

Jiannis Ragoussis

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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.. <i>Nature Communications</i> , 2022 , 13, 843	17.4	5
194	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA).. <i>BMJ Open</i> , 2022 , 12, e059021	3	1
193	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. <i>Genome Medicine</i> , 2021 , 13, 169	14.4	6
192	Lessons learned from understanding chemotherapy resistance in epithelial tubo-ovarian carcinoma from BRCA1 and BRCA2 mutation carriers. <i>Seminars in Cancer Biology</i> , 2021 , 77, 110-126	12.7	9
191	Candidate Markers of Olaparib Response from Genomic Data Analyses of Human Cancer Cell Lines. <i>Cancers</i> , 2021 , 13,	6.6	1
190	Molecular characterization of DICER1-mutated pituitary blastoma. <i>Acta Neuropathologica</i> , 2021 , 141, 929-944	14.3	6
189	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021 , 12, 1749	17.4	7
188	Nanopore long-read RNA-seq and absolute quantification delineate transcription dynamics in early embryo development of an insect pest. <i>Scientific Reports</i> , 2021 , 11, 7878	4.9	3
187	Extraction of nuclei from archived postmortem tissues for single-nucleus sequencing applications. <i>Nature Protocols</i> , 2021 , 16, 2788-2801	18.8	3
186	Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3953-3971	8.3	5
185	A coordinated progression of progenitor cell states initiates urinary tract development. <i>Nature Communications</i> , 2021 , 12, 2627	17.4	5
184	Modeling High-Grade Serous Ovarian Carcinoma Using a Combination of Fallopian Tube Electroporation and CRISPR-Cas9-Mediated Genome Editing. <i>Cancer Research</i> , 2021 , 81, 5147-5160	10.1	3
183	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	25
182	The genetic landscape of choroid plexus tumors in children and adults. <i>Neuro-Oncology</i> , 2021 , 23, 650-660		3
181	Whole-exome sequencing of non-BRCA1/BRCA2 mutation carrier cases at high-risk for hereditary breast/ovarian cancer. <i>Human Mutation</i> , 2021 , 42, 290-299	4.7	9
180	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. <i>Nature Communications</i> , 2021 , 12, 491	17.4	7
179	Haplotype-resolved de novo assembly of the Vero cell line genome. <i>Npj Vaccines</i> , 2021 , 6, 106	9.5	5

178	A chromosome-anchored genome assembly for Lake Trout (<i>Salvelinus namaycush</i>). <i>Molecular Ecology Resources</i> , 2021 ,	8.4	2
177	Oviduct epithelial cells constitute two developmentally distinct lineages that are spatially separated along the distal-proximal axis. <i>Cell Reports</i> , 2021 , 36, 109677	10.6	5
176	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. <i>Neuro-Oncology</i> , 2021 , 23, 1470-1480	1	10
175	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. <i>Methods in Molecular Biology</i> , 2021 , 2381, 285-303	1.4	
174	Effects of the Sex Chromosome Complement, XX, XO, or XY, on the Transcriptome and Development of Mouse Oocytes During Follicular Growth.. <i>Frontiers in Genetics</i> , 2021 , 12, 792604	4.5	1
173	A functionally impaired missense variant identified in French Canadian families implicates FANCI as a candidate ovarian cancer-predisposing gene. <i>Genome Medicine</i> , 2021 , 13, 186	14.4	2
172	Single-cell analysis of childhood leukemia reveals a link between developmental states and ribosomal protein expression as a source of intra-individual heterogeneity. <i>Scientific Reports</i> , 2020 , 10, 8079	4.9	9
171	Model-based analysis of sample index hopping reveals its widespread artifacts in multiplexed single-cell RNA-sequencing. <i>Nature Communications</i> , 2020 , 11, 2704	17.4	9
170	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. <i>Nature Communications</i> , 2020 , 11, 3406	17.4	88
