Juan Ramn Gonzlez

List of Publications by Year in Descending Order

156 papers	10,943 citations	42 h-index	103 g-index
172 ext. papers	13,104 ext. citations	6.8 avg, IF	5.21 L-index

#	Paper	IF	Citations
156	Meta-analysis of epigenome-wide association studies in newborns and children show widespread sex differences in blood DNA methylation. *Mutation Research - Reviews in Mutation Research*, **2022**, 789, 108415	7	2
155	The early-life exposome modulates the effect of polymorphic inversions on DNA methylation.. *Communications Biology*, **2022**, 5, 455	6.7	0
154	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. *Molecular Psychiatry*, **2021**, 26, 2056-2069	15.1	25
153	Advancing tools for human early lifecourse exposome research and translation (ATHLETE): Project overview.. *Environmental Epidemiology*, **2021**, 5, e166	0.2	2
152	methylclock: a Bioconductor package to estimate DNA methylation age. *Bioinformatics*, **2021**, 37, 1759-1760	7.6	9
151	Orchestrating privacy-protected big data analyses of data from different resources with R and DataSHIELD. *PLoS Computational Biology*, **2021**, 17, e1008880	5	5
150	Urinary metabolite quantitative trait loci in children and their interaction with dietary factors. *Human Molecular Genetics*, **2021**, 29, 3830-3844	5.6	1
149	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. *Molecular Psychiatry*, **2021**, 26, 2148-2162	15.1	7
148	MLIP genotype as a predictor of pharmacological response in primary open-angle glaucoma and ocular hypertension. *Scientific Reports*, **2021**, 11, 1583	4.9	0
147	Early-life environmental exposure determinants of child behavior in Europe: A longitudinal, population-based study. *Environment International*, **2021**, 153, 106523	12.9	15
146	Performance of approaches relying on multidimensional intermediary data to decipher causal relationships between the exposome and health: A simulation study under various causal structures. *Environment International*, **2021**, 153, 106509	12.9	1
145	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. *Nature Genetics*, **2021**, 53, 1311-1321	36.3	27
144	The early-life exposome and epigenetic age acceleration in children. *Environment International*, **2021**, 155, 106683	12.9	5
143	Polymorphic Inversions Underlie the Shared Genetic Susceptibility of Obesity-Related Diseases. *American Journal of Human Genetics*, **2020**, 106, 846-858	11	3
142	Using methylome data to inform exposome-health association studies: An application to the identification of environmental drivers of child body mass index. *Environment International*, **2020**, 138, 105622	12.9	10
141	Association between the pregnancy exposome and fetal growth. *International Journal of Epidemiology*, **2020**, 49, 572-586	7.8	16
140	Extreme downregulation of chromosome Y and Alzheimer's disease in men. *Neurobiology of Aging*, **2020**, 90, 150.e1-150.e4	5.6	9

