

Katia Nones

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

16,190
citations

76196

40
h-index

45213

90
g-index

98
all docs

98
docs citations

98
times ranked

26341
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. <i>Gastroenterology</i> , 2022, 162, 320-324.e4.	0.6	26
2	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. <i>Genome Medicine</i> , 2022, 14, 3.	3.6	16
3	Whole genome deep sequencing analysis of cell-free DNA in samples with low tumour content. <i>BMC Cancer</i> , 2022, 22, 85.	1.1	9
4	Multioomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. <i>Cancer Cell</i> , 2022, 40, 88-102.e7.	7.7	64
5	qmotif: determination of telomere content from whole-genome sequence data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	5
6	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. <i>Genome Medicine</i> , 2022, 14, .	3.6	24
7	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. <i>Gastroenterology</i> , 2021, 160, 362-377.e13.	0.6	90
8	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, 155.	2.0	26
9	The Genomic Landscape of Lobular Breast Cancer. <i>Cancers</i> , 2021, 13, 1950.	1.7	13
10	Acquired <i>RAD51C</i> Promoter Methylation Loss Causes PARP Inhibitor Resistance in High-Grade Serous Ovarian Carcinoma. <i>Cancer Research</i> , 2021, 81, 4709-4722.	0.4	42
11	Verifying explainability of a deep learning tissue classifier trained on RNA-seq data. <i>Scientific Reports</i> , 2021, 11, 2641.	1.6	32
12	ROR1 and ROR2 expression in pancreatic cancer. <i>BMC Cancer</i> , 2021, 21, 1199.	1.1	4
13	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	5.8	102
14	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. <i>Scientific Reports</i> , 2020, 10, 17687.	1.6	14
15	The Impact of Next Generation Sequencing in Cancer Research. <i>Cancers</i> , 2020, 12, 2928.	1.7	7
16	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. <i>Npj Breast Cancer</i> , 2020, 6, 33.	2.3	19
17	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020, 31, 107625.	2.9	78
18	Estimating the costs of genomic sequencing in cancer control. <i>BMC Health Services Research</i> , 2020, 20, 492.	0.9	18

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19	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
20	Abstract 224: Evaluation of next generation sequencing of DNA and RNA from archival formalin-fixed, paraffin-embedded pancreatic cancer tissue: A pilot study of the SEER-linked virtual tissue repository. , 2020, , .		0
21	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	5.8	205
22	Mechanisms of Genomic Instability in Breast Cancer. <i>Trends in Molecular Medicine</i> , 2019, 25, 595-611.	3.5	109
23	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. <i>Annals of Oncology</i> , 2019, 30, 1071-1079.	0.6	64
24	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 8, 269-290.	2.3	42
25	Diff-Quik Cytology Smears from Endobronchial Ultrasound Transbronchial Needle Aspiration Lymph Node Specimens as a Source of DNA for Next-Generation Sequencing Instead of Cell Blocks. <i>Respiration</i> , 2019, 97, 525-539.	1.2	25
26	Patterns of Genomic Instability in Breast Cancer. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 198-211.	4.0	68
27	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	0.7	19
28	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. <i>Cancers</i> , 2019, 11, 190.	1.7	39
29	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. <i>International Journal of Cancer</i> , 2019, 144, 1049-1060.	2.3	54
30	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. <i>Journal of Pathology</i> , 2019, 247, 214-227.	2.1	73
31	Abstract 479: BRAF and KRAS mutation define distinct subtypes of the CpG island methylator phenotype in colorectal cancers. , 2019, , .		0
32	Characterization of a novel breast cancer cell line derived from a metastatic bone lesion of a breast cancer patient. <i>Breast Cancer Research and Treatment</i> , 2018, 170, 179-188.	1.1	5
33	Mixed ductal-lobular carcinomas: evidence for progression from ductal to lobular morphology. <i>Journal of Pathology</i> , 2018, 244, 460-468.	2.1	31
34	Telomere sequence content can be used to determine ALT activity in tumours. <i>Nucleic Acids Research</i> , 2018, 46, 4903-4918.	6.5	40
35	<sc>CEP</sc> 55 is a determinant of cell fate during perturbed mitosis in breast cancer. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	59
36	Early Changes in CD4+ T-Cell Activation During Blood-Stage Plasmodium falciparum Infection. <i>Journal of Infectious Diseases</i> , 2018, 218, 1119-1129.	1.9	17

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37	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	1.1	57
38	Copy number profiles of paired primary and metastatic colorectal cancers. Oncotarget, 2018, 9, 3394-3405.	0.8	14
39	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
40	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
41	Next-Generation Sequencing of Endobronchial Ultrasound Transbronchial Needle Aspiration Specimens in Lung Cancer. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 388-391.	2.5	14
42	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	3.6	27
43	DNA methylation in schizophrenia in different patient-derived cell types. NPJ Schizophrenia, 2017, 3, 6.	2.0	25
44	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
45	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
46	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. Carcinogenesis, 2016, 37, 356-365.	1.3	46
47	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
48	Quantitative trait loci with sex-specific effects for internal organs weights and hematocrit value in a broiler-layer cross. Journal of Applied Genetics, 2016, 57, 215-224.	1.0	6
49	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
50	Whole-genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
51	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
52	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. Journal of Proteome Research, 2015, 14, 2255-2266.	1.8	52
53	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. PLoS ONE, 2015, 10, e0126911.	1.1	42
54	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0

