Jack A Taylor

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.

211 papers	12,140 citations	56 h-index	105 g-index
233 ext. papers	15,006 ext. citations	8.9 avg, IF	5.99 L-index

#	Paper	IF	Citations
211	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
210	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
209	Vitamin D Supplement Use and Risk of Breast Cancer by Race-Ethnicity. *Epidemiology*, **2022**, 33, 37-47	3.1	1
208	Breast Cancer Screening Strategies for Women With ATM, CHEK2, and PALB2 Pathogenic Variants: A Comparative Modeling Analysis.. *JAMA Oncology*, **2022**,	13.4	5
207	A Genome-Wide Gene-Based Gene Environment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications*, **2022**, 2, 211-219		0
206	Vitamin D concentrations and breast cancer incidence among Black/African American and non-Black Hispanic/Latina women.. *Cancer*, **2022**,	6.4	1
205	Differential Gene Expression in Bladder Tumors from Workers Occupationally Exposed to Arylamines. *BioMed Research International*, **2021**, 2021, 2624433	3	0
204	Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast. *Journal of Clinical Oncology*, **2021**, 39, 3918-3926	2.2	6
203	Associations of Body Composition and Physical Activity Level With Multiple Measures of Epigenetic Age Acceleration. *American Journal of Epidemiology*, **2021**, 190, 984-993	3.8	9
202	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. *Journal of the National Cancer Institute*, **2021**, 113, 1168-1176	9.7	9
201	Wavelet Screening identifies regions highly enriched for differentially methylated loci for orofacial clefts. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab035	3.7	
200	Alcohol Consumption and Methylation-Based Measures of Biological Age. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2021**, 76, 2107-2111	6.4	4
199	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
198	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. *Nature Communications*, **2021**, 12, 4198	17.4	1
197	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. *American Journal of Human Genetics*, **2021**, 108, 1190-1203	11	1
196	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. *Journal of Clinical Oncology*, **2021**, 39, 3430-3440	2.2	3
195	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. *Journal of the National Cancer Institute*, **2021**, 113, 329-337	9.7	14

194	Reliability of DNA methylation measures using Illumina methylation BeadChip. *Epigenetics*, **2021**, 16, 495-502	5.7	4
193	African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. *International Journal of Cancer*, **2021**, 148, 99-105	7.5	7
192	ipDMR: identification of differentially methylated regions with interval P-values. *Bioinformatics*, **2021**, 37, 711-713	7.2	5
191	Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2021**, 186, 173-182	3.5	6
190	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. *British Journal of Cancer*, **2021**, 124, 842-854	8.7	2
189	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. *Nature Genetics*, **2021**, 53, 65-75	36.3	62
188	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078	17.4	4
187	A Population-Based Study of Genes Previously Implicated in Breast Cancer. *New England Journal of Medicine*, **2021**, 384, 440-451	59.2	115
186	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. *Journal of Clinical Oncology*, **2021**, 39, 2564-2573	2.2	12
185	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145	8.7	0
184	Blood DNA methylation profiles improve breast cancer prediction. *Molecular Oncology*, **2021**,	7.9	3
183	The ENmix DNA methylation analysis pipeline for Illumina BeadChip and comparisons with seven other preprocessing pipelines. *Clinical Epigenetics*, **2021**, 13, 216	7.7	2
182	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581	36.3	76
181	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. *European Urology*, **2020**, 78, 316-320	10.2	13
180	The Role of Blood Cell Composition in Epidemiologic Studies of Telomeres. *Epidemiology*, **2020**, 31, e34-e36	3.8	1
179	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
178	Prediagnostic Immune Cell Profiles and Breast Cancer. *JAMA Network Open*, **2020**, 3, e1919536	10.4	14
177	A data mining approach to investigate food groups related to incidence of bladder cancer in the BLadder cancer Epidemiology and Nutritional Determinants International Study. *British Journal of Nutrition*, **2020**, 124, 611-619	3.6	2

