

Matthew C Keller

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

16,252
citations

61984

43
h-index

37204

96
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117
all docs

117
docs citations

117
times ranked

19905
citing authors

#	ARTICLE	IF	CITATIONS
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , 2022, 91, 102-117.	1.3	61
2	Assortative mating biases marker-based heritability estimators. <i>Nature Communications</i> , 2022, 13, 660.	12.8	35
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
4	Predicting causal genes from psychiatric genome-wide association studies using high-level etiological knowledge. <i>Molecular Psychiatry</i> , 2022, 27, 3095-3106.	7.9	4
5	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	21.4	142
6	An evolutionary investigation of depressed mood: The relationship between daily stressors and patterns of depressive symptoms. <i>Journal of Behavior Therapy and Experimental Psychiatry</i> , 2022, 76, 101749.	1.2	0
7	Bias and Precision of Parameter Estimates from Models Using Polygenic Scores to Estimate Environmental and Genetic Parental Influences. <i>Behavior Genetics</i> , 2021, 51, 279-288.	2.1	9
8	Estimation of Parental Effects Using Polygenic Scores. <i>Behavior Genetics</i> , 2021, 51, 264-278.	2.1	34
9	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	12.8	19
10	Genetic architecture of four smoking behaviors using partitioned SNP heritability. <i>Addiction</i> , 2021, 116, 2498-2508.	3.3	14
11	Novel approach for parallelizing pairwise comparison problems as applied to detecting segments identical by descent in whole-genome data. <i>Bioinformatics</i> , 2021, 37, 2121-2125.	4.1	3
12	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. <i>Neuropsychopharmacology</i> , 2021, 46, 1788-1801.	5.4	12
13	Genomic partitioning of inbreeding depression in humans. <i>American Journal of Human Genetics</i> , 2021, 108, 1488-1501.	6.2	6
14	Twin studies to GWAS: there and back again. <i>Trends in Cognitive Sciences</i> , 2021, 25, 855-869.	7.8	39
15	No Evidence for Social Genetic Effects or Genetic Similarity Among Friends Beyond that Due to Population Stratification: A Reappraisal of Domingue et al (2018). <i>Behavior Genetics</i> , 2020, 50, 67-71.	2.1	7
16	The Role of A Priori Identified Addiction and Smoking Gene Sets in Smoking Behaviors. <i>Nicotine and Tobacco Research</i> , 2020, 22, 1310-1315.	2.6	5
17	Nick Martin as a Mentor – A Perspective. <i>Twin Research and Human Genetics</i> , 2020, 23, 112-113.	0.6	0
18	Measurement Error Cannot Account for Failed Replications of Historic Candidate Gene-by-Environment Hypotheses: Response to Vrshek-Schallhorn et al.. <i>American Journal of Psychiatry</i> , 2019, 176, 668-669.	7.2	4

