

Shelley B Bull

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

1,791
citations

331670

21
h-index

289244

40
g-index

65
all docs

65
docs citations

65
times ranked

3678
citing authors

#	ARTICLE	IF	CITATIONS
1	New Susceptibility Loci Associated with Kidney Disease in Type 1 Diabetes. <i>PLoS Genetics</i> , 2012, 8, e1002921.	3.5	216
2	Genome-Wide Association Study of Diabetic Kidney Disease Highlights Biology Involved in Glomerular Basement Membrane Collagen. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2000-2016.	6.1	135
3	Comparative Expression of the Mitotic Regulators SAK and PLK in Colorectal Cancer. <i>Annals of Surgical Oncology</i> , 2001, 8, 729-740.	1.5	105
4	A Genome-Wide Association Study Identifies a Novel Major Locus for Glycemic Control in Type 1 Diabetes, as Measured by Both A1C and Glucose. <i>Diabetes</i> , 2010, 59, 539-549.	0.6	103
5	The Combination of p53 Mutation and neu/erbB-2 Amplification Is Associated With Poor Survival in Node-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2004, 22, 86-96.	1.6	90
6	Multiple Superoxide Dismutase 1/Splicing Factor Serine Alanine 15 Variants Are Associated With the Development and Progression of Diabetic Nephropathy. <i>Diabetes</i> , 2008, 57, 218-228.	0.6	89
7	Multiple Variants in Vascular Endothelial Growth Factor (VEGFA) Are Risk Factors for Time to Severe Retinopathy in Type 1 Diabetes. <i>Diabetes</i> , 2007, 56, 2161-2168.	0.6	88
8	MDR1 Gene Expression and Outcome in Osteosarcoma: A Prospective, Multicenter Study. <i>Journal of Clinical Oncology</i> , 2000, 18, 2685-2694.	1.6	80
9	Reduction of selection bias in genomewide studies by resampling. <i>Genetic Epidemiology</i> , 2005, 28, 352-367.	1.3	67
10	Distinguishing luminal breast cancer subtypes by Ki67, progesterone receptor or TP53 status provides prognostic information. <i>Modern Pathology</i> , 2014, 27, 554-561.	5.5	66
11	The association of previously reported polymorphisms for microvascular complications in a meta-analysis of diabetic retinopathy. <i>Human Genetics</i> , 2015, 134, 247-257.	3.8	60
12	BR-squared: a practical solution to the winner's curse in genome-wide scans. <i>Human Genetics</i> , 2011, 129, 545-552.	3.8	56
13	Preferential allelic expression can lead to reduced expression of BRCA1 in sporadic breast cancers. , 1998, 77, 1-6.		46
14	Confidence intervals for multinomial logistic regression in sparse data. <i>Statistics in Medicine</i> , 2007, 26, 903-918.	1.6	44
15	Prognostic Effect of Basal-Like Breast Cancers Is Time Dependent: Evidence from Tissue Microarray Studies on a Lymph Node-Negative Cohort. <i>Clinical Cancer Research</i> , 2008, 14, 4168-4174.	7.0	37
16	The Efficiency of Multinomial Logistic Regression Compared with Multiple Group Discriminant Analysis. <i>Journal of the American Statistical Association</i> , 1987, 82, 1118-1122.	3.1	36
17	Re-Ranking Sequencing Variants in the Post-GWAS Era for Accurate Causal Variant Identification. <i>PLoS Genetics</i> , 2013, 9, e1003609.	3.5	36
18	A flexible genome-wide bootstrap method that accounts for ranking and threshold selection bias in GWAS interpretation and replication study design. <i>Statistics in Medicine</i> , 2011, 30, 1898-1912.	1.6	32

