Jiannis Ragoussis

List of Publications by Year in descending order

192 papers	20,039 citations	12328 69 h-index	11937 134 g-index
219 all docs	219 docs citations	219 times ranked	34275 citing authors

#	Article	IF	Citations
1	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
2	A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers. PLoS Biology, 2010, 8, e1000384.	5.6	762
3	High-resolution genome-wide mapping of HIF-binding sites by ChIP-seq. Blood, 2011, 117, e207-e217.	1.4	623
4	hsa-miR-210 Is Induced by Hypoxia and Is an Independent Prognostic Factor in Breast Cancer. Clinical Cancer Research, 2008, 14, 1340-1348.	7.0	617
5	Identification and Characterization of Enhancers Controlling the Inflammatory Gene Expression Program in Macrophages. Immunity, 2010, 32, 317-328.	14.3	567
6	Direct targeting of Sec23a by miR-200s influences cancer cell secretome and promotes metastatic colonization. Nature Medicine, 2011, 17, 1101-1108.	30.7	552
7	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	2.9	538
8	QuantiSNP: an Objective Bayes Hidden-Markov Model to detect and accurately map copy number variation using SNP genotyping data. Nucleic Acids Research, 2007, 35, 2013-2025.	14.5	525
9	Genome-wide Association of Hypoxia-inducible Factor (HIF)-1Î± and HIF-2Î± DNA Binding with Expression Profiling of Hypoxia-inducible Transcripts. Journal of Biological Chemistry, 2009, 284, 16767-16775.	3.4	516
10	Single nucleotide polymorphisms in TNFSF15 confer susceptibility to Crohn's disease. Human Molecular Genetics, 2005, 14, 3499-3506.	2.9	438
11	Concordant Regulation of Gene Expression by Hypoxia and 2-Oxoglutarate-dependent Dioxygenase Inhibition. Journal of Biological Chemistry, 2006, 281, 15215-15226.	3.4	434
12	ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. Cell, 2010, 143, 367-378.	28.9	365
13	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
14	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	2.9	334
15	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. Nature Communications, 2020, 11, 3406.	12.8	300
16	microRNA-Associated Progression Pathways and Potential Therapeutic Targets Identified by Integrated mRNA and microRNA Expression Profiling in Breast Cancer. Cancer Research, 2011, 71, 5635-5645.	0.9	285
17	MAFG-driven astrocytes promote CNS inflammation. Nature, 2020, 578, 593-599.	27.8	282
18	MicroRNA-210 Regulates Mitochondrial Free Radical Response to Hypoxia and Krebs Cycle in Cancer Cells by Targeting Iron Sulfur Cluster Protein ISCU. PLoS ONE, 2010, 5, e10345.	2.5	276

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19	Polycomb Associates Genome-wide with a Specific RNA Polymerase II Variant, and Regulates Metabolic Genes in ESCs. Cell Stem Cell, 2012, 10, 157-170.	11.1	261
20	Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. Nature Neuroscience, 2020, 23, 771-781.	14.8	258
21	Foxp2 Regulates Gene Networks Implicated in Neurite Outgrowth in the Developing Brain. PLoS Genetics, 2011, 7, e1002145.	3.5	256
22	Tumor hypoxia induces nuclear paraspeckle formation through HIF-2Î± dependent transcriptional activation of NEAT1 leading to cancer cell survival. Oncogene, 2015, 34, 4482-4490.	5.9	245
23	The small-nucleolar RNAs commonly used for microRNA normalisation correlate with tumour pathology and prognosis. British Journal of Cancer, 2011, 104, 1168-1177.	6.4	244
24	Direct reprogramming of fibroblasts into endothelial cells capable of angiogenesis and reendothelialization in tissue-engineered vessels. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13793-13798.	7.1	235
25	hsaâ€miRâ€210 is a marker of tumor hypoxia and a prognostic factor in head and neck cancer. Cancer, 2010, 116, 2148-2158.	4.1	215
26	Genotyping Technologies for Genetic Research. Annual Review of Genomics and Human Genetics, 2009, 10, 117-133.	6.2	194
