Jiannis Ragoussis

List of Publications by Citations

195 papers	15,513 citations	63 h-index	123 g-index
219 ext. papers	18,179 ext. citations	9.8 avg, IF	5.96 L-index

#	Paper	IF	Citations
195	Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, **2010**, 466, 368-72	50.4	1499
194	A large fraction of extragenic RNA pol II transcription sites overlap enhancers. *PLoS Biology*, **2010**, 8, e1000384	9.7	617
193	hsa-miR-210 Is induced by hypoxia and is an independent prognostic factor in breast cancer. *Clinical Cancer Research*, **2008**, 14, 1340-8	12.9	555
192	Identification and characterization of enhancers controlling the inflammatory gene expression program in macrophages. *Immunity*, **2010**, 32, 317-28	32.3	497
191	Direct targeting of Sec23a by miR-200s influences cancer cell secretome and promotes metastatic colonization. *Nature Medicine*, **2011**, 17, 1101-8	50.5	486
190	High-resolution genome-wide mapping of HIF-binding sites by ChIP-seq. *Blood*, **2011**, 117, e207-17	2.2	484
189	QuantiSNP: an Objective Bayes Hidden-Markov Model to detect and accurately map copy number variation using SNP genotyping data. *Nucleic Acids Research*, **2007**, 35, 2013-25	20.1	462
188	A genome-wide scan for common alleles affecting risk for autism. *Human Molecular Genetics*, **2010**, 19, 4072-82	5.6	443
187	Genome-wide association of hypoxia-inducible factor (HIF)-1alpha and HIF-2alpha DNA binding with expression profiling of hypoxia-inducible transcripts. *Journal of Biological Chemistry*, **2009**, 284, 16767-16775	5.4	406
186	Single nucleotide polymorphisms in TNFSF15 confer susceptibility to Crohn's disease. *Human Molecular Genetics*, **2005**, 14, 3499-506	5.6	376
185	Concordant regulation of gene expression by hypoxia and 2-oxoglutarate-dependent dioxygenase inhibition: the role of HIF-1alpha, HIF-2alpha, and other pathways. *Journal of Biological Chemistry*, **2006**, 281, 15215-26	5.4	351
184	ATR-X syndrome protein targets tandem repeats and influences allele-specific expression in a size-dependent manner. *Cell*, **2010**, 143, 367-78	56.2	297
183	Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nature Genetics*, **2009**, 41, 657-65	36.3	297
182	Individual common variants exert weak effects on the risk for autism spectrum disorders. *Human Molecular Genetics*, **2012**, 21, 4781-92	5.6	279
181	microRNA-associated progression pathways and potential therapeutic targets identified by integrated mRNA and microRNA expression profiling in breast cancer. *Cancer Research*, **2011**, 71, 5635-45	10.1	253
180	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	3.7	243
179	Polycomb associates genome-wide with a specific RNA polymerase II variant, and regulates metabolic genes in ESCs. *Cell Stem Cell*, **2012**, 10, 157-70	18	221

