William Bush

List of Publications by Citations

150 papers	5,181 citations	31 h-index	70 g-index
183 ext. papers	7,340 ext. citations	6.3 avg, IF	5.5 L-index

#	Paper	IF	Citations
150	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
149	Chapter 11: Genome-wide association studies. *PLoS Computational Biology*, **2012**, 8, e1002822	5	708
148	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. *Genetic Epidemiology*, **2007**, 31, 306-15	2.6	261
147	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. *Nature Genetics*, **2017**, 49, 1126-1132	36.3	246
146	The phenotypic legacy of admixture between modern humans and Neandertals. *Science*, **2016**, 351, 737-41	33.3	172
145	Unravelling the human genome-phenome relationship using phenome-wide association studies. *Nature Reviews Genetics*, **2016**, 17, 129-45	30.1	167
144	Evidence for polygenic susceptibility to multiple sclerosis--the shape of things to come. *American Journal of Human Genetics*, **2010**, 86, 621-5	11	146
143	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. *JAMA Neurology*, **2018**, 75, 989-998	17.2	142
142	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. *JAMA - Journal of the American Medical Association*, **2016**, 315, 47-57	27.4	115
141	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. *Molecular Psychiatry*, **2020**, 25, 1859-1875	15.1	106
140	ICD-9 tobacco use codes are effective identifiers of smoking status. *Journal of the American Medical Informatics Association: JAMIA*, **2013**, 20, 652-8	8.6	102
139	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	1.3	76
138	Cystic fibrosis-related diabetes is caused by islet loss and inflammation. *JCI Insight*, **2018**, 3,	9.9	75
137	eMERGEing progress in genomics-the first seven years. *Frontiers in Genetics*, **2014**, 5, 184	4.5	65
136	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	36.3	62
135	Human islet preparations distributed for research exhibit a variety of insulin-secretory profiles. *American Journal of Physiology - Endocrinology and Metabolism*, **2015**, 308, E592-602	6	56
134	A comparison of cataloged variation between International HapMap Consortium and 1000 Genomes Project data. *Journal of the American Medical Informatics Association: JAMIA*, **2012**, 19, 289-94	8.6	56

133	Parallel multifactor dimensionality reduction: a tool for the large-scale analysis of gene-gene interactions. *Bioinformatics*, **2006**, 22, 2173-4	7.2	54
132	Is Isolated Low High-Density Lipoprotein Cholesterol a Cardiovascular Disease Risk Factor? New Insights From the Framingham Offspring Study. *Circulation: Cardiovascular Quality and Outcomes*, **2016**, 9, 206-212	5.8	53
131	Antiepileptic activity of preferential inhibitors of persistent sodium current. *Epilepsia*, **2014**, 55, 1274-83	6.4	50
130	Genetic Programming Neural Networks: A Powerful Bioinformatics Tool for Human Genetics. *Applied Soft Computing Journal*, **2007**, 7, 471-479	7.5	50
129	Genetic analysis of biological pathway data through genomic randomization. *Human Genetics*, **2011**, 129, 563-71	6.3	48
128	Sex-specific genetic predictors of Alzheimer's disease biomarkers. *Acta Neuropathologica*, **2018**, 136, 857-872	14.3	48
127	Alternative contingency table measures improve the power and detection of multifactor dimensionality reduction. *BMC Bioinformatics*, **2008**, 9, 238	3.6	45
126	Automated extraction of clinical traits of multiple sclerosis in electronic medical records. *Journal of the American Medical Informatics Association: JAMIA*, **2013**, 20, e334-40	8.6	40
125	Interrogating the complex role of chromosome 16p13.13 in multiple sclerosis susceptibility: independent genetic signals in the CIITA-CLEC16A-SOCS1 gene complex. *Human Molecular Genetics*, **2011**, 20, 3517-24	5.6	39
124	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
123	Comprehensive Analysis of Constraint on the Spatial Distribution of Missense Variants in Human Protein Structures. *American Journal of Human Genetics*, **2018**, 102, 415-426	11	35
122	Are Interactions between cis-Regulatory Variants Evidence for Biological Epistasis or Statistical Artifacts?. *American Journal of Human Genetics*, **2016**, 99, 817-830	11	32
121	Sex differences in the genetic predictors of Alzheimer's pathology. *Brain*, **2019**, 142, 2581-2589	11.2	32
120	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	5.6	31
119	Bioinformatics challenges in genome-wide association studies (GWAS). *Methods in Molecular Biology*, **2014**, 1168, 63-81	1.4	31
118	Associations between KCNJ6 (GIRK2) gene polymorphisms and pain-related phenotypes. *Pain*, **2013**, 154, 2853-2859	8	30
117	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. *Nature Communications*, **2018**, 9, 3221	17.4	29
116	Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA **2008**, 24-35		29