27	Substantial Histone Reduction Modulates Genomewide Nucleosomal Occupancy and Global Transcriptional Output. PLoS Biology, 2011, 9, e1001086.	5.6	193
28	Subchromosomal Positioning of the Epidermal Differentiation Complex (EDC) in Keratinocyte and Lymphoblast Interphase Nuclei. Experimental Cell Research, 2002, 272, 163-175.	2.6	188
29	Principles of dimer-specific gene regulation revealed by a comprehensive characterization of NF-ÎºB family DNA binding. Nature Immunology, 2012, 13, 95-102.	14.5	188
30	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. Human Genetics, 2012, 131, 565-579.	3.8	180
31	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery inArabidopsis. EMBO Journal, 2012, 31, 4359-4370.	7.8	178
32	CMIP and ATP2C2 Modulate Phonological Short-Term Memory in Language Impairment. American Journal of Human Genetics, 2009, 85, 264-272.	6.2	173
33	The Histone Demethylase JMJD2B Is Regulated by Estrogen Receptor Î± and Hypoxia, and Is a Key Mediator of Estrogen Induced Growth. Cancer Research, 2010, 70, 6456-6466.	0.9	167
34	Comparing CNV detection methods for SNP arrays. Briefings in Functional Genomics & Proteomics, 2009, 8, 353-366.	3.8	166
35	Next generation sequencing for molecular diagnosis of neurological disorders using ataxias as a model. Brain, 2013, 136, 3106-3118.	7.6	146
36	Extensive regulation of the nonâ€coding transcriptome by hypoxia: role of <scp>HIF</scp> in releasing paused <scp>RNA</scp> pol2. EMBO Reports, 2014, 15, 70-76.	4.5	146

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37	Benchmarking of the Oxford Nanopore MinION sequencing for quantitative and qualitative assessment of cDNA populations. Scientific Reports, 2016, 6, 31602.	3.3	146
38	Extensive characterization of NF-ÎºB binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. Genome Biology, 2011, 12, R70.	9.6	137
39	Stalled developmental programs at the root of pediatric brain tumors. Nature Genetics, 2019, 51, 1702-1713.	21.4	136
40	Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. Molecular Cancer, 2014, 13, 28.	19.2	135
41	MicroRNA-10b and breast cancer metastasis. Nature, 2008, 455, E8-E9.	27.8	134
42	miR-210 is a target of hypoxia-inducible factors 1 and 2 in renal cancer, regulates ISCU and correlates with good prognosis. British Journal of Cancer, 2013, 108, 1133-1142.	6.4	134
43	Characterization of a Family with Rare Deletions in CNTNAP5 and DOCK4 Suggests Novel Risk Loci for Autism and Dyslexia. Biological Psychiatry, 2010, 68, 320-328.	1.3	131
44	A 15q13.3 microdeletion segregating with autism. European Journal of Human Genetics, 2009, 17, 687-692.	2.8	129
45	De novopoint mutations in patients diagnosed with ataxic cerebral palsy. Brain, 2015, 138, 1817-1832.	7.6	129
46	Recurrent noncoding U1ÂsnRNA mutations drive cryptic splicing in SHH medulloblastoma. Nature, 2019, 574, 707-711.	27.8	129
47	A statistical approach for detecting genomic aberrations in heterogeneous tumor samples from single nucleotide polymorphism genotyping data. Genome Biology, 2010, 11, R92.	8.8	125
48	Association of theKIAA0319Dyslexia Susceptibility Gene With Reading Skills in the General Population. American Journal of Psychiatry, 2008, 165, 1576-1584.	7.2	120
49	Genome-wide analysis of mutations in mutant lineages selected following fast-neutron irradiation mutagenesis of Arabidopsis thaliana. Genome Research, 2012, 22, 1306-1315.	5.5	119
50	Next-generation sequencing (NGS) as a diagnostic tool for retinal degeneration reveals a much higher detection rate in early-onset disease. European Journal of Human Genetics, 2013, 21, 274-280.	2.8	119
51	VACTERL/caudal regression/Currarino syndrome-like malformations in mice with mutation in the proprotein convertasePcsk5. Genes and Development, 2008, 22, 1465-1477.	5.9	110
52	Estrogen receptor-Î± directly regulates the hypoxia-inducible factor 1 pathway associated with antiestrogen response in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15172-15177.	7.1	110