169	Methodologies for Transcript Profiling Using Long-Read Technologies. <i>Frontiers in Genetics</i> , 2020 , 11, 606	4.5	24
168	Developmental trajectory of oligodendrocyte progenitor cells in the human brain revealed by single cell RNA sequencing. <i>Glia</i> , 2020 , 68, 1291-1303	9	22
167	Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. <i>Nature Neuroscience</i> , 2020 , 23, 771-781	25.5	91
166	Single-Cell Transcriptomic Profiling of De Novo and Relapsed Acute Myeloid Leukemia Identifies a Leukemic Stemness Program Shared across Diverse Phenotypes. <i>Blood</i> , 2020 , 136, 1-1	2.2	
165	DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. <i>Journal of Clinical Investigation</i> , 2020 , 130, 1479-1490	15.9	15
164	Integration of Transcriptome and Metabolome Provides Unique Insights to Pathways Associated With Obese Breast Cancer Patients. <i>Frontiers in Oncology</i> , 2020 , 10, 804	5.3	13
163	MAFG-driven astrocytes promote CNS inflammation. <i>Nature</i> , 2020 , 578, 593-599	50.4	125
162	Failure to replicate the association of rare loss-of-function variants in type I IFN immunity genes with severe COVID-19 2020 ,		5
161	Metagenomic analysis of planktonic riverine microbial consortia using nanopore sequencing reveals insight into river microbe taxonomy and function. <i>GigaScience</i> , 2020 , 9,	7.6	11

160	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. <i>PLoS ONE</i> , 2020 , 15, e0236187	3.7	6
159	Regulation of cellular sterol homeostasis by the oxygen responsive noncoding RNA lincNORS. <i>Nature Communications</i> , 2020 , 11, 4755	17.4	7
158	A Distributed Whole Genome Sequencing Benchmark Study. <i>Frontiers in Genetics</i> , 2020 , 11, 612515	4.5	2
157	De novo assembly of the olive fruit fly (<i>Bactrocera oleae</i>) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. <i>BMC Genomics</i> , 2020 , 21, 259	4.5	10
156	() orchestrates male sex determination in major agricultural fruit fly pests. <i>Science</i> , 2019 , 365, 1457-1460	33.3	47
155	Gene Ontology and Expression Studies of Strigolactone Analogues on a Hepatocellular Carcinoma Cell Line. <i>Analytical Cellular Pathology</i> , 2019 , 2019, 1598182	3.4	2
154	Next-generation HLA typing of 382 International Histocompatibility Working Group reference B-lymphoblastoid cell lines: Report from the 17th International HLA and Immunogenetics Workshop. <i>Human Immunology</i> , 2019 , 80, 449-460	2.3	13
153	Quality control project of NGS HLA genotyping for the 17th International HLA and Immunogenetics Workshop. <i>Human Immunology</i> , 2019 , 80, 228-236	2.3	19
152	Analysis of head and neck carcinoma progression reveals novel and relevant stage-specific changes associated with immortalisation and malignancy. <i>Scientific Reports</i> , 2019 , 9, 11992	4.9	13
151	Exome Sequencing in and -Negative Greek Families Identifies and as Candidate Risk Genes for Hereditary Breast Cancer. <i>Frontiers in Genetics</i> , 2019 , 10, 1005	4.5	7
150	Genome-wide analysis of androgen receptor binding and transcriptomic analysis in mesenchymal subsets during prostate development. <i>DMM Disease Models and Mechanisms</i> , 2019 , 12,	4.1	4
149	Stalled developmental programs at the root of pediatric brain tumors. <i>Nature Genetics</i> , 2019 , 51, 1702-1713	16.3	58
148	Recurrent noncoding U1'snRNA mutations drive cryptic splicing in SHH medulloblastoma. <i>Nature</i> , 2019 , 574, 707-711	50.4	78
147	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , 2018 , 5, e333-e345	14.6	38
146	Regulators of Asymmetric Cell Division in Breast Cancer. <i>Trends in Cancer</i> , 2018 , 4, 798-801	12.5	2
145	Global long non-coding RNA expression in the rostral anterior cingulate cortex of depressed suicides. <i>Translational Psychiatry</i> , 2018 , 8, 224	8.6	30
