William Bush

List of Publications by Year
in descending order

161 papers	9,149 citations	101384 36 h-index	53109 85 g-index
183 all docs	183 docs citations	183 times ranked	15886 citing authors

#	Article	IF	Citations
1	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
2	Chapter 11: Genome-Wide Association Studies. PLoS Computational Biology, 2012, 8, e1002822.	1.5	950
3	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
4	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	9.4	472
5	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. Genetic Epidemiology, 2007, 31, 306-315.	0.6	337
6	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	6.0	269
7	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
8	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. JAMA Neurology, 2018, 75, 989.	4.5	223
9	Unravelling the human genomeâ€“phenome relationship using phenome-wide association studies. Nature Reviews Genetics, 2016, 17, 129-145.	7.7	222
10	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
11	Evidence for Polygenic Susceptibility to Multiple Sclerosisâ€”The Shape of Things to Come. American Journal of Human Genetics, 2010, 86, 621-625.	2.6	162
12	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	3.8	148
13	ICD-9 tobacco use codes are effective identifiers of smoking status. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 652-658.	2.2	127
14	Cystic fibrosisâ€“related diabetes is caused by islet loss and inflammation. JCI Insight, 2018, 3, .	2.3	127
15	Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575.	3.7	93
16	Sex-specific genetic predictors of Alzheimerâ€™s disease biomarkers. Acta Neuropathologica, 2018, 136, 857-872.	3.9	87
17	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	1.1	79
18	Biofilter: a knowledge-integration system for the multi-locus analysis of genome-wide association studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 368-79.	0.7	79

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19	Is Isolated Low High-Density Lipoprotein Cholesterol a Cardiovascular Disease Risk Factor?. Circulation: Cardiovascular Quality and Outcomes, 2016, 9, 206-212.	0.9	71
20	Human islet preparations distributed for research exhibit a variety of insulin-secretory profiles. American Journal of Physiology - Endocrinology and Metabolism, 2015, 308, E592-E602.	1.8	69
21	Parallel multifactor dimensionality reduction: a tool for the large-scale analysis of gene-gene interactions. Bioinformatics, 2006, 22, 2173-2174.	1.8	67
22	Sex differences in the genetic predictors of Alzheimerâ€™s pathology. Brain, 2019, 142, 2581-2589.	3.7	65
23	A comparison of cataloged variation between International HapMap Consortium and 1000 Genomes Project data. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 289-294.	2.2	64
24	Comprehensive Analysis of Constraint on the Spatial Distribution of Missense Variants in Human Protein Structures. American Journal of Human Genetics, 2018, 102, 415-426.	2.6	61
25	Genetic programming neural networks: A powerful bioinformatics tool for human genetics. Applied Soft Computing Journal, 2007, 7, 471-479.	4.1	60
26	Antiepileptic activity of preferential inhibitors of persistent sodium current. Epilepsia, 2014, 55, 1274-1283.	2.6	60
27	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	5.8	60
28	Alternative contingency table measures improve the power and detection of multifactor dimensionality reduction. BMC Bioinformatics, 2008, 9, 238.	1.2	57
29	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
30	BIOFILTER: A KNOWLEDGE-INTEGRATION SYSTEM FOR THE MULTI-LOCUS ANALYSIS OF GENOME-WIDE ASSOCIATION STUDIES. , 2008, , .		53
31	Interrogating the complex role of chromosome 16p13.13 in multiple sclerosis susceptibility: independent genetic signals in the CIITAâ€“CLEC16Aâ€“SOCS1 gene complex. Human Molecular Genetics, 2011, 20, 3517-3524.	1.4	50
32	Genetic analysis of biological pathway data through genomic randomization. Human Genetics, 2011, 129, 563-571.	1.8	50
33	Genetic and Clinical Risk Prediction Model for Postoperative Atrial Fibrillation. Circulation: Arrhythmia and Electrophysiology, 2015, 8, 25-31.	2.1	49
34	Automated extraction of clinical traits of multiple sclerosis in electronic medical records. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e334-e340.	2.2	45
35	Associations between KCNJ6 (GIRK2) gene polymorphisms and pain-related phenotypes. Pain, 2013, 154, 2853-2859.	2.0	42
36	Whole genome sequencing of Caribbean Hispanic families with lateâ€onset Alzheimer's disease. Annals of Clinical and Translational Neurology, 2018, 5, 406-417.	1.7	42

