Diego Vozzi

List of Publications by Year
in descending order

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	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
2	Next-generation sequencing identified SPATC1L as a possible candidate gene for both early-onset and age-related hearing loss. European Journal of Human Genetics, 2019, 27, 70-79.	2.8	22
3	The Challenge of Next Generation Sequencing in a Boy With Severe Mononucleosis and EBV-related Lymphoma. Journal of Pediatric Hematology/Oncology, 2018, 40, e323-e326.	0.6	2
4	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
5	Targeted sequencing identifies novel variants involved in autosomal recessive hereditary hearing loss in Qatari families. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2017, 800-802, 29-36.	1.0	23
6	Putative modifier genes in mevalonate kinase deficiency. Molecular Medicine Reports, 2016, 13, 3181-3189.	2.4	4
7	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
8	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
9	Two-gene mutation in a single patient: Biochemical and functional analysis for a correct interpretation of exome results. Molecular Medicine Reports, 2015, 12, 6128-6132.	2.4	2
10	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
11	Increased Rate of Deleterious Variants in Long Runs of Homozygosity of an Inbred Population from Qatar. Human Heredity, 2015, 79, 14-19.	0.8	28
12	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
13	Genome-wide association analysis on normal hearing function identifiesPCDH20andSLC28A3as candidates for hearing function and loss. Human Molecular Genetics, 2015, 24, 5655-5664.	2.9	37
14	Mevalonate kinase deficiency and IBD: shared genetic background. Gut, 2014, 63, 1367-1368.	12.1	30
15	Consanguinity and Hereditary Hearing Loss in Qatar. Human Heredity, 2014, 77, 175-182.	0.8	15
16	Linkage Study and Exome Sequencing Identify a BDP1 Mutation Associated with Hereditary Hearing Loss. PLoS ONE, 2013, 8, e80323.	2.5	50
17	Molecular Diagnosis of Usher Syndrome: Application of Two Different Next Generation Sequencing-Based Procedures. PLoS ONE, 2012, 7, e43799.	2.5	29
18	Molecular epidemiology of Usher syndrome in Italy. Molecular Vision, 2011, 17, 1662-8.	1.1	27