176	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
175	Long-term ambient fine particulate matter and DNA methylation in inflammation pathways: results from the Sister Study. *Epigenetics*, **2020**, 15, 524-535	5.7	10
174	Gene-methylation interactions: discovering region-wise DNA methylation levels that modify SNP-associated disease risk. *Clinical Epigenetics*, **2020**, 12, 109	7.7	5
173	Blood DNA Methylation and Breast Cancer: A Prospective Case-Cohort Analysis in the Sister Study. *Journal of the National Cancer Institute*, **2020**, 112, 87-94	9.7	41
172	Association of Neighborhood Deprivation With Epigenetic Aging Using 4 Clock Metrics. *JAMA Network Open*, **2020**, 3, e2024329	10.4	17
171	Zebrafish behavioural profiling identifies GABA and serotonin receptor ligands related to sedation and paradoxical excitation. *Nature Communications*, **2019**, 10, 4078	17.4	12
170	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. *Epigenomics*, **2019**, 11, 1487-1500	4.4	24
169	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019** , 10, 431	17.4	45
168	RE: "SOCIOECONOMIC POSITION AND DNA METHYLATION AGE ACCELERATION ACROSS THE LIFE COURSE". *American Journal of Epidemiology*, **2019**, 188, 487-488	3.8	4
167	The association between coffee consumption and bladder cancer in the bladder cancer epidemiology and nutritional determinants (BLEND) international pooled study. *Cancer Causes and Control*, **2019**, 30, 859-870	2.8	8
166	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. *Cancer Medicine*, **2019**, 8, 2503-2513	4.8	4
165	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
164	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. *Nature Communications*, **2019**, 10, 1893	17.4	79
163	Shift work, DNA methylation and epigenetic age. *International Journal of Epidemiology*, **2019**, 48, 1536-1544	7.4	21
162	A comparison of DNA methylation in newborn blood samples from infants with and without orofacial clefts. *Clinical Epigenetics*, **2019**, 11, 40	7.7	10
161	Hormone therapy use and breast tissue DNA methylation: analysis of epigenome wide data from the normal breast study. *Epigenetics*, **2019**, 14, 146-157	5.7	4
160	Persistent epigenetic changes in adult daughters of older mothers. *Epigenetics*, **2019**, 14, 467-476	5.7	6
159	Alcohol and DNA Methylation: An Epigenome-Wide Association Study in Blood and Normal Breast Tissue. *American Journal of Epidemiology*, **2019**, 188, 1055-1065	3.8	25

158	Methylation-Based Biological Age and Breast Cancer Risk. *Journal of the National Cancer Institute*, **2019**, 111, 1051-1058	9.7	67
157	Air pollution, particulate matter composition and methylation-based biologic age. *Environment International*, **2019**, 132, 105071	12.9	33
156	Reproduction, DNA methylation and biological age. *Human Reproduction*, **2019**, 34, 1965-1973	5.7	15
155	Epigenetic mortality predictors and incidence of breast cancer. *Aging*, **2019**, 11, 11975-11987	5.6	14
154	Hazardous air pollutants and telomere length in the Sister Study. *Environmental Epidemiology*, **2019**, 3,	0.2	2
153	Modeling the Complex Exposure History of Smoking in Predicting Bladder Cancer: A Pooled Analysis of 15 Case-Control Studies. *Epidemiology*, **2019**, 30, 458-465	3.1	5
152	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
151	Genome-wide association study of anti-M□lerian hormone levels in pre-menopausal women of late reproductive age and relationship with genetic determinants of reproductive lifespan. *Human Molecular Genetics*, **2019**, 28, 1392-1401	5.6	9
150	The Association of a Breast Cancer Diagnosis With Serum 25-Hydroxyvitamin D Concentration Over Time. *American Journal of Epidemiology*, **2019**, 188, 637-645	3.8	4
149	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52
148	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. *International Journal of Epidemiology*, **2018**, 47, 22-23u	7.8	62
147	Roadmap for investigating epigenome deregulation and environmental origins of cancer. *International Journal of Cancer*, **2018**, 142, 874-882	7.5	46
146	Genome-Wide Association Study of Serum 25-Hydroxyvitamin D in US Women. *Frontiers in Genetics*, **2018**, 9, 67	4.5	21
145	Vitamin D, DNA methylation, and breast cancer. *Breast Cancer Research*, **2018**, 20, 70	8.3	34
144	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
143	Reproductive history and blood cell telomere length. *Aging*, **2018**, 10, 2383-2393	5.6	7
142	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
141	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643

