

Diego Vozzi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11121485/publications.pdf>

Version: 2024-02-01

18
papers

2,699
citations

623734

14
h-index

888059

17
g-index

18
all docs

18
docs citations

18
times ranked

7851
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
2	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
3	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
4	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	21.4	215
5	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
6	Linkage Study and Exome Sequencing Identify a BDP1 Mutation Associated with Hereditary Hearing Loss. <i>PLoS ONE</i> , 2013, 8, e80323.	2.5	50
7	Genome-wide association analysis on normal hearing function identifies <i>PCDH20</i> and <i>SLC28A3</i> as candidates for hearing function and loss. <i>Human Molecular Genetics</i> , 2015, 24, 5655-5664.	2.9	37
8	Mevalonate kinase deficiency and IBD: shared genetic background. <i>Gut</i> , 2014, 63, 1367-1368.	12.1	30
9	Molecular Diagnosis of Usher Syndrome: Application of Two Different Next Generation Sequencing-Based Procedures. <i>PLoS ONE</i> , 2012, 7, e43799.	2.5	29
10	Increased Rate of Deleterious Variants in Long Runs of Homozygosity of an Inbred Population from Qatar. <i>Human Heredity</i> , 2015, 79, 14-19.	0.8	28
11	Molecular epidemiology of Usher syndrome in Italy. <i>Molecular Vision</i> , 2011, 17, 1662-8.	1.1	27
12	Targeted sequencing identifies novel variants involved in autosomal recessive hereditary hearing loss in Qatari families. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2017, 800-802, 29-36.	1.0	23
13	Next-generation sequencing identified SPATC1L as a possible candidate gene for both early-onset and age-related hearing loss. <i>European Journal of Human Genetics</i> , 2019, 27, 70-79.	2.8	22
14	Consanguinity and Hereditary Hearing Loss in Qatar. <i>Human Heredity</i> , 2014, 77, 175-182.	0.8	15
15	Putative modifier genes in mevalonate kinase deficiency. <i>Molecular Medicine Reports</i> , 2016, 13, 3181-3189.	2.4	4
16	Two-gene mutation in a single patient: Biochemical and functional analysis for a correct interpretation of exome results. <i>Molecular Medicine Reports</i> , 2015, 12, 6128-6132.	2.4	2
17	The Challenge of Next Generation Sequencing in a Boy With Severe Mononucleosis and EBV-related Lymphoma. <i>Journal of Pediatric Hematology/Oncology</i> , 2018, 40, e323-e326.	0.6	2
18	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015, 70, 758-762.	0.4	0