William Bush

List of Publications by Year in Descending Order

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	Packaging Biocomputing Software to Maximize Distribution and Reuse. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2022**, 27, 412-416	1.3	
149	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
148	New insights into the genetic etiology of Alzheimer's disease and related dementias.. *Nature Genetics*, **2022**,	36.3	27
147	Complex Genetic Interactions/Data Mining/Dimensionality Reduction **2021**, 265-277		
146	Replication of European hypertension associations in a case-control study of 9,534 African Americans. *PLoS ONE*, **2021**, 16, e0259962	3.7	1
145	Large-scale sequencing studies expand the known genetic architecture of Alzheimer's disease.. *Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring*, **2021**, 13, e12255	5.2	
144	Modeling transcriptional regulation using gene regulatory networks based on multi-omics data sources. *BMC Bioinformatics*, **2021**, 22, 200	3.6	1
143	Higher CSF Ferritin Heavy-Chain (Fth1) and Transferrin Predict Better Neurocognitive Performance in People with HIV. *Molecular Neurobiology*, **2021**, 58, 4842-4855	6.2	
142	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
141	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
140	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	
139	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. *Nature Communications*, **2021**, 12, 1236	17.4	14
138	Gene Variants and Related Soluble TNFR2 Levels Impact Resilience in Alzheimer's Disease. *Frontiers in Aging Neuroscience*, **2021**, 13, 638922	5.3	2
137	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
136	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
135	Multiple viruses detected in human DNA are associated with Alzheimer disease risk.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e054585	1.2	
134	Sex differences in the genetic architecture underlying resilience in AD.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e055010	1.2	

133	Sex-specific genetic predictors of memory performance.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e056083	1.2	
132	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	
131	Admixture mapping identifies novel regions influencing Alzheimer disease in African Americans.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e056443	1.2	
130	Comparative trans-ethnic meta-analysis of whole exome sequencing variation for Alzheimer's disease (AD) in 18,402 individuals of the Alzheimer's Disease Sequencing Project (ADSP). *Alzheimer's and Dementia*, **2020**, 16, e041583	1.2	
129	Sex differences in genetic predictors of resilience to Alzheimer's disease. *Alzheimer's and Dementia*, **2020**, 16, e043259	1.2	
128	Using linkage analysis to identify novel gene-gene interactions in Alzheimer's disease. *Alzheimer's and Dementia*, **2020**, 16, e043435	1.2	
127	A multiancestry analysis of Alzheimer's disease coexpressed gene networks identifies a common immune signaling pathway regulated by granulocyte-colony stimulating factor (G-CSF). *Alzheimer's and Dementia*, **2020**, 16, e045361	1.2	
126	Mapping Alzheimer disease's associated regions in the African American population. *Alzheimer's and Dementia*, **2020**, 16, e046072	1.2	
125	Structural characterization of rare missense variants within known neurodegenerative disease proteins. *Alzheimer's and Dementia*, **2020**, 16, e046405	1.2	
124	Interplay between traumatic brain injury and intimate partner violence: data driven analysis utilizing electronic health records. *BMC Women's Health*, **2020**, 20, 269	2.9	5
123	Protein-altering germline mutations implicate novel genes related to lung cancer development. *Nature Communications*, **2020**, 11, 2220	17.4	6
122	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
121	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
120	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
119	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	
118	Genetic variants and functional pathways associated with resilience to Alzheimer's disease. *Brain*, **2020**, 143, 2561-2575	11.2	25
117	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
116	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

115	Packaging Biocomputing Software to Maximize Distribution and Reuse. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2020**, 25, 739-742	1.3	
114	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
113	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
112	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. *Oncotarget*, **2019**, 10, 1760-1774	3.3	12
111	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. *Current Genetic Medicine Reports*, **2019**, 7, 30-40	2.2	0
110	Genome-Wide Association Studies **2019**, 235-241		3
109	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
108	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
107	Sex differences in the genetic predictors of Alzheimer's pathology. *Brain*, **2019**, 142, 2581-2589	11.2	32
106	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
105	Catechol-O-methyltransferase polymorphism Val158Met is associated with distal neuropathic pain in HIV-associated sensory neuropathy. *Aids*, **2019**, 33, 1575-1582	3.5	4
104	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
103	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
102	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
101	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
100	Functional annotation of genomic variants in studies of late-onset Alzheimer's disease. *Bioinformatics*, **2018**, 34, 2724-2731	7.2	13
99	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
98	Racial Disparities in Lung Cancer Survival: The Contribution of Stage, Treatment, and Ancestry. *Journal of Thoracic Oncology*, **2018**, 13, 1464-1473	8.9	16

