Eric K Moses

List of Publications by Year
in descending order

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		87843	71651
126	6,701	38	76
papers	citations	h-index	g-index

130	130	130	13863
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	1.1	696
2	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	9.4	594
3	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
4	Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. Nature Genetics, 2007, 39, 1208-1216.	9.4	456
5	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
6	Chemerin, a Novel Adipokine in the Regulation of Angiogenesis. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 2476-2485.	1.8	184
7	High Dimensional Endophenotype Ranking in the Search for Major Depression Risk Genes. Biological Psychiatry, 2012, 71, 6-14.	0.7	170
8	A Genome Scan in Families from Australia and New Zealand Confirms the Presence of a Maternal Susceptibility Locus for Pre-Eclampsia, on Chromosome 2. American Journal of Human Genetics, 2000, 67, 1581-1585.	2.6	163
9	Crystal structure of HLA-G: A nonclassical MHC class I molecule expressed at the fetal-maternal interface. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3360-3365.	3.3	139
10	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	9.4	138
11	Genome-Wide Association Scan Identifies a Risk Locus for Preeclampsia on 2q14, Near the Inhibin, Beta B Gene. PLoS ONE, 2012, 7, e33666.	1.1	110
12	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109
13	Transcriptomic epidemiology of smoking: the effect of smoking on gene expression in lymphocytes. BMC Medical Genomics, 2010, 3, 29.	0.7	100
14	Inherited Thrombophilia Polymorphisms and Pregnancy Outcomes in Nulliparous Women. Obstetrics and Gynecology, 2010, 115, 5-13.	1.2	98
15	Meta-analysis of human methylation data for evidence of sex-specific autosomal patterns. BMC Genomics, 2014, 15, 981.	1.2	94
16	The ERAP2 gene is associated with preeclampsia in Australian and Norwegian populations. Human Genetics, 2009, 126, 655-666.	1.8	93
17	A Genome-Wide Integrative Genomic Study Localizes Genetic Factors Influencing Antibodies against Epstein-Barr Virus Nuclear Antigen 1 (EBNA-1). PLoS Genetics, 2013, 9, e1003147.	1.5	92
18	High-coverage plasma lipidomics reveals novel sex-specific lipidomic fingerprints of age and BMI: Evidence from two large population cohort studies. PLoS Biology, 2020, 18, e3000870.	2.6	89

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19	Increased endoplasmic reticulum stress in decidual tissue from pregnancies complicated by fetal growth restriction with and without pre-eclampsia. Placenta, 2011, 32, 823-829.	0.7	82
20	A transcriptional profile of the decidua in preeclampsia. American Journal of Obstetrics and Gynecology, 2011, 204, 84.e1-84.e27.	0.7	81
21	Objective prioritization of positional candidate genes at a quantitative trait locus for pre-eclampsia on 2q22. Molecular Human Reproduction, 2006, 12, 505-512.	1.3	71
22	Impact of DISC1 variation on neuroanatomical and neurocognitive phenotypes. Molecular Psychiatry, 2011, 16, 1096-1104.	4.1	71
23	Association between the candidate susceptibility gene ACVR2A on chromosome 2q22 and pre-eclampsia in a large Norwegian population-based study (the HUNT study). European Journal of Human Genetics, 2009, 17, 250-257.	1.4	67
24	Diverse biological activities of the vascular non-inflammatory molecules â€“ The Vanin pantetheinases. Biochemical and Biophysical Research Communications, 2012, 417, 653-658.	1.0	65
25	Genetic association of preeclampsia to the inflammatory response gene SEPS1. American Journal of Obstetrics and Gynecology, 2008, 198, 336.e1-336.e5.	0.7	62
26	Genome-Wide Transcriptome Directed Pathway Analysis of Maternal Pre-Eclampsia Susceptibility Genes. PLoS ONE, 2015, 10, e0128230.	1.1	61
27	Endogenous factor VIII synthesis from the intron 22â€“inverted F8 locus may modulate the immunogenicity of replacement therapy for hemophilia A. Nature Medicine, 2013, 19, 1318-1324.	15.2	59
28	Genetic determinants of mitochondrial content. Human Molecular Genetics, 2007, 16, 1504-1514.	1.4	54
29	Genetic dissection of the pre-eclampsia susceptibility locus on chromosome 2q22 reveals shared novel risk factors for cardiovascular disease. Molecular Human Reproduction, 2013, 19, 423-437.	1.3	54
30	A critical assessment of the factors affecting reporter gene assays for promoter SNP function: a reassessment of â^'308 TNF polymorphism function using a novel integrated reporter system. European Journal of Human Genetics, 2009, 17, 1454-1462.	1.4	52
31	A low COMT activity haplotype is associated with recurrent preeclampsia in a Norwegian population cohort (HUNT2). Molecular Human Reproduction, 2011, 17, 439-446.	1.3	52
32	5Î²-Dihydroprogesterone and steroid 5Î²â€“reductase decrease in association with human parturition at term. Molecular Human Reproduction, 2005, 11, 495-501.	1.3	49
33	Genetic Variation at the FTO Locus Influences RBL2 Gene Expression. Diabetes, 2010, 59, 726-732.	0.3	49
34	MACROD2 gene associated with autistic-like traits in a general population sample. Psychiatric Genetics, 2014, 24, 241-248.	0.6	48
35	A genome-wide association study for malignant mesothelioma risk. Lung Cancer, 2013, 82, 1-8.	0.9	45
36	Molecular Markers of Preterm Labor in the Choriodecidua. Reproductive Sciences, 2010, 17, 297-310.	1.1	43

