

Wilson W L Sung

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4647306/publications.pdf>

Version: 2024-02-01

17
papers

3,913
citations

758635

12
h-index

887659

17
g-index

17
all docs

17
docs citations

17
times ranked

7613
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibiotic resistance is ancient. <i>Nature</i> , 2011, 477, 457-461.	13.7	1,967
2	Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. <i>Nature Neuroscience</i> , 2017, 20, 602-611.	7.1	691
3	Improved diagnostic yield compared with targeted gene sequencing panels suggests a role for whole-genome sequencing as a first-tier genetic test. <i>Genetics in Medicine</i> , 2018, 20, 435-443.	1.1	404
4	Molecular Diagnostic Yield of Chromosomal Microarray Analysis and Whole-Exome Sequencing in Children With Autism Spectrum Disorder. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 895.	3.8	352
5	A Comprehensive Workflow for Read Depth-Based Identification of Copy-Number Variation from Whole-Genome Sequence Data. <i>American Journal of Human Genetics</i> , 2018, 102, 142-155.	2.6	156
6	A microcosting and cost-consequence analysis of clinical genomic testing strategies in autism spectrum disorder. <i>Genetics in Medicine</i> , 2017, 19, 1268-1275.	1.1	62
7	The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 56 participants. <i>Cmaj</i> , 2018, 190, E126-E136.	0.9	57
8	Genome Sequencing as a Diagnostic Test in Children With Unexplained Medical Complexity. <i>JAMA Network Open</i> , 2020, 3, e2018109.	2.8	47
9	Proteomic analysis of the response of the plant growth-promoting bacterium <i>Pseudomonas putida</i> UW4 to nickel stress. <i>Proteome Science</i> , 2009, 7, 18.	0.7	38
10	Impact of DNA source on genetic variant detection from human whole-genome sequencing data. <i>Journal of Medical Genetics</i> , 2019, 56, 809-817.	1.5	32
11	Acclimation of the crucifer <i>Eutrema salsugineum</i> to phosphate limitation is associated with constitutively high expression of phosphate-starvation genes. <i>Plant, Cell and Environment</i> , 2016, 39, 1818-1834.	2.8	24
12	De Novo Genome and Transcriptome Assembly of the Canadian Beaver (<i>Castor canadensis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 755-773.	0.8	18
13	Clinical Genetic Risk Variants Inform a Functional Protein Interaction Network for Tetralogy of Fallot. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003410.	1.6	15
14	Long-Read Sequencing Improves the Detection of Structural Variations Impacting Complex Non-Coding Elements of the Genome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2060.	1.8	14
15	Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. <i>Npj Genomic Medicine</i> , 2022, 7, 18.	1.7	14
16	Exposure of two <i>Eutrema salsugineum</i> (<i>Thellungiella salsuginea</i>) accessions to water deficits reveals different coping strategies in response to drought. <i>Physiologia Plantarum</i> , 2015, 155, 267-280.	2.6	13
17	Coding and long non-coding RNAs provide evidence of distinct transcriptional reprogramming for two ecotypes of the extremophile plant <i>Eutrema salsugineum</i> undergoing water deficit stress. <i>BMC Genomics</i> , 2020, 21, 396.	1.2	9