemical Journal</i> , 2022, 479, 401-424.	1.7	6
2	CLIPreg: constructing translational regulatory networks from CLIP-, Ribo- and RNA-seq. <i>Bioinformatics</i> , 2022, 38, 3651-3653.	1.8	0
3	Intestinal stem cell aging signature reveals a reprogramming strategy to enhance regenerative potential. <i>Npj Regenerative Medicine</i> , 2022, 7, .	2.5	4
4	PKN2 deficiency leads both to prenatal α -congenital β ™ cardiomyopathy and defective angiotensin II stress responses. <i>Biochemical Journal</i> , 2022, 479, 1467-1486.	1.7	4
5	A high-resolution map of human RNA translation. <i>Molecular Cell</i> , 2022, 82, 2885-2899.e8.	4.5	37
6	Computational Stem Cell Biology: Open Questions and Guiding Principles. <i>Cell Stem Cell</i> , 2021, 28, 20-32.	5.2	18
7	Challenges for Computational Stem Cell Biology: A Discussion for the Field. <i>Stem Cell Reports</i> , 2021, 16, 3-9.	2.3	4
8	Evaluating Capture Sequence Performance for Single-Cell CRISPR Activation Experiments. <i>ACS Synthetic Biology</i> , 2021, 10, 640-645.	1.9	3
9	ShinyCell: simple and sharable visualization of single-cell gene expression data. <i>Bioinformatics</i> , 2021, 37, 3374-3376.	1.8	83
10	Modelling human blastocysts by reprogramming fibroblasts into iBlastoids. <i>Nature</i> , 2021, 591, 627-632.	13.7	211
11	Coding and non-coding roles of MOCCI (C15ORF48) coordinate to regulate host inflammation and immunity. <i>Nature Communications</i> , 2021, 12, 2130.	5.8	56
12	Transcriptional signature in microglia associated with $A\beta$ plaque phagocytosis. <i>Nature Communications</i> , 2021, 12, 3015.	5.8	142
13	Synthetic biology: at the crossroads of genetic engineering and human therapeutics—a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, , .	1.8	2
14	EpiMogrify Models H3K4me3 Data to Identify Signaling Molecules that Improve Cell Fate Control and Maintenance. <i>Cell Systems</i> , 2020, 11, 509-522.e10.	2.9	10
15	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
16	Reprogramming roadmap reveals route to human induced trophoblast stem cells. <i>Nature</i> , 2020, 586, 101-107.	13.7	131
17	Characterising the loss-of-function impact of 5'™ untranslated region variants in 15,708 individuals. <i>Nature Communications</i> , 2020, 11, 2523.	5.8	99
18	GeneSwitches: ordering gene expression and functional events in single-cell experiments. <i>Bioinformatics</i> , 2020, 36, 3273-3275.	1.8	27

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19	Whole-Genome Sequencing of Finnish Type 1 Diabetic Siblings Discordant for Kidney Disease Reveals DNA Variants associated with Diabetic Nephropathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 309-323.	3.0	10
20	Integrated systems genetic analyses reveal a network target for delaying glioma progression. <i>Annals of Clinical and Translational Neurology</i> , 2019, 6, 1616-1638.	1.7	8
21	WWP2 regulates pathological cardiac fibrosis by modulating SMAD2 signaling. <i>Nature Communications</i> , 2019, 10, 3616.	5.8	44
22	Widespread Translational Control of Fibrosis in the Human Heart by RNA-Binding Proteins. <i>Circulation</i> , 2019, 140, 937-951.	1.6	95
23	Molecular Interaction Networks to Select Factors for Cell Conversion. <i>Methods in Molecular Biology</i> , 2019, 1975, 333-361.	0.4	2
24	deltaTE: Detection of Translationally Regulated Genes by Integrative Analysis of Ribo-seq and RNA-seq Data. <i>Current Protocols in Molecular Biology</i> , 2019, 129, e108.	2.9	77
25	Potassium channel dysfunction in human neuronal models of Angelman syndrome. <i>Science</i> , 2019, 366, 1486-1492.	6.0	118