144	Current and Future Methods for mRNA Analysis: A Drive Toward Single Molecule Sequencing. <i>Methods in Molecular Biology</i> , 2018 , 1783, 209-241	1.4	22
143	Transcript Profiling Using Long-Read Sequencing Technologies. <i>Methods in Molecular Biology</i> , 2018 , 1783, 121-147	1.4	24

142	Sequencing of DICER1 in sarcomas identifies biallelic somatic DICER1 mutations in an adult-onset embryonal rhabdomyosarcoma. <i>British Journal of Cancer</i> , 2017 , 116, 1621-1626	8.7	24
141	A Targetable EGFR-Dependent Tumor-Initiating Program in Breast Cancer. <i>Cell Reports</i> , 2017 , 21, 1140-1148	4.9	45
140	Update on hypoxia-inducible factors and hydroxylases in oxygen regulatory pathways: from physiology to therapeutics. <i>Hypoxia (Auckland, N Z)</i> , 2017 , 5, 11-20	2.1	17
139	RNA Sequencing Reveals that Kaposi Sarcoma-Associated Herpesvirus Infection Mimics Hypoxia Gene Expression Signature. <i>PLoS Pathogens</i> , 2017 , 13, e1006143	7.6	21
138	The empress of subterfuge: cancer of the fallopian tube presenting with malapropism. <i>Lancet, The</i> , 2017 , 390, 1003-1004	4.0	
137	H3.1 K36M mutation in a congenital-onset soft tissue neoplasm. <i>Pediatric Blood and Cancer</i> , 2017 , 64, e26633	3	3
136	Identification of genes expressed in a mesenchymal subset regulating prostate organogenesis using tissue and single cell transcriptomics. <i>Scientific Reports</i> , 2017 , 7, 16385	4.9	7
135	A multidimensional integration analysis reveals potential bridging targets in the process of colorectal cancer liver metastasis. <i>PLoS ONE</i> , 2017 , 12, e0178760	3.7	6
134	Survival of metastatic melanoma patients after dendritic cell vaccination correlates with expression of leukocyte phosphatidylethanolamine-binding protein 1/Raf kinase inhibitory protein. <i>Oncotarget</i> , 2017 , 8, 67439-67456	3.3	12
133	High-sensitivity sequencing reveals multi-organ somatic mosaicism causing DICER1 syndrome. <i>Journal of Medical Genetics</i> , 2016 , 53, 43-52	5.8	51
132	Weighted gene co-expression network analysis of colorectal cancer liver metastasis genome sequencing data and screening of anti-metastasis drugs. <i>International Journal of Oncology</i> , 2016 , 49, 1108-18	4.4	19
131	Deep Sequencing Reveals Spatially Distributed Distinct Hot Spot Mutations in DICER1-Related Multinodular Goiter. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016 , 101, 3637-3645	5.6	22
130	Benchmarking of the Oxford Nanopore MinION sequencing for quantitative and qualitative assessment of cDNA populations. <i>Scientific Reports</i> , 2016 , 6, 31602	4.9	98
129	Live single-cell laser tag. <i>Nature Communications</i> , 2016 , 7, 11636	17.4	14
128	Pattern recognition receptor mediated downregulation of microRNA-650 fine-tunes MxA expression in dendritic cells infected with influenza A virus. <i>European Journal of Immunology</i> , 2016 , 46, 167-77	6.1	10
127	Tumor hypoxia induces nuclear paraspeckle formation through HIF-2 α -dependent transcriptional activation of NEAT1 leading to cancer cell survival. <i>Oncogene</i> , 2015 , 34, 4482-90	9.2	164
126	De novo point mutations in patients diagnosed with ataxic cerebral palsy. <i>Brain</i> , 2015 , 138, 1817-32	11.2	101
125	Next-Generation Sequencing Analysis Reveals Differential Expression Profiles of MiRNA-mRNA Target Pairs in KSHV-Infected Cells. <i>PLoS ONE</i> , 2015 , 10, e0126439	3.7	16

124	Biomarker discovery: quantification of microRNAs and other small non-coding RNAs using next generation sequencing. <i>BMC Medical Genomics</i> , 2015 , 8, 35	3.7	56
123	Estrogen receptor- β directly regulates the hypoxia-inducible factor 1 pathway associated with antiestrogen response in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 15172-7	11.5	74
122	Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. <i>Molecular Cancer</i> , 2014 , 13, 28	42.1	104
