Denise Harold

List of Publications by Year
in descending order

77 papers	18,854 citations	76294 40 h-index	62565 80 g-index
88 all docs	88 docs citations	88 times ranked	21951 citing authors

#	Article	IF	Citations
1	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	9.4	3,741
2	Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. Nature Genetics, 2009, 41, 1088-1093.	9.4	2,697
3	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
4	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
5	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
6	Genome-wide Analysis of Genetic Loci Associated With Alzheimer Disease. JAMA - Journal of the American Medical Association, 2010, 303, 1832.	3.8	1,064
7	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
8	Identification of Genetic Factors that Modify Clinical Onset of Huntingtonâ€™s Disease. Cell, 2015, 162, 516-526.	13.5	514
9	Common polygenic variation enhances risk prediction for Alzheimerâ€™s disease. Brain, 2015, 138, 3673-3684.	3.7	359
10	Genetic Evidence Implicates the Immune System and Cholesterol Metabolism in the Aetiology of Alzheimer's Disease. PLoS ONE, 2010, 5, e13950.	1.1	347
11	GWAS of Cerebrospinal Fluid Tau Levels Identifies Risk Variants for Alzheimerâ€™s Disease. Neuron, 2013, 78, 256-268.	3.8	344
12	Increased expression of BIN1 mediates Alzheimer genetic risk by modulating tau pathology. Molecular Psychiatry, 2013, 18, 1225-1234.	4.1	321
13	Strong Evidence That KIAA0319 on Chromosome 6p Is a Susceptibility Gene for Developmental Dyslexia. American Journal of Human Genetics, 2005, 76, 581-591.	2.6	260
14	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	4.1	260
15	Remapping the Insulin Gene/IDDM2 Locus in Type 1 Diabetes. Diabetes, 2004, 53, 1884-1889.	0.3	198
16	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. Human Molecular Genetics, 2013, 22, 832-841.	1.4	186
17	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
18	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155

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19	Meta-analysis of the Association Between Variants in SORL1 and Alzheimer Disease. Archives of Neurology, 2011, 68, 99.	4.9	153
20	Further evidence that the KIAA0319 gene confers susceptibility to developmental dyslexia. Molecular Psychiatry, 2006, 11, 1085-1091.	4.1	140
21	Genetic overlap between Alzheimerâ€™s disease and Parkinsonâ€™s disease at the MAPT locus. Molecular Psychiatry, 2015, 20, 1588-1595.	4.1	133
22	Characterization of a Family with Rare Deletions in CNTNAP5 and DOCK4 Suggests Novel Risk Loci for Autism and Dyslexia. Biological Psychiatry, 2010, 68, 320-328.	0.7	131
23	SNPs Associated with Cerebrospinal Fluid Phospho-Tau Levels Influence Rate of Decline in Alzheimer's Disease. PLoS Genetics, 2010, 6, e1001101.	1.5	111
24	Genome-wide association study of Alzheimer's disease with psychotic symptoms. Molecular Psychiatry, 2012, 17, 1316-1327.	4.1	110
25	Missense variant in TREML2 protects against Alzheimer's disease. Neurobiology of Aging, 2014, 35, 1510.e19-1510.e26.	1.5	110
26	Genome-wide haplotype association study identifies the FRMD4A gene as a risk locus for Alzheimer's disease. Molecular Psychiatry, 2013, 18, 461-470.	4.1	103
27	Follow-up of loci from the International Genomics of Alzheimerâ€™s Disease Project identifies TRIP4 as a novel susceptibility gene. Translational Psychiatry, 2014, 4, e358-e358.	2.4	98
28	Determining SNP Allele Frequencies in DNA Pools. BioTechniques, 2000, 28, 464-470.	0.8	91
29	A modifier of Huntington's disease onset at the MLH1 locus. Human Molecular Genetics, 2017, 26, 3859-3867.	1.4	88
30	A review of pharmaceutical occurrence and pathways in the aquatic environment in the context of a changing climate and the COVID-19 pandemic. Analytical Methods, 2021, 13, 575-594.	1.3	82
31	Alzheimer's disease genetics: current knowledge and future challenges. International Journal of Geriatric Psychiatry, 2011, 26, 793-802.	1.3	79
32	Genetic evidence for the involvement of lipid metabolism in Alzheimer's disease. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2010, 1801, 754-761.	1.2	66
33	Genome-wide association interaction analysis for Alzheimer's disease. Neurobiology of Aging, 2014, 35, 2436-2443.	1.5	61
34	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
35	The Role of Variation at AÎ²PP, PSEN1, PSEN2, and MAPT in Late Onset Alzheimer's Disease. Journal of Alzheimer's Disease, 2012, 28, 377-387.	1.2	53
36	No consistent evidence for association between mtDNA variants and Alzheimer disease. Neurology, 2012, 78, 1038-1042.	1.5	52

