

David A Eccles

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9400053/publications.pdf>

Version: 2024-02-01

37
papers

9,119
citations

361413

20
h-index

315739

38
g-index

110
all docs

110
docs citations

110
times ranked

18314
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioenergetic and Metabolic Adaptation in Tumor Progression and Metastasis. <i>Frontiers in Oncology</i> , 2022, 12, 857686.	2.8	8
2	Capturing SNP Association across the NK Receptor and HLA Gene Regions in Multiple Sclerosis by Targeted Penalised Regression Models. <i>Genes</i> , 2022, 13, 87.	2.4	1
3	Towards inclusive funding practices for early career researchers. <i>Journal of Science Policy & Governance</i> , 2021, 18, .	0.2	5
4	The MinION as a cost-effective technology for diagnostic screening of the SCN1A gene in epilepsy patients. <i>Epilepsy Research</i> , 2021, 172, 106593.	1.6	1
5	Expanding the conservation genomics toolbox: Incorporating structural variants to enhance genomic studies for species of conservation concern. <i>Molecular Ecology</i> , 2021, 30, 5949-5965.	3.9	26
6	Transcription Factors Active in the Anterior Blastema of <i>Schmidtea mediterranea</i> . <i>Biomolecules</i> , 2021, 11, 1782.	4.0	4
7	Homeostatic IL-13 in healthy skin directs dendritic cell differentiation to promote TH2 and inhibit TH17 cell polarization. <i>Nature Immunology</i> , 2021, 22, 1538-1550.	14.5	61
8	Metagenomic analysis of planktonic riverine microbial consortia using nanopore sequencing reveals insight into river microbe taxonomy and function. <i>GigaScience</i> , 2020, 9, .	6.4	28
9	Mitochondrial DNA Affects the Expression of Nuclear Genes Involved in Immune and Stress Responses in a Breast Cancer Model. <i>Frontiers in Physiology</i> , 2020, 11, 543962.	2.8	6
10	A semi-automated technique for adenoma quantification in the ApcMin mouse using FeatureCounter. <i>Scientific Reports</i> , 2020, 10, 3064.	3.3	2
11	Harnessing the MinION: An example of how to establish long-read sequencing in a laboratory using challenging plant tissue from <i>Eucalyptus pauciflora</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 77-89.	4.8	53
12	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
13	Tree Lab: Portable genomics for Early Detection of Plant Viruses and Pests in Sub-Saharan Africa. <i>Genes</i> , 2019, 10, 632.	2.4	81
14	Exome Sequencing Diagnoses X-Linked Moesin-Associated Immunodeficiency in a Primary Immunodeficiency Case. <i>Frontiers in Immunology</i> , 2018, 9, 420.	4.8	24
15	Expression QTL analysis of glaucoma endophenotypes in the Norfolk Island isolate provides evidence that immune-related genes are associated with optic disc size. <i>Journal of Human Genetics</i> , 2018, 63, 83-87.	2.3	1
16	De novo assembly of the complex genome of <i>Nippostrongylus brasiliensis</i> using MinION long reads. <i>BMC Biology</i> , 2018, 16, 6.	3.8	35
17	Th2 responses are primed by skin dendritic cells with distinct transcriptional profiles. <i>Journal of Experimental Medicine</i> , 2017, 214, 125-142.	8.5	69
18	Gene-centric analysis implicates nuclear encoded mitochondrial protein gene variants in migraine susceptibility. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 157-163.	1.2	6

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19	Genomic, Transcriptomic, and Phenotypic Analyses of <i>Neisseria meningitidis</i> Isolates from Disease Patients and Their Household Contacts. <i>MSystems</i> , 2017, 2, .	3.8	3
20	Annotated mitochondrial genome with Nanopore R9 signal for <i>Nippostrongylus brasiliensis</i> . <i>F1000Research</i> , 2017, 6, 56.	1.6	14
21	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. <i>F1000Research</i> , 2017, 6, 760.	1.6	107
22	Investigation of chimeric reads using the MinION. <i>F1000Research</i> , 2017, 6, 631.	1.6	38
23	Investigation of chimeric reads using the MinION. <i>F1000Research</i> , 2017, 6, 631.	1.6	32
24	“Mutiny on the Bounty”: the genetic history of Norfolk Island reveals extreme gender-biased admixture. <i>Investigative Genetics</i> , 2015, 6, 11.	3.3	9
25	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.	1.6	270
26	MinION nanopore sequencing of an influenza genome. <i>Frontiers in Microbiology</i> , 2015, 6, 766.	3.5	85
27	Mitochondrial Genome Acquisition Restores Respiratory Function and Tumorigenic Potential of Cancer Cells without Mitochondrial DNA. <i>Cell Metabolism</i> , 2015, 21, 81-94.	16.2	582
28	An analysis of DNA methylation in human adipose tissue reveals differential modification of obesity genes before and after gastric bypass and weight loss. <i>Genome Biology</i> , 2015, 16, 8.	8.8	200
29	β -Catenin-Dependent Control of Positional Information along the AP Body Axis in Planarians Involves a Teashirt Family Member. <i>Cell Reports</i> , 2015, 10, 253-265.	6.4	66
30	A Phenomic Scan of the Norfolk Island Genetic Isolate Identifies a Major Pleiotropic Effect Locus Associated with Metabolic and Renal Disorder Markers. <i>PLoS Genetics</i> , 2015, 11, e1005593.	3.5	3
31	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
32	The p.Ala510Val mutation in the SPG7 (paraplegin) gene is the most common mutation causing adult onset neurogenetic disease in patients of British ancestry. <i>Journal of Neurology</i> , 2013, 260, 1286-1294.	3.6	45
33	Mapping eQTLs in the Norfolk Island Genetic Isolate Identifies Candidate Genes for CVD Risk Traits. <i>American Journal of Human Genetics</i> , 2013, 93, 1087-1099.	6.2	28
34	A unique demographic history exists for the MAO-A gene in Polynesians. <i>Journal of Human Genetics</i> , 2012, 57, 294-300.	2.3	4
35	Complete Mitochondrial Genome Sequencing Reveals Novel Haplotypes in a Polynesian Population. <i>PLoS ONE</i> , 2012, 7, e35026.	2.5	23
36	Testing the thrifty gene hypothesis: the Gly482Ser variant in PPARGC1A is associated with BMI in Tongans. <i>BMC Medical Genetics</i> , 2011, 12, 10.	2.1	38

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37	Estimation of genomic ancestry in admixed populations. F1000Research, 0, 5, 779.	1.6	0