121	Methods of quantifying microRNAs for hypoxia research: classic and next generation. <i>Antioxidants and Redox Signaling</i> , 2014 , 21, 1239-48	8.4	4
120	Microarray-based ultra-high resolution discovery of genomic deletion mutations. <i>BMC Genomics</i> , 2014 , 15, 224	4.5	4
119	Microarray-based optimization to detect genomic deletion mutations. <i>Genomics Data</i> , 2014 , 2, 53-54		4
118	Extensive regulation of the non-coding transcriptome by hypoxia: role of HIF in releasing paused RNAPol2. <i>EMBO Reports</i> , 2014 , 15, 70-6	6.5	125
117	The molecular biology of the olive fly comes of age. <i>BMC Genetics</i> , 2014 , 15 Suppl 2, S8	2.6	13
116	Intestinal myofibroblast-specific Tpl2-Cox-2-PGE2 pathway links innate sensing to epithelial homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4658-67	11.5	52
115	IRF5:RelA interaction targets inflammatory genes in macrophages. <i>Cell Reports</i> , 2014 , 8, 1308-17	10.6	70
114	Olive fly transcriptomics analysis implicates energy metabolism genes in spinosad resistance. <i>BMC Genomics</i> , 2014 , 15, 714	4.5	20
113	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in Arabidopsis. <i>EMBO Journal</i> , 2013 , 32, 914-914	13	5
112	Next-generation sequencing (NGS) as a diagnostic tool for retinal degeneration reveals a much higher detection rate in early-onset disease. <i>European Journal of Human Genetics</i> , 2013 , 21, 274-80	5.3	107
111	miR-210 is a target of hypoxia-inducible factors 1 and 2 in renal cancer, regulates ISCU and correlates with good prognosis. <i>British Journal of Cancer</i> , 2013 , 108, 1133-42	8.7	112
110	MicroRNA expression profile in head and neck cancer: HOX-cluster embedded microRNA-196a and microRNA-10b dysregulation implicated in cell proliferation. <i>BMC Cancer</i> , 2013 , 13, 533	4.8	58
109	Next generation sequencing for molecular diagnosis of neurological disorders using ataxias as a model. <i>Brain</i> , 2013 , 136, 3106-18	11.2	128
108	High-resolution analysis of cis-acting regulatory networks at the β globin locus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120361	5.8	11
107	GATA-1 genome-wide occupancy associates with distinct epigenetic profiles in mouse fetal liver erythropoiesis. <i>Nucleic Acids Research</i> , 2013 , 41, 4938-48	20.1	19

106	Smooth muscle cells differentiated from reprogrammed embryonic lung fibroblasts through DKK3 signaling are potent for tissue engineering of vascular grafts. <i>Circulation Research</i> , 2013 , 112, 1433-43	15.7	63
105	Cellular interference in craniofrontonasal syndrome: males mosaic for mutations in the X-linked EFNB1 gene are more severely affected than true hemizygotes. <i>Human Molecular Genetics</i> , 2013 , 22, 1654-62	5.6	50
104	Cross-species analysis reveals evolving and conserved features of the nuclear factor B (NF- B) proteins. <i>Journal of Biological Chemistry</i> , 2013 , 288, 11546-54	5.4	13
103	Regulation of Hypoxia Responses by MicroRNA Expression 2013 , 267-285		
102	TGF- β /Smad2/3 signaling directly regulates several miRNAs in mouse ES cells and early embryos. <i>PLoS ONE</i> , 2013 , 8, e55186	3.7	12
101	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in Arabidopsis. <i>EMBO Journal</i> , 2012 , 31, 4359-70	13	120
100	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. <i>Human Genetics</i> , 2012 , 131, 565-79	6.3	150
99	Direct reprogramming of fibroblasts into endothelial cells capable of angiogenesis and reendothelialization in tissue-engineered vessels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13793-8	11.5	194
98	Association of microRNA-221/222 and -323-3p with rheumatoid arthritis via predictions using the human TNF transgenic mouse model. <i>Arthritis Research and Therapy</i> , 2012 , 14,	5.7	1
