Jeroen Gj Van Rooij

List of Publications by Year
in descending order

31 papers	3,404 citations	430442 18 h-index	525886 27 g-index
31 all docs	31 docs citations	31 times ranked	8377 citing authors

#	Article	IF	Citations
1	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
2	Genome-wide association study of frontotemporal dementia identifies a C9ORF72 haplotype with a median of 12-G4C2 repeats that predisposes to pathological repeat expansions. Translational Psychiatry, 2021, 11, 451.	2.4	6
3	SomaticTARDBPvariants as a cause of semantic dementia. Brain, 2020, 143, 3827-3841.	3.7	12
4	Reduced penetrance of pathogenic ACMG variants in a deeply phenotyped cohort study and evaluation of ClinVar classification over time. Genetics in Medicine, 2020, 22, 1812-1820.	1.1	24
5	Deep Learning for Assessing the Corneal Endothelium from Specular Microscopy Images up to 1 Year after Ultrathin-DSAEK Surgery. Translational Vision Science and Technology, 2020, 9, 49.	1.1	26
6	Exome sequencing identifies three novel ADâ€associated genes. Alzheimer's and Dementia, 2020, 16, e041592.	0.4	6
7	SORL1 â€variant carriers in ADESâ€ADSP: A higher level of variant pathogenicity associates with earlier age at onset of Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e044492.	0.4	1
8	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. Genetics in Medicine, 2020, 22, 1803-1811.	1.1	49
9	EIF2AK3 variants in Dutch patients with Alzheimer's disease. Neurobiology of Aging, 2019, 73, 229.e11-229.e18.	1.5	25
10	Fully convolutional architecture vs sliding-window CNN for corneal endothelium cell segmentation. BMC Biomedical Engineering, 2019, 1, 4.	1.7	47
11	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. Genome Biology, 2019, 20, 235.	3.8	26
12	Convolutional neural network-based regression for biomarker estimation in corneal endothelium microscopy images. , 2019, 2019, 876-881.		7
13	Hippocampal transcriptome profiling combined with protein-protein interaction analysis elucidates Alzheimer's disease pathways and genes. Neurobiology of Aging, 2019, 74, 225-233.	1.5	30
14	Automatic detection of the region of interest in corneal endothelium images using dense convolutional neural networks. , 2019, , .		6
15	A C6orf10/LOC101929163 locus is associated with age of onset in C9orf72 carriers. Brain, 2018, 141, 2895-2907.	3.7	39
16	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	5.8	43
17	Rare gene deletions in genetic generalized and Rolandic epilepsies. PLoS ONE, 2018, 13, e0202022.	1.1	6
18	Improved Accuracy and Robustness of a Corneal Endothelial Cell Segmentation Method Based on Merging Superpixels. Lecture Notes in Computer Science, 2018, , 631-638.	1.0	3

#	Article	IF	Citations
19	Corneal Endothelial Cell Segmentation by Classifier-Driven Merging of Oversegmented Images. IEEE Transactions on Medical Imaging, 2018, 37, 2278-2289.	5.4	33
20	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	9.4	390
21	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	9.4	363
22	Characterization of pathogenic SORL1 genetic variants for association with Alzheimerâ€™s disease: a clinical interpretation strategy. European Journal of Human Genetics, 2017, 25, 973-981.	1.4	102
23	Establishing the role of rare coding variants in known Parkinson's disease risk loci. Neurobiology of Aging, 2017, 59, 220.e11-220.e18.	1.5	15
24	Lack of evidence for a role of genetic variation in TMEM230 in the risk for Parkinson's disease in the Caucasian population. Neurobiology of Aging, 2017, 50, 167.e11-167.e13.	1.5	24
25	Excessive burden of lysosomal storage disorder gene variants in Parkinsonâ€™s disease. Brain, 2017, 140, 3191-3203.	3.7	323
26	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. PLoS Genetics, 2016, 12, e1006260.	1.5	76
27	P1â€¢123: Differential Expression in Hippocampus of Alzheimer's Disease Patients. Alzheimer's and Dementia, 2016, 12, P451.	0.4	0
28	P2-024: Whole-exome sequencing in dutch families with Alzheimer's disease. , 2015, 11, P490-P490.		0
29	The dystrophin gene and cognitive function in the general population. European Journal of Human Genetics, 2015, 23, 837-843.	1.4	6
30	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
31	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483