139	Extreme Downregulation of Chromosome Y and Cancer Risk in Men. *Journal of the National Cancer Institute*, **2020**, 112, 913-920	9.7	20
138	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. *Allergy: European Journal of Allergy and Clinical Immunology*, **2020**, 75, 3248-3260	9.3	27
137	MADloy: robust detection of mosaic loss of chromosome Y from genotype-array-intensity data. *BMC Bioinformatics*, **2020**, 21, 533	3.6	1
136	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. *Translational Psychiatry*, **2020**, 10, 398	8.6	17
135	Female-specific risk of Alzheimer's disease is associated with tau phosphorylation processes: A transcriptome-wide interaction analysis. *Neurobiology of Aging*, **2020**, 96, 104-108	5.6	5
134	In utero and childhood exposure to tobacco smoke and multi-layer molecular signatures in children. *BMC Medicine*, **2020**, 18, 243	11.4	6
133	Identifying chromosomal subpopulations based on their recombination histories advances the study of the genetic basis of phenotypic traits. *Genome Research*, **2020**, 30, 1802-1814	9.7	2
132	Independent Multiple Factor Association Analysis for Multiblock Data in Imaging Genetics. *Neuroinformatics*, **2019**, 17, 583-592	3.2	2
131	Comprehensive study of the exposome and omic data using rexposome Bioconductor Packages. *Bioinformatics*, **2019**, 35, 5344-5345	7.2	11
130	scoreInvHap: Inversion genotyping for genome-wide association studies. *PLoS Genetics*, **2019**, 15, e1008203	6	7
129	Common polymorphic inversions at 17q21.31 and 8p23.1 associate with cancer prognosis. *Human Genomics*, **2019**, 13, 57	6.8	3
128	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nature Genetics*, **2019**, 51, 245-257	36.3	259
127	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. *Nature Communications*, **2018**, 9, 321	17.4	50
126	CTDquerier: a bioconductor R package for Comparative Toxicogenomics DatabaseTM data extraction, visualization and enrichment of environmental and toxicological studies. *Bioinformatics*, **2018**, 34, 3235-3237	7.2	5
125	Characterization of Proteins in Plasma-Derived Exosomes From Malaria-Infected Liver-Chimeric Humanized Mice. *Frontiers in Microbiology*, **2018**, 9, 1271	5.7	20
124	A systemic approach to identify signaling pathways activated during short-term exposure to traffic-related urban air pollution from human blood. *Environmental Science and Pollution Research*, **2018**, 25, 29572-29583	5.1	1
123	Sparse multiple factor analysis to integrate genetic data, neuroimaging features, and attention-deficit/hyperactivity disorder domains. *International Journal of Methods in Psychiatric Research*, **2018**, 27, e1738	4.3	5
122	The first in vivo multiparametric comparison of different radiation exposure biomarkers in human blood. *PLoS ONE*, **2018**, 13, e0193412	3.7	29

121	Circulating miRNAs, isomiRs and small RNA clusters in human plasma and breast milk. *PLoS ONE*, **2018**, 13, e0193527	3.7	32
120	When pitch adds to volume: coregulation of transcript diversity predicts gene function. *BMC Genomics*, **2018**, 19, 926	4.5	
119	Variability of urinary concentrations of non-persistent chemicals in pregnant women and school-aged children. *Environment International*, **2018**, 121, 561-573	12.9	61
118	In-utero and childhood chemical exposome in six European mother-child cohorts. *Environment International*, **2018**, 121, 751-763	12.9	79
117	Human Early Life Exposome (HELIX) study: a European population-based exposome cohort. *BMJ Open*, **2018**, 8, e021311	3	88
116	Strategies for integrated analysis in imaging genetics studies. *Neuroscience and Biobehavioral Reviews*, **2018**, 93, 57-70	9	5
115	APOE and MS4A6A interact with GnRH signaling in Alzheimer's disease: Enrichment of epistatic effects. *Alzheimer's and Dementia*, **2017**, 13, 493-497	1.2	5
114	Polymorphisms in the SNRPN gene are associated with obesity susceptibility in a Spanish population. *Journal of Gene Medicine*, **2017**, 19, e2956	3.5	1
113	MultiDataSet: an R package for encapsulating multiple data sets with application to omic data integration. *BMC Bioinformatics*, **2017**, 18, 36	3.6	18
112	Imaging genetics in attention-deficit/hyperactivity disorder and related neurodevelopmental domains: state of the art. *Brain Imaging and Behavior*, **2017**, 11, 1922-1931	4.1	7
111	The acute effects of ultraviolet radiation on the blood transcriptome are independent of plasma 25OHD. *Environmental Research*, **2017**, 159, 239-248	7.9	9
110	Computational analysis of multimorbidity between asthma, eczema and rhinitis. *PLoS ONE*, **2017**, 12, e0179125	3.7	26
109	Novel genes involved in severe early-onset obesity revealed by rare copy number and sequence variants. *PLoS Genetics*, **2017**, 13, e1006657	6	22
108	A systematic comparison of statistical methods to detect interactions in exposome-health associations. *Environmental Health*, **2017**, 16, 74	6	32
107	Redundancy analysis allows improved detection of methylation changes in large genomic regions. *BMC Bioinformatics*, **2017**, 18, 553	3.6	7
106	Genes Interacting with Occupational Exposures to Low Molecular Weight Agents and Irritants on Adult-Onset Asthma in Three European Studies. *Environmental Health Perspectives*, **2017**, 125, 207-214	8.4	17
105	psygenet2r: a R/Bioconductor package for the analysis of psychiatric disease genes. *Bioinformatics*, **2017**, 33, 4004-4006	7.2	2
104	Detectable clonal mosaicism in blood as a biomarker of cancer risk in Fanconi anemia. *Blood Advances*, **2017**, 1, 319-329	7.8	13