115	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	9.7	28
114	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. *Human Heredity*, **2015**, 79, 137-46	1.1	27
113	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. *Gut*, **2014**, 63, 800-7	19.2	27
112	New insights into the genetic etiology of Alzheimer's disease and related dementias.. *Nature Genetics*, **2022**,	36.3	27
111	SecureMA: protecting participant privacy in genetic association meta-analysis. *Bioinformatics*, **2014**, 30, 3334-41	7.2	26
110	Accuracy of administratively-assigned ancestry for diverse populations in an electronic medical record-linked biobank. *PLoS ONE*, **2014**, 9, e99161	3.7	26
109	Whole genome sequencing of Caribbean Hispanic families with late-onset Alzheimer's disease. *Annals of Clinical and Translational Neurology*, **2018**, 5, 406-417	5.3	25
108	New insights on the genetic etiology of Alzheimer and related dementia		25
107	Genetic variants and functional pathways associated with resilience to Alzheimer's disease. *Brain*, **2020**, 143, 2561-2575	11.2	25
106	Genetic and clinical risk prediction model for postoperative atrial fibrillation. *Circulation: Arrhythmia and Electrophysiology*, **2015**, 8, 25-31	6.4	24
105	Antibody-specific detection of caveolin-1 in subapical compartments of MDCK cells. *Histochemistry and Cell Biology*, **2006**, 126, 27-34	2.4	24
104	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	6.3	23
103	Genome-wide association study of HIV-associated neurocognitive disorder (HAND): A CHARTER group study. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 413-426	3.5	23
102	Mitochondrial DNA Haplogroups and Neurocognitive Impairment During HIV Infection. *Clinical Infectious Diseases*, **2015**, 61, 1476-84	11.6	23
101	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. *BMC Medical Genomics*, **2016**, 9 Suppl 1, 32	3.7	23
100	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	5.6	22
99	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, 2568-78	4	21
98	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. *Carcinogenesis*, **2014**, 35, 2068-73	4.6	17