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19	Elevated expression of podocalyxin is associated with lymphatic invasion, basal-like phenotype, and clinical outcome in axillary lymph node-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 137, 709-719.	2.5	30
20	Incorporation of covariates into genome scanning using sib-pair analysis in bipolar affective disorder. <i>Genetic Epidemiology</i> , 1997, 14, 635-640.	1.3	28
21	Menacalc, a quantitative method of metastasis assessment, as a prognostic marker for axillary node-negative breast cancer. <i>BMC Cancer</i> , 2015, 15, 483.	2.6	27
22	Validation of Intratumoral T-bet+ Lymphoid Cells as Predictors of Disease-Free Survival in Breast Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 41-48.	3.4	25
23	Insights From Mixture Cure Modeling of Molecular Markers for Prognosis in Breast Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 2047-2054.	1.6	23
24	Molecular and Epidemiologic Study of Multiresistant <i>Serratia marcescens</i> Infections in a Spinal Cord Injury Rehabilitation Unit. <i>Infection Control and Hospital Epidemiology</i> , 1988, 9, 20-27.	1.8	17
25	Type of TP53 mutation and ERBB2 amplification affects survival in node-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2007, 105, 255-265.	2.5	17
26	JACKKNIFE BIAS REDUCTION FOR POLYCHOTOMOUS LOGISTIC REGRESSION. <i>Statistics in Medicine</i> , 1997, 16, 545-560.	1.6	16
27	A hierarchical clustering method for estimating copy number variation. <i>Biostatistics</i> , 2007, 8, 632-653.	1.5	16
28	Bivariate genetic association analysis of systolic and diastolic blood pressure by copula models. <i>BMC Proceedings</i> , 2014, 8, S72.	1.6	16
29	Multiple linear combination (MLC) regression tests for common variants adapted to linkage disequilibrium structure. <i>Genetic Epidemiology</i> , 2017, 41, 108-121.	1.3	14
30	Tumoral BRD4 expression in lymph node-negative breast cancer: association with T-bet+ tumor-infiltrating lymphocytes and disease-free survival. <i>BMC Cancer</i> , 2018, 18, 750.	2.6	13
31	Genome-wide association analyses of North American Rheumatoid Arthritis Consortium and Framingham Heart Study data utilizing genome-wide linkage results. <i>BMC Proceedings</i> , 2009, 3, S103.	1.6	12
32	Resampling to Address the Winner's Curse in Genetic Association Analysis of Time to Event. <i>Genetic Epidemiology</i> , 2015, 39, 518-528.	1.3	11
33	Region-based analysis in genome-wide association study of Framingham Heart Study blood lipid phenotypes. <i>BMC Proceedings</i> , 2009, 3, S127.	1.6	10
34	New Locus for Skin Intrinsic Fluorescence in Type 1 Diabetes Also Associated With Blood and Skin Glycated Proteins. <i>Diabetes</i> , 2016, 65, 2060-2071.	0.6	10
35	Fine mapping by linkage and association in nuclear family and case-control designs. <i>Genetic Epidemiology</i> , 2005, 29, S48-S58.	1.3	9
36	Gene-based multiple regression association testing for combined examination of common and low frequency variants in quantitative trait analysis. <i>Frontiers in Genetics</i> , 2013, 4, 233.	2.3	9