103	Exploration of large, rare copy number variants associated with psychiatric and neurodevelopmental disorders in individuals with anorexia nervosa. *Psychiatric Genetics*, **2017**, 27, 152-158	2.9	11
102	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. *Sleep*, **2016**, 39, 1859-1869	1.1	22
101	Efficient and Powerful Method for Combining P-Values in Genome-Wide Association Studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2016**, 13, 1100-1106	3	3
100	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
99	Combined Treatment With Environmental Enrichment and (-)-Epigallocatechin-3-Gallate Ameliorates Learning Deficits and Hippocampal Alterations in a Mouse Model of Down Syndrome. *ENeuro*, **2016**, 3,	3.9	26
98	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. *PLoS ONE*, **2016**, 11, e0157739	3.7	0
97	A Systematic Comparison of Linear Regression-Based Statistical Methods to Assess Exposome-Health Associations. *Environmental Health Perspectives*, **2016**, 124, 1848-1856	8.4	111
96	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. *American Journal of Human Genetics*, **2016**, 98, 680-96	11	489
95	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
94	The Pregnancy Exposome: Multiple Environmental Exposures in the INMA-Sabadell Birth Cohort. *Environmental Science & Technology*, **2015**, 49, 10632-41	10.3	66
93	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. *Nature Genetics*, **2015**, 47, 1449-1456	36.3	329
92	A novel common variant in DCST2 is associated with length in early life and height in adulthood. *Human Molecular Genetics*, **2015**, 24, 1155-68	5.6	77
91	A Decision Aid to Support Informed Choices for Patients Recently Diagnosed With Prostate Cancer: A Randomized Controlled Trial. *Cancer Nursing*, **2015**, 38, E42-50	2.6	37
90	Interaction association analysis of imputed SNPs in case-control and follow-up studies. *Genetic Epidemiology*, **2015**, 39, 185-96	2.6	
89	Principal Component Analysis of the Effects of Environmental Enrichment and (-)-epigallocatechin-3-gallate on Age-Associated Learning Deficits in a Mouse Model of Down Syndrome. *Frontiers in Behavioral Neuroscience*, **2015**, 9, 330	3.5	32
88	Genetic polymorphisms associated with increased risk of developing chronic myelogenous leukemia. *Oncotarget*, **2015**, 6, 36269-77	3.3	23
87	DNA methylation levels and long-term trihalomethane exposure in drinking water: an epigenome-wide association study. *Epigenetics*, **2015**, 10, 650-61	5.7	19
86	Following the footprints of polymorphic inversions on SNP data: from detection to association tests. *Nucleic Acids Research*, **2015**, 43, e53	20.1	27

