John S K Kauwe

List of Publications by Year
in descending order

136 papers	24,787 citations	38660 50 h-index	11581 135 g-index
156 all docs	156 docs citations	156 times ranked	23824 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	TREM2 Variants in Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 117-127.	13.9	2,385
4	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
5	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
6	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	9.4	1,676
7	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
8	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
9	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
10	Rare coding variants in the phospholipase D3 gene confer risk for Alzheimerâ€™s disease. Nature, 2014, 505, 550-554.	13.7	425
11	Genetic Evidence Implicates the Immune System and Cholesterol Metabolism in the Aetiology of Alzheimer's Disease. PLoS ONE, 2010, 5, e13950.	1.1	347
12	GWAS of Cerebrospinal Fluid Tau Levels Identifies Risk Variants for Alzheimerâ€™s Disease. Neuron, 2013, 78, 256-268.	3.8	344
13	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	7.1	330
14	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	4.1	260
15	Alzheimerâ€™s Disease: Analyzing the Missing Heritability. PLoS ONE, 2013, 8, e79771.	1.1	257
16	Genetic studies of quantitative MCI and AD phenotypes in ADNI: Progress, opportunities, and plans. Alzheimer's and Dementia, 2015, 11, 792-814.	0.4	241
17	Genome-wide association study identifies four novel loci associated with Alzheimerâ€™s endophenotypes and disease modifiers. Acta Neuropathologica, 2017, 133, 839-856.	3.9	199
18	Cerebrospinal fluid APOE levels: an endophenotype for genetic studies for Alzheimer's disease. Human Molecular Genetics, 2012, 21, 4558-4571.	1.4	196

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19	HDDD2 is a familial frontotemporal lobar degeneration with ubiquitin-positive, tau-negative inclusions caused by a missense mutation in the signal peptide of progranulin. Annals of Neurology, 2006, 60, 314-322.	2.8	186
20	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	1.5	174
21	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
22	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166
23	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.4	166
24	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. Brain Imaging and Behavior, 2014, 8, 183-207.	1.1	161
25	A Scan of Chromosome 10 Identifies a Novel Locus Showing Strong Association with Late-Onset Alzheimer Disease. American Journal of Human Genetics, 2006, 78, 78-88.	2.6	157
26	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
27	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.5	144
28	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	4.5	144
29	Association of late-onset Alzheimer's disease with genetic variation in multiple members of the GAPD gene family. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15688-15693.	3.3	134
30	DAPK1 variants are associated with Alzheimer's disease and allele-specific expression. Human Molecular Genetics, 2006, 15, 2560-2568.	1.4	125
31	Evaluating the necessity of PCR duplicate removal from next-generation sequencing data and a comparison of approaches. BMC Bioinformatics, 2016, 17, 239.	1.2	124
32	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. Genome Biology, 2019, 20, 97.	3.8	122
33	SNPs Associated with Cerebrospinal Fluid Phospho-Tau Levels Influence Rate of Decline in Alzheimer's Disease. PLoS Genetics, 2010, 6, e1001101.	1.5	111
34	Missense variant in TREML2 protects against Alzheimer's disease. Neurobiology of Aging, 2014, 35, 1510.e19-1510.e26.	1.5	110
35	Genome-Wide Association Study of CSF Levels of 59 Alzheimer's Disease Candidate Proteins: Significant Associations with Proteins Involved in Amyloid Processing and Inflammation. PLoS Genetics, 2014, 10, e1004758.	1.5	109
36	Association and Expression Analyses With Single-Nucleotide Polymorphisms in <emph type="ital">TOMM40</emph> in Alzheimer Disease. Archives of Neurology, 2011, 68, 1013.	4.9	97

