Alfredo Iacoangeli

List of Publications by Year
in descending order

33	1,414	516710 16	414414 32
papers	citations	h-index	g-index

49	49	49	2439
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural variation analysis of 6,500 whole genome sequences in amyotrophic lateral sclerosis. Npj Genomic Medicine, 2022, 7, 8.	3.8	23
2	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
3	Whole-genome sequencing reveals that variants in the Interleukin 18 Receptor Accessory Protein 3â€²UTR protect against ALS. Nature Neuroscience, 2022, 25, 433-445.	14.8	16
4	GEOexplorer: a webserver for gene expression analysis and visualisation. Nucleic Acids Research, 2022, 50, W367-W374.	14.5	17
5	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	8.8	49
6	DGLinker: flexible knowledge-graph prediction of diseaseâ€“gene associations. Nucleic Acids Research, 2021, 49, W153-W161.	14.5	19
7	A HML6 endogenous retrovirus on chromosome 3 is upregulated in amyotrophic lateral sclerosis motor cortex. Scientific Reports, 2021, 11, 14283.	3.3	13
8	Association of Variants in the SPTLC1 Gene With Juvenile Amyotrophic Lateral Sclerosis. JAMA Neurology, 2021, 78, 1236.	9.0	46
9	Advances in the genetic classification of amyotrophic lateral sclerosis. Current Opinion in Neurology, 2021, 34, 756-764.	3.6	12
10	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
11	SCFD1 expression quantitative trait loci in amyotrophic lateral sclerosis are differentially expressed. Brain Communications, 2021, 3, fcab236.	3.3	14
12	Enrichment of SARM1 alleles encoding variants with constitutively hyperactive NADase in patients with ALS and other motor nerve disorders. ELife, 2021, 10, .	6.0	44
13	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
14	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. Cell Reports, 2020, 33, 108456.	6.4	24
15	Frequency and methylation status of selected retrotransposition competent L1 loci in amyotrophic lateral sclerosis. Molecular Brain, 2020, 13, 154.	2.6	7
16	Genome-wide Meta-analysis Finds the ACSL5-ZDHHC6 Locus Is Associated with ALS and Links Weight Loss to the Disease Genetics. Cell Reports, 2020, 33, 108323.	6.4	41
17	Relationship between smoking and ALS: Mendelian randomisation interrogation of causality. Journal of Neurology, Neurosurgery and Psychiatry, 2020, 91, 1312-1315.	1.9	11
18	A Knowledge-Based Machine Learning Approach to Gene Prioritisation in Amyotrophic Lateral Sclerosis. Genes, 2020, 11, 668.	2.4	16

#	Article	IF	Citations
19	UK case control study of smoking and risk of amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2020, 21, 222-227.	1.7	10
20	ATXN1 repeat expansions confer risk for amyotrophic lateral sclerosis and contribute to TDP-43 mislocalization. Brain Communications, 2020, 2, fcaa064.	3.3	33
21	Cross-reactive probes on Illumina DNA methylation arrays: a large study on ALS shows that a cautionary approach is warranted in interpreting epigenome-wide association studies. NAR Genomics and Bioinformatics, 2020, 2, lqaa105.	3.2	13
22	C9orf72 intermediate expansions of 24â€“30 repeats are associated with ALS. Acta Neuropathologica Communications, 2019, 7, 115.	5.2	75
23	DNAscan: personal computer compatible NGS analysis, annotation and visualisation. BMC Bioinformatics, 2019, 20, 213.	2.6	14
24	ALSgeneScanner: a pipeline for the analysis and interpretation of DNA sequencing data of ALS patients. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2019, 20, 207-215.	1.7	11
25	Telomere length is greater in ALS than in controls: a whole genome sequencing study. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2019, 20, 229-234.	1.7	18
26	Exome sequencing in amyotrophic lateral sclerosis implicates a novel gene, DNAJC7, encoding a heat-shock protein. Nature Neuroscience, 2019, 22, 1966-1974.	14.8	101
27	Association of NIPA1 repeat expansions with amyotrophic lateral sclerosis in a large international cohort. Neurobiology of Aging, 2019, 74, 234.e9-234.e15.	3.1	26
28	Younger age of onset in familial amyotrophic lateral sclerosis is a result of pathogenic gene variants, rather than ascertainment bias. Journal of Neurology, Neurosurgery and Psychiatry, 2019, 90, 268-271.	1.9	38
29	Reconsidering the causality of TIA1 mutations in ALS. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2018, 19, 1-3.	1.7	22
30	Project MinE: study design and pilot analyses of a large-scale whole-genome sequencing study in amyotrophic lateral sclerosis. European Journal of Human Genetics, 2018, 26, 1537-1546.	2.8	129
31	PepComposer: computational design of peptides binding to a given protein surface. Nucleic Acids Research, 2016, 44, W522-W528.	14.5	52
32	Exploiting Homology Information in Nontemplate Based Prediction of Protein Structures. Journal of Chemical Theory and Computation, 2015, 11, 5045-5051.	5.3	1
33	Mutations in the Sphingolipid Pathway Gene <i>SPTLC1</i> are a Cause of Amyotrophic Lateral Sclerosis. SSRN Electronic Journal, 0, , .	0.4	0