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	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
2	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	9.4	1,272
3	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	2.6	819
4	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	1.4	538
5	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	1.4	334
6	Incorporating language phenotypes strengthens evidence of linkage to autism. American Journal of Medical Genetics Part A, 2001, 105, 539-547.	2.4	192
7	PEDSnet: a National Pediatric Learning Health System. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 602-606.	2.2	168
8	Adequacy of single-locus approximations for linkage analyses of oligogenic traits. Genetic Epidemiology, 1992, 9, 45-59.	0.6	104
9	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
10	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
11	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
12	The replication requirement. Nature Genetics, 2001, 29, 244-245.	9.4	83
13	SRGAP1Is a Candidate Gene for Papillary Thyroid Carcinoma Susceptibility. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E973-E980.	1.8	74
14	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
15	New segregation analysis of panic disorder. American Journal of Medical Genetics Part A, 1996, 67, 147-153.	2.4	61
16	Identification of a Schizophrenia-Associated Functional Noncoding Variant inNOS1AP. American Journal of Psychiatry, 2009, 166, 434-441.	4.0	59
17	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
18	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

#	Article	IF	Citations
19	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
20	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
21	Statistical Evidence: A Likelihood Paradigm. American Journal of Human Genetics, 1998, 63, 283-289.	2.6	41
22	HLODs, Trait Models, and Ascertainment: Implications of Admixture for Parameter Estimation and Linkage Detection. Human Heredity, 2002, 53, 23-35.	0.4	40
23	Thermometers: Something for Statistical Geneticists to Think about. Human Heredity, 2006, 61, 144-156.	0.4	35
24	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
25	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
26	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
27	KELVIN: A Software Package for Rigorous Measurement of Statistical Evidence in Human Genetics. Human Heredity, 2011, 72, 276-288.	0.4	32
28	A new statistical test for age-of-onset anticipation: Application to bipolar disorder. Genetic Epidemiology, 1997, 14, 1091-1096.	0.6	31
29	The Autism Simplex Collection: an international, expertly phenotyped autism sample for genetic and phenotypic analyses. Molecular Autism, 2014, 5, 34.	2.6	31
30	[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
31	A bayesian approach to replication of linkage findings. Genetic Epidemiology, 1999, 17, S749-54.	0.6	28
32	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
33	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
34	A molecular genetic study of autism and related phenotypes in extended pedigrees. Journal of Neurodevelopmental Disorders, 2013, 5, 30.	1.5	23
35	Accumulating quantitative trait linkage evidence across multiple datasets using the posterior probability of linkage. Genetic Epidemiology, 2007, 31, 91-102.	0.6	22
36	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

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37	Using extended pedigrees to identify novel autism spectrum disorder (ASD) candidate genes. Human Genetics, 2015, 134, 191-201.	1.8	20
38	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
39	A New Method for Computing the Multipoint Posterior Probability of Linkage. Human Heredity, 2004, 57, 90-99.	0.4	19
40	Investigating the numerical effects of ascertainment bias in linkage analysis: Development of methods and preliminary results. , 1997, 14, 1119-1124.		16
41	Association statistics under the PPL framework. Genetic Epidemiology, 2010, 34, 835-845.	0.6	14
42	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
43	Reply to Cordell and Farrall. American Journal of Human Genetics, 2003, 73, 1471-1473.	2.6	12
44	Combined Multipoint Analysis of Multiple Asthma Data Sets Based on the Posterior Probability of Linkage. Genetic Epidemiology, 2001, 21, S73-8.	0.6	11
45	Fast and Accurate Calculation of a Computationally Intensive Statistic for Mapping Disease Genes. Journal of Computational Biology, 2009, 16, 659-676.	0.8	11
46	Exploiting gene Ã— gene interaction in linkage analysis. BMC Proceedings, 2007, 1, S64.	1.8	10
47	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
48	Measurement of Evidence and Evidence of Measurement. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.2	8
49	Whereâ€™s the Evidence?. Human Heredity, 2011, 71, 59-66.	0.4	8
50	Statistical Evidence Measured on a Properly Calibrated Scale for Multinomial Hypothesis Comparisons. Entropy, 2016, 18, 114.	1.1	8
51	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
52	No evidence amalgamation without evidence measurement. SynthÃˆse, 2019, 196, 3139-3161.	0.6	8
53	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
54	Discussing gene-gene interaction: Warning â€" translating equations to English may result in Jabberwocky. Genetic Epidemiology, 2007, 31, S61-S67.	0.6	7

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55	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
56	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
57	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
58	Expected Monotonicity â€“ A Desirable Property for Evidence Measures?. Human Heredity, 2010, 70, 151-166.	0.4	6
59	Employing MCMC under the PPL framework to analyze sequence data in large pedigrees. Frontiers in Genetics, 2013, 4, 59.	1.1	6
60	Next-Generation Linkage Analysis. Human Heredity, 2011, 72, 227-227.	0.4	5
61	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
62	Ascertainment bias in linkage analysis: Comments on Ginsburg et al.. Genetic Epidemiology, 2005, 28, 283-285.	0.6	4
63	Evidence, Temperature, and the Laws of Thermodynamics. Human Heredity, 2015, 78, 153-163.	0.4	4
64	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
65	Calculation of multipoint likelihoods using flanking marker data: a simulation study. BMC Genetics, 2005, 6, S44.	2.7	3
66	Using projection and 2D plots to visually reveal genetic mechanisms of complex human disorders. , 2009, , .		3
67	The Value of Regenotyping Older Linkage Data Sets with Denser Marker Panels. Human Heredity, 2014, 78, 9-16.	0.4	3
68	Fast Computation of Human Genetic Linkage. , 2007, , .		2
69	Statistical Evidence Measured on a Properly Calibrated Scale across Nested and Non-nested Hypothesis Comparisons. Entropy, 2015, 17, 5333-5352.	1.1	2
70	A new statistical test for age-of-onset anticipation: Application to bipolar disorder. , 1997, 14, 1091.		1
71	Meta-Analysis of Repository Data: Impact of Data Regularization on NIMH Schizophrenia Linkage Results. PLoS ONE, 2014, 9, e84696.	1.1	1
72	Bronchopulmonary Dysplasiaâ€associated Pulmonary Hypertension and Mutations in the DDAH1 Gene. FASEB Journal, 2015, 29, 1017.1.	0.2	0