26	A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. <i>Nature Neuroscience</i> , 2019, 22, 2087-2097.	7.1	591
27	Let it RE : IN : integrating experimental observations to predict pluripotency network behaviour. <i>EMBO Journal</i> , 2019, 38, .	3.5	0
28	A Bayesian Approach for Analysis of Whole-Genome Bisulfite Sequencing Data Identifies Disease-Associated Changes in DNA Methylation. <i>Genetics</i> , 2017, 205, 1443-1458.	1.2	14
29	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
30	RNA polymerase II primes Polycomb-repressed developmental genes throughout terminal neuronal differentiation. <i>Molecular Systems Biology</i> , 2017, 13, 946.	3.2	44
31	Cell Type of Origin Dictates the Route to Pluripotency. <i>Cell Reports</i> , 2017, 21, 2649-2660.	2.9	49
32	IL-11 is a crucial determinant of cardiovascular fibrosis. <i>Nature</i> , 2017, 552, 110-115.	13.7	451
33	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	6.5	116
34	Titin-truncating variants affect heart function in disease cohorts and the general population. <i>Nature Genetics</i> , 2017, 49, 46-53.	9.4	255
35	Computational methods for direct cell conversion. <i>Cell Cycle</i> , 2016, 15, 3343-3354.	1.3	13
36	Web-based Gene Pathogenicity Analysis (WGPA): a web platform to interpret gene pathogenicity from personal genome data. <i>Bioinformatics</i> , 2016, 32, 635-637.	1.8	1

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37	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	9.4	263
38	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. <i>Nature Neuroscience</i> , 2016, 19, 223-232.	7.1	131
39	Function-selective domain architecture plasticity potentials in eukaryotic genome evolution. <i>Biochimie</i> , 2015, 119, 269-277.	1.3	5
40	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	6.5	42
41	WGBSSuite: simulating whole-genome bisulphite sequencing data and benchmarking differential DNA methylation analysis tools. <i>Bioinformatics</i> , 2015, 31, 2371-2373.	1.8	30
42	EvoTol: a protein-sequence based evolutionary intolerance framework for disease-gene prioritization. <i>Nucleic Acids Research</i> , 2015, 43, e33-e33.	6.5	33
43	The SUPERFAMILY 1.75 database in 2014: a doubling of data. <i>Nucleic Acids Research</i> , 2015, 43, D227-D233.	6.5	74
44	A <sc>P</sc>roteome <sc>Q</sc>uality <sc>I</sc>ndex. <i>Environmental Microbiology</i> , 2015, 17, 4-9.	1.8	6
45	The Evolution of Human Cells in Terms of Protein Innovation. <i>Molecular Biology and Evolution</i> , 2014, 31, 1364-1374.	3.5	13
46	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
47	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
48	A daily-updated tree of (sequenced) life as a reference for genome research. <i>Scientific Reports</i> , 2013, 3, 2015.	1.6	47
49	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. <i>Nucleic Acids Research</i> , 2012, 41, D499-D507.	6.5	53
50	Exploring uncertainties in the relationship between temperature, ice volume, and sea level over the past 50 million years. <i>Reviews of Geophysics</i> , 2012, 50, .	9.0	33
51	SUPERFAMILY 1.75 including a domain-centric gene ontology method. <i>Nucleic Acids Research</i> , 2011, 39, D427-D434.	6.5	147
52	A Ca ²⁺ -based computational model for NMDA receptor-dependent synaptic plasticity at individual post-synaptic spines in the hippocampus. <i>Frontiers in Synaptic Neuroscience</i> , 2010, 2, 31.	1.3	25
53	The Evolution and Structure Prediction of Coiled Coils across All Genomes. <i>Journal of Molecular Biology</i> , 2010, 403, 480-493.	2.0	85
54	Cell Type of Origin Dictates the Route to Pluripotency. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0