178	The small-nucleolar RNAs commonly used for microRNA normalisation correlate with tumour pathology and prognosis. *British Journal of Cancer*, **2011**, 104, 1168-77	8.7	217
177	Foxp2 regulates gene networks implicated in neurite outgrowth in the developing brain. *PLoS Genetics*, **2011**, 7, e1002145	6	198
176	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, 13793-8	11.5	194
175	hsa-mir-210 is a marker of tumor hypoxia and a prognostic factor in head and neck cancer. *Cancer*, **2010**, 116, 2148-58	6.4	193
174	Subchromosomal positioning of the epidermal differentiation complex (EDC) in keratinocyte and lymphoblast interphase nuclei. *Experimental Cell Research*, **2002**, 272, 163-75	4.2	170
173	Tumor hypoxia induces nuclear paraspeckle formation through HIF-2 dependent transcriptional activation of NEAT1 leading to cancer cell survival. *Oncogene*, **2015**, 34, 4482-90	9.2	164
172	Genotyping technologies for genetic research. *Annual Review of Genomics and Human Genetics*, **2009**, 10, 117-33	9.7	164
171	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. *Human Genetics*, **2012**, 131, 565-79	6.3	150
170	Comparing CNV detection methods for SNP arrays. *Briefings in Functional Genomics & Proteomics*, **2009**, 8, 353-66		150
169	Principles of dimer-specific gene regulation revealed by a comprehensive characterization of NF- B family DNA binding. *Nature Immunology*, **2011**, 13, 95-102	19.1	143
168	CMIP and ATP2C2 modulate phonological short-term memory in language impairment. *American Journal of Human Genetics*, **2009**, 85, 264-72	11	142
167	The histone demethylase JMJD2B is regulated by estrogen receptor alpha and hypoxia, and is a key mediator of estrogen induced growth. *Cancer Research*, **2010**, 70, 6456-66	10.1	141
166	Substantial histone reduction modulates genomewide nucleosomal occupancy and global transcriptional output. *PLoS Biology*, **2011**, 9, e1001086	9.7	140
165	Next generation sequencing for molecular diagnosis of neurological disorders using ataxias as a model. *Brain*, **2013**, 136, 3106-18	11.2	128
164	Extensive regulation of the non-coding transcriptome by hypoxia: role of HIF in releasing paused RNApol2. *EMBO Reports*, **2014**, 15, 70-6	6.5	125
163	MAFG-driven astrocytes promote CNS inflammation. *Nature*, **2020**, 578, 593-599	50.4	125
162	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in Arabidopsis. *EMBO Journal*, **2012**, 31, 4359-70	13	120
161	A 15q13.3 microdeletion segregating with autism. *European Journal of Human Genetics*, **2009**, 17, 687-92	5.3	114

160	MicroRNA-10b and breast cancer metastasis. *Nature*, **2008**, 455, E8-9; author reply E9	50.4	113
159	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, 1133-42	8.7	112
158	A statistical approach for detecting genomic aberrations in heterogeneous tumor samples from single nucleotide polymorphism genotyping data. *Genome Biology*, **2010**, 11, R92	18.3	111
157	Extensive characterization of NF-B binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. *Genome Biology*, **2011**, 12, R70	18.3	110
156	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, 274-80	5.3	107
155	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	42.1	104
154	Association of the KIAA0319 dyslexia susceptibility gene with reading skills in the general population. *American Journal of Psychiatry*, **2008**, 165, 1576-84	11.9	104
153	Characterization of a family with rare deletions in CNTNAP5 and DOCK4 suggests novel risk loci for autism and dyslexia. *Biological Psychiatry*, **2010**, 68, 320-8	7.9	103
152	De novo point mutations in patients diagnosed with ataxic cerebral palsy. *Brain*, **2015**, 138, 1817-32	11.2	101
151	VACTERL/caudal regression/Currarino syndrome-like malformations in mice with mutation in the proprotein convertase Pcsk5. *Genes and Development*, **2008**, 22, 1465-77	12.6	99
150	Benchmarking of the Oxford Nanopore MinION sequencing for quantitative and qualitative assessment of cDNA populations. *Scientific Reports*, **2016**, 6, 31602	4.9	98
149	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. *BMC Medical Genomics*, **2009**, 2, 54	3.7	96
148	Matrix-assisted laser desorption/ionisation, time-of-flight mass spectrometry in genomics research. *PLoS Genetics*, **2006**, 2, e100	6	92
147	Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. *Nature Neuroscience*, **2020**, 23, 771-781	25.5	91
146	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. *Nature Communications*, **2020**, 11, 3406	17.4	88
145	Genome-wide analysis of mutations in mutant lineages selected following fast-neutron irradiation mutagenesis of Arabidopsis thaliana. *Genome Research*, **2012**, 22, 1306-15	9.7	87
144	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, 1716-23	2.4	83
143	Evaluating the effects of imputation on the power, coverage, and cost efficiency of genome-wide SNP platforms. *American Journal of Human Genetics*, **2008**, 83, 112-9	11	80