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37	Analysis of Genome-Wide Association Studies of Alzheimer Disease and of Parkinson Disease to Determine If These 2 Diseases Share a Common Genetic Risk. JAMA Neurology, 2013, 70, 1268-76.	4.5	51
38	No support for association between Dyslexia Susceptibility 1 Candidate 1 and developmental dyslexia. Molecular Psychiatry, 2005, 10, 237-238.	4.1	49
39	Suggestive synergy between genetic variants in TF and HFE as risk factors for Alzheimer's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 955-959.	1.1	47
40	Cognitive analysis of schizophrenia risk genes that function as epigenetic regulators of gene expression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 1170-1179.	1.1	43
41	Î±-T-Catenin Is Expressed in Human Brain and Interacts With the Wnt Signaling Pathway But Is Not Responsible for Linkage to Chromosome 10 in Alzheimer's Disease. NeuroMolecular Medicine, 2004, 5, 133-146.	1.8	41
42	Polymorphisms in BACE2 may affect the age of onset Alzheimer's dementia in Down syndrome. Neurobiology of Aging, 2014, 35, 1513.e1-1513.e5.	1.5	41
43	Association analysis of 528 intraâ€genic SNPs in a region of chromosome 10 linked to late onset Alzheimer's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 727-731.	1.1	40
44	A single nucleotide polymorphism in CHAT influences response to acetylcholinesterase inhibitors in Alzheimer's disease. Pharmacogenetics and Genomics, 2006, 16, 75-77.	0.7	36
45	Evidence that PICALM affects age at onset of Alzheimer's dementia in Down syndrome. Neurobiology of Aging, 2013, 34, 2441.e1-2441.e5.	1.5	35
46	Genetic variation at the CELF1 (CUGBP, elavâ€like family member 1 gene) locus is genomeâ€wide associated with Alzheimer's disease and obesity. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 283-293.	1.1	35
47	MiR-137-derived polygenic risk: effects on cognitive performance in patients with schizophrenia and controls. Translational Psychiatry, 2017, 7, e1012-e1012.	2.4	34
48	Sequence variation in the CHAT locus shows no association with late-onset Alzheimer's disease. Human Genetics, 2003, 113, 258-267.	1.8	33
49	A genome-wide study shows a limited contribution of rare copy number variants to Alzheimer's disease risk. Human Molecular Genetics, 2013, 22, 816-824.	1.4	33
50	The Genetic Modifiers of Motor OnsetAgeÂ(GeM MOA) Website: Genome-wide Association Analysis for Genetic Modifiers of Huntingtonâ€™s Disease. Journal of Huntington's Disease, 2015, 4, 279-284.	0.9	30
51	Can Studies of Neuroinflammation in a TSPO Genetic Subgroup (HAB or MAB) Be Applied to the Entire AD Cohort?. Journal of Nuclear Medicine, 2015, 56, 707-713.	2.8	30
52	Genetically predicted complement component 4A expression: effects on memory function and middle temporal lobe activation. Psychological Medicine, 2018, 48, 1608-1615.	2.7	29
53	Cognitive Characterization of Schizophrenia Risk Variants Involved in Synaptic Transmission: Evidence of CACNA1C's Role in Working Memory. Neuropsychopharmacology, 2017, 42, 2612-2622.	2.8	28
54	Interaction between theADAM12 andSH3MD1 genes may confer susceptibility to late-onset Alzheimer's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 448-452.	1.1	27