53	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. BMC Medical Genomics, 2009, 2, 54.	1.5	105
54	Matrix-Assisted Laser Desorption/Ionisation, Time-of-Flight Mass Spectrometry in Genomics Research. PLoS Genetics, 2006, 2, e100.	3.5	103

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55	Identification of microRNA-221/222 and microRNA-323-3p association with rheumatoid arthritis via predictions using the human tumour necrosis factor transgenic mouse model. Annals of the Rheumatic Diseases, 2012, 71, 1716-1723.	0.9	103
56	Recessive Mutations in SPTBN2 Implicate Î²-III Spectrin in Both Cognitive and Motor Development. PLoS Genetics, 2012, 8, e1003074.	3.5	94
57	IRF5:RelA Interaction Targets Inflammatory Genes in Macrophages. Cell Reports, 2014, 8, 1308-1317.	6.4	94
58	Evaluating the Effects of Imputation on the Power, Coverage, and Cost Efficiency of Genome-wide SNP Platforms. American Journal of Human Genetics, 2008, 83, 112-119.	6.2	93
59	Animal models for arthritis: innovative tools for prevention and treatment. Annals of the Rheumatic Diseases, 2011, 70, 1357-1362.	0.9	92
60	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology,the, 2018, 5, e333-e345.	4.6	90
61	Maleness-on-the-Y (MoY) orchestrates male sex determination in major agricultural fruit fly pests. Science, 2019, 365, 1457-1460.	12.6	88
62	SW-ARRAY: a dynamic programming solution for the identification of copy-number changes in genomic DNA using array comparative genome hybridization data. Nucleic Acids Research, 2005, 33, 3455-3464.	14.5	87
63	Seeing clearly: the dominant and recessive nature ofFOXE3in eye developmental anomalies. Human Mutation, 2009, 30, 1378-1386.	2.5	84
64	Smooth Muscle Cells Differentiated From Reprogrammed Embryonic Lung Fibroblasts Through DKK3 Signaling Are Potent for Tissue Engineering of Vascular Grafts. Circulation Research, 2013, 112, 1433-1443.	4.5	83
65	Intestinal myofibroblast-specific Tpl2-Cox-2-PGE ₂ pathway links innate sensing to epithelial homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4658-67.	7.1	83
66	Regenerant Arabidopsis Lineages Display a Distinct Genome-Wide Spectrum of Mutations Conferring Variant Phenotypes. Current Biology, 2011, 21, 1385-1390.	3.9	82
67	Î±â€Haemoglobin stabilising protein is a quantitative trait gene that modifies the phenotype of Î²â€thalassaemia. British Journal of Haematology, 2006, 133, 675-682.	2.5	79
68	Quantitative high-throughput analysis of transcription factor binding specificities. Nucleic Acids Research, 2004, 32, 44e-44.	14.5	70
69	The Leukocyte Receptor Complex in Chicken Is Characterized by Massive Expansion and Diversification of Immunoglobulin-Like Loci. PLoS Genetics, 2006, 2, e73.	3.5	70
70	A Targetable EGFR-Dependent Tumor-Initiating Program in Breast Cancer. Cell Reports, 2017, 21, 1140-1149.	6.4	70
71	Methodologies for Transcript Profiling Using Long-Read Technologies. Frontiers in Genetics, 2020, 11, 606.	2.3	70
72	Genomic organization of the human folate receptor genes on chromosome 11q13. Genomics, 1992, 14, 423-430.	2.9	69

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73	MicroRNA expression profile in head and neck cancer: HOX-cluster embedded microRNA-196a and microRNA-10b dysregulation implicated in cell proliferation. BMC Cancer, 2013, 13, 533.	2.6	68
74	Biomarker discovery: quantification of microRNAs and other small non-coding RNAs using next generation sequencing. BMC Medical Genomics, 2015, 8, 35.	1.5	67
75	High-sensitivity sequencing reveals multi-organ somatic mosaicism causing DICER1 syndrome. Journal of Medical Genetics, 2016, 53, 43-52.	3.2	67
76	Cellular interference in craniofrontonasal syndrome: males mosaic for mutations in the X-linked EFNB1 gene are more severely affected than true hemizygotes. Human Molecular Genetics, 2013, 22, 1654-1662.	2.9	66