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37	Are Interactions between cis-Regulatory Variants Evidence for Biological Epistasis or Statistical Artifacts?. American Journal of Human Genetics, 2016, 99, 817-830.	2.6	40
38	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	5.8	40
39	Bioinformatics Challenges in Genome-Wide Association Studies (GWAS). Methods in Molecular Biology, 2014, 1168, 63-81.	0.4	40
40	Discovery of gene-gene interactions across multiple independent data sets of late onset Alzheimer disease from the Alzheimer Disease Genetics Consortium. Neurobiology of Aging, 2016, 38, 141-150.	1.5	39
41	Racial Disparities in Lung Cancer Survival: The Contribution of Stage, Treatment, and Ancestry. Journal of Thoracic Oncology, 2018, 13, 1464-1473.	0.5	38
42	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. Gut, 2014, 63, 800-807.	6.1	35
43	Pleiotropic Associations of Risk Variants Identified for Other Cancers With Lung Cancer Risk: The PAGE and TRICL Consortia. Journal of the National Cancer Institute, 2014, 106, dju061.	3.0	35
44	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. Human Heredity, 2015, 79, 137-146.	0.4	34
45	SecureMA: protecting participant privacy in genetic association meta-analysis. Bioinformatics, 2014, 30, 3334-3341.	1.8	32
46	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. European Urology, 2020, 78, 316-320.	0.9	32
47	Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA. , 2008, , 24-35.		31
48	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	1.8	31
49	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	5.8	31
50	Accuracy of Administratively-Assigned Ancestry for Diverse Populations in an Electronic Medical Record-Linked Biobank. PLoS ONE, 2014, 9, e99161.	1.1	31
51	Functional annotation of genomic variants in studies of late-onset Alzheimerâ€™s disease. Bioinformatics, 2018, 34, 2724-2731.	1.8	30
52	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. Human Molecular Genetics, 2016, 25, 5500-5512.	1.4	29
53	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. Carcinogenesis, 2018, 39, 336-346.	1.3	29
54	Mitochondrial DNA Haplogroups and Neurocognitive Impairment During HIV Infection. Clinical Infectious Diseases, 2015, 61, 1476-1484.	2.9	27

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55	Rare genetic variation implicated in non-Hispanic white families with Alzheimer disease. Neurology: Genetics, 2018, 4, e286.	0.9	27
56	Antibody-specific detection of caveolin-1 in subapical compartments of MDCK cells. Histochemistry and Cell Biology, 2006, 126, 27-34.	0.8	26
57	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. BMC Medical Genomics, 2016, 9, 32.	0.7	26
58	Genomeâ€wide association study of HIVâ€associated neurocognitive disorder (HAND): A CHARTER group study. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 413-426.	1.1	26
59	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. Genomics, 2019, 111, 808-818.	1.3	26
60	Sex differences in the genetic architecture of cognitive resilience to Alzheimerâ€™s disease. Brain, 2022, 145, 2541-2554.	3.7	26
61	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. Oncotarget, 2019, 10, 1760-1774.	0.8	25
62	Africanâ€specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. International Journal of Cancer, 2021, 148, 99-105.	2.3	24
63	Association of Cancer Susceptibility Variants with Risk of Multiple Primary Cancers: The Population Architecture using Genomics and Epidemiology Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2568-2578.	1.1	23
64	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	0.7	22
65	A Rare Germline HOXB13 Variant Contributes to Risk of Prostate Cancer in Men of African Ancestry. European Urology, 2022, 81, 458-462.	0.9	22
66	Replication of Associations between GWAS SNPs and Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. Journal of Investigative Dermatology, 2014, 134, 2049-2052.	0.3	21
67	Cerebrospinal fluid (CSF) biomarkers of iron status are associated with CSF viral load, antiretroviral therapy, and demographic factors in HIV-infected adults. Fluids and Barriers of the CNS, 2017, 14, 11.	2.4	21
68	In Silico Functional Annotation of Genomic Variation. Current Protocols in Human Genetics, 2016, 88, 6.15.1-6.15.17.	3.5	20
69	Automated quantification of pancreatic Î²-cell mass. American Journal of Physiology - Endocrinology and Metabolism, 2014, 306, E1460-E1467.	1.8	19
70	Pleiotropic and Sex-Specific Effects of Cancer GWAS SNPs on Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. PLoS ONE, 2015, 10, e0120491.	1.1	19
71	RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. Human Molecular Genetics, 2019, 28, 3053-3061.	1.4	19
72	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. Carcinogenesis, 2014, 35, 2068-2073.	1.3	18

