Joep de Ligt

List of Publications by Year in descending order

56 papers	9,883 citations	101543 36 h-index	155660 55 g-index
63 all docs	63 docs citations	63 times ranked	20396 citing authors

#	Article	IF	Citations
1	Airborne Transmission of SARS-CoV-2 Delta Variant within Tightly Monitored Isolation Facility, New Zealand (Aotearoa). Emerging Infectious Diseases, 2022, 28, 501-509.	4.3	21
2	Genomic epidemiology of Delta SARS-CoV-2 during transition from elimination to suppression in Aotearoa New Zealand. Nature Communications, 2022, 13, .	12.8	17
3	Use of Genomics to Track Coronavirus Disease Outbreaks, New Zealand. Emerging Infectious Diseases, 2021, 27, 1317-1322.	4.3	28
4	Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 during Border Quarantine and Air Travel, New Zealand (Aotearoa). Emerging Infectious Diseases, 2021, 27, 1274-1278.	4.3	68
5	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	1.8	115
6	Identification of novel human Wnt target genes using adult endodermal tissue-derived organoids. Developmental Biology, 2021, 474, 37-47.	2.0	23
7	Real-Time Genomics for Tracking Severe Acute Respiratory Syndrome Coronavirus 2 Border Incursions after Virus Elimination, New Zealand. Emerging Infectious Diseases, 2021, 27, 2361-2368.	4.3	27
8	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. Wellcome Open Research, 2021, 6, 121.	1.8	129
9	COVID-19 vaccine strategies for Aotearoa New Zealand: a mathematical modelling study. The Lancet Regional Health - Western Pacific, 2021, 15, 100256.	2.9	15
10	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. Nature Communications, 2020, 11, 6351.	12.8	100
11	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. Virus Evolution, 2020, 6, veaa027.	4.9	119
12	Scalable Workflows and Reproducible Data Analysis for Genomics. Methods in Molecular Biology, 2019, 1910, 723-745.	0.9	25
13	Deficiency of nucleotide excision repair is associated with mutational signature observed in cancer. Genome Research, 2019, 29, 1067-1077.	5.5	66
14	Natural helix 9 mutants of PPARÎ³ differently affect its transcriptional activity. Molecular Metabolism, 2019, 20, 115-127.	6.5	12
15	Longâ€term expanding human airway organoids for disease modeling. EMBO Journal, 2019, 38, .	7.8	619
16	The molecular genetic make-up of male breast cancer. Endocrine-Related Cancer, 2019, 26, 779-794.	3.1	27
17	A Living Biobank of Breast Cancer Organoids Captures Disease Heterogeneity. Cell, 2018, 172, 373-386.e10.	28.9	1,201
18	A Single Complex Agpat2 Allele in a Patient With Partial Lipodystrophy. Frontiers in Physiology, 2018, 9, 1363.	2.8	7

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19	A System-wide Approach to Monitor Responses to Synergistic BRAF and EGFR Inhibition in Colorectal Cancer Cells. Molecular and Cellular Proteomics, 2018, 17, 1892-1908.	3.8	13
20	Cancer cells copy migratory behavior and exchange signaling networks via extracellular vesicles. EMBO Journal, 2018, 37, .	7.8	58
21	Genetic dissection of colorectal cancer progression by orthotopic transplantation of engineered cancer organoids. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2357-E2364.	7.1	198
22	Unraveling genetic predisposition to familial or early onset gastric cancer using germline whole-exome sequencing. European Journal of Human Genetics, 2017, 25, 1246-1252.	2.8	34
23	Use of CRISPR-modified human stem cell organoids to study the origin of mutational signatures in cancer. Science, 2017, 358, 234-238.	12.6	337
24	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. Nature Communications, 2017, 8, 1326.	12.8	315
25	Molecular dissection of germline chromothripsis in a developmental context using patient-derived iPS cells. Genome Medicine, 2017, 9, 9.	8.2	25
26	The Genomic Scrapheap Challenge; Extracting Relevant Data from Unmapped Whole Genome Sequencing Reads, Including Strain Specific Genomic Segments, in Rats. PLoS ONE, 2016, 11, e0160036.	2.5	5
27	Tissue-specific mutation accumulation in human adult stem cells during life. Nature, 2016, 538, 260-264.	27.8	759
28	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
29	Novel mutations in LRP6 highlight the role of WNT signaling in tooth agenesis. Genetics in Medicine, 2016, 18, 1158-1162.	2.4	58
30	Novel genetic causes for cerebral visual impairment. European Journal of Human Genetics, 2016, 24, 660-665.	2.8	127
31	Genomic landscape of rat strain and substrain variation. BMC Genomics, 2015, 16, 357.	2.8	84
32	Cerebral visual impairment and intellectual disability caused by PGAP1 variants. European Journal of Human Genetics, 2015, 23, 1689-1693.	2.8	15
33	Long-Term Culture of Genome-Stable Bipotent Stem Cells from Adult Human Liver. Cell, 2015, 160, 299-312.	28.9	1,166
34	Next-generation sequencing-based genome diagnostics across clinical genetics centers: implementation choices and their effects. European Journal of Human Genetics, 2015, 23, 1142-1150.	2.8	56
35	Toward effective software solutions for big biology. Nature Biotechnology, 2015, 33, 686-687.	17.5	46
36	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115