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19	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. <i>American Journal of Human Genetics</i> , 2019, 105, 334-350.	6.2	86
20	The etiology of DSM-5 alcohol use disorder: Evidence of shared and non-shared additive genetic effects. <i>Drug and Alcohol Dependence</i> , 2019, 201, 147-154.	3.2	7
21	No Support for Historical Candidate Gene or Candidate Gene-by-Interaction Hypotheses for Major Depression Across Multiple Large Samples. <i>American Journal of Psychiatry</i> , 2019, 176, 376-387.	7.2	436
22	Imputation of behavioral candidate gene repeat variants in 486,551 publicly-available UK Biobank individuals. <i>European Journal of Human Genetics</i> , 2019, 27, 963-969.	2.8	15
23	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	21.4	1,307
24	Shared additive genetic variation for alcohol dependence among subjects of African and European ancestry. <i>Addiction Biology</i> , 2019, 24, 132-144.	2.6	18
25	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018, 121, 616-630.	2.6	20
26	Evolutionary Perspectives on Genetic and Environmental Risk Factors for Psychiatric Disorders. <i>Annual Review of Clinical Psychology</i> , 2018, 14, 471-493.	12.3	31
27	Using partitioned heritability methods to explore genetic architecture. <i>Nature Reviews Genetics</i> , 2018, 19, 185-185.	16.3	9
28	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. <i>Nature Genetics</i> , 2018, 50, 737-745.	21.4	205
29	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.	12.0	97
30	Relationships between estimated autozygosity and complex traits in the UK Biobank. <i>PLoS Genetics</i> , 2018, 14, e1007556.	3.5	33
31	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	12.8	484
32	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	6.2	119
33	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <i>Nature Genetics</i> , 2018, 50, 912-919.	21.4	893
34	Multi-Trait Analysis of GWAS and Biological Insights Into Cognition: A Response to Hill (2018). <i>Twin Research and Human Genetics</i> , 2018, 21, 394-397.	0.6	3
35	A fast and accurate method for detection of IBD shared haplotypes in genome-wide SNP data. <i>European Journal of Human Genetics</i> , 2017, 25, 617-624.	2.8	18
36	Commentary: Fundamental problems with candidate gene-by-environment interaction studies – reflections on Moore and Thoenes (2016). <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2017, 58, 328-330.	5.2	26

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37	Facial Trustworthiness is Associated with Heritable Aspects of Face Shape. <i>Adaptive Human Behavior and Physiology</i> , 2017, 3, 351-364.	1.1	8
38	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. <i>Cell Reports</i> , 2017, 21, 2597-2613.	6.4	103
39	No Evidence That Schizophrenia Candidate Genes Are More Associated With Schizophrenia Than Noncandidate Genes. <i>Biological Psychiatry</i> , 2017, 82, 702-708.	1.3	170
40	Assessing the accuracy of perceptions of intelligence based on heritable facial features. <i>Intelligence</i> , 2017, 64, 1-8.	3.0	3
41	Predicting Cognitive Executive Functioning with Polygenic Risk Scores for Psychiatric Disorders. <i>Behavior Genetics</i> , 2017, 47, 11-24.	2.1	20
42	GeneEvolve: a fast and memory efficient forward-time simulator of realistic whole-genome sequence and SNP data. <i>Bioinformatics</i> , 2017, 33, 294-296.	4.1	16
43	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
44	Genetic influences on the human oral microbiome. <i>BMC Genomics</i> , 2017, 18, 659.	2.8	66
45	Evidence of Shared Genome-Wide Additive Genetic Effects on Interpersonal Trauma Exposure and Generalized Vulnerability to Drug Dependence in a Population of Substance Users. <i>Journal of Traumatic Stress</i> , 2016, 29, 197-204.	1.8	4
46	Facial averageness and genetic quality: testing heritability, genetic correlation with attractiveness, and the paternal age effect. <i>Evolution and Human Behavior</i> , 2016, 37, 61-66.	2.2	29
47	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. <i>PLoS Genetics</i> , 2016, 12, e1006343.	3.5	24
48	Shared additive genetic influences on DSM-IV criteria for alcohol dependence in subjects of European ancestry. <i>Addiction</i> , 2015, 110, 1922-1931.	3.3	20
49	Independent evidence for an association between general cognitive ability and a genetic locus for educational attainment. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 363-373.	1.7	25
50	Candidate Gene-Environment Interaction Research. <i>Perspectives on Psychological Science</i> , 2015, 10, 37-59.	9.0	310
51	Genetic variation links creativity to psychiatric disorders. <i>Nature Neuroscience</i> , 2015, 18, 928-929.	14.8	21
52	Evolutionary behavioral genetics. <i>Current Opinion in Behavioral Sciences</i> , 2015, 2, 73-80.	3.9	26
53	Genome-Wide Association Study of Behavioral Disinhibition in a Selected Adolescent Sample. <i>Behavior Genetics</i> , 2015, 45, 375-381.	2.1	55
54	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015, 47, 1114-1120.	21.4	709