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37	Genome-Wide Association Study of Autistic-Like Traits in a General Population Study of Young Adults. Frontiers in Human Neuroscience, 2013, 7, 658.	1.0	43
38	Genetic association of the activin A receptor gene (ACVR2A) and pre-eclampsia. Molecular Human Reproduction, 2009, 15, 195-204.	1.3	40
39	Thrombomodulin Ala455Val Dimorphism Is Not Associated with Pre-Eclampsia in Australian and New Zealand Women. Gynecologic and Obstetric Investigation, 2002, 54, 43-45.	0.7	39
40	An emerging role for comprehensive proteome analysis in human pregnancy research. Reproduction, 2005, 129, 685-696.	1.1	39
41	Identification of a native Dichelobacter nodosus plasmid and implications for the evolution of the vap regions. Gene, 1996, 172, 111-116.	1.0	37
42	C677T Methylenetetrahydrofolate Reductase Polymorphism Is Not a Risk Factor for Pre-Eclampsia/Eclampsia among Australian Women. Human Heredity, 2001, 51, 20-22.	0.4	37
43	Identification of ACOX2 as a shared genetic risk factor for preeclampsia and cardiovascular disease. European Journal of Human Genetics, 2011, 19, 796-800.	1.4	37
44	Inherited thrombophilias and adverse pregnancy outcomes: a caseâ€“control study in an Australian population. Acta Obstetricia Et Gynecologica Scandinavica, 2012, 91, 250-255.	1.3	36
45	Prothrombin G20210A Mutation: Is It Associated with Pre-Eclampsia?. Gynecologic and Obstetric Investigation, 2000, 50, 254-257.	0.7	35
46	Clinical significance of circulating microRNAs as markers in detecting and predicting congenital heart defects in children. Journal of Translational Medicine, 2018, 16, 42.	1.8	34
47	Methylenetetrahydrofolate Reductase Polymorphisms Are Not a Risk Factor for Pre-Eclampsia/Eclampsia in Australian Women. Gynecologic and Obstetric Investigation, 2000, 50, 100-102.	0.7	33
48	The eNos Gene: A Candidate for the Preeclampsia Susceptibility Locus?. Hypertension in Pregnancy, 1999, 18, 81-93.	0.5	32
49	Proteomic approaches in endometriosis research. Proteomics, 2004, 4, 1897-1902.	1.3	32
50	Genetic Approaches in Preeclampsia. Methods in Molecular Biology, 2018, 1710, 53-72.	0.4	32
51	GenotypeÃ—age interaction in human transcriptional ageing. Mechanisms of Ageing and Development, 2012, 133, 581-590.	2.2	31
52	Genome-wide association analysis confirms and extends the association of SLC2A9 with serum uric acid levels to Mexican Americans. Frontiers in Genetics, 2013, 4, 279.	1.1	30
53	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. Nature Communications, 2022, 13, .	5.8	30
54	A multiple site-specific DNA-inversion model for the control of Ompi phase and antigenic variation in Dichelobacter nodosus. Molecular Microbiology, 1995, 17, 183-196.	1.2	29

