Joni L Rutter

List of Publications by Year in descending order

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49 papers

4,633 citations

26 h-index 253896 43 g-index

51 all docs

51 docs citations

51 times ranked

6871 citing authors

#	Article	IF	CITATIONS
1	The "All of Us―Research Program. New England Journal of Medicine, 2019, 381, 668-676.	13.9	955
2	Cholinergic nicotinic receptor genes implicated in a nicotine dependence association study targeting 348 candidate genes with 3713 SNPs. Human Molecular Genetics, 2007, 16, 36-49.	1.4	784
3	Novel genes identified in a high-density genome wide association study for nicotine dependence. Human Molecular Genetics, 2007, 16, 24-35.	1.4	596
4	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 427-443.	2.2	342
5	Isolation of genes from complex sources of mammalian genomic DNA using exon amplification. Nature Genetics, 1994, 6, 98-105.	9.4	291
6	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. JAMA Network Open, 2021, 4, e2116901.	2.8	179
7	Diversity and inclusion for the All of Us research program: A scoping review. PLoS ONE, 2020, 15, e0234962.	1.1	128
8	p53 Down-regulates Human Matrix Metalloproteinase-1 (Collagenase-1) Gene Expression. Journal of Biological Chemistry, 1999, 274, 11535-11540.	1.6	119
9	Cell-type specific regulation of human interstitial collagenase-1 gene expression by interleukin- $1\hat{l}^2$ (IL- $1\hat{l}^2$) in human fibroblasts and BC-8701 breast cancer cells. Journal of Cellular Biochemistry, 1997, 66, 322-336.	1.2	115
10	Frequent loss of chromosome 14 in atypical and malignant meningioma: identification of a putative `tumor progression' locus. Oncogene, 1997, 14, 611-616.	2.6	109
11	Geneâ €e nvironment interplay in common complex diseases: forging an integrative modelâ€"recommendations from an NIH workshop. Genetic Epidemiology, 2011, 35, 217-225.	0.6	95
12	A Novel Host/Tumor Cell Interaction Activates Matrix Metalloproteinase 1 and Mediates Invasion through Type I Collagen. Journal of Biological Chemistry, 1999, 274, 25371-25378.	1.6	91
13	Kin-cohort estimates for familial breast cancer risk in relation to variants in DNA base excision repair, BRCA1 interacting and growth factor genes. BMC Cancer, 2004, 4, 9.	1.1	73
14	An ontology-driven semantic mashup of gene and biological pathway information: Application to the domain of nicotine dependence. Journal of Biomedical Informatics, 2008, 41, 752-765.	2.5	65
15	Mutational analysis of the BRCA1-interacting genes ZNF350/ZBRK1 and BRIP1/BACH1 among BRCA1 and BRCA2-negative probands from breast-ovarian cancer families and among early-onset breast cancer cases and reference individuals. Human Mutation, 2003, 22, 121-128.	1.1	49
16	Candidate Single Nucleotide Polymorphism Selection using Publicly Available Tools: A Guide for Epidemiologists. American Journal of Epidemiology, 2006, 164, 794-804.	1.6	49
17	Measuring addiction propensity and severity: The need for a new instrument \hat{a} . Drug and Alcohol Dependence, 2010, 111, 4-12.	1.6	41
18	A collaborative translational research framework for evaluating and implementing the appropriate use of human genome sequencing to improve health. PLoS Medicine, 2018, 15, e1002631.	3.9	40