142	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, 3455-64	20.1	79
141	Animal models for arthritis: innovative tools for prevention and treatment. *Annals of the Rheumatic Diseases*, **2011**, 70, 1357-62	2.4	78
140	Seeing clearly: the dominant and recessive nature of FOXE3 in eye developmental anomalies. *Human Mutation*, **2009**, 30, 1378-86	4.7	78
139	Recurrent noncoding U1´snRNA mutations drive cryptic splicing in SHH medulloblastoma. *Nature*, **2019**, 574, 707-711	50.4	78
138	Estrogen receptor-□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, 15172-7	11.5	74
137	Recessive mutations in SPTBN2 implicate □II spectrin in both cognitive and motor development. *PLoS Genetics*, **2012**, 8, e1003074	6	74
136	IRF5:RelA interaction targets inflammatory genes in macrophages. *Cell Reports*, **2014**, 8, 1308-17	10.6	70
135	Alpha-haemoglobin stabilising protein is a quantitative trait gene that modifies the phenotype of beta-thalassaemia. *British Journal of Haematology*, **2006**, 133, 675-82	4.5	70
134	Quantitative high-throughput analysis of transcription factor binding specificities. *Nucleic Acids Research*, **2004**, 32, e44	20.1	67
133	Regenerant Arabidopsis lineages display a distinct genome-wide spectrum of mutations conferring variant phenotypes. *Current Biology*, **2011**, 21, 1385-90	6.3	65
132	Smooth muscle cells differentiated from reprogrammed embryonic lung fibroblasts through DKK3 signaling are potent for tissue engineering of vascular grafts. *Circulation Research*, **2013**, 112, 1433-43	15.7	63
131	Genomic organization of the human folate receptor genes on chromosome 11q13. *Genomics*, **1992**, 14, 423-30	4.3	63
130	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	4.8	58
129	The leukocyte receptor complex in chicken is characterized by massive expansion and diversification of immunoglobulin-like Loci. *PLoS Genetics*, **2006**, 2, e73	6	58
128	Stalled developmental programs at the root of pediatric brain tumors. *Nature Genetics*, **2019**, 51, 1702-1713	36.3	58
127	Biomarker discovery: quantification of microRNAs and other small non-coding RNAs using next generation sequencing. *BMC Medical Genomics*, **2015**, 8, 35	3.7	56
126	CpG methylation profiling in VHL related and VHL unrelated renal cell carcinoma. *Molecular Cancer*, **2009**, 8, 31	42.1	56
125	GenoSNP: a variational Bayes within-sample SNP genotyping algorithm that does not require a reference population. *Bioinformatics*, **2008**, 24, 2209-14	7.2	56

