Brendan J Keating

List of Publications by Year
in descending order

140 papers	11,771 citations	34016 52 h-index	30848 102 g-index
142 all docs	142 docs citations	142 times ranked	21760 citing authors

#	Article	IF	Citations
1	Whole transcriptome profiling of prospective endomyocardial biopsies reveals prognostic and diagnostic signatures of cardiac allograft rejection. Journal of Heart and Lung Transplantation, 2022, 41, 840-848.	0.3	9
2	Donor and recipient polygenic risk scores influence the risk of post-transplant diabetes. Nature Medicine, 2022, 28, 999-1005.	15.2	15
3	The Impact of Donor and Recipient Genetic Variation on Outcomes After Solid Organ Transplantation: A Scoping Review and Future Perspectives. