Juan RamÃ³n GonzÃ¡lez

List of Publications by Year
in descending order

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152 papers	14,590 citations	53939 47 h-index	24511 114 g-index
172 all docs	172 docs citations	172 times ranked	28923 citing authors

#	Article	IF	Citations
1	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	3.2	11
2	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.	2.4	24
3	teff: estimation of Treatment EFFects on transcriptomic data using causal random forest. Bioinformatics, 2022, 38, 3124-3125.	1.8	4
4	The early-life exposome modulates the effect of polymorphic inversions on DNA methylation. Communications Biology, 2022, 5, 455.	2.0	6
5	methylclock: a Bioconductor package to estimate DNA methylation age. Bioinformatics, 2021, 37, 1759-1760.	1.8	67
6	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. Molecular Psychiatry, 2021, 26, 2056-2069.	4.1	79
7	Urinary metabolite quantitative trait loci in children and their interaction with dietary factors. Human Molecular Genetics, 2021, 29, 3830-3844.	1.4	7
8	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.	4.1	21
9	MLIP genotype as a predictor of pharmacological response in primary open-angle glaucoma and ocular hypertension. Scientific Reports, 2021, 11, 1583.	1.6	5
10	Orchestrating privacy-protected big data analyses of data from different resources with R and DataSHIELD. PLoS Computational Biology, 2021, 17, e1008880.	1.5	25
11	Early-life environmental exposure determinants of child behavior in Europe: A longitudinal, population-based study. Environment International, 2021, 153, 106523.	4.8	52
12	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.	4.8	4
13	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
14	The early-life exposome and epigenetic age acceleration in children. Environment International, 2021, 155, 106683.	4.8	47
15	Advancing tools for human early lifecourse exposome research and translation (ATHLETE). Environmental Epidemiology, 2021, 5, e166.	1.4	24
16	MADloy: robust detection of mosaic loss of chromosome Y from genotype-array-intensity data. BMC Bioinformatics, 2020, 21, 533.	1.2	7
17	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. Translational Psychiatry, 2020, 10, 398.	2.4	54
18	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.	1.5	11

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19	In utero and childhood exposure to tobacco smoke and multi-layer molecular signatures in children. BMC Medicine, 2020, 18, 243.	2.3	22
20	Identifying chromosomal subpopulations based on their recombination histories advances the study of the genetic basis of phenotypic traits. Genome Research, 2020, 30, 1802-1814.	2.4	4
21	Polymorphic Inversions Underlie the Shared Genetic Susceptibility of Obesity-Related Diseases. American Journal of Human Genetics, 2020, 106, 846-858.	2.6	11
22	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.	4.8	22
23	Association between the pregnancy exposome and fetal growth. International Journal of Epidemiology, 2020, 49, 572-586.	0.9	28
24	Extreme downregulation of chromosome Y and Alzheimer's disease in men. Neurobiology of Aging, 2020, 90, 150.e1-150.e4.	1.5	26
25	Extreme Downregulation of Chromosome Y and Cancer Risk in Men. Journal of the National Cancer Institute, 2020, 112, 913-920.	3.0	46
26	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.	2.7	55
27	Comprehensive study of the exposome and omic data using rexposome Bioconductor Packages. Bioinformatics, 2019, 35, 5344-5345.	1.8	27
28	scoreInvHap: Inversion genotyping for genome-wide association studies. PLoS Genetics, 2019, 15, e1008203.	1.5	17
29	Independent Multiple Factor Association Analysis for Multiblock Data in Imaging Genetics. Neuroinformatics, 2019, 17, 583-592.	1.5	2
30	Common polymorphic inversions at 17q21.31 and 8p23.1 associate with cancer prognosis. Human Genomics, 2019, 13, 57.	1.4	4
31	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.	9.4	536
32	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	5.8	85
33	<tt>CTDquerier</tt>: a bioconductor R package for Comparative Toxicogenomics DatabaseTM data extraction, visualization and enrichment of environmental and toxicological studies. Bioinformatics, 2018, 34, 3235-3237.	1.8	9
34	When pitch adds to volume: coregulation of transcript diversity predicts gene function. BMC Genomics, 2018, 19, 926.	1.2	1
35	Variability of urinary concentrations of non-persistent chemicals in pregnant women and school-aged children. Environment International, 2018, 121, 561-573.	4.8	106
36	In-utero and childhood chemical exposome in six European mother-child cohorts. Environment International, 2018, 121, 751-763.	4.8	122

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37	Human Early Life Exposome (HELIX) study: a European population-based exposome cohort. BMJ Open, 2018, 8, e021311.	0.8	161
38	Strategies for integrated analysis in imaging genetics studies. Neuroscience and Biobehavioral Reviews, 2018, 93, 57-70.	2.9	7
39	Characterization of Plasmodium vivax Proteins in Plasma-Derived Exosomes From Malaria-Infected Liver-Chimeric Humanized Mice. Frontiers in Microbiology, 2018, 9, 1271.	1.5	43
40	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.	2.7	1
41	Sparse multiple factor analysis to integrate genetic data, neuroimaging features, and attentionâ€deficit/hyperactivity disorder domains. International Journal of Methods in Psychiatric Research, 2018, 27, e1738.	1.1	10
42	The first in vivo multiparametric comparison of different radiation exposure biomarkers in human blood. PLoS ONE, 2018, 13, e0193412.	1.1	34
43	Circulating miRNAs, isomiRs and small RNA clusters in human plasma and breast milk. PLoS ONE, 2018, 13, e0193527.	1.1	51
44	APOE and MS4A6A interact with GnRH signaling in Alzheimer's disease: Enrichment of epistatic effects. Alzheimer's and Dementia, 2017, 13, 493-497.	0.4	10
45	Polymorphisms in the SNRPN gene are associated with obesity susceptibility in a Spanish population. Journal of Gene Medicine, 2017, 19, e2956.	1.4	4
46	MultiDataSet: an R package for encapsulating multiple data sets with application to omic data integration. BMC Bioinformatics, 2017, 18, 36.	1.2	20
47	Imaging genetics in attention-deficit/hyperactivity disorder and related neurodevelopmental domains: state of the art. Brain Imaging and Behavior, 2017, 11, 1922-1931.	1.1	10
48	The acute effects of ultraviolet radiation on the blood transcriptome are independent of plasma 25OHD3. Environmental Research, 2017, 159, 239-248.	3.7	13
49	psygenet2r: a R/Bioconductor package for the analysis of psychiatric disease genes. Bioinformatics, 2017, 33, 4004-4006.	1.8	3
50	Detectable clonal mosaicism in blood as a biomarker of cancer risk in Fanconi anemia. Blood Advances, 2017, 1, 319-329.	2.5	18
51	Computational analysis of multimorbidity between asthma, eczema and rhinitis. PLoS ONE, 2017, 12, e0179125.	1.1	33
52	Novel genes involved in severe early-onset obesity revealed by rare copy number and sequence variants. PLoS Genetics, 2017, 13, e1006657.	1.5	28
53	A systematic comparison of statistical methods to detect interactions in exposome-health associations. Environmental Health, 2017, 16, 74.	1.7	51
54	Redundancy analysis allows improved detection of methylation changes in large genomic regions. BMC Bioinformatics, 2017, 18, 553.	1.2	8

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55	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.	2.8	23
56	Exploration of large, rare copy number variants associated with psychiatric and neurodevelopmental disorders in individuals with anorexia nervosa. Psychiatric Genetics, 2017, 27, 152-158.	0.6	18
57	A Systematic Comparison of Linear Regressionâ€“Based Statistical Methods to Assess Exposome-Health Associations. Environmental Health Perspectives, 2016, 124, 1848-1856.	2.8	151
58	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
59	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
60	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
61	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.	1.9	4
62	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	1.4	275
63	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, ENEURO.0103-16.2016.	0.9	42
64	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. PLoS ONE, 2016, 11, e0157739.	1.1	2
65	A Decision Aid to Support Informed Choices for Patients Recently Diagnosed With Prostate Cancer. Cancer Nursing, 2015, 38, E42-E50.	0.7	51
66	Interaction Association Analysis of Imputed SNPs in Caseâ€Control and Followâ€Up Studies. Genetic Epidemiology, 2015, 39, 185-196.	0.6	0
67	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.	1.0	44
68	Genetic polymorphisms associated with increased risk of developing chronic myelogenous leukemia. Oncotarget, 2015, 6, 36269-36277.	0.8	27
69	DNA methylation levels and long-term trihalomethane exposure in drinking water: an epigenome-wide association study. Epigenetics, 2015, 10, 650-661.	1.3	22
70	Following the footprints of polymorphic inversions on SNP data: from detection to association tests. Nucleic Acids Research, 2015, 43, e53-e53.	6.5	45
71	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.	1.2	3
72	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108

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73	The Pregnancy Exposome: Multiple Environmental Exposures in the INMA-Sabadell Birth Cohort. Environmental Science & Technology, 2015, 49, 10632-10641.	4.6	81
74	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.	9.4	529
75	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
76	The Human Early-Life Exposome (HELIX): Project Rationale and Design. Environmental Health Perspectives, 2014, 122, 535-544.	2.8	280
77	Genetic heterogeneity of asthma phenotypes identified by a clustering approach. European Respiratory Journal, 2014, 43, 439-452.	3.1	57
78	A Common 16p11.2 Inversion Underlies the Joint Susceptibility to Asthma and Obesity. American Journal of Human Genetics, 2014, 94, 361-372.	2.6	66
79	Worldwide population distribution of the common LCE3C-LCE3B deletion associated with psoriasis and other autoimmune disorders. BMC Genomics, 2013, 14, 261.	1.2	9
80	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.	1.2	48
81	Genetic factors conferring an increased susceptibility to develop Crohn's disease also influence disease phenotype: results from the IBDchip European Project. Gut, 2013, 62, 1556-1565.	6.1	221
82	Genomeâ€wide association study of body mass index in 23Â000 individuals with and without asthma. Clinical and Experimental Allergy, 2013, 43, 463-474.	1.4	68
83	Prenatal Methylmercury Exposure and Genetic Predisposition to Cognitive Deficit at Age 8 Years. Epidemiology, 2013, 24, 643-650.	1.2	59
84	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, 243-260.	0.7	44
85	Genetic Association Analysis and Metaâ€Analysis of Imputed SNPs in Longitudinal Studies. Genetic Epidemiology, 2013, 37, 465-477.	0.6	3
86	HLA Distribution in COPD Patients. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2013, 10, 138-146.	0.7	15
87	FTO Risk Haplotype Among Early Onset and Severe Obesity Cases in a Population of Western Spain. Obesity, 2012, 20, 909-915.	1.5	29
88	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	1.4	33
89	Aberrant brain microRNA target and miRISC gene expression in the anx/anx anorexia mouse model. Gene, 2012, 497, 181-190.	1.0	12
90	Transient receptor potential genes, smoking, occupational exposures and cough in adults. Respiratory Research, 2012, 13, 26.	1.4	84

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91	Identification of polymorphic inversions from genotypes. BMC Bioinformatics, 2012, 13, 28.	1.2	46
92	Genome-wide association study of lung function decline in adults with and without asthma. Journal of Allergy and Clinical Immunology, 2012, 129, 1218-1228.	1.5	94
93	Bayesian model to detect phenotype-specific genes for copy number data. BMC Bioinformatics, 2012, 13, 130.	1.2	0
94	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	9.4	519
95	Hypothesis-Based Analysis of Gene-Gene Interactions and Risk of Myocardial Infarction. PLoS ONE, 2012, 7, e41730.	1.1	17
96	The Î²-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, 275-287.	1.1	14
97	Genetic Variants of the FADS Gene Cluster and ELOVL Gene Family, Colostrums LC-PUFA Levels, Breastfeeding, and Child Cognition. PLoS ONE, 2011, 6, e17181.	1.1	111
98	A recurrent-events survival analysis of the duration of Olympic records. IMA Journal of Management Mathematics, 2011, 22, 115-128.	1.1	3
99	CNVassoc: Association analysis of CNV data using R. BMC Medical Genomics, 2011, 4, 47.	0.7	16
100	MLPAstats: An R GUI package for the integrated analysis of copy number alterations using MLPA data. BMC Bioinformatics, 2011, 12, 147.	1.2	4
101	A fast and accurate method to detect allelic genomic imbalances underlying mosaic rearrangements using SNP array data. BMC Bioinformatics, 2011, 12, 166.	1.2	52
102	NT-proBNP: A cardiac biomarker to assess prognosis in non-Hodgkin lymphoma. Leukemia Research, 2011, 35, 715-720.	0.4	29
103	Role of the neurotrophin network in eating disordersâ€™ subphenotypes: Body mass index and age at onset of the disease. Journal of Psychiatric Research, 2010, 44, 834-840.	1.5	10
104	R-Gada: a fast and flexible pipeline for copy number analysis in association studies. BMC Bioinformatics, 2010, 11, 380.	1.2	46
105	Confidence intervals for median survival time with recurrent event data. Computational Statistics and Data Analysis, 2010, 54, 78-89.	0.7	5
106	Multiple correspondence discriminant analysis: An application to detect stratification in copy number variation. Statistics in Medicine, 2010, 29, 3284-3293.	0.8	9
107	Tag-SNP analysis of the GFI1-EVI5-RPL5-FAM69 risk locus for multiple sclerosis. European Journal of Human Genetics, 2010, 18, 827-831.	1.4	25
108	The autoimmune disease-associated KIF5A, CD226 and SH2B3 gene variants confer susceptibility for multiple sclerosis. Genes and Immunity, 2010, 11, 439-445.	2.2	79

