

Nicholas J Dickens

List of Publications by Year in descending order

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54
papers

12,848
citations

236925

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315739

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docs citations

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times ranked

17762
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional differentiation of <i>Trypanosoma brucei</i> during in vitro acquisition of resistance to acoziborole. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009939.	3.0	2
2	Zygote morphogenesis but not the establishment of cell polarity in <i>Plasmodium berghei</i> is controlled by the small GTPase, RAB11A. <i>PLoS Pathogens</i> , 2020, 16, e1008091.	4.7	3
3	<i>Trypanosoma brucei</i> ATR Links DNA Damage Signaling during Antigenic Variation with Regulation of RNA Polymerase I-Transcribed Surface Antigens. <i>Cell Reports</i> , 2020, 30, 836-851.e5.	6.4	24
4	Defining the sediment prokaryotic communities of the Indian River Lagoon, FL, USA, an Estuary of National Significance. <i>PLoS ONE</i> , 2020, 15, e0236305.	2.5	9
5	Title is missing!. , 2020, 16, e1008091.		0
6	Title is missing!. , 2020, 16, e1008091.		0
7	Title is missing!. , 2020, 16, e1008091.		0
8	Title is missing!. , 2020, 16, e1008091.		0
9	Title is missing!. , 2020, 16, e1008091.		0
10	Title is missing!. , 2020, 16, e1008091.		0
11	Genomic instability at the locus of sterol C24-methyltransferase promotes amphotericin B resistance in <i>Leishmania</i> parasites. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007052.	3.0	39
12	A <i>Leishmania infantum</i> genetic marker associated with miltefosine treatment failure for visceral leishmaniasis. <i>EBioMedicine</i> , 2018, 36, 83-91.	6.1	56
13	Comparative genomics of Tunisian <i>Leishmania major</i> isolates causing human cutaneous leishmaniasis with contrasting clinical severity. <i>Infection, Genetics and Evolution</i> , 2017, 50, 110-120.	2.3	16
14	Sterol 14 α -demethylase mutation leads to amphotericin B resistance in <i>Leishmania mexicana</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005649.	3.0	43
15	Mapping replication dynamics in <i>Trypanosoma brucei</i> reveals a link with telomere transcription and antigenic variation. <i>ELife</i> , 2016, 5, .	6.0	51
16	Genome-wide mapping reveals single-origin chromosome replication in <i>Leishmania</i> , a eukaryotic microbe. <i>Genome Biology</i> , 2015, 16, 230.	8.8	46
17	Regulators of <i>Trypanosoma brucei</i> Cell Cycle Progression and Differentiation Identified Using a Kinome-Wide RNAi Screen. <i>PLoS Pathogens</i> , 2014, 10, e1003886.	4.7	176
18	The Streamlined Genome of <i>Phytomonas</i> spp. Relative to Human Pathogenic Kinetoplastids Reveals a Parasite Tailored for Plants. <i>PLoS Genetics</i> , 2014, 10, e1004007.	3.5	66