97	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimer's Disease Sequencing Project. *Dementia and Geriatric Cognitive Disorders*, **2018**, 45, 1-17	2.6	16
96	Racial Disparities in Lung Cancer Survival: The Contribution of Stage, Treatment, and Ancestry. *Journal of Thoracic Oncology*, **2018**, 13, 1464-1473	8.9	16
95	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	4.3	16
94	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	4.3	16
93	Automated quantification of pancreatic β-cell mass. *American Journal of Physiology - Endocrinology and Metabolism*, **2014**, 306, E1460-7	6	15
92	Rare genetic variation implicated in non-Hispanic white families with Alzheimer disease. *Neurology: Genetics*, **2018**, 4, e286	3.8	15
91	In Silico Functional Annotation of Genomic Variation. *Current Protocols in Human Genetics*, **2016**, 88, 6.15.1-6.15.17	3.2	14
90	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	3.7	14
89	Pleiotropy of cancer susceptibility variants on the risk of non-Hodgkin lymphoma: the PAGE consortium. *PLoS ONE*, **2014**, 9, e89791	3.7	14
88	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. *Nature Communications*, **2021**, 12, 1236	17.4	14
87	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. *European Urology*, **2020**, 78, 316-320	10.2	13
86	Functional annotation of genomic variants in studies of late-onset Alzheimer's disease. *Bioinformatics*, **2018**, 34, 2724-2731	7.2	13
85	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. *Oncotarget*, **2019**, 10, 1760-1774	3.3	12
84	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	1.3	12
83	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. *Carcinogenesis*, **2018**, 39, 336-346	4.6	11
82	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	4.4	11
81	Genome simulation approaches for synthesizing in silico datasets for human genomics. *Advances in Genetics*, **2010**, 72, 1-24	3.3	11
80	BIOFILTER: A KNOWLEDGE-INTEGRATION SYSTEM FOR THE MULTI-LOCUS ANALYSIS OF GENOME-WIDE ASSOCIATION STUDIES **2008**,		11

79	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	1.1	11
78	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	4.3	10
77	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	7	10
76	Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. *BioData Mining*, **2015**, 8, 35	4.3	9
75	LD-spline: mapping SNPs on genotyping platforms to genomic regions using patterns of linkage disequilibrium. *BioData Mining*, **2009**, 2, 7	4.3	9
74	Exploring epistasis in candidate genes for rheumatoid arthritis. *BMC Proceedings*, **2007**, 1 Suppl 1, S70	2.3	9
73	GSK3Interactions with Amyloid Genes: An Autopsy Verification and Extension. *Neurotoxicity Research*, **2015**, 28, 232-8	4.3	8
72	Evidence for extensive pleiotropy among pharmacogenes. *Pharmacogenomics*, **2016**, 17, 853-66	2.6	8
71	Visualizing SNP statistics in the context of linkage disequilibrium using LD-Plus. *Bioinformatics*, **2010**, 26, 578-9	7.2	8
70	Genetic variation in the rhythmonome: ethnic variation and haplotype structure in candidate genes for arrhythmias. *Pharmacogenomics*, **2009**, 10, 1043-53	2.6	8
69	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	1.9	7
68	RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. *Human Molecular Genetics*, **2019**, 28, 3053-3061	5.6	7
67	A small number of candidate gene SNPs reveal continental ancestry in African Americans. *Annals of Human Genetics*, **2013**, 77, 56-66	2.2	7
66	Estimating cumulative pathway effects on risk for age-related macular degeneration using mixed linear models. *BMC Bioinformatics*, **2015**, 16, 329	3.6	7
65	Overview of linkage analysis in complex traits. *Current Protocols in Human Genetics*, **2010**, Chapter 1, Unit 1.9.1-18	3.2	7
64	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	1.3	7
63	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	1.3	7
62	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	1.1	7