140	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
139	Soy Formula and Epigenetic Modifications: Analysis of Vaginal Epithelial Cells from Infant Girls in the IFED Study. *Environmental Health Perspectives*, **2017**, 125, 447-452	8.4	28
138	Serum Vitamin D and Risk of Breast Cancer within Five Years. *Environmental Health Perspectives*, **2017**, 125, 077004	8.4	46
137	The Sister Study Cohort: Baseline Methods and Participant Characteristics. *Environmental Health Perspectives*, **2017**, 125, 127003	8.4	103
136	Single-Nucleotide Polymorphisms in Vitamin D-Related Genes May Modify Vitamin D-Breast Cancer Associations. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1761-1771	4	12
135	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. *Human Molecular Genetics*, **2017**, 26, 4067-4085	5.6	151
134	RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip. *BMC Genomics*, **2017**, 18, 4	4.5	53
133	Previous GWAS hits in relation to young-onset breast cancer. *Breast Cancer Research and Treatment*, **2017**, 161, 333-344	4.4	9
132	An epigenome-wide study of body mass index and DNA methylation in blood using participants from the Sister Study cohort. *International Journal of Obesity*, **2017**, 41, 194-199	5.5	35
131	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
130	Systemic Levels of Estrogens and PGE Synthesis in Relation to Postmenopausal Breast Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 383-388	4	10
129	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
128	oxBS-MLE: an efficient method to estimate 5-methylcytosine and 5-hydroxymethylcytosine in paired bisulfite and oxidative bisulfite treated DNA. *Bioinformatics*, **2016**, 32, 3667-3669	7.2	13
127	Long-term use of calcium channel blocking drugs and breast cancer risk in a prospective cohort of US and Puerto Rican women. *Breast Cancer Research*, **2016**, 18, 61	8.3	17
126	RCP: a novel probe design bias correction method for Illumina Methylation BeadChip. *Bioinformatics*, **2016**, 32, 2659-63	7.2	64
125	Zebrafish behavioral profiling identifies multitarget antipsychotic-like compounds. *Nature Chemical Biology*, **2016**, 12, 559-66	11.7	81
124	A family-based, genome-wide association study of young-onset breast cancer: inherited variants and maternally mediated effects. *European Journal of Human Genetics*, **2016**, 24, 1316-23	5.3	10
123	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. *Human Molecular Genetics*, **2016**, 25, 1203-14	5.6	20

122	ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. *Nucleic Acids Research*, **2016**, 44, e20	20.1	157
121	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. *PLoS Genetics*, **2016**, 12, e1006385	6	55
120	Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. *PLoS ONE*, **2016**, 11, e0156361	3.7	37
119	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. *Human Molecular Genetics*, **2016**, 25, 3600-3612	5.6	9
118	International pooled study on diet and bladder cancer: the bladder cancer, epidemiology and nutritional determinants (BLEND) study: design and baseline characteristics. *Archives of Public Health*, **2016**, 74, 30	2.6	16
117	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
116	Associations of prostate cancer risk variants with disease aggressiveness: results of the NCI-SPORE Genetics Working Group analysis of 18,343 cases. *Human Genetics*, **2015**, 134, 439-50	6.3	34
115	Lifetime use of nonsteroidal anti-inflammatory drugs and breast cancer risk: results from a prospective study of women with a sister with breast cancer. *BMC Cancer*, **2015**, 15, 960	4.8	29
114	In utero exposure to diethylstilbestrol and blood DNA methylation in women ages 40-59 years from the sister study. *PLoS ONE*, **2015**, 10, e0118757	3.7	12
113	Body mass index associated with genome-wide methylation in breast tissue. *Breast Cancer Research and Treatment*, **2015**, 151, 453-63	4.4	21
112	Non-Steroidal Anti-Inflammatory Drug Use and Genomic DNA Methylation in Blood. *PLoS ONE*, **2015**, 10, e0138920	3.7	7
111	Learning phenotype densities conditional on many interacting predictors. *Bioinformatics*, **2014**, 30, 1562-82	7.8	3
110	Genome-wide age-related DNA methylation changes in blood and other tissues relate to histone modification, expression and cancer. *Carcinogenesis*, **2014**, 35, 356-64	4.6	86
109	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. *ELife*, **2014**, 3,	8.9	229
108	Processed pseudogenes acquired somatically during cancer development. *Nature Communications*, **2014**, 5, 3644	17.4	68
107	CpG sites associated with cigarette smoking: analysis of epigenome-wide data from the Sister Study. *Environmental Health Perspectives*, **2014**, 122, 673-8	8.4	79
106	Identification of DNA methylation changes in newborns related to maternal smoking during pregnancy. *Environmental Health Perspectives*, **2014**, 122, 1147-53	8.4	153
105	Asymmetry in family history implicates nonstandard genetic mechanisms: application to the genetics of breast cancer. *PLoS Genetics*, **2014**, 10, e1004174	6	4

