

# Jeroen Gj Van Rooij

## List of Publications by Year in descending order

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Version: 2024-02-01

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 Alzheimer's disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	9.4	700
2	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
3	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
4	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017, 49, 131-138.	9.4	390
5	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017, 49, 139-145.	9.4	363
6	Excessive burden of lysosomal storage disorder gene variants in Parkinson's disease. <i>Brain</i> , 2017, 140, 3191-3203.	3.7	323
7	Characterization of pathogenic SORL1 genetic variants for association with Alzheimer's disease: a clinical interpretation strategy. <i>European Journal of Human Genetics</i> , 2017, 25, 973-981.	1.4	102
8	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. <i>PLoS Genetics</i> , 2016, 12, e1006260.	1.5	76
9	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. <i>Genetics in Medicine</i> , 2020, 22, 1803-1811.	1.1	49
10	Fully convolutional architecture vs sliding-window CNN for corneal endothelium cell segmentation. <i>BMC Biomedical Engineering</i> , 2019, 1, 4.	1.7	47
11	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. <i>Nature Communications</i> , 2018, 9, 4228.	5.8	43
12	A C6orf10/LOC101929163 locus is associated with age of onset in C9orf72 carriers. <i>Brain</i> , 2018, 141, 2895-2907.	3.7	39
13	Corneal Endothelial Cell Segmentation by Classifier-Driven Merging of Oversegmented Images. <i>IEEE Transactions on Medical Imaging</i> , 2018, 37, 2278-2289.	5.4	33
14	Hippocampal transcriptome profiling combined with protein-protein interaction analysis elucidates Alzheimer's disease pathways and genes. <i>Neurobiology of Aging</i> , 2019, 74, 225-233.	1.5	30
15	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. <i>Genome Biology</i> , 2019, 20, 235.	3.8	26
16	Deep Learning for Assessing the Corneal Endothelium from Specular Microscopy Images up to 1 Year after Ultrathin-DSEK Surgery. <i>Translational Vision Science and Technology</i> , 2020, 9, 49.	1.1	26
17	EIF2AK3 variants in Dutch patients with Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019, 73, 229.e11-229.e18.	1.5	25
18	Lack of evidence for a role of genetic variation in TMEM230 in the risk for Parkinson's disease in the Caucasian population. <i>Neurobiology of Aging</i> , 2017, 50, 167.e11-167.e13.	1.5	24

#	ARTICLE	IF	CITATIONS
19	Reduced penetrance of pathogenic ACMG variants in a deeply phenotyped cohort study and evaluation of ClinVar classification over time. <i>Genetics in Medicine</i> , 2020, 22, 1812-1820.	1.1	24
20	Establishing the role of rare coding variants in known Parkinson's disease risk loci. <i>Neurobiology of Aging</i> , 2017, 59, 220.e11-220.e18.	1.5	15
21	Somatic <i>TARDBP</i> variants as a cause of semantic dementia. <i>Brain</i> , 2020, 143, 3827-3841.	3.7	12
22	Convolutional neural network-based regression for biomarker estimation in corneal endothelium microscopy images. , 2019, 2019, 876-881.		7
23	The dystrophin gene and cognitive function in the general population. <i>European Journal of Human Genetics</i> , 2015, 23, 837-843.	1.4	6
24	Rare gene deletions in genetic generalized and Rolandic epilepsies. <i>PLoS ONE</i> , 2018, 13, e0202022.	1.1	6
25	Exome sequencing identifies three novel AD-associated genes. <i>Alzheimer's and Dementia</i> , 2020, 16, e041592.	0.4	6
26	Genome-wide association study of frontotemporal dementia identifies a C9ORF72 haplotype with a median of 12-G4C2 repeats that predisposes to pathological repeat expansions. <i>Translational Psychiatry</i> , 2021, 11, 451.	2.4	6
27	Automatic detection of the region of interest in corneal endothelium images using dense convolutional neural networks. , 2019, , .		6
28	Improved Accuracy and Robustness of a Corneal Endothelial Cell Segmentation Method Based on Merging Superpixels. <i>Lecture Notes in Computer Science</i> , 2018, , 631-638.	1.0	3
29	<i>SORL1</i> variant carriers in ADESADSP: A higher level of variant pathogenicity associates with earlier age at onset of Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e044492.	0.4	1
30	P2-024: Whole-exome sequencing in dutch families with Alzheimer's disease. , 2015, 11, P490-P490.		0
31	P1123: Differential Expression in Hippocampus of Alzheimer's Disease Patients. <i>Alzheimer's and Dementia</i> , 2016, 12, P451.	0.4	0