61	European Mitochondrial DNA Haplogroups are Associated with Cerebrospinal Fluid Biomarkers of Inflammation in HIV Infection. *Pathogens and Immunity*, **2016**, 1, 330-351	4.9	7
60	African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. *International Journal of Cancer*, **2021**, 148, 99-105	7.5	7
59	Protein-altering germline mutations implicate novel genes related to lung cancer development. *Nature Communications*, **2020**, 11, 2220	17.4	6
58	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,	3.6	6
57	Three-dimensional spatial analysis of missense variants in RTEL1 identifies pathogenic variants in patients with Familial Interstitial Pneumonia. *BMC Bioinformatics*, **2018**, 19, 18	3.6	6
56	Putting pleiotropy and selection into context defines a new paradigm for interpreting genetic data. *Circulation: Cardiovascular Genetics*, **2013**, 6, 299-307		6
55	Discussing gene-gene interaction: warning--translating equations to English may result in jabberwocky. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S61-7	2.6	6
54	Evaluating power and type 1 error in large pedigree analyses of binary traits. *PLoS ONE*, **2013**, 8, e62615	3.7	6
53	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	0.9	6
52	Sex-Specific Parental Effects on Offspring Lipid Levels. *Journal of the American Heart Association*, **2015**, 4,	6	5
51	Interplay between traumatic brain injury and intimate partner violence: data driven analysis utilizing electronic health records. *BMC Womens Health*, **2020**, 20, 269	2.9	5
50	Analysis of Heritability Using Genome-Wide Data. *Current Protocols in Human Genetics*, **2016**, 91, 1.30.1-1.30.10	3.3	5
49	Can Neural Network Constraints in GP Provide Power to Detect Genes Associated with Human Disease?. *Lecture Notes in Computer Science*, **2005**, 44-53	0.9	5
48	Phenotyping Adverse Drug Reactions: Statin-Related Myotoxicity. *AMIA Summits on Translational Science Proceedings*, **2015**, 2015, 466-70	1.1	5
47	Germline Genetic Variants and Lung Cancer Survival in African Americans. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1288-1295	4	4
46	Gene expression in cell lines from propionic acidemia patients, carrier parents, and controls. *Molecular Genetics and Metabolism*, **2015**, 115, 174-9	3.7	4
45	Local ancestry transitions modify snp-trait associations. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 424-435	1.3	4
44	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	1.1	4

43	PSCAN: Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. *Genome Biology*, **2020**, 21, 217	18.3	4
42	Catechol-O-methyltransferase polymorphism Val158Met is associated with distal neuropathic pain in HIV-associated sensory neuropathy. *Aids*, **2019**, 33, 1575-1582	3.5	4
41	Genome-Wide Association Studies **2019**, 235-241		3
40	Multivariate analysis of regulatory SNPs: empowering personal genomics by considering cis-epistasis and heterogeneity. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2011**, 276-87	1.3	3
39	Immune and Inflammatory Pathways Implicated by Whole Blood Transcriptomic Analysis in a Diverse Ancestry Alzheimer's Disease Cohort. *Journal of Alzheimer's Disease*, **2020**, 76, 1047-1060	4.3	2
38	UTILIZATION OF AN EMR-BIOREPOSITORY TO IDENTIFY THE GENETIC PREDICTORS OF CALCINEURIN-INHIBITOR TOXICITY IN HEART TRANSPLANT RECIPIENTS **2013**,		2
37	Association Rule Discovery Has the Ability to Model Complex Genetic Effects **2007**, 2007, 624-629		2
36	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	1.1	2
35	Genome-Wide Meta-Analysis of Late-Onset Alzheimer's Disease Using Rare Variant Imputation in 65,602 Subjects Identifies Novel Rare Variant Locus NCK2: The International Genomics of Alzheimer's Project (IGAP)		2
34	Gene Variants and Related Soluble TNFR2 Levels Impact Resilience in Alzheimer's Disease. *Frontiers in Aging Neuroscience*, **2021**, 13, 638922	5.3	2
33	Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. *Translational Psychiatry*, **2021**, 11, 618	8.6	2
32	Introducing COCOS: codon consequence scanner for annotating reading frame changes induced by stop-lost and frame shift variants. *Bioinformatics*, **2017**, 33, 1561-1562	7.2	1
31	[O2–08–03]: WHOLE-GENOME SEQUENCING IN FAMILIAL LATE-ONSET ALZHEIMER's DISEASE IDENTIFIES RARE VARIATION IN AD CANDIDATE GENES **2017**, 13, P571-P572		1
30	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	5	1
29	Genetic Variants and Functional Pathways Associated with Resilience to Alzheimer's Disease		1
28	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	1.3	1
27	Replication of European hypertension associations in a case-control study of 9,534 African Americans. *PLoS ONE*, **2021**, 16, e0259962	3.7	1
26	African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer		1

