Samantha N Mcnulty

List of Publications by Year in descending order

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759233 677142 23 525 12 22 citations h-index g-index papers 23 23 23 939 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Endosymbiont DNA in Endobacteria-Free Filarial Nematodes Indicates Ancient Horizontal Genetic Transfer. PLoS ONE, 2010, 5, e11029.	2.5	105
2	Genomic heterogeneity of ALK fusion breakpoints in non-small-cell lung cancer. Modern Pathology, 2018, 31, 791-808.	5 . 5	79
3	Helminth.net: expansions to Nematode.net and an introduction to Trematode.net. Nucleic Acids Research, 2015, 43, D698-D706.	14.5	58
4	Comparing the mitochondrial genomes of Wolbachia-dependent and independent filarial nematode species. BMC Genomics, 2012, 13, 145.	2.8	39
5	Inter and intra-specific diversity of parasites that cause lymphatic filariasis. Infection, Genetics and Evolution, 2013, 14, 137-146.	2.3	34
6	Beyond sequence variation: assessment of copy number variation in adult glioblastoma through targeted tumor somatic profiling. Human Pathology, 2019, 86, 170-181.	2.0	24
7	Diagnostic Utility of Next-Generation Sequencing for Disorders of Somatic Mosaicism: A Five-Year Cumulative Cohort. American Journal of Human Genetics, 2019, 105, 734-746.	6.2	23
8	Transcriptomic and Proteomic Analyses of a Wolbachia-Free Filarial Parasite Provide Evidence of Trans-Kingdom Horizontal Gene Transfer. PLoS ONE, 2012, 7, e45777.	2. 5	20
9	Analysis of point mutations and copy number variation in Grade II and III meningioma. Experimental and Molecular Pathology, 2018, 105, 328-333.	2.1	18
10	Discriminating a common somatic ASXL1 mutation (c.1934dup; p.G646Wfs*12) from artifact in myeloid malignancies using NGS. Leukemia, 2018, 32, 1874-1878.	7.2	18
11	Pediatric meningioma: a clinicopathologic and molecular study with potential grading implications. Brain Pathology, 2020, 30, 1134-1143.	4.1	17
12	Localization of Wolbachia-like gene transcripts and peptides in adult Onchocerca flexuosa worms indicates tissue specific expression. Parasites and Vectors, 2013, 6, 2.	2. 5	15
13	BRAF mutations may identify a clinically distinct subset of glioblastoma. Scientific Reports, 2021, 11, 19999.	3.3	15
14	Optimization of Population Frequency Cutoffs for Filtering Common Germline Polymorphisms from Tumor-Only Next-Generation Sequencing Data. Journal of Molecular Diagnostics, 2019, 21, 903-912.	2.8	13
15	Absence of Wolbachia Endobacteria in Chandlerella quiscali, an Avian Filarial Parasite. Journal of Parasitology, 2012, 98, 382-387.	0.7	9
16	Impact of Reducing DNA Input on Next-Generation Sequencing Library Complexity and Variant Detection. Journal of Molecular Diagnostics, 2020, 22, 720-727.	2.8	9
17	Beyond Panel-Based Testing: Exome Analysis Increases Sensitivity for Diagnosis of Genetic Kidney Disease. Kidney360, 2020, 1, 772-780.	2.1	7
18	Brugia malayi: Whole genome amplification for genomic characterization of filarial parasites. Experimental Parasitology, 2008, 119, 256-263.	1.2	6

#	Article	IF	CITATIONS
19	Direct experimental manipulation of intestinal cells in Ascaris suum, with minor influences on the global transcriptome. International Journal for Parasitology, 2017, 47, 271-279.	3.1	6
20	Clinical Implications of a Targeted RNA-Sequencing Panel in the Detection of Gene Fusions in Solid Tumors. Journal of Molecular Diagnostics, 2021, 23, 1749-1760.	2.8	5
21	Comparison of gene fusion detection methods in salivary gland tumors. Human Pathology, 2022, 123, 1-10.	2.0	3
22	A Next-Generation Sequencing Test for Severe Congenital Neutropenia. Journal of Molecular Diagnostics, 2021, 23, 200-211.	2.8	2
23	Utility of copy number variants in the classification of intracranial ependymoma. Cancer Genetics, 2020, 240, 66-72.	0.4	0