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19	A cascade of DNA-binding proteins for sexual commitment and development in Plasmodium. Nature, 2014, 507, 253-257.	27.8	366
20	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. Evolutionary Bioinformatics, 2014, 10, EBO.S13759.	1.2	23
21	Genome-wide Analysis Reveals Extensive Functional Interaction between DNA Replication Initiation and Transcription in the Genome of Trypanosoma brucei. Cell Reports, 2012, 2, 185-197.	6.4	93
22	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . Genome Research, 2011, 21, 2129-2142.	5.5	380
23	Genetic Factors Underlying the Risk of Thalidomide-Related Neuropathy in Patients With Multiple Myeloma. Journal of Clinical Oncology, 2011, 29, 797-804.	1.6	95
24	XBP1s levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. Blood, 2010, 116, 250-253.	1.4	107
25	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. Blood, 2010, 116, e56-e65.	1.4	315
26	Homozygous Deletion Mapping in Myeloma Samples Identifies Genes and an Expression Signature Relevant to Pathogenesis and Outcome. Clinical Cancer Research, 2010, 16, 1856-1864.	7.0	124
27	MMSET deregulation affects cell cycle progression and adhesion regulons in t(4;14) myeloma plasma cells. Haematologica, 2009, 94, 78-86.	3.5	106
28	Genetic Variations Associated with Overall and Progression-Free Survival in Multiple Myeloma Patients Treated with Thalidomide Combinations.. Blood, 2009, 114, 426-426.	1.4	2
29	Gene Expression Profiling Classifies Splenic Marginal Zone Lymphoma and Hairy Cell Leukemia-Variant as Related Diseases That Are Distinct From Typical Hairy Cell Leukemia.. Blood, 2009, 114, 3467-3467.	1.4	0
30	Global Methylation Array Analysis of Multiple Myeloma Samples Indicate An Alteration of Epigenetics During the Transition From MGUS to Myeloma and An Increased Frequency of Gene Methylation in t(4;14) Myeloma.. Blood, 2009, 114, 121-121.	1.4	0
31	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling.. Blood, 2009, 114, 1793-1793.	1.4	0
32	UTX, a Histone Demethylase, Is Inactivated through Homozygous Deletion, Mutation, and DNA Methylation in Multiple Myeloma.. Blood, 2009, 114, 1798-1798.	1.4	0
33	Deletions of <i>CDKN2C</i> in Multiple Myeloma: Biological and Clinical Implications. Clinical Cancer Research, 2008, 14, 6033-6041.	7.0	88
34	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. Blood, 2008, 112, 4924-4934.	1.4	65
35	Genome-Wide Co-Expression Analysis in Multiple Tissues. PLoS ONE, 2008, 3, e4033.	2.5	21
36	The Impact of Constitutional Copy Number Variants in Myeloma. Blood, 2008, 112, 496-496.	1.4	1

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37	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling Identifies Kinase Pathway Alterations.. Blood, 2008, 112, 1694-1694.	1.4	0
38	High Resolution Genomic Profiling Using Single Nucleotide Polymorphism Microarrays Identifies Multiple Novel Genomic Minimally Deleted Regions in Multiple Myeloma. Blood, 2008, 112, 625-625.	1.4	0
39	Homozygous Deletions Can Be Used to Define a Cell Death Specific Gene Expression Signature Able to Predict Outcome in Myeloma. Blood, 2008, 112, 2725-2725.	1.4	0
40	Gene mapping and expression analysis of 16q loss of heterozygosity identifies WWOX and CYLD as being important in determining clinical outcome in multiple myeloma. Blood, 2007, 110, 3291-3300.	1.4	133
41	Integration of Gene Mapping and Expression Arrays Identifies Mechanisms by Which Genes Are Dysregulated as a Result of Copy Number Loss and Gain Associated with IgH Translocations in Multiple Myeloma.. Blood, 2007, 110, 395-395.	1.4	1
42	Genome-Wide Identification of Gene Expression Networks Affected by Genomic Changes in Multiple Myeloma.. Blood, 2007, 110, 2494-2494.	1.4	4
43	Mutation and Methylation Analysis of WWOX and CYLD on 16q; Potential Tumor Suppressor Genes in Myeloma.. Blood, 2007, 110, 2473-2473.	1.4	0
44	Screening of Homozygous Deletions Identifies Key Deregulated Genes and Pathways in Multiple Myeloma.. Blood, 2007, 110, 2474-2474.	1.4	0
45	An Integrated Pharmacogenomic Strategy for the Definition of Thalidomide Response Signatures in Presenting Cases of Multiple Myeloma.. Blood, 2007, 110, 2493-2493.	1.4	0
46	Heritability and Tissue Specificity of Expression Quantitative Trait Loci. PLoS Genetics, 2006, 2, e172.	3.5	183
47	eQTL Explorer: integrated mining of combined genetic linkage and expression experiments. Bioinformatics, 2006, 22, 509-511.	4.1	22
48	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
49	The Tudor domain â€”Royal Familyâ€™: Tudor, plant Agenet, Chromo, PWWP and MBT domains. Trends in Biochemical Sciences, 2003, 28, 69-74.	7.5	448
50	Positional cloning of a novel gene influencing asthma from Chromosome 2q14. Nature Genetics, 2003, 35, 258-263.	21.4	326
51	THoR: a tool for domain discovery and curation of multiple alignments. Genome Biology, 2003, 4, R52.	9.6	3
52	Recent improvements to the SMART domain-based sequence annotation resource. Nucleic Acids Research, 2002, 30, 242-244.	14.5	613
53	Cadherin-like domains in Î±-dystroglycan, Î±/Î²-sarcoglycan and yeast and bacterial proteins. Current Biology, 2002, 12, R197-R199.	3.9	58
54	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319