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37	Clique-Based Clustering of Correlated SNPs in a Gene Can Improve Performance of Gene-Based Multi-Bin Linear Combination Test. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	9
38	Regression models for allele sharing: analysis of accumulating data in affected sib pair studies. <i>Statistics in Medicine</i> , 2002, 21, 431-444.	1.6	8
39	Are quantitative trait-dependent sampling designs cost-effective for analysis of rare and common variants?. <i>BMC Proceedings</i> , 2011, 5, S111.	1.6	8
40	Does Familial Clustering of Risk Factors for Long-Term Diabetic Complications Leave Any Place for Genes That Act independently?. <i>Journal of Cardiovascular Translational Research</i> , 2012, 5, 388-398.	2.4	8
41	Statistical power in COVID-19 case-control host genomic study design. <i>Genome Medicine</i> , 2020, 12, 115.	8.2	7
42	Heterogeneity in IBD Allele Sharing among Covariate-Defined Subgroups: Issues and Findings for Affected Relatives. <i>Human Heredity</i> , 2003, 56, 94-106.	0.8	6
43	Regression models, scan statistics and reappearance probabilities to detect regions of association between gene expression and copy number. <i>Statistics in Medicine</i> , 2011, 30, 1157-1178.	1.6	6
44	Two-phase designs for joint quantitative-trait-dependent and genotype-dependent sampling in post-GWAS regional sequencing. <i>Genetic Epidemiology</i> , 2018, 42, 104-116.	1.3	6
45	The Efficiency of Multinomial Logistic Regression Compared With Multiple Group Discriminant Analysis. <i>Journal of the American Statistical Association</i> , 1987, 82, 1118.	3.1	6
46	Two-phase Stratified Sampling Designs for Regional Sequencing. <i>Genetic Epidemiology</i> , 2012, 36, 320-332.	1.3	5
47	A 2-step strategy for detecting pleiotropic effects on multiple longitudinal traits. <i>Frontiers in Genetics</i> , 2014, 5, 357.	2.3	5
48	Efficiency of reduced logistic regression models. <i>Canadian Journal of Statistics</i> , 1994, 22, 319-334.	0.9	4
49	Non-invasive Electroarthrography Measures Load-Induced Cartilage Streaming Potentials via Electrodes Placed on Skin Surrounding an Articular Joint. <i>Cartilage</i> , 2020, , 194760352092858.	2.7	3
50	Sequence kernel association test for survival outcomes in the presence of a non-susceptible fraction. <i>Biostatistics</i> , 2020, 21, 518-530.	1.5	3
51	Disease-marker associations: Power and heterogeneity in independent population samples. <i>Genetic Epidemiology</i> , 1999, 17, S509-S514.	1.3	2
52	Modeling Complex Disease with Demographic and Environmental Covariates and a Candidate Gene Marker. <i>Genetic Epidemiology</i> , 2001, 21, S423-S428.	1.3	2
53	A Note on the Efficiencies of Sampling Strategies in Two-stage Bayesian Regional Fine Mapping of a Quantitative Trait. <i>Genetic Epidemiology</i> , 2014, 38, 599-609.	1.3	2
54	Multiphase analysis by linkage, quantitative transmission disequilibrium, and measured genotype: systolic blood pressure in complex Mexican American pedigrees. <i>BMC Proceedings</i> , 2014, 8, S108.	1.6	2

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55	Two-phase sample selection strategies for design and analysis in post-genome-wide association fine-mapping studies. <i>Statistics in Medicine</i> , 2021, 40, 6792-6817.	1.6	2
56	Comparative Expression of the Mitotic Regulators SAK and PLK in Colorectal Cancer. <i>Annals of Surgical Oncology</i> , 2001, 8, 729-740.	1.5	2
57	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. <i>Cancers</i> , 2022, 14, 3363.	3.7	2
58	Comparison of evidence for linkage from different analytic methods. <i>Genetic Epidemiology</i> , 1997, 14, 965-970.	1.3	1
59	Does Simultaneous Consideration of Multiple Regions Improve Disease Gene Localization?. <i>Genetic Epidemiology</i> , 2001, 21, S504-S509.	1.3	1
60	An exploration of heterogeneity in genetic analysis of complex pedigrees: linkage and association using whole genome sequencing data in the MAP4 region. <i>BMC Proceedings</i> , 2014, 8, S107.	1.6	1
61	Gene-based and pathway-based testing for rare-variant association in affected sib pairs. <i>Genetic Epidemiology</i> , 2020, 44, 368-381.	1.3	1
62	Statistical challenges in high-dimensional molecular and genetic epidemiology. <i>Canadian Journal of Statistics</i> , 2018, 46, 24-40.	0.9	0