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55	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015, 44, 1706-1721.	1.9	53
56	A test of the facultative calibration/reactive heritability model of extraversion. <i>Evolution and Human Behavior</i> , 2015, 36, 414-419.	2.2	10
57	No relationship between intelligence and facial attractiveness in a large, genetically informative sample. <i>Evolution and Human Behavior</i> , 2015, 36, 240-247.	2.2	17
58	Whole-Genome Pathway Analysis on 132,497 Individuals Identifies Novel Gene-Sets Associated with Body Mass Index. <i>PLoS ONE</i> , 2014, 9, e78546.	2.5	4
59	The Association of Genotype-Based Inbreeding Coefficient with a Range of Physical and Psychological Human Traits. <i>PLoS ONE</i> , 2014, 9, e103102.	2.5	31
60	A recessive genetic model and runs of homozygosity in major depressive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2014, 165, 157-166.	1.7	20
61	Gene × Environment Interaction Studies Have Not Properly Controlled for Potential Confounders: The Problem and the (Simple) Solution. <i>Biological Psychiatry</i> , 2014, 75, 18-24.	1.3	510
62	Genetic Factors That Increase Male Facial Masculinity Decrease Facial Attractiveness of Female Relatives. <i>Psychological Science</i> , 2014, 25, 476-484.	3.3	46
63	Large-scale genomics unveils the genetic architecture of psychiatric disorders. <i>Nature Neuroscience</i> , 2014, 17, 782-790.	14.8	321
64	Estimating the Sex-Specific Effects of Genes on Facial Attractiveness and Sexual Dimorphism. <i>Behavior Genetics</i> , 2014, 44, 270-281.	2.1	23
65	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	21.4	2,067
66	Additive Genetic Variation in Schizophrenia Risk Is Shared by Populations of African and European Descent. <i>American Journal of Human Genetics</i> , 2013, 93, 463-470.	6.2	72
67	The Genetic Correlation between Height and IQ: Shared Genes or Assortative Mating?. <i>PLoS Genetics</i> , 2013, 9, e1003451.	3.5	61
68	Runs of Homozygosity Implicate Autozygosity as a Schizophrenia Risk Factor. <i>PLoS Genetics</i> , 2012, 8, e1002656.	3.5	109
69	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , 2012, 44, 247-250.	21.4	578
70	MAINTENANCE OF GENETIC VARIATION IN HUMAN PERSONALITY: TESTING EVOLUTIONARY MODELS BY ESTIMATING HERITABILITY DUE TO COMMON CAUSAL VARIANTS AND INVESTIGATING THE EFFECT OF DISTANT INBREEDING. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3238-3251.	2.3	166
71	Recent methods for polygenic analysis of genome-wide data implicate an important effect of common variants on cardiovascular disease risk. <i>BMC Medical Genetics</i> , 2011, 12, 146.	2.1	51
72	Mutational load analysis of unrelated individuals. <i>BMC Proceedings</i> , 2011, 5, S55.	1.6	6