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37	Extreme cerebrospinal fluid amyloid Î² levels identify family with late-onset Alzheimer's disease presenilin 1 mutation. Annals of Neurology, 2007, 61, 446-453.	2.8	87
38	Variation in MAPT is associated with cerebrospinal fluid tau levels in the presence of amyloid-beta deposition. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8050-8054.	3.3	84
39	Alzheimerâ€™s disease risk variants show association with cerebrospinal fluid amyloid beta. Neurogenetics, 2009, 10, 13-17.	0.7	80
40	Genetics of Alzheimerâ€™s Disease. BioMed Research International, 2013, 2013, 1-13.	0.9	75
41	Phosphorylated Tau-AÎ²42 Ratio as a Continuous Trait for Biomarker Discovery for Early-Stage Alzheimerâ€™s Disease in Multiplex Immunoassay Panels of Cerebrospinal Fluid. Biological Psychiatry, 2014, 75, 723-731.	0.7	72
42	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.4	72
43	Molecular characterization of novel progranulin (GRN) mutations in frontotemporal dementia. Human Mutation, 2008, 29, 512-521.	1.1	71
44	Apolipoprotein E levels in cerebrospinal fluid and the effects of ABCA1 polymorphisms. Molecular Neurodegeneration, 2007, 2, 7.	4.4	68
45	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimerâ€™s disease resilience. Genome Medicine, 2017, 9, 100.	3.6	67
46	Fine-mapping of the human leukocyte antigen locus as a risk factor for Alzheimer disease: A caseâ€“control study. PLoS Medicine, 2017, 14, e1002272.	3.9	67
47	Identification and validation of novel CSF biomarkers for early stages of Alzheimer's disease. Proteomics - Clinical Applications, 2007, 1, 1373-1384.	0.8	66
48	Fine Mapping of Genetic Variants in BIN1, CLU, CR1 and PICALM for Association with Cerebrospinal Fluid Biomarkers for Alzheimer's Disease. PLoS ONE, 2011, 6, e15918.	1.1	64
49	Genome-wide, high-content siRNA screening identifies the Alzheimerâ€™s genetic risk factor FERMT2 as a major modulator of APP metabolism. Acta Neuropathologica, 2017, 133, 955-966.	3.9	60
50	Rs5848 Variant Influences GRN mRNA Levels in Brain and Peripheral Mononuclear Cells in Patients with Alzheimer's Disease. Journal of Alzheimer's Disease, 2009, 18, 603-612.	1.2	59
51	Association of Rare Coding Mutations With Alzheimer Disease and Other Dementias Among Adults of European Ancestry. JAMA Network Open, 2019, 2, e191350.	2.8	58
52	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
53	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
54	Performances on the CogState and Standard Neuropsychological Batteries Among HIV Patients Without Dementia. AIDS and Behavior, 2011, 15, 1902-1909.	1.4	52

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55	A Versatile Omnibus Test for Detecting Mean and Variance Heterogeneity. Genetic Epidemiology, 2014, 38, 51-59.	0.6	52
56	Population-based Analysis of Alzheimerâ€™s Disease Risk Alleles Implicates Genetic Interactions. Biological Psychiatry, 2014, 75, 732-737.	0.7	52
57	Assessment of TREM2 rs75932628 association with Alzheimer's disease in a population-based sample: the Cache County Study. Neurobiology of Aging, 2013, 34, 2889.e11-2889.e13.	1.5	47
58	Genetically predicted body mass index and Alzheimer's diseaseâ€“related phenotypes in three large samples: Mendelian randomization analyses. Alzheimer's and Dementia, 2015, 11, 1439-1451.	0.4	46
59	Haplotype-based association analysis of the MAPT locus in late onset Alzheimer's disease. BMC Genetics, 2007, 8, 3.	2.7	45
60	Mitochondria and Alzheimerâ€™s Disease: the Role of Mitochondrial Genetic Variation. Current Genetic Medicine Reports, 2018, 6, 1-10.	1.9	45
61	Relative risk for Alzheimer disease based on complete family history. Neurology, 2019, 92, e1745-e1753.	1.5	45
62	Mitochondrial Genomic Analysis of Late Onset Alzheimerâ€™s Disease Reveals Protective Haplogroups H6A1A/H6A1B: The Cache County Study on Memory in Aging. PLoS ONE, 2012, 7, e45134.	1.1	44
63	A potential endophenotype for Alzheimer's disease: cerebrospinal fluid clusterin. Neurobiology of Aging, 2016, 37, 208.e1-208.e9.	1.5	44
64	A Common Variant of IL-6R is Associated with Elevated IL-6 Pathway Activity in Alzheimerâ€™s Disease Brains. Journal of Alzheimer's Disease, 2017, 56, 1037-1054.	1.2	44
65	Calibrating Longitudinal Cognition in Alzheimer's Disease Across Diverse Test Batteries and Datasets. Neuroepidemiology, 2014, 43, 194-205.	1.1	43
66	Validating predicted biological effects of Alzheimer's disease associated SNPs using CSF biomarker levels. Journal of Alzheimer's Disease, 2010, 21, 833-42.	1.2	43
67	Rarity of the Alzheimer Diseaseâ€“ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	4.5	41
68	Observed Changes in Radiographic Measurements of the First Ray after Frontal Plane Rotation of the First Metatarsal in a Cadaveric Foot Model. Journal of Foot and Ankle Surgery, 2014, 53, 274-278.	0.5	40
69	Systems biology approach to late-onset Alzheimer's disease genome-wide association study identifies novel candidate genes validated using brain expression data and Caenorhabditis elegans experiments. , 2017, 13, 1133-1142.		40
70	Knowledge Gaps, Challenges, and Opportunities in Health and Prevention Research for Asian Americans, Native Hawaiians, and Pacific Islanders: A Report From the 2021 National Institutes of Health Workshop. Annals of Internal Medicine, 2022, 175, 574-589.	2.0	40
71	Ubiquilin 1 polymorphisms are not associated with late-onset Alzheimer's disease. Annals of Neurology, 2006, 59, 21-26.	2.8	37
72	RAB10: an Alzheimer’s disease resilience locus and potential drug target. Clinical Interventions in Aging, 2019, Volume 14, 73-79.	1.3	37