124	Comparison of human chromosome 6p25 with mouse chromosome 13 reveals a greatly expanded ov-serpin gene repertoire in the mouse. *Genomics*, **2002**, 79, 349-62	4.3	55
123	Intestinal myofibroblast-specific Tpl2-Cox-2-PGE2 pathway links innate sensing to epithelial homeostasis. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E4658-67	11.5	52
122	High-sensitivity sequencing reveals multi-organ somatic mosaicism causing DICER1 syndrome. *Journal of Medical Genetics*, **2016**, 53, 43-52	5.8	51
121	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, 1654-62	5.6	50
120	Positional cloning identifies a novel cyclophilin as a candidate amplified oncogene in 1q21. *Oncogene*, **2002**, 21, 2261-9	9.2	50
119	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, 272-80	4.3	50
118	Refined genotype-phenotype correlations in cases of chromosome 6p deletion syndromes. *European Journal of Human Genetics*, **2004**, 12, 718-28	5.3	49
117	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, 910-8	4.3	48
116	() orchestrates male sex determination in major agricultural fruit fly pests. *Science*, **2019**, 365, 1457-1460	33.3	47
115	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, 673-9	4.3	47
114	Characterization and mapping of the human SOX4 gene. *Mammalian Genome*, **1993**, 4, 577-84	3.2	47
113	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, 7069-76	12.9	46
112	A Targetable EGFR-Dependent Tumor-Initiating Program in Breast Cancer. *Cell Reports*, **2017**, 21, 1140-1148	8.8	45
111	Preparation of high-quality next-generation sequencing libraries from picogram quantities of target DNA. *Genome Research*, **2012**, 22, 125-33	9.7	45
110	An oncogenic role of eIF3e/INT6 in human breast cancer. *Oncogene*, **2010**, 29, 4080-9	9.2	41
109	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 18q21-q23 and 6p25. *Genomics*, **1999**, 62, 490-9	4.3	40
108	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	14.6	38
107	Transcriptional signature of human adipose tissue-derived stem cells (hASCs) preconditioned for chondrogenesis in hypoxic conditions. *Experimental Cell Research*, **2009**, 315, 1937-52	4.2	37

106	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	3.7	35
105	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. *EMBO Journal*, **2009**, 28, 3400-12	13	34
104	The role of hypoxia regulated microRNAs in cancer. *Current Topics in Microbiology and Immunology*, **2010**, 345, 47-70	3.3	33
103	Association of the aromatase gene with Alzheimer's disease in women. *Neuroscience Letters*, **2010**, 468, 202-6	3.3	31
102	Variations within oxygen-regulated gene expression in humans. *Journal of Applied Physiology*, **2009**, 106, 212-20	3.7	31
101	Affymetrix GeneChip system: moving from research to the clinic. *Expert Review of Molecular Diagnostics*, **2006**, 6, 145-52	3.8	31
100	Global long non-coding RNA expression in the rostral anterior cingulate cortex of depressed suicides. *Translational Psychiatry*, **2018**, 8, 224	8.6	30
99	Development and evaluation of real competitive PCR for high-throughput quantitative applications. *Analytical Biochemistry*, **2005**, 339, 231-41	3.1	28
98	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, 12477-82	11.5	26
97	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. *Journal of Clinical Investigation*, **2021**, 131,	15.9	25
96	Sequencing of DICER1 in sarcomas identifies biallelic somatic DICER1 mutations in an adult-onset embryonal rhabdomyosarcoma. *British Journal of Cancer*, **2017**, 116, 1621-1626	8.7	24
95	Methodologies for Transcript Profiling Using Long-Read Technologies. *Frontiers in Genetics*, **2020**, 11, 606	4.5	24
94	Transcript Profiling Using Long-Read Sequencing Technologies. *Methods in Molecular Biology*, **2018**, 1783, 121-147	1.4	24
93	Developmental trajectory of oligodendrocyte progenitor cells in the human brain revealed by single cell RNA sequencing. *Glia*, **2020**, 68, 1291-1303	9	22
92	Deep Sequencing Reveals Spatially Distributed Distinct Hot Spot Mutations in DICER1-Related Multinodular Goiter. *Journal of Clinical Endocrinology and Metabolism*, **2016**, 101, 3637-3645	5.6	22
91	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. *Genome Research*, **2005**, 15, 1503-10	9.7	22
90	New vector for transfer of yeast artificial chromosomes to mammalian cells. *Somatic Cell and Molecular Genetics*, **1993**, 19, 161-9		22
89	Altered intra-nuclear organisation of heterochromatin and genes in ICF syndrome. *PLoS ONE*, **2010**, 5, e11364	3.7	22