85	affy2sv: an R package to pre-process Affymetrix CytoScan HD and 750K arrays for SNP, CNV, inversion and mosaicism calling. *BMC Bioinformatics*, **2015**, 16, 167	3.6	2
84	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
83	A common 16p11.2 inversion underlies the joint susceptibility to asthma and obesity. *American Journal of Human Genetics*, **2014**, 94, 361-72	11	46
82	The human early-life exposome (HELIX): project rationale and design. *Environmental Health Perspectives*, **2014**, 122, 535-44	8.4	219
81	Genetic heterogeneity of asthma phenotypes identified by a clustering approach. *European Respiratory Journal*, **2014**, 43, 439-52	13.6	43
80	Worldwide population distribution of the common LCE3C-LCE3B deletion associated with psoriasis and other autoimmune disorders. *BMC Genomics*, **2013**, 14, 261	4.5	8
79	A flexible count data model to fit the wide diversity of expression profiles arising from extensively replicated RNA-seq experiments. *BMC Bioinformatics*, **2013**, 14, 254	3.6	41
78	Genetic factors conferring an increased susceptibility to develop Crohn's disease also influence disease phenotype: results from the IBDchip European Project. *Gut*, **2013**, 62, 1556-65	19.2	184
77	Genome-wide association study of body mass index in 23 000 individuals with and without asthma. *Clinical and Experimental Allergy*, **2013**, 43, 463-74	4.1	54
76	Prenatal methylmercury exposure and genetic predisposition to cognitive deficit at age 8 years. *Epidemiology*, **2013**, 24, 643-50	3.1	41
75	Cure frailty models for survival data: application to recurrences for breast cancer and to hospital readmissions for colorectal cancer. *Statistical Methods in Medical Research*, **2013**, 22, 243-60	2.3	40
74	Genetic association analysis and meta-analysis of imputed SNPs in longitudinal studies. *Genetic Epidemiology*, **2013**, 37, 465-77	2.6	3
73	HLA distribution in COPD patients. *COPD: Journal of Chronic Obstructive Pulmonary Disease*, **2013**, 10, 138-46	2	11
72	FTO risk haplotype among early onset and severe obesity cases in a population of western Spain. *Obesity*, **2012**, 20, 909-15	8	27
71	Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15	5.6	24
70	Aberrant brain microRNA target and miRISC gene expression in the anx/anx anorexia mouse model. *Gene*, **2012**, 497, 181-90	3.8	11
69	Transient receptor potential genes, smoking, occupational exposures and cough in adults. *Respiratory Research*, **2012**, 13, 26	7.3	77
68	Identification of polymorphic inversions from genotypes. *BMC Bioinformatics*, **2012**, 13, 28	3.6	33

67	Genome-wide association study of lung function decline in adults with and without asthma. *Journal of Allergy and Clinical Immunology*, **2012**, 129, 1218-28	11.5	78
66	Bayesian model to detect phenotype-specific genes for copy number data. *BMC Bioinformatics*, **2012**, 13, 130	3.6	
65	Detectable clonal mosaicism and its relationship to aging and cancer. *Nature Genetics*, **2012**, 44, 651-8	36.3	409
64	Hypothesis-based analysis of gene-gene interactions and risk of myocardial infarction. *PLoS ONE*, **2012**, 7, e41730	3.7	15
63	The Interferon scaffold attachment region confers high-level transgene expression and avoids extinction by epigenetic modifications of integrated provirus in adipose tissue-derived human mesenchymal stem cells. *Tissue Engineering - Part C: Methods*, **2011**, 17, 275-87	2.9	12
62	Genetic variants of the FADS gene cluster and ELOVL gene family, colostrums LC-PUFA levels, breastfeeding, and child cognition. *PLoS ONE*, **2011**, 6, e17181	3.7	94
61	A recurrent-events survival analysis of the duration of Olympic records. *IMA Journal of Management Mathematics*, **2011**, 22, 115-128	1.4	2
60	CNVassoc: Association analysis of CNV data using R. *BMC Medical Genomics*, **2011**, 4, 47	3.7	15
59	MLPAstats: an R GUI package for the integrated analysis of copy number alterations using MLPA data. *BMC Bioinformatics*, **2011**, 12, 147	3.6	4
58	A fast and accurate method to detect allelic genomic imbalances underlying mosaic rearrangements using SNP array data. *BMC Bioinformatics*, **2011**, 12, 166	3.6	43
57	NT-proBNP: a cardiac biomarker to assess prognosis in non-Hodgkin lymphoma. *Leukemia Research*, **2011**, 35, 715-20	2.7	19
56	Tag-SNP analysis of the GFI1-EVI5-RPL5-FAM69 risk locus for multiple sclerosis. *European Journal of Human Genetics*, **2010**, 18, 827-31	5.3	24
55	The autoimmune disease-associated KIF5A, CD226 and SH2B3 gene variants confer susceptibility for multiple sclerosis. *Genes and Immunity*, **2010**, 11, 439-45	4.4	71
54	Loss of function of transient receptor potential vanilloid 1 (TRPV1) genetic variant is associated with lower risk of active childhood asthma. *Journal of Biological Chemistry*, **2010**, 285, 27532-5	5.4	95
53	Susceptibility genetic variants associated with colorectal cancer risk correlate with cancer phenotype. *Gastroenterology*, **2010**, 139, 788-96, 796.e1-6	13.3	41
52	Role of the neurotrophin network in eating disordersRsubphenotypes: body mass index and age at onset of the disease. *Journal of Psychiatric Research*, **2010**, 44, 834-40	5.2	7
51	R-Gada: a fast and flexible pipeline for copy number analysis in association studies. *BMC Bioinformatics*, **2010**, 11, 380	3.6	44
50	Confidence intervals for median survival time with recurrent event data. *Computational Statistics and Data Analysis*, **2010**, 54, 78-89	1.6	5