77	Human Epidermal Differentiation Complex in a Single 2.5 Mbp Long Continuum of Overlapping DNA Cloned in Bacteria Integrating Physical and Transcript Maps. Journal of Investigative Dermatology, 1999, 112, 910-918.	0.7	65
78	GenoSNP: a variational Bayes within-sample SNP genotyping algorithm that does not require a reference population. Bioinformatics, 2008, 24, 2209-2214.	4.1	65
79	CpG methylation profiling in VHL related and VHL unrelated renal cell carcinoma. Molecular Cancer, 2009, 8, 31.	19.2	65
80	Single-cell RNA sequencing reveals time- and sex-specific responses of mouse spinal cord microglia to peripheral nerve injury and links ApoE to chronic pain. Nature Communications, 2022, 13, 843.	12.8	62
81	Comparison of Human Chromosome 6p25 with Mouse Chromosome 13 Reveals a Greatly Expanded Ov-Serpin Gene Repertoire in the Mouse. Genomics, 2002, 79, 349-362.	2.9	57
82	Isolation and Characterization of Human and Mouse ZIRTL, a Member of the IRT1 Family of Transporters, Mapping within the Epidermal Differentiation Complex. Genomics, 1999, 62, 272-280.	2.9	56
83	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. Journal of Clinical Investigation, 2021, 131, .	8.2	56
84	Refined genotypeâ€“phenotype correlations in cases of chromosome 6p deletion syndromes. European Journal of Human Genetics, 2004, 12, 718-728.	2.8	55
85	Preparation of high-quality next-generation sequencing libraries from picogram quantities of target DNA. Genome Research, 2012, 22, 125-133.	5.5	55
86	A testis-expressed Zn finger gene (ZNF76) in human 6p21.3 centromeric to the MHC is closely linked to the human homolog of the t-complex gene tcp-11. Genomics, 1992, 14, 673-679.	2.9	54
87	An oncogenic role of eIF3e/INT6 in human breast cancer. Oncogene, 2010, 29, 4080-4089.	5.9	53
88	Positional cloning identifies a novel cyclophilin as a candidate amplified oncogene in 1q21. Oncogene, 2002, 21, 2261-2269.	5.9	52
89	Phase I/II Trial of Bevacizumab and Radiotherapy for Locally Advanced Inoperable Colorectal Cancer: Vasculature-Independent Radiosensitizing Effect of Bevacizumab. Clinical Cancer Research, 2009, 15, 7069-7076.	7.0	52
90	Characterization and mapping of the human SOX4 gene. Mammalian Genome, 1993, 4, 577-584.	2.2	51

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91	Global long non-coding RNA expression in the rostral anterior cingulate cortex of depressed suicides. Translational Psychiatry, 2018, 8, 224.	4.8	50
92	Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly. Molecular Biology and Evolution, 2021, 38, 3953-3971.	8.9	48
93	The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749.	12.8	47
94	Transcriptional signature of human adipose tissue-derived stem cells (hASCs) preconditioned for chondrogenesis in hypoxic conditions. Experimental Cell Research, 2009, 315, 1937-1952.	2.6	46
95	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. EMBO Journal, 2009, 28, 3400-3412.	7.8	46
96	Current and Future Methods for mRNA Analysis: A Drive Toward Single Molecule Sequencing. Methods in Molecular Biology, 2018, 1783, 209-241.	0.9	46
97	Developmental trajectory of oligodendrocyte progenitor cells in the human brain revealed by single cell RNA sequencing. Glia, 2020, 68, 1291-1303.	4.9	44
98	Human Ovalbumin Serpin Evolution: Phylogenic Analysis, Gene Organization, and Identification of New PI8-Related Genes Suggest That Two Interchromosomal and Several Intrachromosomal Duplications Generated the Gene Clusters at 18q21â€“q23 and 6p25. Genomics, 1999, 62, 490-499.	2.9	43
99	Transcript Profiling Using Long-Read Sequencing Technologies. Methods in Molecular Biology, 2018, 1783, 121-147.	0.9	41
100	Single-Cell RNA-Seq Analysis of Cells from Degenerating and Non-Degenerating Intervertebral Discs from the Same Individual Reveals New Biomarkers for Intervertebral Disc Degeneration. International Journal of Molecular Sciences, 2022, 23, 3993.	4.1	39
