

Wouter van Rheenen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5200691/publications.pdf>

Version: 2024-02-01

58
papers

7,745
citations

126907

33
h-index

133252

59
g-index

66
all docs

66
docs citations

66
times ranked

16913
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. <i>European Journal of Human Genetics</i> , 2022, 30, 532-539.	2.8	16
2	Structural variation analysis of 6,500 whole genome sequences in amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2022, 7, 8.	3.8	23
3	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. <i>Genome Medicine</i> , 2022, 14, 7.	8.2	12
4	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. <i>Science Translational Medicine</i> , 2022, 14, eabj0264.	12.4	38
5	Major advances in neuromuscular disorders in the past two decades. <i>Lancet Neurology</i> , The, 2022, 21, 585-587.	10.2	2
6	Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. <i>Biological Psychiatry</i> , 2021, 89, 11-19.	1.3	59
7	The Effect of <i>SMN</i> Gene Dosage on ALS Risk and Disease Severity. <i>Annals of Neurology</i> , 2021, 89, 686-697.	5.3	10
8	Distinctive pattern of temporal atrophy in patients with frontotemporal dementia and the I383V variant in <i>TARDBP</i> . <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2021, 92, 787-789.	1.9	5
9	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	8.8	49
10	Genotype-phenotype correlations of <i>KIF5A</i> stalk domain variants. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2021, 22, 561-570.	1.7	9
11	Associations between lifestyle and amyotrophic lateral sclerosis stratified by <i>C9orf72</i> genotype: a longitudinal, population-based, case-control study. <i>Lancet Neurology</i> , The, 2021, 20, 373-384.	10.2	35
12	Association of Variants in the <i>SPTLC1</i> Gene With Juvenile Amyotrophic Lateral Sclerosis. <i>JAMA Neurology</i> , 2021, 78, 1236.	9.0	46
13	<i>SCFD1</i> expression quantitative trait loci in amyotrophic lateral sclerosis are differentially expressed. <i>Brain Communications</i> , 2021, 3, fcb236.	3.3	14
14	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021, 53, 1636-1648.	21.4	223
15	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. <i>Nature Genetics</i> , 2020, 52, 1303-1313.	21.4	163
16	Dutch population structure across space, time and GWAS design. <i>Nature Communications</i> , 2020, 11, 4556.	12.8	21
17	Analysis of FUS, PFN2, TDP-43, and PLS3 as potential disease severity modifiers in spinal muscular atrophy. <i>Neurology: Genetics</i> , 2020, 6, e386.	1.9	13
18	ALS in Danish Registries. <i>Neurology: Genetics</i> , 2020, 6, e398.	1.9	34

#	ARTICLE	IF	CITATIONS
19	Analysis of shared common genetic risk between amyotrophic lateral sclerosis and epilepsy. <i>Neurobiology of Aging</i> , 2020, 92, 153.e1-153.e5.	3.1	4
20	The project MinE databrowser: bringing large-scale whole-genome sequencing in ALS to researchers and the public. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2019, 20, 432-440.	1.7	60
21	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
22	Genetic correlations of polygenic disease traits: from theory to practice. <i>Nature Reviews Genetics</i> , 2019, 20, 567-581.	16.3	236
23	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
24	Exome array analysis of rare and low frequency variants in amyotrophic lateral sclerosis. <i>Scientific Reports</i> , 2019, 9, 5931.	3.3	16
25	Association of NIPA1 repeat expansions with amyotrophic lateral sclerosis in a large international cohort. <i>Neurobiology of Aging</i> , 2019, 74, 234.e9-234.e15.	3.1	26
26	Prognosis for patients with amyotrophic lateral sclerosis: development and validation of a personalised prediction model. <i>Lancet Neurology</i> , The, 2018, 17, 423-433.	10.2	342
27	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. <i>Neuron</i> , 2018, 97, 1268-1283.e6.	8.1	517
28	Reconsidering the causality of TIA1 mutations in ALS. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2018, 19, 1-3.	1.7	22
29	Whole blood transcriptome analysis in amyotrophic lateral sclerosis: A biomarker study. <i>PLoS ONE</i> , 2018, 13, e0198874.	2.5	37
30	ATXN2 trinucleotide repeat length correlates with risk of ALS. <i>Neurobiology of Aging</i> , 2017, 51, 178.e1-178.e9.	3.1	86
31	No association between gluten sensitivity and amyotrophic lateral sclerosis. <i>Journal of Neurology</i> , 2017, 264, 694-700.	3.6	4
32	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , 2017, 8, 14774.	12.8	114
33	Meta-analysis of pharmacogenetic interactions in amyotrophic lateral sclerosis clinical trials. <i>Neurology</i> , 2017, 89, 1915-1922.	1.1	82
34	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2017, 8, 611.	12.8	93
35	Circulating microRNAs in patients with intracranial aneurysms. <i>PLoS ONE</i> , 2017, 12, e0176558.	2.5	26
36	Autoantibody pathogenicity in a multifocal motor neuropathy induced pluripotent stem cell-derived model. <i>Annals of Neurology</i> , 2016, 80, 71-88.	5.3	53