104	Global DNA methylation and one-carbon metabolism gene polymorphisms and the risk of breast cancer in the Sister Study. *Carcinogenesis*, **2014**, 35, 333-8	4.6	44
103	Admixture mapping of prostate cancer in African Americans participating in the North Carolina-Louisiana Prostate Cancer Project (PCaP). *Prostate*, **2014**, 74, 1-9	4.2	20
102	Author response: Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer **2014**,		3
101	Genetic polymorphism and prostate cancer aggressiveness: a case-only study of 1,536 GWAS and candidate SNPs in African-Americans and European-Americans. *Prostate*, **2013**, 73, 11-22	4.2	57
100	Serum microRNA expression as an early marker for breast cancer risk in prospectively collected samples from the Sister Study cohort. *Breast Cancer Research*, **2013**, 15, R42	8.3	81
99	Epigenome-wide association study of breast cancer using prospectively collected sister study samples. *Journal of the National Cancer Institute*, **2013**, 105, 694-700	9.7	103
98	Recreational and household physical activity at different time points and DNA global methylation. *European Journal of Cancer*, **2013**, 49, 2199-206	7.5	59
97	Polymorphisms in CYP17 and CYP3A4 and prostate cancer in men of African descent. *Prostate*, **2013**, 73, 668-76	4.2	28
96	Association between urinary prostaglandin E2 metabolite and breast cancer risk: a prospective, case-cohort study of postmenopausal women. *Cancer Prevention Research*, **2013**, 6, 511-8	3.2	36
95	No association between DNA repair gene XRCC1 and amyotrophic lateral sclerosis. *Neurobiology of Aging*, **2012**, 33, 1015.e25-6	5.6	5
94	Genetic ancestry, self-reported race and ethnicity in African Americans and European Americans in the PCaP cohort. *PLoS ONE*, **2012**, 7, e30950	3.7	25
93	Association between genetic variants in DNA and histone methylation and telomere length. *PLoS ONE*, **2012**, 7, e40504	3.7	23
92	Inhibition of fried meat-induced colorectal DNA damage and altered systemic genotoxicity in humans by crucifera, chlorophyllin, and yogurt. *PLoS ONE*, **2011**, 6, e18707	3.7	38
91	Reliability and short-term intra-individual variability of telomere length measurement using monochrome multiplexing quantitative PCR. *PLoS ONE*, **2011**, 6, e25774	3.7	13
90	Genome-wide analysis of loss of heterozygosity and copy number amplification in uterine leiomyomas using the 100K single nucleotide polymorphism array. *Experimental and Molecular Pathology*, **2011**, 91, 434-9	4.4	4
89	Telomere length in peripheral blood and breast cancer risk in a prospective case-cohort analysis: results from the Sister Study. *Cancer Causes and Control*, **2011**, 22, 1061-6	2.8	34
88	GWAS SNP Replication among African American and European American men in the North Carolina-Louisiana prostate cancer project (PCaP). *Prostate*, **2011**, 71, 881-91	4.2	26
87	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. *Nature Genetics*, **2010**, 42, 978-84	36.3	408