101	Variations within oxygen-regulated gene expression in humans. Journal of Applied Physiology, 2009, 106, 212-220.	2.5	37
102	Single-cell analysis of childhood leukemia reveals a link between developmental states and ribosomal protein expression as a source of intra-individual heterogeneity. Scientific Reports, 2020, 10, 8079.	3.3	37
103	Affymetrix GeneChipÂ® system: moving from research to the clinic. Expert Review of Molecular Diagnostics, 2006, 6, 145-152.	3.1	36
104	The Use of Genome-Wide eQTL Associations in Lymphoblastoid Cell Lines to Identify Novel Genetic Pathways Involved in Complex Traits. PLoS ONE, 2011, 6, e22070.	2.5	36
105	Integration of Transcriptome and Metabolome Provides Unique Insights to Pathways Associated With Obese Breast Cancer Patients. Frontiers in Oncology, 2020, 10, 804.	2.8	36
106	Association of the aromatase gene with Alzheimer's disease in women. Neuroscience Letters, 2010, 468, 202-206.	2.1	34
107	The Role of Hypoxia Regulated microRNAs in Cancer. Current Topics in Microbiology and Immunology, 2010, 345, 47-70.	1.1	34
108	Analysis of head and neck carcinoma progression reveals novel and relevant stage-specific changes associated with immortalisation and malignancy. Scientific Reports, 2019, 9, 11992.	3.3	32

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109	Wholeâ€exome sequencing of nonâ€•BRCA1/BRCA2 mutation carrier cases at highâ€risk for hereditary breast/ovarian cancer. Human Mutation, 2021, 42, 290-299.	2.5	32
110	DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. Journal of Clinical Investigation, 2020, 130, 1479-1490.	8.2	31
111	Deep Sequencing Reveals Spatially Distributed Distinct Hot Spot Mutations in DICER1-Related Multinodular Goiter. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 3637-3645.	3.6	30
112	Sequencing of DICER1 in sarcomas identifies biallelic somatic DICER1 mutations in an adult-onset embryonal rhabdomyosarcoma. British Journal of Cancer, 2017, 116, 1621-1626.	6.4	30
113	Development and evaluation of real competitive PCR for high-throughput quantitative applications. Analytical Biochemistry, 2005, 339, 231-241.	2.4	28
114	Dissecting the genetic complexity of human 6p deletion syndromes by using a region-specific, phenotype-driven mouse screen. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12477-12482.	7.1	28
115	RNA Sequencing Reveals that Kaposi Sarcoma-Associated Herpesvirus Infection Mimics Hypoxia Gene Expression Signature. PLoS Pathogens, 2017, 13, e1006143.	4.7	28
116	Metagenomic analysis of planktonic riverine microbial consortia using nanopore sequencing reveals insight into river microbe taxonomy and function. GigaScience, 2020, 9, .	6.4	28
117	New vector for transfer of yeast artificial chromosomes to mammalian cells. Somatic Cell and Molecular Genetics, 1993, 19, 161-169.	0.7	27
118	Olive fly transcriptomics analysis implicates energy metabolism genes in spinosad resistance. BMC Genomics, 2014, 15, 714.	2.8	27
119	Quality control project of NGS HLA genotyping for the 17th International HLA and Immunogenetics Workshop. Human Immunology, 2019, 80, 228-236.	2.4	27
120	Oviduct epithelial cells constitute two developmentally distinct lineages that are spatially separated along the distal-proximal axis. Cell Reports, 2021, 36, 109677.	6.4	27
121	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. Genome Research, 2005, 15, 1503-1510.	5.5	26
122	Genotyping technologies for all. Drug Discovery Today: Technologies, 2006, 3, 115-122.	4.0	26
123	Update on hypoxia-inducible factors and hydroxylases in oxygen regulatory pathways: from physiology to therapeutics. Hypoxia (Auckland, N Z), 2017, Volume 5, 11-20.	1.9	26
124	Model-based analysis of sample index hopping reveals its widespread artifacts in multiplexed single-cell RNA-sequencing. Nature Communications, 2020, 11, 2704.	12.8	26