49	Multiple correspondence discriminant analysis: an application to detect stratification in copy number variation. *Statistics in Medicine*, **2010**, 29, 3284-93	2.3	6
48	Traffic-related air pollution, oxidative stress genes, and asthma (ECHRS). *Environmental Health Perspectives*, **2009**, 117, 1919-24	8.4	65
47	Joint effect of obesity and TNFA variability on asthma: two international cohort studies. *European Respiratory Journal*, **2009**, 33, 1003-9	13.6	39
46	Accounting for uncertainty when assessing association between copy number and disease: a latent class model. *BMC Bioinformatics*, **2009**, 10, 172	3.6	18
45	Identification of new putative susceptibility genes for several psychiatric disorders by association analysis of regulatory and non-synonymous SNPs of 306 genes involved in neurotransmission and neurodevelopment. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2009**, 150B, 808-16	3.5	79
44	A pooling-based genome-wide analysis identifies new potential candidate genes for atopy in the European Community Respiratory Health Survey (ECRHS). *BMC Medical Genetics*, **2009**, 10, 128	2.1	41
43	Boundary sequences stabilize transgene expression from subtle position effects in retroviral vectors. *Blood Cells, Molecules, and Diseases*, **2009**, 43, 214-20	2.1	7
42	Brain-derived neurotrophic factor modulates the severity of cognitive alterations induced by mutant huntingtin: involvement of phospholipaseCgamma activity and glutamate receptor expression. *Neuroscience*, **2009**, 158, 1234-50	3.9	91
41	Urokinase-type plasminogen activator receptor transcriptionally controlled adenoviruses eradicate pancreatic tumors and liver metastasis in mouse models. *Neoplasia*, **2009**, 11, 518-28, 4 p following 528	6.4	29
40	Identification of copy number variants defining genomic differences among major human groups. *PLoS ONE*, **2009**, 4, e7230	3.7	28
39	Analysis of Population-Based Genetic Association Studies Applied to Cancer Susceptibility and Prognosis **2009**, 149-191		
38	Probe-specific mixed-model approach to detect copy number differences using multiplex ligation-dependent probe amplification (MLPA). *BMC Bioinformatics*, **2008**, 9, 261	3.6	11
37	Extensive genotyping of the BDNF and NTRK2 genes define protective haplotypes against obsessive-compulsive disorder. *Biological Psychiatry*, **2008**, 63, 619-28	7.9	63
36	Association of NTRK3 and its interaction with NGF suggest an altered cross-regulation of the neurotrophin signaling pathway in eating disorders. *Human Molecular Genetics*, **2008**, 17, 1234-44	5.6	42
35	TNFA -308G>A in two international population-based cohorts and risk of asthma. *European Respiratory Journal*, **2008**, 32, 350-61	13.6	27
34	A brain-derived neurotrophic factor (BDNF) haplotype is associated with antidepressant treatment outcome in mood disorders. *Pharmacogenomics Journal*, **2008**, 8, 101-12	3.5	68
33	Restricted transgene persistence after lentiviral vector-mediated fetal gene transfer in the pregnant rabbit model. *Journal of Gene Medicine*, **2008**, 10, 951-64	3.5	8
32	Maximizing association statistics over genetic models. *Genetic Epidemiology*, **2008**, 32, 246-54	2.6	93