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19	Efficiency of DNA pooling to estimate joint allele frequencies and measure linkage disequilibrium. Genetic Epidemiology, 2002, 22, 94-102.	0.6	39
20	Thyroid Nodules, Polymorphic Variants in DNA Repair and RET-Related Genes, and Interaction with lonizing Radiation Exposure from Nuclear Tests in Kazakhstan. Radiation Research, 2009, 171, 77-88.	0.7	38
21	Symbiotic relationship of pharmacogenetics and drugs of abuse. AAPS Journal, 2006, 8, E174-E184.	2.2	35
22	Development of the Initial Surveys for the All of Us Research Program. Epidemiology, 2019, 30, 597-608.	1.2	35
23	Heterogeneity of risk for melanoma and pancreatic and digestive malignancies. Cancer, 2004, 101, 2809-2816.	2.0	33
24	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. JAMA Network Open, 2022, 5, e223890.	2.8	31
25	CDKN2A point mutations D153spl(c.457G>T) and IVS2+1G>T result in aberrant splice products affecting both p16INK4a and p14ARF. Oncogene, 2003, 22, 4444-4448.	2.6	29
26	The HER2 I655V Polymorphism and Breast Cancer Risk in Ashkenazim. Epidemiology, 2003, 14, 694-700.	1.2	27
27	Supplementing High-Density SNP Microarrays for Additional Coverage of Disease-Related Genes: Addiction as a Paradigm. PLoS ONE, 2009, 4, e5225.	1.1	27
28	Retinoid-Mediated Suppression of Tumor Invasion and Matrix Metalloproteinase Synthesis. Annals of the New York Academy of Sciences, 1999, 878, 466-486.	1.8	26
29	Cannabinoid Receptor-2 and HIV-Associated Neurocognitive Disorders. Journal of NeuroImmune Pharmacology, 2014, 9, 447-453.	2.1	26
30	Similar prevalence of founder BRCA1 and BRCA2 mutations among Ashkenazi and non-Ashkenazi men with breast cancer: Evidence from 261 cases in Israel, 1976–1999. European Journal of Medical Genetics, 2008, 51, 141-147.	0.7	20
31	Do Opioids Activate Latent HIV-1 by Down-Regulating Anti-HIV microRNAs?. Journal of NeuroImmune Pharmacology, 2012, 7, 519-523.	2.1	20
32	Posttranscriptional regulation of collagenase-1 gene expression in synoviocytes by adenosine receptor stimulation. Arthritis and Rheumatism, 1997, 40, 1772-1779.	6.7	19
33	Setting Priorities for Genomic Research. Science, 2004, 304, 1445c-1447c.	6.0	19
34	Genetic Research and Smoking Behavior. JAMA - Journal of the American Medical Association, 2007, 297, 809.	3.8	16
35	Human Metalloproteinase-1 (Collagenase-1) Is a Tumor Suppressor Protein p53 Target Gene. Annals of the New York Academy of Sciences, 1999, 878, 638-641.	1.8	14
36	Two approaches to mutation detection based on functional data. Statistics in Medicine, 2002, 21, 3447-3464.	0.8	13

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37	Identification and characterization of novel human transcripts embedded within HMGA2 in $t(12;14)(q15;q24.1)$ uterine leiomyoma. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2006, 602, 43-53.	0.4	10
38	Demonstrating an approach for evaluating synthetic geospatial and temporal epidemiologic data utility: results from analyzing & mp;gt;1.8 million SARS-CoV-2 tests in the United States National COVID Cohort Collaborative (N3C). Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1350-1365.	2.2	8
39	Cellâ€type specific regulation of human interstitial collagenaseâ€1 gene expression by interleukinâ€1β (ILâ€1β) in human fibroblasts and BCâ€8701 breast cancer cells. Journal of Cellular Biochemistry, 1997, 66, 322-336.	n 1.2	5
40	Reâ€definin G A ddi C CH3 T ion: genomics and epigenomics on substance use disorders. Molecular Genetics & Cenetics & Genomic Medicine, 2014, 2, 273-279.	0.6	2
41	Emerging trends in the abuse of designer drugs and their catastrophic health effects: Update on chemistry, pharmacology, toxicology and addiction potential. Life Sciences, 2014, 97, 1.	2.0	1
42	The Nuts and Bolts of Gene Array Technology and its Application to Drug Abuse Research. Drug and Alcohol Dependence, 2007, 91, 102-106.	1.6	0
43	TRP channels, GPCRs, endolipids and natural products: A tetrad that makes sense. Life Sciences, 2013, 92, 393.	2.0	O
44	Symbiotic Relationship of Pharmacogenetics and Drugs of Abuse. , 2008, , 69-86.		0
45	The Genetics of Addiction: A Global Problem with Global Opportunities. , 2015, , 39-63.		0
46	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		0
47	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		O
48	Diversity and inclusion for the All of Us research program: A scoping review., 2020, 15, e0234962.		0
49	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		0