

# Nicholas J Dickens

## List of Publications by Year in descending order

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54  
papers

12,848  
citations

236925

25  
h-index

315739

38  
g-index

56  
all docs

56  
docs citations

56  
times ranked

17762  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
2	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	27.8	2,421
3	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002, 30, 242-244.	14.5	613
4	The Tudor domain "Royal Family": Tudor, plant Agenet, Chromo, PWWP and MBT domains. <i>Trends in Biochemical Sciences</i> , 2003, 28, 69-74.	7.5	448
5	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . <i>Genome Research</i> , 2011, 21, 2129-2142.	5.5	380
6	A cascade of DNA-binding proteins for sexual commitment and development in <i>Plasmodium</i> . <i>Nature</i> , 2014, 507, 253-257.	27.8	366
7	Positional cloning of a novel gene influencing asthma from Chromosome 2q14. <i>Nature Genetics</i> , 2003, 35, 258-263.	21.4	326
8	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. <i>Blood</i> , 2010, 116, e56-e65.	1.4	315
9	Heritability and Tissue Specificity of Expression Quantitative Trait Loci. <i>PLoS Genetics</i> , 2006, 2, e172.	3.5	183
10	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
11	Gene mapping and expression analysis of 16q loss of heterozygosity identifies <i>WWOX</i> and <i>CYLD</i> as being important in determining clinical outcome in multiple myeloma. <i>Blood</i> , 2007, 110, 3291-3300.	1.4	133
12	Homozygous Deletion Mapping in Myeloma Samples Identifies Genes and an Expression Signature Relevant to Pathogenesis and Outcome. <i>Clinical Cancer Research</i> , 2010, 16, 1856-1864.	7.0	124
13	<i>XBP1s</i> levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. <i>Blood</i> , 2010, 116, 250-253.	1.4	107
14	<i>MMSET</i> deregulation affects cell cycle progression and adhesion regulons in t(4;14) myeloma plasma cells. <i>Haematologica</i> , 2009, 94, 78-86.	3.5	106
15	Genetic Factors Underlying the Risk of Thalidomide-Related Neuropathy in Patients With Multiple Myeloma. <i>Journal of Clinical Oncology</i> , 2011, 29, 797-804.	1.6	95
16	Genome-wide Analysis Reveals Extensive Functional Interaction between DNA Replication Initiation and Transcription in the Genome of <i>Trypanosoma brucei</i> . <i>Cell Reports</i> , 2012, 2, 185-197.	6.4	93
17	Deletions of <i>CDKN2C</i> in Multiple Myeloma: Biological and Clinical Implications. <i>Clinical Cancer Research</i> , 2008, 14, 6033-6041.	7.0	88
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	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. <i>Blood</i> , 2008, 112, 4924-4934.	1.4	65
20	Cadherin-like domains in $\beta$ -dystroglycan, $\beta$ - $\mu$ -sarcoglycan and yeast and bacterial proteins. <i>Current Biology</i> , 2002, 12, R197-R199.	3.9	58
21	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
22	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
23	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
24	Sterol 14 $\alpha$ -demethylase mutation leads to amphotericin B resistance in <i>Leishmania mexicana</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005649.	3.0	43
25	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
26	<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
27	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13759.	1.2	23
28	eQTL Explorer: integrated mining of combined genetic linkage and expression experiments. <i>Bioinformatics</i> , 2006, 22, 509-511.	4.1	22
29	Genome-Wide Co-Expression Analysis in Multiple Tissues. <i>PLoS ONE</i> , 2008, 3, e4033.	2.5	21
30	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
31	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
32	Genome-Wide Identification of Gene Expression Networks Affected by Genomic Changes in Multiple Myeloma.. <i>Blood</i> , 2007, 110, 2494-2494.	1.4	4
33	THoR: a tool for domain discovery and curation of multiple alignments. <i>Genome Biology</i> , 2003, 4, R52.	9.6	3
34	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
35	Genetic Variations Associated with Overall and Progression-Free Survival in Multiple Myeloma Patients Treated with Thalidomide Combinations.. <i>Blood</i> , 2009, 114, 426-426.	1.4	2
36	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

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37	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
38	The Impact of Constitutional Copy Number Variants in Myeloma. Blood, 2008, 112, 496-496.	1.4	1
39	Mutation and Methylation Analysis of WWOX and CYLD on 16q; Potential Tumor Suppressor Genes in Myeloma.. Blood, 2007, 110, 2473-2473.	1.4	0
40	Screening of Homozygous Deletions Identifies Key Deregulated Genes and Pathways in Multiple Myeloma.. Blood, 2007, 110, 2474-2474.	1.4	0
41	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
42	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling Identifies Kinase Pathway Alterations.. Blood, 2008, 112, 1694-1694.	1.4	0
43	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
44	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
45	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
46	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
47	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling.. Blood, 2009, 114, 1793-1793.	1.4	0
48	UTX, a Histone Demethylase, Is Inactivated through Homozygous Deletion, Mutation, and DNA Methylation in Multiple Myeloma.. Blood, 2009, 114, 1798-1798.	1.4	0
49	Title is missing!. , 2020, 16, e1008091.		0
50	Title is missing!. , 2020, 16, e1008091.		0
51	Title is missing!. , 2020, 16, e1008091.		0
52	Title is missing!. , 2020, 16, e1008091.		0
53	Title is missing!. , 2020, 16, e1008091.		0
54	Title is missing!. , 2020, 16, e1008091.		0