Veronica J Vieland

List of Publications by Year
in descending order

72	6,815	185998 28	98622 67
papers	citations	h-index	g-index

76	76	76	9214
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The PPLD has advantages over conventional regression methods in application to moderately sized genome-wide association studies. PLoS ONE, 2021, 16, e0257164.	1.1	4
2	A new linear regression-like residual for survival analysis, with application to genome wide association studies of time-to-event data. PLoS ONE, 2020, 15, e0232300.	1.1	7
3	Segregating patterns of copy number variations in extended autism spectrum disorder (ASD) pedigrees. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 268-276.	1.1	7
4	No evidence amalgamation without evidence measurement. SynthÃˆse, 2019, 196, 3139-3161.	0.6	8
5	A genome-wide linkage study of autism spectrum disorder and the broad autism phenotype in extended pedigrees. Journal of Neurodevelopmental Disorders, 2018, 10, 20.	1.5	20
6	Longâ€range genomic regulators of THBS1 and LTBP4 modify disease severity in duchenne muscular dystrophy. Annals of Neurology, 2018, 84, 234-245.	2.8	53
7	Validation of a microRNA target site polymorphism in H3F3B that is potentially associated with a broad schizophrenia phenotype. PLoS ONE, 2018, 13, e0194233.	1.1	8
8	Statistical Evidence Measured on a Properly Calibrated Scale for Multinomial Hypothesis Comparisons. Entropy, 2016, 18, 114.	1.1	8
9	A single nucleotide polymorphism in the dimethylarginine dimethylaminohydrolase gene is associated with lower risk of pulmonary hypertension in bronchopulmonary dysplasia. Acta Paediatrica, International Journal of Paediatrics, 2016, 105, e170-5.	0.7	24
10	Statistical Evidence Measured on a Properly Calibrated Scale across Nested and Non-nested Hypothesis Comparisons. Entropy, 2015, 17, 5333-5352.	1.1	2
11	Evidence, Temperature, and the Laws of Thermodynamics. Human Heredity, 2015, 78, 153-163.	0.4	4
12	Using extended pedigrees to identify novel autism spectrum disorder (ASD) candidate genes. Human Genetics, 2015, 134, 191-201.	1.8	20
13	Bronchopulmonary Dysplasiaâ€associated Pulmonary Hypertension and Mutations in the DDAH1 Gene. FASEB Journal, 2015, 29, 1017.1.	0.2	0
14	The Value of Regenotyping Older Linkage Data Sets with Denser Marker Panels. Human Heredity, 2014, 78, 9-16.	0.4	3
15	Revisiting Schizophrenia Linkage Data in the NIMH Repository: Reanalysis of Regularized Data Across Multiple Studies. American Journal of Psychiatry, 2014, 171, 350-359.	4.0	7
16	The Autism Simplex Collection: an international, expertly phenotyped autism sample for genetic and phenotypic analyses. Molecular Autism, 2014, 5, 34.	2.6	31
17	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	2.6	819
18	PEDSnet: a National Pediatric Learning Health System. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 602-606.	2.2	168

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19	Next-generation linkage and association methods applied to hypertension: a multifaceted approach to the analysis of sequence data. BMC Proceedings, 2014, 8, S111.	1.8	5
20	Meta-Analysis of Repository Data: Impact of Data Regularization on NIMH Schizophrenia Linkage Results. PLoS ONE, 2014, 9, e84696.	1.1	1
21	A molecular genetic study of autism and related phenotypes in extended pedigrees. Journal of Neurodevelopmental Disorders, 2013, 5, 30.	1.5	23
22	SRGAP1Is a Candidate Gene for Papillary Thyroid Carcinoma Susceptibility. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E973-E980.	1.8	74
23	Employing MCMC under the PPL framework to analyze sequence data in large pedigrees. Frontiers in Genetics, 2013, 4, 59.	1.1	6
24	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	1.4	334
25	Novel method for combined linkage and genome-wide association analysis finds evidence of distinct genetic architecture for two subtypes of autism. Journal of Neurodevelopmental Disorders, 2011, 3, 113-123.	1.5	22
26	Measurement of Evidence and Evidence of Measurement. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.2	8
27	Whereâ€™s the Evidence?. Human Heredity, 2011, 71, 59-66.	0.4	8
28	KELVIN: A Software Package for Rigorous Measurement of Statistical Evidence in Human Genetics. Human Heredity, 2011, 72, 276-288.	0.4	32
29	Next-Generation Linkage Analysis. Human Heredity, 2011, 72, 227-227.	0.4	5
30	Rare familial 16q21 microdeletions under a linkage peak implicate cadherin 8 (CDH8) in susceptibility to autism and learning disability. Journal of Medical Genetics, 2011, 48, 48-54.	1.5	94
31	Combined linkage and linkage disequilibrium analysis of a motor speech phenotype within families ascertained for autism risk loci. Journal of Neurodevelopmental Disorders, 2010, 2, 210-223.	1.5	10
32	Association statistics under the PPL framework. Genetic Epidemiology, 2010, 34, 835-845.	0.6	14
33	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
34	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	1.4	538
35	Expected Monotonicity â€“ A Desirable Property for Evidence Measures?. Human Heredity, 2010, 70, 151-166.	0.4	6
36	Fast and Accurate Calculation of a Computationally Intensive Statistic for Mapping Disease Genes. Journal of Computational Biology, 2009, 16, 659-676.	0.8	11