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55	Alzheimer's disease and age-related macular degeneration have different genetic models for complement gene variation. Neurobiology of Aging, 2012, 33, 1843.e9-1843.e17.	1.5	24
56	Haplotype-based stratification of Huntington's disease. European Journal of Human Genetics, 2017, 25, 1202-1209.	1.4	24
57	Deep Sequencing of the Nicastrin Gene in Pooled DNA, the Identification of Genetic Variants That Affect Risk of Alzheimer's Disease. PLoS ONE, 2011, 6, e17298.	1.1	21
58	Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. Biological Psychiatry, 2021, 90, 28-34.	0.7	20
59	No evidence that extended tracts of homozygosity are associated with Alzheimer's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 764-771.	1.1	17
60	Monitoring of emerging contaminants of concern in the aquatic environment: a review of studies showing the application of effect-based measures. Analytical Methods, 2021, 13, 5120-5143.	1.3	17
61	Linkage disequilibrium structure of KIAA0319 and DCDC2, two candidate susceptibility genes for developmental dyslexia. Molecular Psychiatry, 2006, 11, 1061-1061.	4.1	13
62	Beyond C4: Analysis of the complement gene pathway shows enrichment for IQ in patients with psychotic disorders and healthy controls. Genes, Brain and Behavior, 2019, 18, e12602.	1.1	13
63	Identifying schizophrenia patients who carry pathogenic genetic copy number variants using standard clinical assessment: retrospective cohort study. British Journal of Psychiatry, 2020, 216, 275-279.	1.7	12
64	Effects of MiRâ€137 genetic risk score on brain volume and cortical measures in patients with schizophrenia and controls. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 369-376.	1.1	10
65	Characterisation and Validation of Insertions and Deletions in 173 Patient Exomes. PLoS ONE, 2012, 7, e51292.	1.1	8
66	The Differential Influence of Immune, Endocytotic, and Lipid Metabolism Genes on Amyloid Deposition and Neurodegeneration in Subjects at Risk of Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2021, 79, 127-139.	1.2	8
67	Effects of complement geneâ€set polygenic risk score on brain volume and cortical measures in patients with psychotic disorders and healthy controls. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 445-453.	1.1	6
68	From Molecule to Clinic and Community for Neurodegeneration: Research to Bridge Translational Gaps. Journal of Alzheimer's Disease, 2012, 33, S385-S396.	1.2	5
69	Genetically elevated highâ€density lipoprotein cholesterol through the cholesteryl ester transfer protein gene does not associate with risk of Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 595-598.	1.2	2
70	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
71	A03 Genetic Modifiers Affecting The Age At Motor Onset In Huntington's Disease. Journal of Neurology, Neurosurgery and Psychiatry, 2014, 85, A1-A2.	0.9	1
72	Biomarkers for Psychosis: the Molecular Genetics of Psychosis. Current Behavioral Neuroscience Reports, 2015, 2, 112-118.	0.6	1

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73	RNA-seq analysis of murine peyerâ€™s patches at 6 and 18 h post infection with Fasciola hepatica metacecariae. Veterinary Parasitology, 2022, 302, 109643.	0.7	1
74	A COGNITIVE AND MOLECULAR ANALYSIS OF SDCCAG8, A SCHIZOPHRENIA RISK GENE THAT FUNCTIONS IN THE CENTROSOME. European Neuropsychopharmacology, 2019, 29, S876-S877.	0.3	0
75	O51. Beyond C4: Analysis of the Complement Gene Pathway Shows Enrichment for IQ in Patients With Schizophrenia and Healthy Controls. Biological Psychiatry, 2019, 85, S126-S127.	0.7	0
76	Genetic Risk Variants Interacting With MIR137: Effects On Cognition, Brain Structure And Brain Function In Patients And Healthy Participants. European Neuropsychopharmacology, 2019, 29, S729-S730.	0.3	0
77	43RARE COPY NUMBER VARIATIONS ARE ASSOCIATED WITH POORER COGNITION IN SCHIZOPHRENIA. European Neuropsychopharmacology, 2019, 29, S1091-S1092.	0.3	0