William Sproviero

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6862610/publications.pdf

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31 papers	2,140 citations	361413 20 h-index	454955 30 g-index
34 all docs	34 docs citations	34 times ranked	4131 citing authors

#	Article	IF	Citations
1	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
2	Lipidomic traits of plasma and cerebrospinal fluid in amyotrophic lateral sclerosis correlate with disease progression. Brain Communications, 2021, 3, fcab143.	3.3	29
3	High Blood Pressure and Risk of Dementia: A Two-Sample Mendelian Randomization Study in the UK Biobank. Biological Psychiatry, 2021, 89, 817-824.	1.3	35
4	Associations Between Brain Volumes and Cognitive Tests with Hypertensive Burden in UK Biobank. Journal of Alzheimer's Disease, 2021, 84, 1373-1389.	2.6	19
5	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
6	ATXN1 repeat expansions confer risk for amyotrophic lateral sclerosis and contribute to TDP-43 mislocalization. Brain Communications, 2020, 2, fcaa064.	3.3	33
7	C9orf72 intermediate expansions of 24â€“30 repeats are associated with ALS. Acta Neuropathologica Communications, 2019, 7, 115.	5.2	75
8	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
9	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
10	Opioid use, postoperative complications, and implant survival after unicompartmental versus total knee replacement: a population-based network study. Lancet Rheumatology, The, 2019, 1, e229-e236.	3.9	18
11	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
12	Identification of new risk factors for rolandic epilepsy: CNV at Xp22.31 and alterations at cholinergic synapses. Journal of Medical Genetics, 2018, 55, 607-616.	3.2	22
13	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
14	The multistep hypothesis of ALS revisited. Neurology, 2018, 91, e635-e642.	1.1	146
15	CHCHD10 variants in amyotrophic lateral sclerosis: Where is the evidence?. Annals of Neurology, 2018, 84, 110-116.	5.3	24
16	ATXN2 trinucleotide repeat length correlates with risk of ALS. Neurobiology of Aging, 2017, 51, 178.e1-178.e9.	3.1	86
17	A comprehensive analysis of rare genetic variation in amyotrophic lateral sclerosis in the UK. Brain, 2017, 140, 1611-1618.	7.6	71
18	Meta-analysis of pharmacogenetic interactions in amyotrophic lateral sclerosis clinical trials. Neurology, 2017, 89, 1915-1922.	1.1	82

#	Article	IF	Citations
19	Detection of long repeat expansions from PCR-free whole-genome sequence data. Genome Research, 2017, 27, 1895-1903.	5.5	277
20	Targeted Genetic Screen in Amyotrophic Lateral Sclerosis Reveals Novel Genetic Variants with Synergistic Effect on Clinical Phenotype. Frontiers in Molecular Neuroscience, 2017, 10, 370.	2.9	24
21	Rare genetic variation in UNC13A may modify survival in amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2016, 17, 593-599.	1.7	22
22	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	21.4	494
23	NEK1 variants confer susceptibility to amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1037-1042.	21.4	218
24	Association of a Locus in theCAMTA1Gene With Survival in Patients With Sporadic Amyotrophic Lateral Sclerosis. JAMA Neurology, 2016, 73, 812.	9.0	57
25	Investigation of next-generation sequencing technologies as a diagnostic tool for amyotrophic lateral sclerosis. Neurobiology of Aging, 2015, 36, 1600.e5-1600.e8.	3.1	32
26	Residual association at C9orf72 suggests an alternative amyotrophic lateral sclerosis-causing hexanucleotide repeat. Neurobiology of Aging, 2013, 34, 2234.e1-2234.e7.	3.1	22
27	Ataxin-1 and ataxin-2 intermediate-length PolyQ expansions in amyotrophic lateral sclerosis. Neurology, 2012, 79, 2315-2320.	1.1	70
28	FUS mutations in sporadic amyotrophic lateral sclerosis: Clinical and genetic analysis. Neurobiology of Aging, 2012, 33, 837.e1-837.e5.	3.1	32
29	The p.Arg416Cys mutation in SPG3a gene associated with a pure form of spastic paraplegia. Muscle and Nerve, 2012, 45, 919-920.	2.2	5
30	SMN1 gene copy number analyses for SMA healthy carriers in Italian population. Journal of Pediatric Genetics, 2012, 1, 99-102.	0.7	0
31	A novel NF1 gene mutation in an Italian family with neurofibromatosis type 1. Child's Nervous System, 2011, 27, 635-638.	1.1	4