86	Maternal alcohol consumption, alcohol metabolism genes, and the risk of oral clefts: a population-based case-control study in Norway, 1996-2001. *American Journal of Epidemiology*, **2010**, 172, 924-31	3.8	48
85	Obesity and weight gain in adulthood and telomere length. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 816-20	4	140
84	Polymorphisms in DNA repair genes, smoking, and bladder cancer risk: findings from the international consortium of bladder cancer. *Cancer Research*, **2009**, 69, 6857-64	10.1	94
83	Oral facial clefts and gene polymorphisms in metabolism of folate/one-carbon and vitamin A: a pathway-wide association study. *Genetic Epidemiology*, **2009**, 33, 247-55	2.6	43
82	SNPinfo: integrating GWAS and candidate gene information into functional SNP selection for genetic association studies. *Nucleic Acids Research*, **2009**, 37, W600-5	20.1	537
81	Bayesian hierarchically weighted finite mixture models for samples of distributions. *Biostatistics*, **2009**, 10, 155-71	3.7	10
80	XRCC1 and DNA polymerase beta in cellular protection against cytotoxic DNA single-strand breaks. *Cell Research*, **2008**, 18, 48-63	24.7	168
79	Maternal smoking and oral clefts: the role of detoxification pathway genes. *Epidemiology*, **2008**, 19, 606-15	3.1	68
78	Assessing Candidate Gene nsSNPs for Phenotypic Differences in Double-Strand Break Repair Using Radiation-Induced gammaH2A.X Foci. *Journal of Cancer Epidemiology*, **2008**, 2008, 387423	2.8	2
77	Folate and one-carbon metabolism gene polymorphisms and their associations with oral facial clefts. *American Journal of Medical Genetics, Part A*, **2008**, 146A, 440-9	2.5	49
76	Tag SNP selection for candidate gene association studies using HapMap and gene resequencing data. *European Journal of Human Genetics*, **2007**, 15, 1063-70	5.3	35
75	Antimutagenicity of cinnamaldehyde and vanillin in human cells: Global gene expression and possible role of DNA damage and repair. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **2007**, 616, 60-9	3.3	55
74	Val153Met polymorphism of catechol-O-methyltransferase and prevalence of uterine leiomyomata. *Reproductive Sciences*, **2007**, 14, 117-20	3	17
73	Folic acid supplements and risk of facial clefts: national population based case-control study. *BMJ, The*, **2007**, 334, 464	5.9	263
72	TAGster: efficient selection of LD tag SNPs in single or multiple populations. *Bioinformatics*, **2007**, 23, 3254-5	7.2	30
71	Detection of pre-invasive lung cancer: technical aspects of the LIFE project. *Toxicologic Pathology*, **2007**, 35, 65-74	2.1	7
70	Smoking is associated with increased telomerase activity in short-term cultures of human bronchial epithelial cells. *Cancer Letters*, **2007**, 246, 24-33	9.9	20
69	APE1 genotype and risk of bladder cancer: evidence for effect modification by smoking. *International Journal of Cancer*, **2006**, 118, 3170-3	7.5	26

68	DNA repair gene polymorphisms and probability of p53 mutation in bladder cancer. *Molecular Carcinogenesis*, **2006**, 45, 715-9	5	19
67	Lycopene intake and prostate cancer risk: effect modification by plasma antioxidants and the XRCC1 genotype. *Nutrition and Cancer*, **2006**, 55, 13-20	2.8	31
66	How well do HapMap haplotypes identify common haplotypes of genes? A comparison with haplotypes of 334 genes resequenced in the environmental genome project. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 133-7	4	12
65	Approximate Bayesian inference for quantiles. *Journal of Nonparametric Statistics*, **2005**, 17, 385-400	0.7	56
64	Chromosomal abnormalities in bronchial epithelium from smokers, nonsmokers, and lung cancer patients. *Cancer Genetics and Cytogenetics*, **2005**, 159, 137-42		5
63	Lead exposure as a risk factor for amyotrophic lateral sclerosis. *Neurodegenerative Diseases*, **2005**, 2, 195-201	2.3	83
62	No association between SOD2 or NQO1 genotypes and risk of bladder cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2005**, 14, 753-4	4	19
61	VEGF promoter haplotype and amyotrophic lateral sclerosis (ALS). *Journal of Neurogenetics*, **2004**, 18, 429-34	1.6	34
60	Application of the GA/KNN method to SELDI proteomics data. *Bioinformatics*, **2004**, 20, 1638-40	7.2	65
59	Analytical and statistical methods to evaluate microsatellite allelic imbalance in small amounts of DNA. *Laboratory Investigation*, **2004**, 84, 649-57	5.9	21
58	Mini-and microsatellite mutations in children from Chernobyl accident cleanup workers. *Mutation Research - Genetic Toxicology and Environmental Mutagenesis*, **2004**, 559, 143-51	3	40
57	Exploring the effects of methylenetetrahydrofolate reductase gene variants C677T and A1298C on the risk of orofacial clefts in 261 Norwegian case-parent triads. *American Journal of Epidemiology*, **2003**, 157, 1083-91	3.8	71
56	Amyotrophic lateral sclerosis, lead, and genetic susceptibility: polymorphisms in the delta-aminolevulinic acid dehydratase and vitamin D receptor genes. *Environmental Health Perspectives*, **2003**, 111, 1335-9	8.4	55
55	Variants of developmental genes (TGFA, TGFB3, and MSX1) and their associations with orofacial clefts: a case-parent triad analysis. *Genetic Epidemiology*, **2003**, 24, 230-9	2.6	67
54	Cleft palate, transforming growth factor alpha gene variants, and maternal exposures: assessing gene-environment interactions in case-parent triads. *Genetic Epidemiology*, **2003**, 25, 367-74	2.6	32
53	Cadmium is a mutagen that acts by inhibiting mismatch repair. *Nature Genetics*, **2003**, 34, 326-9	36.3	374
52	Bayesian latent variable models for median regression on multiple outcomes. *Biometrics*, **2003**, 59, 296-304	1.4	22
51	p53 mutations in bladder cancer: evidence for exogenous versus endogenous risk factors. *Cancer Research*, **2003**, 63, 7530-8	10.1	27

