

Julja Burchard

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

10,700
citations

186265

28
h-index

289244

40
g-index

42
all docs

42
docs citations

42
times ranked

13398
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction and Prevention of Preterm Birth: A Prospective, Randomized Intervention Trial. <i>American Journal of Perinatology</i> , 2023, 40, 1071-1080.	1.4	8
2	Performance of a validated spontaneous preterm delivery predictor in South Asian and Sub-Saharan African women: a nested case control study. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2022, 35, 8878-8886.	1.5	2
3	Better Estimation of Spontaneous Preterm Birth Prediction Performance through Improved Gestational Age Dating. <i>Journal of Clinical Medicine</i> , 2022, 11, 2885.	2.4	3
4	Cost-Effectiveness of a Proteomic Test for Preterm Birth Prediction. <i>ClinicoEconomics and Outcomes Research</i> , 2021, Volume 13, 809-820.	1.9	11
5	Clinical Validation of a Proteomic Biomarker Threshold for Increased Risk of Spontaneous Preterm Birth and Associated Clinical Outcomes: A Replication Study. <i>Journal of Clinical Medicine</i> , 2021, 10, 5088.	2.4	6
6	In Reply. <i>Obstetrics and Gynecology</i> , 2020, 135, 972-972.	2.4	0
7	Performance of a proteomic preterm delivery predictor in a large independent prospective cohort. <i>American Journal of Obstetrics & Gynecology MFM</i> , 2020, 2, 100140.	2.6	27
8	BET bromodomain inhibition blocks the function of a critical AR-independent master regulator network in lethal prostate cancer. <i>Oncogene</i> , 2019, 38, 5658-5669.	5.9	23
9	Effects of Selective Exclusion of Patients on Preterm Birth Test Performance. <i>Obstetrics and Gynecology</i> , 2019, 134, 1333-1338.	2.4	9
10	Discovery of Selective RNA-Binding Small Molecules by Affinity-Selection Mass Spectrometry. <i>ACS Chemical Biology</i> , 2018, 13, 820-831.	3.4	78
11	Cell fusion potentiates tumor heterogeneity and reveals circulating hybrid cells that correlate with stage and survival. <i>Science Advances</i> , 2018, 4, eaat7828.	10.3	203
12	Vitamin C Prevents Offspring DNA Methylation Changes Associated with Maternal Smoking in Pregnancy. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 745-755.	5.6	83
13	Placental Growth Factor (PlGF) Enhances TLR/MK2 Dependent TNF Gene Transcription and Dissociates miRNAs Targeting TNF Regulatory Transcripts from the Polysome. <i>Blood</i> , 2016, 128, 408-408.	1.4	0
14	The genome as pharmacopeia: Association of genetic dose with phenotypic response. <i>Biochemical Pharmacology</i> , 2015, 94, 229-240.	4.4	3
15	A Single Dose of EGLN1 siRNA Yields Increased Erythropoiesis in Nonhuman Primates. <i>Nucleic Acid Therapeutics</i> , 2014, 24, 405-412.	3.6	2
16	Assessing unintended hybridization-induced biological effects of oligonucleotides. <i>Nature Biotechnology</i> , 2012, 30, 920-923.	17.5	86
17	Predictive Genes in Adjacent Normal Tissue Are Preferentially Altered by sCNV during Tumorigenesis in Liver Cancer and May Rate Limiting. <i>PLoS ONE</i> , 2011, 6, e20090.	2.5	68
18	DLK1-DIO3 Genomic Imprinted MicroRNA Cluster at 14q32.2 Defines a Stemlike Subtype of Hepatocellular Carcinoma Associated with Poor Survival. <i>Journal of Biological Chemistry</i> , 2011, 286, 30706-30713.	3.4	147