25	Genotype Correlation Analysis Reveals Pathway-Based Functional Disequilibrium and Potential Epistasis in the Human Interactome. *Lecture Notes in Computer Science*, **2014**, 8602, 890-901	0.9	1
24	Modeling transcriptional regulation using gene regulatory networks based on multi-omics data sources. *BMC Bioinformatics*, **2021**, 22, 200	3.6	1
23	An association test of the spatial distribution of rare missense variants within protein structures identify Alzheimer's disease-related patterns.. *Genome Research*, **2022**,	9.7	1
22	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. *Current Genetic Medicine Reports*, **2019**, 7, 30-40	2.2	0
21	A Haptoglobin Exon Copy Number Variant Associates With HIV-Associated Neurocognitive Impairment in European and African-Descent Populations.. *Frontiers in Genetics*, **2021**, 12, 756685	4.5	0
20	Comparative trans-ethnic meta-analysis of whole exome sequencing variation for Alzheimer disease (AD) in 18,402 individuals of the Alzheimer Disease Sequencing Project (ADSP). *Alzheimer and Dementia*, **2020**, 16, e041583	1.2	
19	Sex differences in genetic predictors of resilience to Alzheimer disease. *Alzheimer and Dementia*, **2020**, 16, e043259	1.2	
18	Using linkage analysis to identify novel gene-gene interactions in Alzheimer disease. *Alzheimer and Dementia*, **2020**, 16, e043435	1.2	
17	A multiancestry analysis of Alzheimer disease coexpressed gene networks identifies a common immune signaling pathway regulated by granulocyte-colony stimulating factor (G-CSF). *Alzheimer and Dementia*, **2020**, 16, e045361	1.2	
16	Mapping Alzheimer diseaseassociated regions in the African American population. *Alzheimer and Dementia*, **2020**, 16, e046072	1.2	
15	Structural characterization of rare missense variants within known neurodegenerative disease proteins. *Alzheimer and Dementia*, **2020**, 16, e046405	1.2	
14	[O2802]: SEX-SPECIFIC ANALYSIS OF THE ADSP CASE-CONTROL WHOLE-EXOME SEQUENCING DATASET **2017**, 13, P571		
13	Hadoop and PySpark for reproducibility and scalability of genomic sequencing studies. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2020**, 25, 523-534	1.3	
12	Complex Genetic Interactions/Data Mining/Dimensionality Reduction **2021**, 265-277		
11	Large-scale sequencing studies expand the known genetic architecture of Alzheimer's disease.. *Alzheimer and Dementia: Diagnosis, Assessment and Disease Monitoring*, **2021**, 13, e12255	5.2	
10	Knowledge-constrained K-medoids Clustering of Regulatory Rare Alleles for Burden Tests. *Lecture Notes in Computer Science*, **2013**, 7833, 35-42	0.9	
9	Higher CSF Ferritin Heavy-Chain (Fth1) and Transferrin Predict Better Neurocognitive Performance in People with HIV. *Molecular Neurobiology*, **2021**, 58, 4842-4855	6.2	
8	Methylome-wide Analysis Reveals Epigenetic Marks Associated With Resistance to Tuberculosis in Human Immunodeficiency Virus-Infected Individuals From East Africa. *Journal of Infectious Diseases*, **2021**, 224, 695-704	7	

7	Packaging Biocomputing Software to Maximize Distribution and Reuse. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2020**, 25, 739-742	1.3
6	Packaging Biocomputing Software to Maximize Distribution and Reuse. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2022**, 27, 412-416	1.3
5	Multiple viruses detected in human DNA are associated with Alzheimer disease risk.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e054585	1.2
4	Sex differences in the genetic architecture underlying resilience in AD.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e055010	1.2
3	Sex-specific genetic predictors of memory performance.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e056083	1.2
2	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	1.2
1	Admixture mapping identifies novel regions influencing Alzheimer disease in African Americans.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e056443	1.2