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73	Alzheimer's disease alters oligodendrocytic glycolytic and ketolytic gene expression. Alzheimer's and Dementia, 2021, 17, 1474-1486.	0.4	37
74	Variants in PPP3R1 and MAPT are associated with more rapid functional decline in Alzheimer's disease: The Cache County Dementia Progression Study. Alzheimer's and Dementia, 2014, 10, 366-371.	0.4	36
75	Association studies between risk for late-onset Alzheimer's disease and variants in insulin degrading enzyme. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 136B, 62-68.	1.1	35
76	Influence of Coding Variability in APP-AÎ² Metabolism Genes in Sporadic Alzheimerâ€™s Disease. PLoS ONE, 2016, 11, e0150079.	1.1	34
77	Seroprevalence and Serointensity of Latent Toxoplasma gondii in a Sample of Elderly Adults With and Without Alzheimer Disease. Alzheimer Disease and Associated Disorders, 2016, 30, 123-126.	0.6	33
78	Distinct clinicopathologic clusters of persons with TDP-43 proteinopathy. Acta Neuropathologica, 2020, 140, 659-674.	3.9	29
79	Mitochondrial Haplotypes Associated with Biomarkers for Alzheimerâ€™s Disease. PLoS ONE, 2013, 8, e74158.	1.1	28
80	Genomeâ€wide association study of rate of cognitive decline in Alzheimer's disease patients identifies novel genes and pathways. Alzheimer's and Dementia, 2020, 16, 1134-1145.	0.4	28
81	Phylogeographic and nested clade analysis of the stonefly Pteronarcys californica (Plecoptera:Pteronarcyidae) in the western USA. Journal of the North American Benthological Society, 2004, 23, 824-838.	3.0	27
82	Bridging the Gap between Statistical and Biological Epistasis in Alzheimerâ€™s Disease. BioMed Research International, 2015, 2015, 1-7.	0.9	26
83	Analysis of genes (TMEM106B, GRN, ABCC9, KCNMB2, and APOE) implicated in risk for LATE-NC and hippocampal sclerosis provides pathogenetic insights: a retrospective genetic association study. Acta Neuropathologica Communications, 2021, 9, 152.	2.4	26
84	Association studies between common variants in prolyl isomerase Pin1 and the risk for late-onset Alzheimer's disease. Neuroscience Letters, 2007, 419, 15-17.	1.0	25
85	Genetic studies of plasma analytes identify novel potential biomarkers for several complex traits. Scientific Reports, 2016, 6, .	1.6	25
86	Discovery and Confirmation of Diagnostic Serum Lipid Biomarkers for Alzheimer's Disease Using Direct Infusion Mass Spectrometry. Journal of Alzheimer's Disease, 2017, 59, 277-290.	1.2	19
87	Single nucleotide polymorphism discovery in cutthroat trout subspecies using genome reduction, barcoding, and 454 pyro-sequencing. BMC Genomics, 2012, 13, 724.	1.2	18
88	Interaction between variants in CLU and MS4A4E modulates Alzheimer's disease risk. Alzheimer's and Dementia, 2016, 12, 121-129.	0.4	18
89	Genome-wide association study for variants that modulate relationships between cerebrospinal fluid amyloid-beta 42, tau, and p-tau levels. Alzheimer's Research and Therapy, 2018, 10, 86.	3.0	18
90	Microsatellites versus single-nucleotide polymorphisms in linkage analysis for quantitative and qualitative measures. BMC Genetics, 2005, 6, S122.	2.7	15