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55	Heritability of 596 lipid species and genetic correlation with cardiovascular traits in the Busselton Family Heart Study. Journal of Lipid Research, 2020, 61, 537-545.	2.0	29
56	Applications of proteomic methodologies to human pregnancy research: A growing gestation approaching delivery?. Proteomics, 2004, 4, 1909-1917.	1.3	28
57	A Chromosome 11q Quantitative-Trait Locus Influences Change of Blood-Pressure Measurements over Time in Mexican Americans of the San Antonio Family Heart Study. American Journal of Human Genetics, 2007, 81, 744-755.	2.6	28
58	STOX2 but not STOX1 is differentially expressed in decidua from pre-eclamptic women: data from the Second Nord-Trondelag Health Study. Molecular Human Reproduction, 2010, 16, 960-968.	1.3	28
59	Absence of germline mutations in BAP1 in sporadic cases of malignant mesothelioma. Gene, 2015, 563, 103-105.	1.0	27
60	TRAK2, a novel regulator of ABCA1 expression, cholesterol efflux and HDL biogenesis. European Heart Journal, 2017, 38, 3579-3587.	1.0	27
61	Identification and sequencing of the groE operon and flanking genes of Lawsonia intracellularis: use in phylogeny. Microbiology (United Kingdom), 1998, 144, 2073-2084.	0.7	25
62	Bivariate genetic association of KIAA1797 with heart rate in American Indians: the Strong Heart Family Study. Human Molecular Genetics, 2010, 19, 3662-3671.	1.4	25
63	Increased decidual mRNA expression levels of candidate maternal pre-eclampsia susceptibility genes are associated with clinical severity. Placenta, 2014, 35, 117-124.	0.7	25
64	Genetic Architecture of Carotid Artery Intima-Media Thickness in Mexican Americans. Circulation: Cardiovascular Genetics, 2013, 6, 211-221.	5.1	24
65	Association of the TNF2 Allele with Eclampsia. Gynecologic and Obstetric Investigation, 2004, 57, 204-209.	0.7	22
66	Genotype Ã— Adiposity Interaction Linkage Analyses Reveal a Locus on Chromosome 1 for Lipoprotein-Associated Phospholipase A2, a Marker of Inflammation and Oxidative Stress. American Journal of Human Genetics, 2007, 80, 168-177.	2.6	22
67	Genetic variation in PARL influences mitochondrial content. Human Genetics, 2010, 127, 183-190.	1.8	22
68	ADAM28 is elevated in humans with the metabolic syndrome and is a novel sheddase of human tumour necrosis factorâ€Î±. Immunology and Cell Biology, 2012, 90, 966-973.	1.0	21
69	Variants in CPT1A, FADS1, and FADS2 are Associated with Higher Levels of Estimated Plasma and Erythrocyte Delta-5 Desaturases in Alaskan Eskimos. Frontiers in Genetics, 2012, 3, 86.	1.1	21
70	Refined phenotyping identifies links between preeclampsia and related diseases in a Norwegian preeclampsia family cohort. Journal of Hypertension, 2015, 33, 2294-2302.	0.3	21
71	Partial correlation network analyses to detect altered gene interactions in human disease: using preeclampsia as a model. Human Genetics, 2011, 129, 25-34.	1.8	20
72	Western oropharyngeal and gut microbial profiles are associated with allergic conditions in Chinese immigrant children. World Allergy Organization Journal, 2019, 12, 100051.	1.6	19