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73	Three-dimensional spatial analysis of missense variants in RTEL1 identifies pathogenic variants in patients with Familial Interstitial Pneumonia. BMC Bioinformatics, 2018, 19, 18.	1.2	18
74	Fine-mapping analysis of a chromosome 2 region linked to resistance to Mycobacterium tuberculosis infection in Uganda reveals potential regulatory variants. Genes and Immunity, 2019, 20, 473-483.	2.2	18
75	Genetically regulated expression in late-onset Alzheimerâ€™s disease implicates risk genes within known and novel loci. Translational Psychiatry, 2021, 11, 618.	2.4	17
76	Pleiotropy of Cancer Susceptibility Variants on the Risk of Non-Hodgkin Lymphoma: The PAGE Consortium. PLoS ONE, 2014, 9, e89791.	1.1	16
77	Investigating the relationship between mitochondrial genetic variation and cardiovascular-related traits to develop a framework for mitochondrial phenome-wide association studies. BioData Mining, 2014, 7, 6.	2.2	16
78	Genome Simulation. Advances in Genetics, 2010, 72, 1-24.	0.8	14
79	Willingness to Participate in a National Precision Medicine Cohort: Attitudes of Chronic Kidney Disease Patients at a Cleveland Public Hospital. Journal of Personalized Medicine, 2018, 8, 21.	1.1	13
80	Reducing Clinical Noise for Body Mass Index Measures Due to Unit and Transcription Errors in the Electronic Health Record. AMIA Summits on Translational Science Proceedings, 2017, 2017, 102-111.	0.4	13
81	Enabling high-throughput genotype-phenotype associations in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project as part of the Population Architecture using Genomics and Epidemiology (PAGE) study. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 373-84.	0.7	12
82	Progranulin mutations in clinical and neuropathological Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 2458-2467.	0.4	12
83	Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. BioData Mining, 2015, 8, 35.	2.2	11
84	PSCAN: Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. Genome Biology, 2020, 21, 217.	3.8	11
85	Exploring epistasis in candidate genes for rheumatoid arthritis. BMC Proceedings, 2007, 1, S70.	1.8	10
86	Evidence for extensive pleiotropy among pharmacogenes. Pharmacogenomics, 2016, 17, 853-866.	0.6	10
87	Genetic variation in the rhythmonome: ethnic variation and haplotype structure in candidate genes for arrhythmias. Pharmacogenomics, 2009, 10, 1043-1053.	0.6	9
88	LD-Spline: Mapping SNPs on genotyping platforms to genomic regions using patterns of linkage disequilibrium. BioData Mining, 2009, 2, 7.	2.2	9
89	Visualizing SNP statistics in the context of linkage disequilibrium using LD-Plus. Bioinformatics, 2010, 26, 578-579.	1.8	9
90	Overview of Linkage Analysis in Complex Traits. Current Protocols in Human Genetics, 2010, 64, Unit 1.9.1-18.	3.5	9