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91	Mitochondrial genomic variation associated with higher mitochondrial copy number: the Cache County Study on Memory Health and Aging. BMC Bioinformatics, 2014, 15, S6.	1.2	15
92	Sex Differences in Risk for Alzheimerâ€™s Disease Related to Neurotrophin Gene Polymorphisms: The Cache County Memory Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, 1607-1613.	1.7	15
93	Lingering Taxonomic Challenges Hinder Conservation and Management of Global Bonefishes. Fisheries, 2020, 45, 347-358.	0.6	15
94	Novel presenilin 1 variant (P117A) causing Alzheimer's disease in the fourth decade of life. Neuroscience Letters, 2008, 438, 257-259.	1.0	14
95	Assembly of 809 whole mitochondrial genomes with clinical, imaging, and fluid biomarker phenotyping. Alzheimer's and Dementia, 2018, 14, 514-519.	0.4	14
96	Strong Evidence for a Genetic Contribution to Late-Onset Alzheimerâ€™s Disease Mortality: A Population-Based Study. PLoS ONE, 2013, 8, e77087.	1.1	14
97	Observed Changes in First Metatarsal and Medial Cuneiform Positions after First Metatarsophalangeal Joint Arthrodesis. Journal of Foot and Ankle Surgery, 2014, 53, 32-35.	0.5	12
98	Association studies testing for risk for late-onset Alzheimer's disease with common variants in the Î²-amyloid precursor protein (APP). American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 469-474.	1.1	11
99	Variant Tool Chest: an improved tool to analyze and manipulate variant call format (VCF) files. BMC Bioinformatics, 2014, 15, S12.	1.2	11
100	Presenilin E318G variant and Alzheimerâ€™s disease risk: the Cache County study. BMC Genomics, 2016, 17, 438.	1.2	11
101	Genetic Discoveries in AD Using CSF Amyloid and Tau. Current Genetic Medicine Reports, 2014, 2, 23-29.	1.9	10
102	Discovery and Subsequent Confirmation of Novel Serum Biomarkers Diagnosing Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2015, 49, 317-327.	1.2	10
103	Predicting Clinical Dementia Rating Using Blood RNA Levels. Genes, 2020, 11, 706.	1.0	10
104	Analysis of highâ€risk pedigrees identifies 11 candidate variants for Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 307-317.	0.4	10
105	Failure to detect synergy between variants in transferrin and hemochromatosis and Alzheimer's disease in large cohort. Neurobiology of Aging, 2020, 89, 142.e9-142.e12.	1.5	9
106	Population-based analysis of cholesteryl ester transfer protein identifies association between I405V and cognitive decline: the Cache County Study. Neurobiology of Aging, 2015, 36, 547.e1-547.e3.	1.5	8
107	Codon Pairs are Phylogenetically Conserved: A comprehensive analysis of codon pairing conservation across the Tree of Life. PLoS ONE, 2020, 15, e0232260.	1.1	8
108	The efficacy of short tandem repeat polymorphisms versus single-nucleotide polymorphisms for resolving population structure. BMC Genetics, 2005, 6, S84.	2.7	7