97	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. *JAMA Neurology*, **2018**, 75, 989-998	17.2	142
96	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
95	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. *Nature Communications*, **2018**, 9, 3221	17.4	29
94	Local ancestry transitions modify snp-trait associations. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 424-435	1.3	4
93	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
92	Rare genetic variation implicated in non-Hispanic white families with Alzheimer disease. *Neurology: Genetics*, **2018**, 4, e286	3.8	15
91	Cystic fibrosis-related diabetes is caused by islet loss and inflammation. *JCI Insight*, **2018**, 3,	9.9	75
90	Sex-specific genetic predictors of Alzheimer's disease biomarkers. *Acta Neuropathologica*, **2018**, 136, 857-872	14.3	48
89	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
88	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
87	Germline Genetic Variants and Lung Cancer Survival in African Americans. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1288-1295	4	4
86	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
85	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
84	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
83	[O2□8□2]: SEX-SPECIFIC ANALYSIS OF THE ADSP CASE-CONTROL WHOLE-EXOME SEQUENCING DATASET **2017**, 13, P571		
82	[O2□8□3]: WHOLE-GENOME SEQUENCING IN FAMILIAL LATE-ONSET ALZHEIMER's DISEASE IDENTIFIES RARE VARIATION IN AD CANDIDATE GENES **2017**, 13, P571-P572		1
81	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
80	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

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	Are Interactions between cis-Regulatory Variants Evidence for Biological Epistasis or Statistical Artifacts?. *American Journal of Human Genetics*, **2016**, 99, 817-830	11	32
77	Analysis of Heritability Using Genome-Wide Data. *Current Protocols in Human Genetics*, **2016**, 91, 1.30.1-1.30.10	3.2	5
76	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
75	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
74	Evidence for extensive pleiotropy among pharmacogenes. *Pharmacogenomics*, **2016**, 17, 853-66	2.6	8
73	In Silico Functional Annotation of Genomic Variation. *Current Protocols in Human Genetics*, **2016**, 88, 6.15.1-6.15.17	3.2	14
72	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
71	The phenotypic legacy of admixture between modern humans and Neandertals. *Science*, **2016**, 351, 737-41	33.3	172
70	Unravelling the human genome-phenome relationship using phenome-wide association studies. *Nature Reviews Genetics*, **2016**, 17, 129-45	30.1	167
69	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
68	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
67	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
66	Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. *Human Heredity*, **2015**, 79, 137-46	1.1	27
65	Mitochondrial DNA Haplogroups and Neurocognitive Impairment During HIV Infection. *Clinical Infectious Diseases*, **2015**, 61, 1476-84	11.6	23
64	Genetic and clinical risk prediction model for postoperative atrial fibrillation. *Circulation: Arrhythmia and Electrophysiology*, **2015**, 8, 25-31	6.4	24
63	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
62	GSK3β Interactions with Amyloid Genes: An Autopsy Verification and Extension. *Neurotoxicity Research*, **2015**, 28, 232-8	4.3	8

61	Sex-Specific Parental Effects on Offspring Lipid Levels. *Journal of the American Heart Association*, **2015**, 4,	6	5
60	Estimating cumulative pathway effects on risk for age-related macular degeneration using mixed linear models. *BMC Bioinformatics*, **2015**, 16, 329	3.6	7
59	Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. *BioData Mining*, **2015**, 8, 35	4.3	9
58	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
57	Gene expression in cell lines from propionic acidemia patients, carrier parents, and controls. *Molecular Genetics and Metabolism*, **2015**, 115, 174-9	3.7	4
56	Phenotyping Adverse Drug Reactions: Statin-Related Myotoxicity. *AMIA Summits on Translational Science Proceedings*, **2015**, 2015, 466-70	1.1	5
55	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. *Carcinogenesis*, **2014**, 35, 2068-73	4.6	17
54	Antiepileptic activity of preferential inhibitors of persistent sodium current. *Epilepsia*, **2014**, 55, 1274-83	6.4	50
53	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
52	Pleiotropy of cancer susceptibility variants on the risk of non-Hodgkin lymphoma: the PAGE consortium. *PLoS ONE*, **2014**, 9, e89791	3.7	14
51	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
50	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, 2049-2032	4.3	16
49	eMERGEing progress in genomics-the first seven years. *Frontiers in Genetics*, **2014**, 5, 184	4.5	65
48	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
47	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
46	Automated quantification of pancreatic β-cell mass. *American Journal of Physiology - Endocrinology and Metabolism*, **2014**, 306, E1460-7	6	15
45	SecureMA: protecting participant privacy in genetic association meta-analysis. *Bioinformatics*, **2014**, 30, 3334-41	7.2	26
44	Accuracy of administratively-assigned ancestry for diverse populations in an electronic medical record-linked biobank. *PLoS ONE*, **2014**, 9, e99161	3.7	26