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73	Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes. Journal of Hypertension, 2019, 37, 997-1011.	0.3	19
74	Transcriptomics of cortical gray matter thickness decline during normal aging. NeuroImage, 2013, 82, 273-283.	2.1	18
75	Genome-wide genetic investigation of serological measures of common infections. European Journal of Human Genetics, 2015, 23, 1544-1548.	1.4	18
76	Exome array analysis suggests an increased variant burden in families with schizophrenia. Schizophrenia Research, 2017, 185, 9-16.	1.1	18
77	Genetic and Molecular Functional Characterization of Variants within TNFSF13B, a Positional Candidate Preeclampsia Susceptibility Gene on 13q. PLoS ONE, 2010, 5, e12993.	1.1	18
78	The 57 kb deletion in cystinosis patients extends into TRPV1 causing dysregulation of transcription in peripheral blood mononuclear cells. Journal of Medical Genetics, 2011, 48, 563-566.	1.5	17
79	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.8	17
80	Prevalence of common sleep disorders in a middle-aged community sample. Journal of Clinical Sleep Medicine, 2022, 18, 1503-1514.	1.4	17
81	Whole genome sequencing of 91 multiplex schizophrenia families reveals increased burden of rare, exonic copy number variation in schizophrenia probands and genetic heterogeneity. Schizophrenia Research, 2018, 197, 337-345.	1.1	16
82	APOE Îµ2 resilience for Alzheimer's disease is mediated by plasma lipid species: Analysis of three independent cohort studies. Alzheimer's and Dementia, 2022, 18, 2151-2166.	0.4	16
83	Plasma Levels of Soluble Interleukin 1 Receptor Accessory Protein Are Reduced in Obesity. Journal of Clinical Endocrinology and Metabolism, 2014, 99, 3435-3443.	1.8	15
84	The antihypertensive MTHFR gene polymorphism rs17367504-G is a possible novel protective locus for preeclampsia. Journal of Hypertension, 2017, 35, 132-139.	0.3	15
85	The prevalence of inherited thrombophilic polymorphisms in an asymptomatic Australian antenatal population. Australian and New Zealand Journal of Obstetrics and Gynaecology, 2008, 48, 536-541.	0.4	14
86	Preeclampsia and cardiovascular disease share genetic risk factors on chromosome 2q22. Pregnancy Hypertension, 2014, 4, 178-185.	0.6	14
87	P-selectin Expression Tracks Cerebral Atrophy in Mexican-Americans. Frontiers in Genetics, 2012, 3, 65.	1.1	13
88	GWAS and transcriptional analysis prioritize ITPR1 and CNTN4 for a serum uric acid 3p26 QTL in Mexican Americans. BMC Genomics, 2016, 17, 276.	1.2	13
89	Differential Gene Expression at the Maternal-Fetal Interface in Preeclampsia Is Influenced by Gestational Age. PLoS ONE, 2013, 8, e69848.	1.1	13
90	Assessment of Cognition and Personality as Potential Endophenotypes in the Western Australian Family Study of Schizophrenia. Schizophrenia Bulletin, 2018, 44, 908-921.	2.3	12

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91	Potential role for immune-related genes in autism spectrum disorders: Evidence from genome-wide association meta-analysis of autistic traits. Autism, 2022, 26, 361-372.	2.4	12
92	Molecular analysis of one of multiple protease-encoding genes from the prototype virulent strain of Bacteroides nodosus. Gene, 1989, 77, 219-228.	1.0	11
93	Novel Associations of Nonstructural Loci with Paraoxonase Activity. Journal of Lipids, 2012, 2012, 1-7.	1.9	11
94	Identification of Differentially Methylated CpG Sites in Fibroblasts from Keloid Scars. Biomedicines, 2020, 8, 181.	1.4	11
95	Cascade testing for elevated lipoprotein(a) in relatives of probands with familial hypercholesterolaemia and elevated lipoprotein(a). Atherosclerosis, 2022, 349, 219-226.	0.4	11
96	Divergent Regulation of Decidual Oxidative-Stress Response by NRF2 and KEAP1 in Preeclampsia with and without Fetal Growth Restriction. International Journal of Molecular Sciences, 2022, 23, 1966.	1.8	11
97	Environment Changes Genetic Effects on Respiratory Conditions and Allergic Phenotypes. Scientific Reports, 2017, 7, 6342.	1.6	10
98	Pleiotropy of cardiometabolic syndrome with obesity-related anthropometric traits determined using empirically derived kinships from the Busselton Health Study. Human Genetics, 2018, 137, 45-53.	1.8	10
99	Ethnic Differences in the Prevalence of Inherited Thrombophilic Polymorphisms in an Asymptomatic Australian Prenatal Population. Human Biology, 2006, 78, 403-412.	0.4	9
100	Cross-species replication of a resistin mRNA QTL, but not QTLs for circulating levels of resistin, in human and baboon. Heredity, 2008, 101, 60-66.	1.2	9
101	The characterization of Abelson helper integration siteâ€"1 in skeletal muscle and its links to the metabolic syndrome. Metabolism: Clinical and Experimental, 2010, 59, 1057-1064.	1.5	9
102	Molecular prioritization strategies to identify functional genetic variants in the cardiovascular disease-associated expression QTL Vanin-1. European Journal of Human Genetics, 2014, 22, 688-695.	1.4	9
103	ADAM19: A Novel Target for Metabolic Syndrome in Humans and Mice. Mediators of Inflammation, 2017, 2017, 1-9.	1.4	9
104	Cascade testing for elevated lipoprotein(a) in relatives of probands with high lipoprotein(a). American Journal of Preventive Cardiology, 2022, 10, 100343.	1.3	9
105	Analysis of the Epigenome in Multiplex Pre-eclampsia Families Identifies SORD, DGKI, and ICA1 as Novel Candidate Risk Genes. Frontiers in Genetics, 2019, 10, 227.	1.1	8
106	Genetical genomics of Th1 and Th2 immune response in a baboon model of atherosclerosis risk factors. Atherosclerosis, 2011, 217, 387-394.	0.4	7
107	Effects of copy number variable regions on local gene expression in white blood cells of Mexican Americans. European Journal of Human Genetics, 2015, 23, 1229-1235.	1.4	7
108	The Ark: a customizable web-based data management tool for health and medical research. Bioinformatics, 2017, 33, 624-626.	1.8	6