88	Current and Future Methods for mRNA Analysis: A Drive Toward Single Molecule Sequencing. *Methods in Molecular Biology*, **2018**, 1783, 209-241	1.4	22
87	RNA Sequencing Reveals that Kaposi Sarcoma-Associated Herpesvirus Infection Mimics Hypoxia Gene Expression Signature. *PLoS Pathogens*, **2017**, 13, e1006143	7.6	21
86	Olive fly transcriptomics analysis implicates energy metabolism genes in spinosad resistance. *BMC Genomics*, **2014**, 15, 714	4.5	20
85	Genotyping technologies for all. *Drug Discovery Today: Technologies*, **2006**, 3, 115-22	7.1	20
84	Quality control project of NGS HLA genotyping for the 17th International HLA and Immunogenetics Workshop. *Human Immunology*, **2019**, 80, 228-236	2.3	19
83	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, 1108-18	4.4	19
82	GATA-1 genome-wide occupancy associates with distinct epigenetic profiles in mouse fetal liver erythropoiesis. *Nucleic Acids Research*, **2013**, 41, 4938-48	20.1	19
81	Update on hypoxia-inducible factors and hydroxylases in oxygen regulatory pathways: from physiology to therapeutics. *Hypoxia (Auckland, N Z)*, **2017**, 5, 11-20	2.1	17
80	Next-Generation Sequencing Analysis Reveals Differential Expression Profiles of MiRNA-mRNA Target Pairs in KSHV-Infected Cells. *PLoS ONE*, **2015**, 10, e0126439	3.7	16
79	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	4.5	15
78	DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. *Journal of Clinical Investigation*, **2020**, 130, 1479-1490	15.9	15
77	Mitotic recombination of yeast artificial chromosomes. *Nucleic Acids Research*, **1992**, 20, 3135-8	20.1	14
76	Live single-cell laser tag. *Nature Communications*, **2016**, 7, 11636	17.4	14
75	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	2.3	13
74	Analysis of head and neck carcinoma progression reveals novel and relevant stage-specific changes associated with immortalisation and malignancy. *Scientific Reports*, **2019**, 9, 11992	4.9	13
73	The molecular biology of the olive fly comes of age. *BMC Genetics*, **2014**, 15 Suppl 2, S8	2.6	13
72	Three-dimensional hydrogel structures as optical sensor arrays, for the detection of specific DNA sequences. *Analytical Biochemistry*, **2012**, 421, 1-8	3.1	13
71	Cross-species analysis reveals evolving and conserved features of the nuclear factor B (NF-B) proteins. *Journal of Biological Chemistry*, **2013**, 288, 11546-54	5.4	13

70	Analysis of FGGY as a risk factor for sporadic amyotrophic lateral sclerosis. *Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders*, **2009**, 10, 441-7		13
69	Functional conservation of Rel binding sites in drosophilid genomes. *Genome Research*, **2007**, 17, 1327-35	9.7	13
68	Integration of Transcriptome and Metabolome Provides Unique Insights to Pathways Associated With Obese Breast Cancer Patients. *Frontiers in Oncology*, **2020**, 10, 804	5.3	13
67	TGF-/Smad2/3 signaling directly regulates several miRNAs in mouse ES cells and early embryos. *PLoS ONE*, **2013**, 8, e55186	3.7	12
66	BeadArray-based genotyping. *Methods in Molecular Biology*, **2008**, 439, 53-74	1.4	12
65	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	3.3	12
64	High-resolution analysis of cis-acting regulatory networks at the -globin locus. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2013**, 368, 20120361	5.8	11
63	Metagenomic analysis of planktonic riverine microbial consortia using nanopore sequencing reveals insight into river microbe taxonomy and function. *GigaScience*, **2020**, 9,	7.6	11
62	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	3.7	10
61	Pattern recognition receptor mediated downregulation of microRNA-650 fine-tunes MxA expression in dendritic cells infected with influenza A virus. *European Journal of Immunology*, **2016**, 46, 167-77	6.1	10
60	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	4.5	10
59	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. *Neuro-Oncology*, **2021**, 23, 1470-1480	1	10
58	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	4.9	9
57	Model-based analysis of sample index hopping reveals its widespread artifacts in multiplexed single-cell RNA-sequencing. *Nature Communications*, **2020**, 11, 2704	17.4	9
56	Accuracy and reproducibility of protein-DNA microarray technology. *Advances in Biochemical Engineering/Biotechnology*, **2007**, 104, 87-110	1.7	9
55	Lessons learned from understanding chemotherapy resistance in epithelial tubo-ovarian carcinoma from BRCA1and BRCA2mutation carriers. *Seminars in Cancer Biology*, **2021**, 77, 110-126	12.7	9
54	Whole-exome sequencing of non-BRCA1/BRCA2 mutation carrier cases at high-risk for hereditary breast/ovarian cancer. *Human Mutation*, **2021**, 42, 290-299	4.7	9
53	Exome Sequencing in and -Negative Greek Families Identifies and as Candidate Risk Genes for Hereditary Breast Cancer. *Frontiers in Genetics*, **2019**, 10, 1005	4.5	7