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55	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. <i>International Journal of Cancer</i> , 2014, 135, 1110-1118.	2.3	192
56	Imperfect centered miRNA binding sites are common and can mediate repression of target mRNAs. <i>Genome Biology</i> , 2014, 15, R51.	13.9	111
57	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	5.8	236
58	The long non-coding RNA Gomafu is acutely regulated in response to neuronal activation and involved in schizophrenia-associated alternative splicing. <i>Molecular Psychiatry</i> , 2014, 19, 486-494.	4.1	356
59	Abstract 1715: Elucidating mechanisms of resistance to FGFR inhibitors in endometrial cancer. , 2014, , .		0
60	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. <i>Genome Medicine</i> , 2013, 5, 78.	3.6	97
61	Association of IGF1 and KDM5A polymorphisms with performance, fatness and carcass traits in chickens. <i>Journal of Applied Genetics</i> , 2013, 54, 103-112.	1.0	32
62	Modulation of colonic inflammation in Mdr1a ^{+/+} mice by green tea polyphenols and their effects on the colon transcriptome and proteome. <i>Journal of Nutritional Biochemistry</i> , 2013, 24, 1678-1690.	1.9	34
63	miR-139-5p is a regulator of metastatic pathways in breast cancer. <i>Rna</i> , 2013, 19, 1767-1780.	1.6	137
64	MicroRNA-182-5p targets a network of genes involved in DNA repair. <i>Rna</i> , 2013, 19, 230-242.	1.6	108
65	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	1.1	67
66	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , 2012, 12, 395.	1.1	17
67	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	13.7	1,741
68	Effects of dietary broccoli fibre and corn oil on serum lipids, faecal bile acid excretion and hepatic gene expression in rats. <i>Food Chemistry</i> , 2012, 131, 1272-1278.	4.2	23
69	Quantitative trait loci associated with chemical composition of the chicken carcass. <i>Animal Genetics</i> , 2012, 43, 570-576.	0.6	14
70	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. <i>PLoS ONE</i> , 2012, 7, e45835.	1.1	92
71	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , 2011, 12, R126.	13.9	297
72	Genetic parameters for body weight, carcass chemical composition and yield in a broiler-layer cross developed for QTL mapping. <i>Genetics and Molecular Biology</i> , 2011, 34, 429-434.	0.6	8

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73	QTL for percentage of carcass and carcass parts in a broiler x layer cross. <i>Animal Genetics</i> , 2011, 42, 117-124.	0.6	20
74	Changes in colon gene expression associated with increased colon inflammation in interleukin-10 gene-deficient mice inoculated with <i>Enterococcus</i> species. <i>BMC Immunology</i> , 2010, 11, 39.	0.9	55
75	Mapping quantitative trait loci in <i>Gallus gallus</i> using principal components. <i>Revista Brasileira De Zootecnia</i> , 2010, 39, 2434-2441.	0.3	4
76	Diversity of caecal bacteria is altered in interleukin-10 gene-deficient mice before and after colitis onset and when fed polyunsaturated fatty acids. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3306-3316.	0.7	17
77	Cecal and Colonic Responses in Rats Fed 5 or 30% Corn Oil Diets Containing Either 7.5% Broccoli Dietary Fiber or Microcrystalline Cellulose. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 6510-6515.	2.4	38
78	Maternal Influences on the Transmission of Leukocyte Gene Expression Profiles in Population Samples from Brisbane, Australia. <i>PLoS ONE</i> , 2010, 5, e14479.	1.1	13
79	Genome-Wide Analysis of Dietary Eicosapentaenoic Acid- and Oleic Acid-Induced Modulation of Colon Inflammation in Interleukin-10 Gene-Deficient Mice. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2009, 2, 9-28.	1.8	44
80	Multidrug resistance gene deficient (<i>mdr1a</i> ^{-/-}) mice have an altered caecal microbiota that precedes the onset of intestinal inflammation. <i>Journal of Applied Microbiology</i> , 2009, 107, 557-566.	1.4	42
81	Quantitative trait loci for performance traits in a broiler × layer cross. <i>Animal Genetics</i> , 2009, 40, 200-208.	0.6	46
82	Quantitative trait loci associated with fatness in a broiler × layer cross. <i>Animal Genetics</i> , 2009, 40, 729-736.	0.6	48
83	Initiation and elongation steps of mRNA translation are involved in the increase in milk protein yield caused by growth hormone administration during lactation. <i>Journal of Dairy Science</i> , 2009, 92, 1889-1899.	1.4	40
84	The effects of dietary curcumin and rutin on colonic inflammation and gene expression in multidrug resistance gene-deficient (<i>mdr1a</i> ^{-/-}) mice, a model of inflammatory bowel diseases. <i>British Journal of Nutrition</i> , 2009, 101, 169-181.	1.2	88
85	Investigation of Leptin gene in broiler and layer chicken lines. <i>Scientia Agricola</i> , 2008, 65, 214-219.	0.6	8
86	Genetic linkage maps of chicken chromosomes 6, 7, 8, 11 and 13 from a Brazilian resource population. <i>Scientia Agricola</i> , 2008, 65, 447-452.	0.6	10
87	Associations of myostatin gene polymorphisms with performance and mortality traits in broiler chickens. <i>Genetics Selection Evolution</i> , 2007, 39, 73-89.	1.2	39
88	Mapping QTLs on chicken chromosome 1 for performance and carcass traits in a broiler x layer cross. <i>Animal Genetics</i> , 2006, 37, 95-100.	0.6	74
89	Genetic linkage map of chicken chromosome 1 from a Brazilian resource population. <i>Scientia Agricola</i> , 2005, 62, 12-17.	0.6	11
90	Strategic marker selection to detect quantitative trait loci in chicken. <i>Scientia Agricola</i> , 2005, 62, 111-116.	0.6	7

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91	Formulação das dietas, desempenho e qualidade da carcaça, produção e composição de dejetos de suínos. Scientia Agricola, 2002, 59, 635-644.	0.6	3