31	Genetic susceptibility to obsessive-compulsive hoarding: the contribution of neurotrophic tyrosine kinase receptor type 3 gene. *Genes, Brain and Behavior*, **2008**, 7, 778-85	3.6	38
30	Brain-derived neurotrophic factor Val66Met and psychiatric disorders: meta-analysis of case-control studies confirm association to substance-related disorders, eating disorders, and schizophrenia. *Biological Psychiatry*, **2007**, 61, 911-22	7.9	338
29	Semiparametric Inference for a General Class of Models for Recurrent Events. *Journal of Statistical Planning and Inference*, **2007**, 137, 1727-1747	0.8	42
28	GCV modulates the antitumoural efficacy of a replicative adenovirus expressing the Tat8-TK as a late gene in a pancreatic tumour model. *Gene Therapy*, **2007**, 14, 1471-80	4	24
27	Altered brain-derived neurotrophic factor blood levels and gene variability are associated with anorexia and bulimia. *Genes, Brain and Behavior*, **2007**, 6, 706-16	3.6	67
26	Inter-population variability of DEFA3 gene absence: correlation with haplotype structure and population variability. *BMC Genomics*, **2007**, 8, 14	4.5	20
25	SNPassoc: an R package to perform whole genome association studies. *Bioinformatics*, **2007**, 23, 644-5	7.2	513
24	Blood levels of brain-derived neurotrophic factor correlate with several psychopathological symptoms in anorexia nervosa patients. *Neuropsychobiology*, **2007**, 56, 185-90	4	25
23	A recessive Mendelian model to predict carrier probabilities of DFNB1 for nonsyndromic deafness. *Human Mutation*, **2006**, 27, 1135-42	4.7	4
22	Targeting the CYP2B 1/cyclophosphamide suicide system to fibroblast growth factor receptors results in a potent antitumoral response in pancreatic cancer models. *Human Gene Therapy*, **2006**, 17, 1187-200	4.8	13
21	Global variation in copy number in the human genome. *Nature*, **2006**, 444, 444-54	50.4	3306
20	Tat8-TK/GCV suicide gene therapy induces pancreatic tumor regression in vivo. *Human Gene Therapy*, **2005**, 16, 1377-88	4.8	17
19	Converging patterns of colorectal cancer mortality in Europe. *European Journal of Cancer*, **2005**, 41, 430-7	7.5	44
18	Murine segmental duplications are hot spots for chromosome and gene evolution. *Genomics*, **2005**, 86, 692-700	4.3	25
17	frailtypack: a computer program for the analysis of correlated failure time data using penalized likelihood estimation. *Computer Methods and Programs in Biomedicine*, **2005**, 80, 154-64	6.9	42
16	Use of distress and depression thermometers to measure psychosocial morbidity among southern European cancer patients. *Supportive Care in Cancer*, **2005**, 13, 600-6	3.9	123
15	Modelling intervention effects after cancer relapses. *Statistics in Medicine*, **2005**, 24, 3959-75	2.3	8
14	Sex differences in hospital readmission among colorectal cancer patients. *Journal of Epidemiology and Community Health*, **2005**, 59, 506-11	5.1	48

13	Monitoring falls in gastric cancer mortality in Europe. *Annals of Oncology*, **2004**, 15, 338-45	10.3	54
12	Hla-DPB1 mismatch in HLA-A-B-DRB1 identical sibling donor stem cell transplantation and acute graft-versus-host disease. *Transplantation*, **2004**, 77, 1107-10	1.8	22
11	Lung cancer mortality in European regions (1955-1997). *Annals of Oncology*, **2003**, 14, 159-61	10.3	27
10	Suitability of oligonucleotide-mediated cystic fibrosis gene repair in airway epithelial cells. *Journal of Gene Medicine*, **2003**, 5, 625-39	3.5	4
9	Trends in smoking-related cancer incidence in Tarragona, Spain, 1980-96. *Cancer Causes and Control* , **2001**, 12, 903-8	2.8	25
8	Neurodevelopmental delay, motor abnormalities and cognitive deficits in transgenic mice overexpressing Dyrk1A (minibrain), a murine model of DownR syndrome. *Human Molecular Genetics* , **2001**, 10, 1915-23	5.6	299
7	Omic Association Studies with R and Bioconductor		2
6	Bayesian neural networks for the optimisation of biological clocks in humans		2
5	Immune defects and cardiovascular risk in X chromosome monosomy mosaicism mediated by loss of chromosome Y. A risk factor for SARS-CoV-2 vulnerability in elderly men?		1
4	Identification of blood autosomal cis-expression quantitative trait methylation (cis-eQTMs) in children		2
3	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences1		4
2	MADloy: Robust detection of mosaic loss of chromosome Y from genotype-array-intensity data		1
1	Multi-omics signatures of the human early life exposome		1