52	Identification of genes expressed in a mesenchymal subset regulating prostate organogenesis using tissue and single cell transcriptomics. *Scientific Reports*, **2017**, 7, 16385	4.9	7
51	Regulation of cellular sterol homeostasis by the oxygen responsive noncoding RNA lincNORS. *Nature Communications*, **2020**, 11, 4755	17.4	7
50	The transcriptional landscape of Shh medulloblastoma. *Nature Communications*, **2021**, 12, 1749	17.4	7
49	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. *Nature Communications*, **2021**, 12, 491	17.4	7
48	A multidimensional integration analysis reveals potential bridging targets in the process of colorectal cancer liver metastasis. *PLoS ONE*, **2017**, 12, e0178760	3.7	6
47	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. *Genome Medicine*, **2021**, 13, 169	14.4	6
46	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	3.7	6
45	Molecular characterization of DICER1-mutated pituitary blastoma. *Acta Neuropathologica*, **2021**, 141, 929-944	14.3	6
44	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in Arabidopsis. *EMBO Journal*, **2013**, 32, 914-914	13	5
43	A commonly occurring polymorphism upstream of the estrogen receptor alpha alters transcription and is associated with increased HDL. *Atherosclerosis*, **2008**, 199, 354-61	3.1	5
42	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	17.4	5
41	Failure to replicate the association of rare loss-of-function variants in type I IFN immunity genes with severe COVID-19 **2020**,		5
40	Single-nucleus RNA sequencing shows convergent evidence from different cell types for altered synaptic plasticity in major depressive disorder		5
39	Transcriptome landscape of the developing olive fruit fly embryo delineated by Oxford Nanopore long-read RNA-Seq		5
38	Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly. *Molecular Biology and Evolution*, **2021**, 38, 3953-3971	8.3	5
37	A coordinated progression of progenitor cell states initiates urinary tract development. *Nature Communications*, **2021**, 12, 2627	17.4	5
36	Haplotype-resolved de novo assembly of the Vero cell line genome. *Npj Vaccines*, **2021**, 6, 106	9.5	5
35	Oviduct epithelial cells constitute two developmentally distinct lineages that are spatially separated along the distal-proximal axis. *Cell Reports*, **2021**, 36, 109677	10.6	5