125	The genetic landscape of choroid plexus tumors in children and adults. Neuro-Oncology, 2021, 23, 650-660.	1.2	26
126	Weighted gene co-expression network analysis of colorectal cancer liver metastasis genome sequencing data and screening of anti-metastasis drugs. International Journal of Oncology, 2016, 49, 1108-1118.	3.3	25

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127	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. Nature Communications, 2021, 12, 491.	12.8	25
128	Altered Intra-Nuclear Organisation of Heterochromatin and Genes in ICF Syndrome. PLoS ONE, 2010, 5, e11364.	2.5	25
129	GATA-1 genome-wide occupancy associates with distinct epigenetic profiles in mouse fetal liver erythropoiesis. Nucleic Acids Research, 2013, 41, 4938-4948.	14.5	24
130	Functional conservation of Rel binding sites in drosophilid genomes. Genome Research, 2007, 17, 1327-1335.	5.5	22
131	Live single-cell laser tag. Nature Communications, 2016, 7, 11636.	12.8	22
132	De novo assembly of the olive fruit fly (Bactrocera oleae) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. BMC Genomics, 2020, 21, 259.	2.8	21
133	Next-generation HLA typing of 382 International Histocompatibility Working Group reference B-lymphoblastoid cell lines: Report from the 17th International HLA and Immunogenetics Workshop. Human Immunology, 2019, 80, 449-460.	2.4	20
134	The mevalonate precursor enzyme HMGCS1 is a novel marker and key mediator of cancer stem cell enrichment in luminal and basal models of breast cancer. PLoS ONE, 2020, 15, e0236187.	2.5	20
135	Next-Generation Sequencing Analysis Reveals Differential Expression Profiles of MiRNA-mRNA Target Pairs in KSHV-Infected Cells. PLoS ONE, 2015, 10, e0126439.	2.5	19
136	A coordinated progression of progenitor cell states initiates urinary tract development. Nature Communications, 2021, 12, 2627.	12.8	19
137	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in QuÃ©bec, Canada. Genome Medicine, 2021, 13, 169.	8.2	19
138	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. Neuro-Oncology, 2021, 23, 1470-1480.	1.2	18
139	Three-dimensional hydrogel structures as optical sensor arrays, for the detection of specific DNA sequences. Analytical Biochemistry, 2012, 421, 1-8.	2.4	17
140	TGF-Î²/Smad2/3 Signaling Directly Regulates Several miRNAs in Mouse ES Cells and Early Embryos. PLoS ONE, 2013, 8, e55186.	2.5	17
141	The molecular biology of the olive fly comes of age. BMC Genetics, 2014, 15, S8.	2.7	17
142	Pattern recognition receptor mediated downregulation of microRNAâ€650 fineâ€tunes MxA expression in dendritic cells infected with influenza A virus. European Journal of Immunology, 2016, 46, 167-177.	2.9	17
143	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA). BMJ Open, 2022, 12, e059021.	1.9	17
144	Mitotic recombination of yeast artificial chromosomes. Nucleic Acids Research, 1992, 20, 3135-3138.	14.5	16

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145	Comparative analysis of methods for gene transcription profiling data derived from different microarray technologies in rat and mouse models of diabetes. BMC Genomics, 2009, 10, 63.	2.8	16
146	Lessons learned from understanding chemotherapy resistance in epithelial tubo-ovarian carcinoma from BRCA1and BRCA2mutation carriers. Seminars in Cancer Biology, 2020, 77, 110-126.	9.6	16
147	A chromosomeâ€anchored genome assembly for Lake Trout (Salvelinus namaycush). Molecular Ecology Resources, 2022, 22, 679-694.	4.8	16
148	Analysis ofFGGYas a risk factor for sporadic amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders, 2009, 10, 441-447.	2.1	15
149	Cross-species Analysis Reveals Evolving and Conserved Features of the Nuclear Factor ÎºB (NF-ÎºB) Proteins. Journal of Biological Chemistry, 2013, 288, 11546-11554.	3.4	15