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19	RNA-Induced Silencing Complex-Bound Small Interfering RNA Is a Determinant of RNA Interference-Mediated Gene Silencing in Mice. <i>Molecular Pharmacology</i> , 2011, 79, 953-963.	2.3	44
20	Gene expression signature of c-MYC-immortalized human fibroblasts reveals loss of growth inhibitory response to TGF β 2. <i>Cell Cycle</i> , 2011, 10, 2540-2548.	2.6	10
21	Global Regulation on microRNA in Hepatitis B Virus-Associated Hepatocellular Carcinoma. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 187-191.	2.0	36
22	microRNA miR-22 as a regulator of mitochondrial metabolic gene network in hepatocellular carcinoma. <i>Molecular Systems Biology</i> , 2010, 6, 402.	7.2	169
23	MicroRNA miR-210 modulates cellular response to hypoxia through the MYC antagonist MNT. <i>Cell Cycle</i> , 2009, 8, 2756-2768.	2.6	274
24	MicroRNA-like off-target transcript regulation by siRNAs is species specific. <i>Rna</i> , 2009, 15, 308-315.	3.5	71
25	MicroRNA 21 Promotes Glioma Invasion by Targeting Matrix Metalloproteinase Regulators. <i>Molecular and Cellular Biology</i> , 2008, 28, 5369-5380.	2.3	828
26	MicroRNAs in the miR-106b Family Regulate p21/CDKN1A and Promote Cell Cycle Progression. <i>Molecular and Cellular Biology</i> , 2008, 28, 2167-2174.	2.3	513
27	Transcripts Targeted by the MicroRNA-16 Family Cooperatively Regulate Cell Cycle Progression. <i>Molecular and Cellular Biology</i> , 2007, 27, 2240-2252.	2.3	516
28	Genome-wide resources of endoribonuclease-prepared short interfering RNAs for specific loss-of-function studies. <i>Nature Methods</i> , 2007, 4, 337-344.	19.0	167
29	Designing siRNA That Distinguish between Genes That Differ by a Single Nucleotide. <i>PLoS Genetics</i> , 2006, 2, e140.	3.5	237
30	A genome wide analysis of ubiquitin ligases in APP processing identifies a novel regulator of BACE1 mRNA levels. <i>Molecular and Cellular Neurosciences</i> , 2006, 33, 227-235.	2.2	24
31	LRRTM3 promotes processing of amyloid-precursor protein by BACE1 and is a positional candidate gene for late-onset Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17967-17972.	7.1	94
32	Small Interfering RNA Screens Reveal Enhanced Cisplatin Cytotoxicity in Tumor Cells Having both BRCA Network and TP53 Disruptions. <i>Molecular and Cellular Biology</i> , 2006, 26, 9377-9386.	2.3	176
33	Position-specific chemical modification of siRNAs reduces "off-target" transcript silencing. <i>Rna</i> , 2006, 12, 1197-1205.	3.5	686
34	Widespread siRNA "off-target" transcript silencing mediated by seed region sequence complementarity. <i>Rna</i> , 2006, 12, 1179-1187.	3.5	817
35	Synthetic shRNAs as potent RNAi triggers. <i>Nature Biotechnology</i> , 2005, 23, 227-231.	17.5	416
36	Production of complex nucleic acid libraries using highly parallel in situ oligonucleotide synthesis. <i>Nature Methods</i> , 2004, 1, 241-248.	19.0	96

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37	T lymphocyte activation gene identification by coregulated expression on DNA microarrays. <i>Genomics</i> , 2004, 83, 989-999.	2.9	73
38	Expression profiling reveals off-target gene regulation by RNAi. <i>Nature Biotechnology</i> , 2003, 21, 635-637.	17.5	2,101
39	Modulation of TCR-induced transcriptional profiles by ligation of CD28, ICOS, and CTLA-4 receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11790-11795.	7.1	279
40	Expression profiling using microarrays fabricated by an ink-jet oligonucleotide synthesizer. <i>Nature Biotechnology</i> , 2001, 19, 342-347.	17.5	1,225
41	Widespread aneuploidy revealed by DNA microarray expression profiling. <i>Nature Genetics</i> , 2000, 25, 333-337.	21.4	454
42	Drug target validation and identification of secondary drug target effects using DNA microarrays. <i>Nature Medicine</i> , 1998, 4, 1293-1301.	30.7	635