34	Methods of quantifying microRNAs for hypoxia research: classic and next generation. *Antioxidants and Redox Signaling*, **2014**, 21, 1239-48	8.4	4
33	Microarray-based ultra-high resolution discovery of genomic deletion mutations. *BMC Genomics*, **2014**, 15, 224	4.5	4
32	Microarray-based optimization to detect genomic deletion mutations. *Genomics Data*, **2014**, 2, 53-54		4
31	Quantitative profiling of protein-DNA binding on microarrays. *Methods in Molecular Biology*, **2006**, 338, 261-80	1.4	4
30	Genome-wide analysis of androgen receptor binding and transcriptomic analysis in mesenchymal subsets during prostate development. *DMM Disease Models and Mechanisms*, **2019**, 12,	4.1	4
29	H3.1 K36M mutation in a congenital-onset soft tissue neoplasm. *Pediatric Blood and Cancer*, **2017**, 64, e26633	3	3
28	Nanopore long-read RNA-seq and absolute quantification delineate transcription dynamics in early embryo development of an insect pest. *Scientific Reports*, **2021**, 11, 7878	4.9	3
27	Extraction of nuclei from archived postmortem tissues for single-nucleus sequencing applications. *Nature Protocols*, **2021**, 16, 2788-2801	18.8	3
26	Modeling High-Grade Serous Ovarian Carcinoma Using a Combination of Fallopian Tube Electroporation and CRISPR-Cas9-Mediated Genome Editing. *Cancer Research*, **2021**, 81, 5147-5160	10.1	3
25	The genetic landscape of choroid plexus tumors in children and adults. *Neuro-Oncology*, **2021**, 23, 650-660		3
24	Gene Ontology and Expression Studies of Strigolactone Analogues on a Hepatocellular Carcinoma Cell Line. *Analytical Cellular Pathology*, **2019**, 2019, 1598182	3.4	2
23	De novo genome assembly of the olive fruit fly (Bactrocera oleae) developed through a combination of linked-reads and long-read technologies		2
22	A Distributed Whole Genome Sequencing Benchmark Study. *Frontiers in Genetics*, **2020**, 11, 612515	4.5	2
21	Regulators of Asymmetric Cell Division in Breast Cancer. *Trends in Cancer*, **2018**, 4, 798-801	12.5	2
20	A chromosome-anchored genome assembly for Lake Trout (Salvelinus namaycush). *Molecular Ecology Resources*, **2021**,	8.4	2
19	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. *Genome Medicine*, **2021**, 13, 186	14.4	2
18	Association of microRNA-221/222 and -323-3p with rheumatoid arthritis via predictions using the human TNF transgenic mouse model. *Arthritis Research and Therapy*, **2012**, 14,	5.7	1
17	Algorithm implementation for CNV discovery using Affymetrix and Illumina SNP array data. *Methods in Molecular Biology*, **2012**, 838, 291-310	1.4	1

16	Single-cell RNA-seq reveals that glioblastoma recapitulates normal brain development		1
15	Statistical modeling, estimation, and remediation of sample index hopping in multiplexed droplet-based single-cell RNA-seq data		1
14	The genetic analysis of a founder Northern American population of European descent identifies FANCI as a candidate familial ovarian cancer risk gene		1
13	Oviduct epithelial cells constitute two developmentally distinct lineages that are spatially separated along the distal-proximal axis		1
12	Single-cell RNA sequencing reveals time- and sex-specific responses of spinal cord microglia to peripheral nerve injury and links ApoE to neuropathic pain		1
11	Maleness-on-the-Y (MoY) orchestrates male sex determination in major agricultural fruit fly pests		1
10	Candidate Markers of Olaparib Response from Genomic Data Analyses of Human Cancer Cell Lines. *Cancers*, **2021**, 13,	6.6	1
9	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA).. *BMJ Open*, **2022**, 12, e059021	3	1
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6	Regulation of Hypoxia Responses by MicroRNA Expression **2013**, 267-285		
5	Genomic reconstruction by serial mitotic recombination of yeast artificial chromosomes. *Methods in Molecular Biology*, **2006**, 349, 117-26	1.4	
4	Single-Cell Transcriptomic Profiling of De Novo and Relapsed Acute Myeloid Leukemia Identifies a Leukemic Stemness Program Shared across Diverse Phenotypes. *Blood*, **2020**, 136, 1-1	2.2	
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