97	Polycomb associates genome-wide with a specific RNA polymerase II variant, and regulates metabolic genes in ESCs. <i>Cell Stem Cell</i> , 2012 , 10, 157-70	18	221
96	Algorithm implementation for CNV discovery using Affymetrix and Illumina SNP array data. <i>Methods in Molecular Biology</i> , 2012 , 838, 291-310	1.4	1
95	Identification of microRNA-221/222 and microRNA-323-3p association with rheumatoid arthritis via predictions using the human tumour necrosis factor transgenic mouse model. <i>Annals of the Rheumatic Diseases</i> , 2012 , 71, 1716-23	2.4	83
94	Three-dimensional hydrogel structures as optical sensor arrays, for the detection of specific DNA sequences. <i>Analytical Biochemistry</i> , 2012 , 421, 1-8	3.1	13
93	Recessive mutations in SPTBN2 implicate β III spectrin in both cognitive and motor development. <i>PLoS Genetics</i> , 2012 , 8, e1003074	6	74
92	Preparation of high-quality next-generation sequencing libraries from picogram quantities of target DNA. <i>Genome Research</i> , 2012 , 22, 125-33	9.7	45
91	Individual common variants exert weak effects on the risk for autism spectrum disorders. <i>Human Molecular Genetics</i> , 2012 , 21, 4781-92	5.6	279
90	Genome-wide analysis of mutations in mutant lineages selected following fast-neutron irradiation mutagenesis of Arabidopsis thaliana. <i>Genome Research</i> , 2012 , 22, 1306-15	9.7	87
89	Principles of dimer-specific gene regulation revealed by a comprehensive characterization of NF- B family DNA binding. <i>Nature Immunology</i> , 2011 , 13, 95-102	19.1	143

88	Direct targeting of Sec23a by miR-200s influences cancer cell secretome and promotes metastatic colonization. <i>Nature Medicine</i> , 2011 , 17, 1101-8	50.5	486
87	Animal models for arthritis: innovative tools for prevention and treatment. <i>Annals of the Rheumatic Diseases</i> , 2011 , 70, 1357-62	2.4	78
86	Extensive characterization of NF- κ B binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. <i>Genome Biology</i> , 2011 , 12, R70	18.3	110
85	High-resolution genome-wide mapping of HIF-binding sites by CHIP-seq. <i>Blood</i> , 2011 , 117, e207-17	2.2	484
84	The small-nucleolar RNAs commonly used for microRNA normalisation correlate with tumour pathology and prognosis. <i>British Journal of Cancer</i> , 2011 , 104, 1168-77	8.7	217
83	Regenerant Arabidopsis lineages display a distinct genome-wide spectrum of mutations conferring variant phenotypes. <i>Current Biology</i> , 2011 , 21, 1385-90	6.3	65
82	microRNA-associated progression pathways and potential therapeutic targets identified by integrated mRNA and microRNA expression profiling in breast cancer. <i>Cancer Research</i> , 2011 , 71, 5635-45	10.1	253
81	Foxp2 regulates gene networks implicated in neurite outgrowth in the developing brain. <i>PLoS Genetics</i> , 2011 , 7, e1002145	6	198
80	Substantial histone reduction modulates genomewide nucleosomal occupancy and global transcriptional output. <i>PLoS Biology</i> , 2011 , 9, e1001086	9.7	140
79	The use of genome-wide eQTL associations in lymphoblastoid cell lines to identify novel genetic pathways involved in complex traits. <i>PLoS ONE</i> , 2011 , 6, e22070	3.7	35
78	An oncogenic role of eIF3e/INT6 in human breast cancer. <i>Oncogene</i> , 2010 , 29, 4080-9	9.2	41
77	Functional impact of global rare copy number variation in autism spectrum disorders. <i>Nature</i> , 2010 , 466, 368-72	50.4	1499
76	A large fraction of extragenic RNA pol II transcription sites overlap enhancers. <i>PLoS Biology</i> , 2010 , 8, e1000384	9.7	617
75	MicroRNA-210 regulates mitochondrial free radical response to hypoxia and krebs cycle in cancer cells by targeting iron sulfur cluster protein ISCU. <i>PLoS ONE</i> , 2010 , 5, e10345	3.7	243