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109	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, 27532-27535.	1.6	105
110	Susceptibility Genetic Variants Associated With Colorectal Cancer Risk Correlate With Cancer Phenotype. Gastroenterology, 2010, 139, 788-796.e6.	0.6	47
111	Traffic-Related Air Pollution, Oxidative Stress Genes, and Asthma (ECHRS). Environmental Health Perspectives, 2009, 117, 1919-1924.	2.8	78
112	Joint effect of obesity and TNFA variability on asthma: two international cohort studies. European Respiratory Journal, 2009, 33, 1003-1009.	3.1	43
113	Accounting for uncertainty when assessing association between copy number and disease: a latent class model. BMC Bioinformatics, 2009, 10, 172.	1.2	22
114	Identification of new putative susceptibility genes for several psychiatric disorders by association analysis of regulatory and nonâ€synonymous SNPs of 306 genes involved in neurotransmission and neurodevelopment. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 808-816.	1.1	98
115	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	43
116	Boundary sequences stabilize transgene expression from subtle position effects in retroviral vectors. Blood Cells, Molecules, and Diseases, 2009, 43, 214-220.	0.6	7
117	Brain-derived neurotrophic factor modulates the severity of cognitive alterations induced by mutant huntingtin: Involvement of phospholipaseCÎ³ activity and glutamate receptor expression. Neuroscience, 2009, 158, 1234-1250.	1.1	98
118	Urokinase-Type Plasminogen Activator Receptor Transcriptionally Controlled Adenoviruses Eradicate Pancreatic Tumors and Liver Metastasis in Mouse Models. Neoplasia, 2009, 11, 518-IN6.	2.3	31
119	Identification of Copy Number Variants Defining Genomic Differences among Major Human Groups. PLoS ONE, 2009, 4, e7230.	1.1	32
120	Analysis of Population-Based Genetic Association Studies Applied to Cancer Susceptibility and Prognosis. , 2009, , 149-191.		0
121	Restricted transgene persistence after lentiviral vectorâ€mediated fetal gene transfer in the pregnant rabbit model. Journal of Gene Medicine, 2008, 10, 951-964.	1.4	8
122	Maximizing association statistics over genetic models. Genetic Epidemiology, 2008, 32, 246-254.	0.6	101
123	Genetic susceptibility to obsessiveâ€compulsive hoarding: the contribution of neurotrophic tyrosine kinase receptor type 3 gene¹. Genes, Brain and Behavior, 2008, 7, 778-785.	1.1	43
124	Probe-specific mixed-model approach to detect copy number differences using multiplex ligation-dependent probe amplification (MLPA). BMC Bioinformatics, 2008, 9, 261.	1.2	16
125	Extensive Genotyping of the BDNF and NTRK2 Genes Define Protective Haplotypes Against Obsessive-Compulsive Disorder. Biological Psychiatry, 2008, 63, 619-628.	0.7	66
126	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, 1234-1244.	1.4	50

