Matthew D Wilkerson

List of Publications by Year
in descending order

38	6,443	430754	360920
papers	citations	18 h-index	35 g-index

40	40	40	15626
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rare variant association study of veteran twin whole-genomes links severe depression with a nonsynonymous change in the neuronal gene BHLHE22. World Journal of Biological Psychiatry, 2022, 23, 295-306.	1.3	1
2	Germline mutation landscape of DNA damage repair genes in African Americans with prostate cancer highlights potentially targetable RAD genes. Nature Communications, 2022, 13, 1361.	5.8	8
3	Whole-Genome Sequencing Identifies PPARGC1A as a Putative Modifier of Cancer Risk in BRCA1/2 Mutation Carriers. Cancers, 2022, 14, 2350.	1.7	1
4	Distinguishing Smoking-Related Lung Disease Phenotypes Via Imaging and Molecular Features. Chest, 2021, 159, 549-563.	0.4	6
5	Transcriptomic Analysis of Mouse Brain After Traumatic Brain Injury Reveals That the Angiotensin Receptor Blocker Candesartan Acts Through Novel Pathways. Frontiers in Neuroscience, 2021, 15, 636259.	1.4	13
6	Personalized Single-Cell Proteogenomics to Distinguish Acute Myeloid Leukemia from Nonmalignant Clonal Hematopoiesis. Blood Cancer Discovery, 2021, 2, 319-325.	2.6	24
7	Tensin 1 (TNS1) is a modifier gene for low body mass index (BMI) in homozygous [F508del]CFTR patients. Physiological Reports, 2021, 9, e14886.	0.7	0
8	Abstract 2074: Germline mutation landscape of all DNA repair genes in African American prostate cancer patients. , 2021, , .		0
9	Association of Variants in the SPTLC1 Gene With Juvenile Amyotrophic Lateral Sclerosis. JAMA Neurology, 2021, 78, 1236.	4.5	46
10	Identification of a pathogenic intronic KIF5A mutation in an ALS-FTD kindred. Neurology, 2020, 95, 1015-1018.	1.5	19
11	MutEnricher: a flexible toolset for somatic mutation enrichment analysis of tumor whole genomes. BMC Bioinformatics, 2020, 21, 338.	1.2	6
12	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. Cell Reports, 2020, 31, 107502.	2.9	69
13	Neuroinflammatory astrocytes generated from cord blood-derived human induced pluripotent stem cells. Journal of Neuroinflammation, 2019, 16, 164.	3.1	14
14	Digitoxin Inhibits Epithelial-to-Mesenchymal-Transition in Hereditary Castration Resistant Prostate Cancer. Frontiers in Oncology, 2019, 9, 630.	1.3	11
15	Sleep Deprivation Alters the Pituitary Stress Transcriptome in Male and Female Mice. Frontiers in Endocrinology, 2019, 10, 676.	1.5	7
16	Identification of a Robust Methylation Classifier for Cutaneous Melanoma Diagnosis. Journal of Investigative Dermatology, 2019, 139, 1349-1361.	0.3	23
17	Region- and time-dependent gene regulation in the amygdala and anterior cingulate cortex of a PTSD-like mouse model. Molecular Brain, 2019, 12, 25.	1.3	16
18	A Computational Protocol for Detecting Somatic Mutations by Integrating DNA and RNA Sequencing. Methods in Molecular Biology, 2019, 1878, 109-124.	0.4	0

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19	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
20	Chromaffin cell biology: inferences from The Cancer Genome Atlas. Cell and Tissue Research, 2018, 372, 339-346.	1.5	17
21	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. Nature Communications, 2018, 9, 1048.	5.8	254
22	N eonatal mouse cortical but not isogenic human astrocyte feeder layers enhance the functional maturation of induced pluripotent stem cellâ€derived neurons in culture. Glia, 2018, 66, 725-748.	2.5	23
23	Factor XIIIAâ€"expressing inflammatory monocytes promote lung squamous cancer through fibrin cross-linking. Nature Communications, 2018, 9, 1988.	5.8	69
24	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	7.7	532
25	Tsc2 disruption in mesenchymal progenitors results in tumors with vascular anomalies overexpressing Lgals3. ELife, 2017, 6, .	2.8	13
26	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. Npj Breast Cancer, 2016, 2, 16007.	2.3	33
27	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	13.7	1,384
28	Cafeteria diet-induced obesity causes oxidative damage in white adipose. Biochemical and Biophysical Research Communications, 2016, 473, 545-550.	1.0	44
29	Validation of the Lung Subtyping Panel in Multiple Fresh-Frozen and Formalin-Fixed, Paraffin-Embedded Lung Tumor Gene Expression Data Sets. Archives of Pathology and Laboratory Medicine, 2016, 140, 536-542.	1.2	4
30	Subtyping sub-Saharan esophageal squamous cell carcinoma by comprehensive molecular analysis. JCI Insight, 2016, 1, e88755.	2.3	51
31	Combined Targeted DNA Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using UNCseq and NGScopy, and RNA Sequencing Using UNCqeR for the Detection of Genetic Aberrations in NSCLC. PLoS ONE, 2015, 10, e0129280.	1.1	36
32	Coexistent ARID1Aâ€"PIK3CA mutations promote ovarian clear-cell tumorigenesis through pro-tumorigenic inflammatory cytokine signalling. Nature Communications, 2015, 6, 6118.	5.8	247
33	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
34	Alterations of LKB1 and KRAS and risk of brain metastasis: Comprehensive characterization by mutation analysis, copy number, and gene expression in non-small-cell lung carcinoma. Lung Cancer, 2014, 86, 255-261.	0.9	64
35	SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples. Nucleic Acids Research, 2014, 42, e113-e113.	6.5	17
36	ABRA: improved coding indel detection via assembly-based realignment. Bioinformatics, 2014, 30, 2813-2815.	1.8	140

#	Article	IF	Citations
37	Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. Nucleic Acids Research, 2014, 42, e107-e107.	6.5	76
38	BlackOPs: increasing confidence in variant detection through mappability filtering. Nucleic Acids Research, 2013, 41, e178-e178.	6.5	19