74	A genome-wide scan for common alleles affecting risk for autism. <i>Human Molecular Genetics</i> , 2010 , 19, 4072-82	5.6	443
73	The histone demethylase JMJD2B is regulated by estrogen receptor alpha and hypoxia, and is a key mediator of estrogen induced growth. <i>Cancer Research</i> , 2010 , 70, 6456-66	10.1	141
72	Characterization of a family with rare deletions in CNTNAP5 and DOCK4 suggests novel risk loci for autism and dyslexia. <i>Biological Psychiatry</i> , 2010 , 68, 320-8	7.9	103
71	Association of the aromatase gene with Alzheimer's disease in women. <i>Neuroscience Letters</i> , 2010 , 468, 202-6	3.3	31

70	ATR-X syndrome protein targets tandem repeats and influences allele-specific expression in a size-dependent manner. <i>Cell</i> , 2010 , 143, 367-78	56.2	297
69	The role of hypoxia regulated microRNAs in cancer. <i>Current Topics in Microbiology and Immunology</i> , 2010 , 345, 47-70	3.3	33
68	A statistical approach for detecting genomic aberrations in heterogeneous tumor samples from single nucleotide polymorphism genotyping data. <i>Genome Biology</i> , 2010 , 11, R92	18.3	111
67	hsa-mir-210 is a marker of tumor hypoxia and a prognostic factor in head and neck cancer. <i>Cancer</i> , 2010 , 116, 2148-58	6.4	193
66	Identification and characterization of enhancers controlling the inflammatory gene expression program in macrophages. <i>Immunity</i> , 2010 , 32, 317-28	32.3	497
65	Chemokine gene expression in lung CD8 T cells correlates with protective immunity in mice immunized intra-nasally with Adenovirus-85A. <i>BMC Medical Genomics</i> , 2010 , 3, 46	3.7	10
64	Altered intra-nuclear organisation of heterochromatin and genes in ICF syndrome. <i>PLoS ONE</i> , 2010 , 5, e11364	3.7	22
63	Genome-wide association of hypoxia-inducible factor (HIF)-1alpha and HIF-2alpha DNA binding with expression profiling of hypoxia-inducible transcripts. <i>Journal of Biological Chemistry</i> , 2009 , 284, 16767-16775	5.4	406
62	Phase I/II trial of bevacizumab and radiotherapy for locally advanced inoperable colorectal cancer: vasculature-independent radiosensitizing effect of bevacizumab. <i>Clinical Cancer Research</i> , 2009 , 15, 7069-78	12.8	46
61	Comparative analysis of methods for gene transcription profiling data derived from different microarray technologies in rat and mouse models of diabetes. <i>BMC Genomics</i> , 2009 , 10, 63	4.5	15
60	Transcriptional signature of human adipose tissue-derived stem cells (hASCs) preconditioned for chondrogenesis in hypoxic conditions. <i>Experimental Cell Research</i> , 2009 , 315, 1937-52	4.2	37
59	Seeing clearly: the dominant and recessive nature of FOXE3 in eye developmental anomalies. <i>Human Mutation</i> , 2009 , 30, 1378-86	4.7	78
58	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. <i>BMC Medical Genomics</i> , 2009 , 2, 54	3.7	96
57	A 15q13.3 microdeletion segregating with autism. <i>European Journal of Human Genetics</i> , 2009 , 17, 687-92	5.3	114
56	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. <i>EMBO Journal</i> , 2009 , 28, 3400-12	13	34
55	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009 , 41, 657-65	36.3	297
54	CMIP and ATP2C2 modulate phonological short-term memory in language impairment. <i>American Journal of Human Genetics</i> , 2009 , 85, 264-72	11	142
53	CpG methylation profiling in VHL related and VHL unrelated renal cell carcinoma. <i>Molecular Cancer</i> , 2009 , 8, 31	42.1	56

52	Analysis of FGGY as a risk factor for sporadic amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders</i> , 2009 , 10, 441-7		13
51	Genotyping technologies for genetic research. <i>Annual Review of Genomics and Human Genetics</i> , 2009 , 10, 117-33	9.7	164
50	Comparing CNV detection methods for SNP arrays. <i>Briefings in Functional Genomics & Proteomics</i> , 2009 , 8, 353-66		150