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91	UTILIZATION OF AN EMR-BIOREPOSITORY TO IDENTIFY THE GENETIC PREDICTORS OF CALCINEURIN-INHIBITOR TOXICITY IN HEART TRANSPLANT RECIPIENTS. , 2013, , .		9
92	A Small Number of Candidate Gene SNPs Reveal Continental Ancestry in African Americans. Annals of Human Genetics, 2013, 77, 56-66.	0.3	9
93	Estimating cumulative pathway effects on risk for age-related macular degeneration using mixed linear models. BMC Bioinformatics, 2015, 16, 329.	1.2	9
94	Genome-Wide Association Studies. , 2019, , 235-241.		9
95	Bridging the Gaps in Personalized Medicine Value Assessment: A Review of the Need for Outcome Metrics across Stakeholders and Scientific Disciplines. Public Health Genomics, 2019, 22, 16-24.	0.6	9
96	Interplay between traumatic brain injury and intimate partner violence: data driven analysis utilizing electronic health records. BMC Women's Health, 2020, 20, 269.	0.8	9
97	Performance of African-ancestry-specific polygenic hazard score varies according to local ancestry in 8q24. Prostate Cancer and Prostatic Diseases, 2022, 25, 229-237.	2.0	9
98	GSK3Î² Interactions with Amyloid Genes: An Autopsy Verification and Extension. Neurotoxicity Research, 2015, 28, 232-238.	1.3	8
99	Sexâ€Specific Parental Effects on Offspring Lipid Levels. Journal of the American Heart Association, 2015, 4, .	1.6	8
100	Catechol-O-methyltransferase polymorphism Val158Met is associated with distal neuropathic pain in HIV-associated sensory neuropathy. Aids, 2019, 33, 1575-1582.	1.0	8
101	Editorial: The Importance of Diversity in Precision Medicine Research. Frontiers in Genetics, 2020, 11, 875.	1.1	8
102	Utilization of an EMR-biorepository to identify the genetic predictors of calcineurin-inhibitor toxicity in heart transplant recipients. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 253-64.	0.7	8
103	Creation and Validation of an EMR-based Algorithm for Identifying Major Adverse Cardiac Events while on Statins. AMIA Summits on Translational Science Proceedings, 2014, 2014, 112-9.	0.4	8
104	Discussing gene-gene interaction: Warning â€" translating equations to English may result in Jabberwocky. Genetic Epidemiology, 2007, 31, S61-S67.	0.6	7
105	ENABLING HIGH-THROUGHPUT GENOTYPE-PHENOTYPE ASSOCIATIONS IN THE EPIDEMIOLOGIC ARCHITECTURE FOR GENES LINKED TO ENVIRONMENT (EAGLE) PROJECT AS PART OF THE POPULATION ARCHITECTURE USING GENOMICS AND EPIDEMIOLOGY (PAGE) STUDY. , 2012, , .		7
106	Putting Pleiotropy and Selection Into Context Defines a New Paradigm for Interpreting Genetic Data. Circulation: Cardiovascular Genetics, 2013, 6, 299-307.	5.1	7
107	Analysis of Heritability Using Genomeâ€Wide Data. Current Protocols in Human Genetics, 2016, 91, 1.30.1-1.30.10.	3.5	7
108	Germline Genetic Variants and Lung Cancer Survival in African Americans. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1288-1295.	1.1	7