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73	Detecting autozygosity through runs of homozygosity: A comparison of three autozygosity detection algorithms. <i>BMC Genomics</i> , 2011, 12, 460.	2.8	294
74	A Critical Review of the First 10 Years of Candidate Gene-by-Environment Interaction Research in Psychiatry. <i>American Journal of Psychiatry</i> , 2011, 168, 1041-1049.	7.2	919
75	Quantification of Inbreeding Due to Distant Ancestors and Its Detection Using Dense Single Nucleotide Polymorphism Data. <i>Genetics</i> , 2011, 189, 237-249.	2.9	367
76	Are Extended Twin Family Designs Worth the Trouble? A Comparison of the Bias, Precision, and Accuracy of Parameters Estimated in Four Twin Family Models. <i>Behavior Genetics</i> , 2010, 40, 377-393.	2.1	142
77	Not by Twins Alone: Using the Extended Family Design to Investigate Genetic Influence on Political Beliefs. <i>American Journal of Political Science</i> , 2010, 54, 798-814.	4.5	135
78	Theory and Methods in Evolutionary Behavioral Genetics. , 2010, , 280-302.		2
79	Modeling Extended Twin Family Data II: Power Associated With Different Family Structures. <i>Twin Research and Human Genetics</i> , 2009, 12, 19-25.	0.6	17
80	Modeling Extended Twin Family Data I: Description of the Cascade Model. <i>Twin Research and Human Genetics</i> , 2009, 12, 8-18.	0.6	106
81	Flexible Mx Specification of Various Extended Twin Kinship Designs. <i>Twin Research and Human Genetics</i> , 2009, 12, 26-34.	0.6	24
82	Nonpathological paternal isodisomy of chromosome 2 detected from a genome-wide SNP scan. <i>American Journal of Medical Genetics, Part A</i> , 2009, 149A, 1823-1826.	1.2	16
83	The Evolutionary Persistence of Genes That Increase Mental Disorders Risk. <i>Current Directions in Psychological Science</i> , 2008, 17, 395-399.	5.3	22
84	Problems with the imprinting hypothesis of schizophrenia and autism. <i>Behavioral and Brain Sciences</i> , 2008, 31, 273-274.	0.7	3
85	Dr. Keller Replies. <i>American Journal of Psychiatry</i> , 2008, 165, 533-534.	7.2	0
86	Association of Different Adverse Life Events With Distinct Patterns of Depressive Symptoms. <i>American Journal of Psychiatry</i> , 2007, 164, 1521-1529.	7.2	270
87	Endophenotypes in the Genetic Analyses of Mental Disorders. <i>Annual Review of Clinical Psychology</i> , 2006, 2, 267-290.	12.3	362
88	An evolutionary framework for mental disorders: Integrating adaptationist and evolutionary genetic models. <i>Behavioral and Brain Sciences</i> , 2006, 29, 429-441.	0.7	7
89	The evolutionary significance of depressive symptoms: Different adverse situations lead to different depressive symptom patterns.. <i>Journal of Personality and Social Psychology</i> , 2006, 91, 316-330.	2.8	194
90	Resolving the paradox of common, harmful, heritable mental disorders: Which evolutionary genetic models work best?. <i>Behavioral and Brain Sciences</i> , 2006, 29, 385-404.	0.7	495

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91	Estimating the Extent of Parameter Bias in the Classical Twin Design: A Comparison of Parameter Estimates From Extended Twin-Family and Classical Twin Designs. <i>Twin Research and Human Genetics</i> , 2005, 8, 214-223.	0.6	126
92	Quantifying and Addressing Parameter Indeterminacy in the Classical Twin Design. <i>Twin Research and Human Genetics</i> , 2005, 8, 201-213.	0.6	133
93	Is low mood an adaptation? Evidence for subtypes with symptoms that match precipitants. <i>Journal of Affective Disorders</i> , 2005, 86, 27-35.	4.1	163
94	Widespread Evidence for Non-Additive Genetic Variation in Cloninger's and Eysenck's Personality Dimensions using a Twin Plus Sibling Design. <i>Behavior Genetics</i> , 2005, 35, 707-721.	2.1	196
95	A Warm Heart and a Clear Head: The Contingent Effects of Weather on Mood and Cognition. <i>Psychological Science</i> , 2005, 16, 724-731.	3.3	316
96	Quantifying and Addressing Parameter Indeterminacy in the Classical Twin Design. <i>Twin Research and Human Genetics</i> , 2005, 8, 201-213.	0.6	65
97	Estimating the Extent of Parameter Bias in the Classical Twin Design: A Comparison of Parameter Estimates From Extended Twin-Family and Classical Twin Designs. <i>Twin Research and Human Genetics</i> , 2005, 8, 214-223.	0.6	32
98	Evolutionary theories of schizophrenia must ultimately explain the genes that predispose to it. <i>Behavioral and Brain Sciences</i> , 2004, 27, 861-862.	0.7	12