43	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
42	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
41	Bioinformatics challenges in genome-wide association studies (GWAS). *Methods in Molecular Biology*, **2014**, 1168, 63-81	1.4	31
40	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
39	UTILIZATION OF AN EMR-BIOREPOSITORY TO IDENTIFY THE GENETIC PREDICTORS OF CALCINEURIN-INHIBITOR TOXICITY IN HEART TRANSPLANT RECIPIENTS **2013**,		2
38	A small number of candidate gene SNPs reveal continental ancestry in African Americans. *Annals of Human Genetics*, **2013**, 77, 56-66	2.2	7
37	Associations between KCNJ6 (GIRK2) gene polymorphisms and pain-related phenotypes. *Pain*, **2013** , 154, 2853-2859	8	30
36	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
35	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
34	Putting pleiotropy and selection into context defines a new paradigm for interpreting genetic data. *Circulation: Cardiovascular Genetics*, **2013**, 6, 299-307		6
33	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
32	Evaluating power and type 1 error in large pedigree analyses of binary traits. *PLoS ONE*, **2013**, 8, e62615	3.7	6
31	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
30	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
29	Knowledge-constrained K-medoids Clustering of Regulatory Rare Alleles for Burden Tests. *Lecture Notes in Computer Science*, **2013**, 7833, 35-42	0.9	
28	Chapter 11: Genome-wide association studies. *PLoS Computational Biology*, **2012**, 8, e1002822	5	708
27	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
26	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

25	Genetic analysis of biological pathway data through genomic randomization. *Human Genetics*, **2011**, 129, 563-71	6.3	48
24	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
23	Genome simulation approaches for synthesizing in silico datasets for human genomics. *Advances in Genetics*, **2010**, 72, 1-24	3.3	11
22	Visualizing SNP statistics in the context of linkage disequilibrium using LD-Plus. *Bioinformatics*, **2010**, 26, 578-9	7.2	8
21	Overview of linkage analysis in complex traits. *Current Protocols in Human Genetics*, **2010**, Chapter 1, Unit 1.9.1-18	3.2	7
20	Evidence for polygenic susceptibility to multiple sclerosis--the shape of things to come. *American Journal of Human Genetics*, **2010**, 86, 621-5	11	146
19	Genetic variation in the rhythmonome: ethnic variation and haplotype structure in candidate genes for arrhythmias. *Pharmacogenomics*, **2009**, 10, 1043-53	2.6	8
18	LD-spline: mapping SNPs on genotyping platforms to genomic regions using patterns of linkage disequilibrium. *BioData Mining*, **2009**, 2, 7	4.3	9
17	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
16	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
15	Alternative contingency table measures improve the power and detection of multifactor dimensionality reduction. *BMC Bioinformatics*, **2008**, 9, 238	3.6	45
14	Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA **2008**, 24-35		29
13	BIOFILTER: A KNOWLEDGE-INTEGRATION SYSTEM FOR THE MULTI-LOCUS ANALYSIS OF GENOME-WIDE ASSOCIATION STUDIES **2008**,		11
12	Exploring epistasis in candidate genes for rheumatoid arthritis. *BMC Proceedings*, **2007**, 1 Suppl 1, S70	2.3	9
11	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. *Genetic Epidemiology*, **2007**, 31, 306-15	2.6	261
10	Discussing gene-gene interaction: warning--translating equations to English may result in jabberwocky. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S61-7	2.6	6
9	Genetic Programming Neural Networks: A Powerful Bioinformatics Tool for Human Genetics. *Applied Soft Computing Journal*, **2007**, 7, 471-479	7.5	50
8	Association Rule Discovery Has the Ability to Model Complex Genetic Effects **2007**, 2007, 624-629		2

7	Parallel multifactor dimensionality reduction: a tool for the large-scale analysis of gene-gene interactions. *Bioinformatics*, **2006**, 22, 2173-4	7.2	54
6	Antibody-specific detection of caveolin-1 in subapical compartments of MDCK cells. *Histochemistry and Cell Biology*, **2006**, 126, 27-34	2.4	24
5	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
4	Genetic Variants and Functional Pathways Associated with Resilience to Alzheimer's Disease		1
3	African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer		1
2	New insights on the genetic etiology of Alzheimer's and related dementia		25
1	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