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109	Population substructure in Cache County, Utah: the Cache County study. BMC Bioinformatics, 2014, 15, S8.	1.2	7
110	Genes for a â€˜Wellderlyâ€™ Life. Trends in Molecular Medicine, 2016, 22, 637-639.	3.5	7
111	CSF protein changes associated with hippocampal sclerosis risk gene variants highlight impact of GRN/PGRN. Experimental Gerontology, 2017, 90, 83-89.	1.2	7
112	Interaction Between Physical Activity and Genes Related to Neurotrophin Signaling in Late-Life Cognitive Performance: The Cache County Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 1633-1642.	1.7	7
113	CUBAP: an interactive web portal for analyzing codon usage biases across populations. Nucleic Acids Research, 2020, 48, 11030-11039.	6.5	7
114	Atypical chemokine receptor ACKR2-V41A has decreased CCL2 binding, scavenging, and activation, supporting sustained inflammation and increased Alzheimerâ€™s disease risk. Scientific Reports, 2020, 10, 8019.	1.6	7
115	Identification and genomic analysis of pedigrees with exceptional longevity identifies candidate rare variants. Neurobiology of Disease, 2020, 143, 104972.	2.1	7
116	GenoRisk: A polygenic risk score for Alzheimer's disease. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2021, 7, e12211.	1.8	7
117	An analysis of identical single-nucleotide polymorphisms genotyped by two different platforms. BMC Genetics, 2005, 6, S152.	2.7	6
118	Population genealogy resource shows evidence of familial clustering for Alzheimer disease. Neurology: Genetics, 2018, 4, e249.	0.9	6
119	Phylogeography of two marine predators, giant trevally (Caranx ignobilis) and bluefin trevally (Caranx melampygus), across the Indo-Pacific. Bulletin of Marine Science, 2021, 97, 257-280.	0.4	6
120	Association between WWOX/MAF variants and dementia-related neuropathologic endophenotypes. Neurobiology of Aging, 2022, 111, 95-106.	1.5	6
121	Common DNA Variants Accurately Rank an Individual of Extreme Height. International Journal of Genomics, 2018, 2018, 1-7.	0.8	5
122	Association study of rs3846662 with Alzheimer's disease in a population-based cohort: the Cache County Study. Neurobiology of Aging, 2019, 84, 242.e1-242.e6.	1.5	5
123	Pairwise Correlation Analysis of the Alzheimerâ€™s Disease Neuroimaging Initiative (ADNI) Dataset Reveals Significant Feature Correlation. Genes, 2021, 12, 1661.	1.0	5
124	The Ramp Atlas: facilitating tissue and cell-specific ramp sequence analyses through an intuitive web interface. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	3
125	Genome-wide association study of prolactin levels in blood plasma and cerebrospinal fluid. BMC Genomics, 2016, 17, 436.	1.2	2
126	Using the Health Belief Model to evaluate Samoan caregiver perceptions for rheumatic heart disease follow-up care. International Journal of Health Promotion and Education, 2017, 55, 148-157.	0.4	2

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127	The Opioid Abuse Risk Screener predicts aberrant same-day urine drug tests and 1-year controlled substance database checks: A brief report. Health Psychology Open, 2017, 4, 205510291774845.	0.7	2
128	A comprehensive analysis of the phylogenetic signal in ramp sequences in 211 vertebrates. Scientific Reports, 2021, 11, 622.	1.6	2
129	De novo genome assembly of the marine teleost, bluefin trevally (Caranx melampygus). G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
130	Genome-wide association study of brain arteriolosclerosis. Journal of Cerebral Blood Flow and Metabolism, 2022, 42, 1437-1450.	2.4	2
131	O4-01-01: Association of genetic variants with cerebrospinal fluid protein levels of ACE, MMP3 and other proteins and risk for Alzheimer's disease. , 2013, 9, P677-P678.		1
132	Variants in ACPP are associated with cerebrospinal fluid Prostatic Acid Phosphatase levels. BMC Genomics, 2016, 17, 439.	1.2	1
133	Variants in CCL16 are associated with blood plasma and cerebrospinal fluid CCL16 protein levels. BMC Genomics, 2016, 17, 437.	1.2	1
134	Alzheimer's Disease Alters Oligodendrocytic Glycolytic and Ketolytic Gene Expression. FASEB Journal, 2021, 35, .	0.2	1
135	Genome assembly of the roundjaw bonefish (Albula glossodonta), aÂvulnerable circumtropical sportfish. GigaByte, 0, 2022, 1-29.	0.0	1
136	[O1â€“11â€“03]: CEREBROSPINAL FLUID ENDOPHENOTYPES PROVIDE INSIGHT INTO BIOLOGY UNDERLYING ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2017, 13, P218.	0.4	0