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37	Allelic Mutations of KITLG, Encoding KIT Ligand, Cause Asymmetric and Unilateral Hearing Loss and Waardenburg Syndrome Type 2. American Journal of Human Genetics, 2015, 97, 647-660.	6.2	55
38	Heterozygous germline mutations in A2ML1 are associated with a disorder clinically related to Noonan syndrome. European Journal of Human Genetics, 2015, 23, 317-324.	2.8	61
39	Detecting fetal subchromosomal aberrations by MPS: an unexpected discrepancy between amniocyte DNA and ccffDNA. Prenatal Diagnosis, 2014, 34, 402-405.	2.3	2
40	Mobster: accurate detection of mobile element insertions in next generation sequencing data. Genome Biology, 2014, 15, 488.	8.8	86
41	A Drosophila Genetic Resource of Mutants to Study Mechanisms Underlying Human Genetic Diseases. Cell, 2014, 159, 200-214.	28.9	322
42	Platform comparison of detecting copy number variants with microarrays and whole-exome sequencing. Genomics Data, 2014, 2, 144-146.	1.3	13
43	NR2F1 Mutations Cause Optic Atrophy with Intellectual Disability. American Journal of Human Genetics, 2014, 94, 303-309.	6.2	125
44	Mutations Affecting the SAND Domain of DEAF1 Cause Intellectual Disability with Severe Speech Impairment and Behavioral Problems. American Journal of Human Genetics, 2014, 94, 649-661.	6.2	59
45	Detection of Clinically Relevant Copy Number Variants with Whole-Exome Sequencing. Human Mutation, 2013, 34, 1439-1448.	2.5	105
46	Identification of pathogenic gene variants in small families with intellectually disabled siblings by exome sequencing. Journal of Medical Genetics, 2013, 50, 802-811.	3.2	93
47	Reliable noninvasive prenatal testing by massively parallel sequencing of circulating cell-free DNA from maternal plasma processed up to 24h after venipuncture. Clinical Biochemistry, 2013, 46, 1783-1786.	1.9	15
48	Point mutations as a source of de novo genetic disease. Current Opinion in Genetics and Development, 2013, 23, 257-263.	3.3	44
49	GATAD2Bloss-of-function mutations cause a recognisable syndrome with intellectual disability and are associated with learning deficits and synaptic undergrowth inDrosophila. Journal of Medical Genetics, 2013, 50, 507-514.	3.2	63
50	Mutations inDYNC1H1cause severe intellectual disability with neuronal migration defects. Journal of Medical Genetics, 2012, 49, 179-183.	3.2	151
51	Diagnostic Exome Sequencing in Persons with Severe Intellectual Disability. New England Journal of Medicine, 2012, 367, 1921-1929.	27.0	1,367
52	Non-invasive prenatal diagnosis of fetal aneuploidies using massively parallel sequencing-by-ligation and evidence that cell-free fetal DNA in the maternal plasma originates from cytotrophoblastic cells. Expert Opinion on Biological Therapy, 2012, 12, S19-S26.	3.1	111
53	Nextâ€generation genetic testing for retinitis pigmentosa. Human Mutation, 2012, 33, 963-972.	2.5	258
54	Resolving the Breakpoints of the 17q21.31 Microdeletion Syndrome with Next-Generation Sequencing. American Journal of Human Genetics, 2012, 90, 599-613.	6.2	22

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55	Exome Sequencing of Late Recurrence T-Cell Acute Lymphoblastic Leukemia in Children Confirms Second Leukemia and Exposes Predisposition Candidate Genes. Blood, 2011, 118, 755-755.	1.4	0
56	A de novo paradigm for mental retardation. Nature Genetics, 2010, 42, 1109-1112.	21.4	751