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109	TNFRSF1B Gene Variants and Related Soluble TNFR2 Levels Impact Resilience in Alzheimer's Disease. Frontiers in Aging Neuroscience, 2021, 13, 638922.	1.7	7
110	Modeling transcriptional regulation using gene regulatory networks based on multi-omics data sources. BMC Bioinformatics, 2021, 22, 200.	1.2	7
111	Conquering the Needle-in-a-Haystack: How Correlated Input Variables Beneficially Alter the Fitness Landscape for Neural Networks. Lecture Notes in Computer Science, 2009, , 80-91.	1.0	7
112	Evaluating Power and Type 1 Error in Large Pedigree Analyses of Binary Traits. PLoS ONE, 2013, 8, e62615.	1.1	7
113	European Mitochondrial DNA Haplogroups are Associated with Cerebrospinal Fluid Biomarkers of Inflammation in HIV Infection. Pathogens and Immunity, 2016, 1, 330.	1.4	7
114	Characterization of the Metabochip in diverse populations from the International HapMap Project in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 188-99.	0.7	7
115	Can Neural Network Constraints in GP Provide Power to Detect Genes Associated with Human Disease?. Lecture Notes in Computer Science, 2005, , 44-53.	1.0	6
116	Immune and Inflammatory Pathways Implicated by Whole Blood Transcriptomic Analysis in a Diverse Ancestry Alzheimerâ€™s Disease Cohort. Journal of Alzheimer's Disease, 2020, 76, 1047-1060.	1.2	6
117	Local ancestry transitions modify snp-trait associations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 424-435.	0.7	6
118	Gene expression in cell lines from propionic acidemia patients, carrier parents, and controls. Molecular Genetics and Metabolism, 2015, 115, 174-179.	0.5	5
119	Local ancestry transitions modify snp-trait associations. , 2018, , .		5
120	CHARACTERIZATION OF THE METABOCHIP IN DIVERSE POPULATIONS FROM THE INTERNATIONAL HAPMAP PROJECT IN THE EPIDEMIOLOGIC ARCHITECTURE FOR GENES LINKED TO ENVIRONMENT (EAGLE) PROJECT. , 2012, , .		5
121	Phenotyping Adverse Drug Reactions: Statin-Related Myotoxicity. AMIA Summits on Translational Science Proceedings, 2015, 2015, 466-70.	0.4	5
122	Interaction between M. tuberculosis Lineage and Human Genetic Variants Reveals Novel Pathway Associations with Severity of TB. Pathogens, 2021, 10, 1487.	1.2	5
123	An association test of the spatial distribution of rare missense variants within protein structures identifies Alzheimer's diseaseâ€“related patterns. Genome Research, 2022, 32, 778-790.	2.4	5
124	Association Rule Discovery Has the Ability to Model Complex Genetic Effects. , 2007, 2007, 624-629.		4
125	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. Current Genetic Medicine Reports, 2019, 7, 30-40.	1.9	4
126	MULTIVARIATE ANALYSIS OF REGULATORY SNPS: EMPOWERING PERSONAL GENOMICS BY CONSIDERING CIS-EPISTASIS AND HETEROGENEITY. , 2010, , 276-287.		4

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127	Somatic T-cell Receptor Diversity in a Chronic Kidney Disease PatientPopulation Linked to Electronic Health Records. AMIA Summits on Translational Science Proceedings, 2018, 2017, 63-71.	0.4	4
128	Replication of European hypertension associations in a case-control study of 9,534 African Americans. PLoS ONE, 2021, 16, e0259962.	1.1	4
129	Largeâ€scale sequencing studies expand the known genetic architecture of Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2021, 13, e12255.	1.2	4
130	INTEGRATING COMMUNITY-LEVEL DATA RESOURCES FOR PRECISION MEDICINE RESEARCH. , 2018, , .		3
131	Introducing COCOS: codon consequence scanner for annotating reading frame changes induced by stop-lost and frame shift variants. Bioinformatics, 2017, 33, btw820.	1.8	2
132	Higher CSF Ferritin Heavy-Chain (Fth1) and Transferrin Predict Better Neurocognitive Performance in People with HIV. Molecular Neurobiology, 2021, 58, 4842-4855.	1.9	2
133	Genotype Correlation Analysis Reveals Pathway-Based Functional Disequilibrium and Potential Epistasis in the Human Interactome. Lecture Notes in Computer Science, 2014, 8602, 890-901.	1.0	2
134	Extracting Country-of-Origin from Electronic Health Records for Gene- Environment Studies as Part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) Study. AMIA Summits on Translational Science Proceedings, 2017, 2017, 50-57.	0.4	2
135	Genetic architecture of RNA editing regulation in Alzheimerâ€™s disease across diverse ancestral populations. Human Molecular Genetics, 2022, 31, 2876-2886.	1.4	2
136	Rapid storage and retrieval of genomic intervals from a relational database system using nested containment lists. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat056.	1.4	1
137	Predicting Incident Coronary Heart Disease Many Markers at a Time. Circulation: Cardiovascular Genetics, 2016, 9, 472-473.	5.1	1
138	[O2â€“08â€“03]: WHOLEâ€GENOME SEQUENCING IN FAMILIAL LATEâ€ONSET ALZHEIMER's DISEASE IDENTIFIES RARE VARIATION IN AD CANDIDATE GENES. Alzheimer's and Dementia, 2017, 13, P571.	0.4	1
139	Using linkage analysis to identify novel geneâ€gene interactions in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043435.	0.4	1
140	Methylome-wide Analysis Reveals Epigenetic Marks Associated With Resistance to Tuberculosis in Human Immunodeficiency Virusâ€“Infected Individuals From East Africa. Journal of Infectious Diseases, 2021, 224, 695-704.	1.9	1
141	Frequency of ClinVar Pathogenic Variants in Chronic Kidney Disease Patients Surveyed for Return of Research Results at a Cleveland Public Hospital. , 2019, , .		1
142	Frequency of ClinVar Pathogenic Variants in Chronic Kidney Disease Patients Surveyed for Return of Research Results at a Cleveland Public Hospital. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 575-586.	0.7	1
143	A Haptoglobin Exon Copy Number Variant Associates With HIV-Associated Neurocognitive Impairment in European and African-Descent Populations. Frontiers in Genetics, 2021, 12, 756685.	1.1	1
144	[O2â€“08â€“02]: SEXâ€SPECIFIC ANALYSIS OF THE ADSP CASEâ€CONTROL WHOLEâ€EXOME SEQUENCING DATASET. Alzheimer's and Dementia, 2017, 13, P571.	0.4	0