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37	Identification of a Schizophrenia-Associated Functional Noncoding Variant inNOS1AP. American Journal of Psychiatry, 2009, 166, 434-441.	4.0	59
38	Using projection and 2D plots to visually reveal genetic mechanisms of complex human disorders. , 2009, , .		3
39	A Multilocus Model of the Genetic Architecture of Autoimmune Thyroid Disorder, with Clinical Implications. American Journal of Human Genetics, 2008, 82, 1349-1356.	2.6	35
40	Fast Computation of Human Genetic Linkage. , 2007, , .		2
41	Exploiting gene Ã— gene interaction in linkage analysis. BMC Proceedings, 2007, 1, S64.	1.8	10
42	Accumulating quantitative trait linkage evidence across multiple datasets using the posterior probability of linkage. Genetic Epidemiology, 2007, 31, 91-102.	0.6	22
43	Discussing gene-gene interaction: Warning â€" translating equations to English may result in Jabberwocky. Genetic Epidemiology, 2007, 31, S61-S67.	0.6	7
44	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	9.4	1,272
45	Thermometers: Something for Statistical Geneticists to Think about. Human Heredity, 2006, 61, 144-156.	0.4	35
46	Ascertainment bias in linkage analysis: Comments on Ginsburg et al.. Genetic Epidemiology, 2005, 28, 283-285.	0.6	4
47	Two novel quantitative trait linkage analysis statistics based on the posterior probability of linkage: application to the COGA families. BMC Genetics, 2005, 6, S121.	2.7	13
48	Calculation of multipoint likelihoods using flanking marker data: a simulation study. BMC Genetics, 2005, 6, S44.	2.7	3
49	The Posterior Probability of Linkage Allowing for Linkage Disequilibrium and a New Estimate of Disequilibrium between a Trait and a Marker. Human Heredity, 2005, 59, 210-219.	0.4	25
50	The Incorporation of Prior Genomic Information Does Not Necessarily Improve the Performance of Bayesian Linkage Methods: An Example Involving Sex-Specific Recombination and the Two-Point PPL. Human Heredity, 2005, 60, 196-205.	0.4	7
51	Effects of Updating Linkage Evidence across Subsets of Data: Reanalysis of the Autism Genetic Resource Exchange Data Set. American Journal of Human Genetics, 2005, 76, 688-695.	2.6	32
52	Examination of Potential Overlap in Autism and Language Loci on Chromosomes 2, 7, and 13 in Two Independent Samples Ascertained for Specific Language Impairment. Human Heredity, 2004, 57, 10-20.	0.4	97
53	A New Method for Computing the Multipoint Posterior Probability of Linkage. Human Heredity, 2004, 57, 90-99.	0.4	19
54	Bayesian analysis of a previously published genome screen for panic disorder reveals new and compelling evidence for linkage to chromosome 7. American Journal of Medical Genetics Part A, 2003, 121B, 95-99.	2.4	51

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55	Two-Locus Heterogeneity Cannot Be Distinguished from Two-Locus Epistasis on the Basis of Affected-Sib-Pair Data. American Journal of Human Genetics, 2003, 73, 223-232.	2.6	32
56	Reply to Cordell and Farrall. American Journal of Human Genetics, 2003, 73, 1471-1473.	2.6	12
57	HLODs, Trait Models, and Ascertainment: Implications of Admixture for Parameter Estimation and Linkage Detection. Human Heredity, 2002, 53, 23-35.	0.4	40
58	Comparison of â€˜Model-Freeâ€™ and â€˜Model-Basedâ€™ Linkage Statistics in the Presence of Locus Heterogeneity: Single Data Set and Multiple Data Set Applications. Human Heredity, 2001, 51, 217-225.	0.4	45
59	Power to Detect Linkage Based on Multiple Sets of Data in the Presence of Locus Heterogeneity: Comparative Evaluation of Model-Based Linkage Methods for Affected Sib Pair Data. Human Heredity, 2001, 51, 199-208.	0.4	65
60	Combined Multipoint Analysis of Multiple Asthma Data Sets Based on the Posterior Probability of Linkage. Genetic Epidemiology, 2001, 21, S73-8.	0.6	11
61	Incorporating language phenotypes strengthens evidence of linkage to autism. American Journal of Medical Genetics Part A, 2001, 105, 539-547.	2.4	192
62	The replication requirement. Nature Genetics, 2001, 29, 244-245.	9.4	83
63	A bayesian approach to replication of linkage findings. Genetic Epidemiology, 1999, 17, S749-54.	0.6	28
64	Bayesian Linkage Analysis, or: How I Learned to Stop Worrying and Love the Posterior Probability of Linkage. American Journal of Human Genetics, 1998, 63, 947-954.	2.6	84
65	Statistical Evidence: A Likelihood Paradigm. American Journal of Human Genetics, 1998, 63, 283-289.	2.6	41
66	[ITAL]Statistical Evidence: A Likelihood Paradigm.[/ITAL] By Richard Royall. London: Chapman & Hall, 1997. Pp. 191. $64.95. American Journal of Human Genetics, 1998, 63, 283-289.	2.6	31
67	A new statistical test for age-of-onset anticipation: Application to bipolar disorder. Genetic Epidemiology, 1997, 14, 1091-1096.	0.6	31
68	Investigating the numerical effects of ascertainment bias in linkage analysis: Development of methods and preliminary results. , 1997, 14, 1119-1124.		16
69	A new statistical test for age-of-onset anticipation: Application to bipolar disorder. , 1997, 14, 1091.		1
70	New segregation analysis of panic disorder. American Journal of Medical Genetics Part A, 1996, 67, 147-153.	2.4	61
71	Adequacy of Single-Locus Approximations for Linkage Analyses of Oligogenic Traits: Extension to Multigenerational Pedigree Structures. Human Heredity, 1993, 43, 329-336.	0.4	52
72	Adequacy of single-locus approximations for linkage analyses of oligogenic traits. Genetic Epidemiology, 1992, 9, 45-59.	0.6	104