150	Exome Sequencing in BRCA1- and BRCA2-Negative Greek Families Identifies MDM1 and NBEAL1 as Candidate Risk Genes for Hereditary Breast Cancer. Frontiers in Genetics, 2019, 10, 1005.	2.3	15
151	Extraction of nuclei from archived postmortem tissues for single-nucleus sequencing applications. Nature Protocols, 2021, 16, 2788-2801.	12.0	15
152	Survival of metastatic melanoma patients after dendritic cell vaccination correlates with expression of leukocyte phosphatidylethanolamine-binding protein 1/Raf kinase inhibitory protein. Oncotarget, 2017, 8, 67439-67456.	1.8	15
153	Haplotype-resolved de novo assembly of the Vero cell line genome. Npj Vaccines, 2021, 6, 106.	6.0	14
154	BeadArray-Based Genotyping. Methods in Molecular Biology, 2008, 439, 53-74.	0.9	13
155	Chromosome-level assembly reveals a putative Y-autosomal fusion in the sex determination system of the Greenland Halibut (Reinhardtius hippoglossoides). G3: Genes, Genomes, Genetics, 2021, , .	1.8	13
156	High-resolution analysis of cis -acting regulatory networks at the Î±-globin locus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120361.	4.0	12
157	Regulation of cellular sterol homeostasis by the oxygen responsive noncoding RNA lincNORS. Nature Communications, 2020, 11, 4755.	12.8	12
158	Nanopore long-read RNA-seq and absolute quantification delineate transcription dynamics in early embryo development of an insect pest. Scientific Reports, 2021, 11, 7878.	3.3	12
159	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. Genome Medicine, 2021, 13, 186.	8.2	12
160	Chemokine gene expression in lung CD8 T cells correlates with protective immunity in mice immunized intra-nasally with Adenovirus-85A. BMC Medical Genomics, 2010, 3, 46.	1.5	11
161	Molecular characterization of DICER1-mutated pituitary blastoma. Acta Neuropathologica, 2021, 141, 929-944.	7.7	11
162	Modeling High-Grade Serous Ovarian Carcinoma Using a Combination ofIn VivoFallopian Tube Electroporation and CRISPR-Cas9â€“Mediated Genome Editing. Cancer Research, 2021, 81, 5147-5160.	0.9	11

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163	Glioblastoma scRNA-seq shows treatment-induced, immune-dependent increase in mesenchymal cancer cells and structural variants in distal neural stem cells. Neuro-Oncology, 2022, 24, 1494-1508.	1.2	11
164	Accuracy and Reproducibility of Proteinâ€“DNA Microarray Technology. , 2007, 104, 87-110.		10
165	Genome-wide analysis of androgen receptor binding and transcriptomic analysis in mesenchymal subsets during prostate development. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	10
166	A commonly occurring polymorphism upstream of the estrogen receptor alpha alters transcription and is associated with increased HDL. Atherosclerosis, 2008, 199, 354-361.	0.8	8
167	H3.1 K36M mutation in a congenitalâ€onset soft tissue neoplasm. Pediatric Blood and Cancer, 2017, 64, e26633.	1.5	7
168	Identification of genes expressed in a mesenchymal subset regulating prostate organogenesis using tissue and single cell transcriptomics. Scientific Reports, 2017, 7, 16385.	3.3	7
169	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in Arabidopsis. EMBO Journal, 2013, 32, 914-914.	7.8	6
170	A Distributed Whole Genome Sequencing Benchmark Study. Frontiers in Genetics, 2020, 11, 612515.	2.3	6
171	A multidimensional integration analysis reveals potential bridging targets in the process of colorectal cancer liver metastasis. PLoS ONE, 2017, 12, e0178760.	2.5	6
172	Methods of Quantifying MicroRNAs for Hypoxia Research: Classic and Next Generation. Antioxidants and Redox Signaling, 2014, 21, 1239-1248.	5.4	5
173	Quantitative Profiling of Protein-DNA Binding on Microarrays. , 2006, 338, 261-280.		4
174	Microarray-based ultra-high resolution discovery of genomic deletion mutations. BMC Genomics, 2014, 15, 224.	2.8	4
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