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145	Comparative transâ€ethnic metaâ€analysis of whole exome sequencing variation for Alzheimerâ€™s disease (AD) in 18,402 individuals of the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e041583.	0.4	0
146	Sex differences in genetic predictors of resilience to Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043259.	0.4	0
147	A multiancestry analysis of Alzheimerâ€™s disease coexpressed gene networks identifies a common immune signaling pathway regulated by granulocyteâ€colony stimulating factor (Gâ€CSF). Alzheimer's and Dementia, 2020, 16, e045361.	0.4	0
148	Mapping Alzheimer diseaseâ€“associated regions in the African American population. Alzheimer's and Dementia, 2020, 16, e046072.	0.4	0
149	Structural characterization of rare missense variants within known neurodegenerative disease proteins. Alzheimer's and Dementia, 2020, 16, e046405.	0.4	0
150	Knowledge-Constrained K-Medoids Clustering of Regulatory Rare Alleles for Burden Tests. Lecture Notes in Computer Science, 2013, 7833, 35-42.	1.0	0
151	Packaging Biocomputing Software to Maximize Distribution and Reuse. , 2019, , .		0
152	Hadoop and PySpark for reproducibility and scalability of genomic sequencing studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 523-534.	0.7	0
153	Packaging Biocomputing Software to Maximize Distribution and Reuse. , 2021, , .		0
154	Packaging Biocomputing Software to Maximize Distribution and Reuse. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 739-742.	0.7	0
155	Packaging Biocomputing Software to Maximize Distribution and Reuse. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 412-416.	0.7	0
156	Multiple viruses detected in human DNA are associated with Alzheimer disease risk.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054585.	0.4	0
157	Sex differences in the genetic architecture underlying resilience in AD.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055010.	0.4	0
158	Sex-specific genetic predictors of memory performance.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056083.	0.4	0
159	Expression quantitative trait loci (eQTL) analysis in a diverse Alzheimer disease cohort reveals ancestry-specific regulatory architectures.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056211.	0.4	0
160	Admixture mapping identifies novel regions influencing Alzheimer disease in African Americans.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056443.	0.4	0
161	Integration of Protein Structure and Population-Scale DNA Sequence Data for Disease Gene Discovery and Variant Interpretation. Annual Review of Biomedical Data Science, 2022, 5, .	2.8	0