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109	Familial and non-familial risk factors associated with incidence of colorectal cancer in young and middle-aged persons in Western Australia. Cancer Epidemiology, 2019, 62, 101591.	0.8	6
110	Association of Known Melanoma Risk Factors with Primary Melanoma of the Scalp and Neck. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2203-2210.	1.1	6
111	Genome-Wide Genetic and Transcriptomic Investigation of Variation in Antibody Response to Dietary Antigens. Genetic Epidemiology, 2014, 38, 439-446.	0.6	4
112	Is Mammographic Breast Density an Endophenotype for Breast Cancer?. Cancers, 2021, 13, 3916.	1.7	4
113	A Methylome and Transcriptome Analysis of Normal Human Scar Cells Reveals a Role for FOXF2 in Scar Maintenance. Journal of Investigative Dermatology, 2022, 142, 1489-1498.e12.	0.3	4
114	The â^'56T HLA-G Promoter Polymorphism is Not Associated with Pre-eclampsia/Eclampsia in Australian and New Zealand Women. Hypertension in Pregnancy, 2006, 25, 63-71.	0.5	3
115	OP006. A preeclampsia genome-wide linkage scan in norwegian families. Pregnancy Hypertension, 2013, 3, 64.	0.6	3
116	Integrating personalised genomics into risk stratification models of population screening for colorectal cancer. Australian and New Zealand Journal of Public Health, 2017, 41, 3-4.	0.8	3
117	Preeclampsia does not share common risk alleles in 9p21 with coronary artery disease and type 2 diabetes. Annals of Medicine, 2016, 48, 330-336.	1.5	2
118	Finding potential cis-regulatory loci using allele-specific chromatin accessibility as weights in a kernel-based variance component test. BMC Proceedings, 2016, 10, 103-108.	1.8	2
119	Identification of novel sarcoma risk genes using a two-stage genome wide DNA sequencing strategy in cancer cluster families and population case and control cohorts. BMC Medical Genetics, 2019, 20, 69.	2.1	2
120	Evaluation of epigenetic age calculators between preeclampsia and normotensive pregnancies in an Australian cohort. Scientific Reports, 2022, 12, 1664.	1.6	2
121	A variant in the fibronectin (FN1) gene, rs1250229-T, is associated with decreased risk of coronary artery disease in familial hypercholesterolaemia. Journal of Clinical Lipidology, 2022, 16, 525-529.	0.6	2
122	Systems genetics of the nuclear factor-Î¹B signal transduction network. I. Detection of several quantitative trait loci potentially relevant to aging. Mechanisms of Ageing and Development, 2012, 133, 11-19.	2.2	1
123	Late/post-term decidual basalis-derived mesenchymal stem/stromal cells show evidence of advanced ageing and downregulation of microRNA-516b-5p. Placenta, 2021, 109, 43-54.	0.7	1
124	Inherited Thrombophilia Polymorphisms and Pregnancy Outcomes in Nulliparous Women. Obstetrics and Gynecology, 2010, 115, 1305-1306.	1.2	0
125	M9.2 Dissecting the allelic architecture of ERAP2: a novel preeclampsia susceptibility gene. Pregnancy Hypertension, 2010, 1, S6.	0.6	0
126	Lipidomic signatures for APOE genotypes provides new insights about mechanisms of resilience in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2021, 17, .	0.4	0