50	HRAS1 variable number of tandem repeats polymorphism and risk of bladder cancer. *International Journal of Cancer*, **2002**, 100, 414-8	7.5	6
49	Pooled analysis and meta-analysis of glutathione S-transferase M1 and bladder cancer: a HuGE review. *American Journal of Epidemiology*, **2002**, 156, 95-109	3.8	159
48	Potential for selection bias with tumor tissue retrieval in molecular epidemiology studies. *Annals of Epidemiology*, **2002**, 12, 1-6	6.4	52
47	DNA repair gene XRCC3 codon 241 polymorphism, its interaction with smoking and XRCC1 polymorphisms, and bladder cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2002**, 11, 939-43	4	25
46	XPD codon 751 polymorphism, metabolism genes, smoking, and bladder cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2002**, 11, 1004-11	4	31
45	Mutations in tetranucleotide repeats following DNA damage depend on repeat sequence and carcinogenic agent. *Cancer Research*, **2002**, 62, 6052-60	10.1	22
44	CTNNB1 mutations and beta-catenin protein accumulation in human hepatocellular carcinomas associated with high exposure to aflatoxin B1. *Molecular Carcinogenesis*, **2001**, 31, 68-73	5	77
43	A novel host cell reactivation assay to assess homologous recombination capacity in human cancer cell lines. *Biochemical and Biophysical Research Communications*, **2001**, 281, 212-9	3.4	33
42	Vitamin D receptor polymorphisms and prostate cancer. *Molecular Carcinogenesis*, **2000**, 27, 18-23	5	49
41	Vitamin D receptor polymorphisms and prostate cancer. *Molecular Carcinogenesis*, **2000**, 27, 18-23	5	17
40	Symposium overview: the role of genetic polymorphism and repair deficiencies in environmental disease. *Toxicological Sciences*, **1999**, 47, 135-43	4.4	16
39	Insulin-like growth factor-I: a key regulator of human cancer risk?. *Journal of the National Cancer Institute*, **1999**, 91, 579-81	9.7	50
38	Prostate cancer risk and polymorphism in 17 hydroxylase (CYP17) and steroid reductase (SRD5A2). *Carcinogenesis*, **1999**, 20, 1727-31	4.6	158
37	Genetic determinism and the overprotection of human subjects. *Nature Genetics*, **1999**, 21, 362	36.3	16
36	Progesterone receptor gene polymorphism and risk for breast and ovarian cancer. *British Journal of Cancer*, **1998**, 78, 277	8.7	40
35	Avoided and avoidable risks of cancer. *Carcinogenesis*, **1997**, 18, 97-105	4.6	85
34	Genetic Analysis of Complex Diseases. *Science*, **1997**, 275, 1327-1330	33.3	51
33	Increased risk for myelodysplastic syndromes in individuals with glutathione transferase theta 1 (GSTT1) gene defect. *Lancet, The*, **1996**, 347, 295-7	40	252

32	Xenobiotic metabolism genes and the risk of recurrent spontaneous abortion. *Epidemiology*, **1996**, 7, 206-8	3.1	18
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2	Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use		2
1	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2