#	ARTICLE	IF	CITATIONS
37	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
38	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016, 48, 1043-1048.	21.4	494
39	NEK1 variants confer susceptibility to amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016, 48, 1037-1042.	21.4	218
40	Association of a Locus in the <i>CAMTA1</i> Gene With Survival in Patients With Sporadic Amyotrophic Lateral Sclerosis. <i>JAMA Neurology</i> , 2016, 73, 812.	9.0	57
41	Large-scale screening in sporadic amyotrophic lateral sclerosis identifies genetic modifiers in C9orf72 repeat carriers. <i>Neurobiology of Aging</i> , 2016, 39, 220.e9-220.e15.	3.1	20
42	Genomic signals of migration and continuity in Britain before the Anglo-Saxons. <i>Nature Communications</i> , 2016, 7, 10326.	12.8	100
43	Serotonin 2B receptor slows disease progression and prevents degeneration of spinal cord mononuclear phagocytes in amyotrophic lateral sclerosis. <i>Acta Neuropathologica</i> , 2016, 131, 465-480.	7.7	41
44	The role of <i>TREM2</i> R47H as a risk factor for Alzheimer's disease, frontotemporal lobar degeneration, amyotrophic lateral sclerosis, and Parkinson's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 1407-1416.	0.8	152
45	Brain morphologic changes in asymptomatic <i>C9orf72</i> repeat expansion carriers. <i>Neurology</i> , 2015, 85, 1780-1788.	1.1	66
46	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	21.4	227
47	Are CHCHD10 mutations indeed associated with familial amyotrophic lateral sclerosis?. <i>Brain</i> , 2014, 137, e313-e313.	7.6	11
48	A blinded international study on the reliability of genetic testing for GGGGCC-repeat expansions in <i>C9orf72</i> reveals marked differences in results among 14 laboratories. <i>Journal of Medical Genetics</i> , 2014, 51, 419-424.	3.2	118
49	Exome-wide Rare Variant Analysis Identifies TUBA4A Mutations Associated with Familial ALS. <i>Neuron</i> , 2014, 84, 324-331.	8.1	308
50	H63D polymorphism in HFE is not associated with amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2013, 34, 1517.e5-1517.e7.	3.1	19
51	Evidence for an oligogenic basis of amyotrophic lateral sclerosis. <i>Human Molecular Genetics</i> , 2012, 21, 3776-3784.	2.9	307
52	Hexanucleotide repeat expansions in <i>C9ORF72</i> in the spectrum of motor neuron diseases. <i>Neurology</i> , 2012, 79, 878-882.	1.1	100
53	<i>SMN1</i> gene duplications are associated with sporadic ALS. <i>Neurology</i> , 2012, 78, 776-780.	1.1	54
54	NIPA1 polyalanine repeat expansions are associated with amyotrophic lateral sclerosis. <i>Human Molecular Genetics</i> , 2012, 21, 2497-2502.	2.9	49

#	ARTICLE	IF	CITATIONS
55	Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. PLoS ONE, 2012, 7, e35333.	2.5	50
56	Angiogenin variants in Parkinson disease and amyotrophic lateral sclerosis. Annals of Neurology, 2011, 70, 964-973.	5.3	168
57	A large genome scan for rare CNVs in amyotrophic lateral sclerosis. Human Molecular Genetics, 2010, 19, 4091-4099.	2.9	51
58	Functional Characterisation of a GWAS Risk Locus Identifies <i>GPX3</i> as a Lead Candidate Gene in ALS. SSRN Electronic Journal, 0, , .	0.4	0