49	Variations within oxygen-regulated gene expression in humans. <i>Journal of Applied Physiology</i> , 2009 , 106, 212-20	3.7	31
48	MicroRNA-10b and breast cancer metastasis. <i>Nature</i> , 2008 , 455, E8-9; author reply E9	50.4	113
47	A commonly occurring polymorphism upstream of the estrogen receptor alpha alters transcription and is associated with increased HDL. <i>Atherosclerosis</i> , 2008 , 199, 354-61	3.1	5
46	GenoSNP: a variational Bayes within-sample SNP genotyping algorithm that does not require a reference population. <i>Bioinformatics</i> , 2008 , 24, 2209-14	7.2	56
45	hsa-miR-210 is induced by hypoxia and is an independent prognostic factor in breast cancer. <i>Clinical Cancer Research</i> , 2008 , 14, 1340-8	12.9	555
44	VACTERL/caudal regression/Currarino syndrome-like malformations in mice with mutation in the proprotein convertase Pcsk5. <i>Genes and Development</i> , 2008 , 22, 1465-77	12.6	99
43	Association of the KIAA0319 dyslexia susceptibility gene with reading skills in the general population. <i>American Journal of Psychiatry</i> , 2008 , 165, 1576-84	11.9	104
42	BeadArray-based genotyping. <i>Methods in Molecular Biology</i> , 2008 , 439, 53-74	1.4	12
41	Evaluating the effects of imputation on the power, coverage, and cost efficiency of genome-wide SNP platforms. <i>American Journal of Human Genetics</i> , 2008 , 83, 112-9	11	80
40	Analysis of DNA Methylation at the Human Alpha Globin Cluster during Hematopoiesis.. <i>Blood</i> , 2008 , 112, 1861-1861	2.2	
39	Functional conservation of Rel binding sites in drosophilid genomes. <i>Genome Research</i> , 2007 , 17, 1327-35.7		13
38	QuantiSNP: an Objective Bayes Hidden-Markov Model to detect and accurately map copy number variation using SNP genotyping data. <i>Nucleic Acids Research</i> , 2007 , 35, 2013-25	20.1	462
37	Accuracy and reproducibility of protein-DNA microarray technology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2007 , 104, 87-110	1.7	9
36	Quantitative profiling of protein-DNA binding on microarrays. <i>Methods in Molecular Biology</i> , 2006 , 338, 261-80	1.4	4
35	Genomic reconstruction by serial mitotic recombination of yeast artificial chromosomes. <i>Methods in Molecular Biology</i> , 2006 , 349, 117-26	1.4	

34	Matrix-assisted laser desorption/ionisation, time-of-flight mass spectrometry in genomics research. <i>PLoS Genetics</i> , 2006 , 2, e100	6	92
33	The leukocyte receptor complex in chicken is characterized by massive expansion and diversification of immunoglobulin-like Loci. <i>PLoS Genetics</i> , 2006 , 2, e73	6	58
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9	Single-cell RNA-seq reveals that glioblastoma recapitulates normal brain development		1
8	Statistical modeling, estimation, and remediation of sample index hopping in multiplexed droplet-based single-cell RNA-seq data		1
7	The genetic analysis of a founder Northern American population of European descent identifies FANCI as a candidate familial ovarian cancer risk gene		1
6	Oviduct epithelial cells constitute two developmentally distinct lineages that are spatially separated along the distal-proximal axis		1
5	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
4	Single-nucleus RNA sequencing shows convergent evidence from different cell types for altered synaptic plasticity in major depressive disorder		5
3	Transcriptome landscape of the developing olive fruit fly embryo delineated by Oxford Nanopore long-read RNA-Seq		5
2	De novo genome assembly of the olive fruit fly (<i>Bactrocera oleae</i>) developed through a combination of linked-reads and long-read technologies		2
1	Maleness-on-the-Y (MoY) orchestrates male sex determination in major agricultural fruit fly pests		1