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127	TNFA -308G>A in two international population-based cohorts and risk of asthma. European Respiratory Journal, 2008, 32, 350-361.	3.1	28
128	A brain-derived neurotrophic factor (BDNF) haplotype is associated with antidepressant treatment outcome in mood disorders. Pharmacogenomics Journal, 2008, 8, 101-112.	0.9	76
129	SNPassoc: an R package to perform whole genome association studies. Bioinformatics, 2007, 23, 654-655.	1.8	607
130	Blood Levels of Brain-Derived Neurotrophic Factor Correlate with Several Psychopathological Symptoms in Anorexia Nervosa Patients. Neuropsychobiology, 2007, 56, 185-190.	0.9	28
131	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, 911-922.	0.7	381
132	Semiparametric inference for a general class of models for recurrent events. Journal of Statistical Planning and Inference, 2007, 137, 1727-1747.	0.4	62
133	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, 1471-1480.	2.3	24
134	Altered brain-derived neurotrophic factor blood levels and gene variability are associated with anorexia and bulimia. Genes, Brain and Behavior, 2007, 6, 706-716.	1.1	73
135	Inter-population variability of DEFA3 gene absence: correlation with haplotype structure and population variability. BMC Genomics, 2007, 8, 14.	1.2	20
136	Global variation in copy number in the human genome. Nature, 2006, 444, 444-454.	13.7	3,831
137	A recessive Mendelian model to predict carrier probabilities of DFNB1 for nonsyndromic deafness. Human Mutation, 2006, 27, 1135-1142.	1.1	4
138	Targeting the CYP2B1/Cyclophosphamide Suicide System to Fibroblast Growth Factor Receptors Results in a Potent Antitumoral Response in Pancreatic Cancer Models. Human Gene Therapy, 2006, 17, 1187-1200.	1.4	14
139	frailtypack: A computer program for the analysis of correlated failure time data using penalized likelihood estimation. Computer Methods and Programs in Biomedicine, 2005, 80, 154-164.	2.6	54
140	Use of distress and depression thermometers to measure psychosocial morbidity among southern European cancer patients. Supportive Care in Cancer, 2005, 13, 600-606.	1.0	141
141	Modelling intervention effects after cancer relapses. Statistics in Medicine, 2005, 24, 3959-3975.	0.8	12
142	Sex differences in hospital readmission among colorectal cancer patients. Journal of Epidemiology and Community Health, 2005, 59, 506-511.	2.0	67
143	Tat8â€“TK/GCV Suicide Gene Therapy Induces Pancreatic Tumor Regression In Vivo. Human Gene Therapy, 2005, 16, 1377-1388.	1.4	17
144	Converging patterns of colorectal cancer mortality in Europe. European Journal of Cancer, 2005, 41, 430-437.	1.3	50

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145	Murine segmental duplications are hot spots for chromosome and gene evolution. Genomics, 2005, 86, 692-700.	1.3	28
146	Monitoring falls in gastric cancer mortality in Europe. Annals of Oncology, 2004, 15, 338-345.	0.6	65
147	HLA-DPB1 MISMATCH IN HLA-A-B-DRB1 IDENTICAL SIBLING DONOR STEM CELL TRANSPLANTATION AND ACUTE GRAFT-VERSUS-HOST DISEASE. Transplantation, 2004, 77, 1107-1110.	0.5	23
148	Suitability of oligonucleotide-mediated cystic fibrosis gene repair in airway epithelial cells. Journal of Gene Medicine, 2003, 5, 625-639.	1.4	5
149	Lung cancer mortality in European regions (1955â€“1997). Annals of Oncology, 2003, 14, 159-161.	0.6	34
150	Trends in smoking-related cancer incidence in Tarragona, Spain, 1980-96. Cancer Causes and Control, 2001, 12, 903-908.	0.8	32
151	Neurodevelopmental delay, motor abnormalities and cognitive deficits in transgenic mice overexpressing Dyrk1A (minibrain), a murine model of Down's syndrome. Human Molecular Genetics, 2001, 10, 1915-1923.	1.4	357
152	Omic Association Studies with R and Bioconductor. , 0, , .		2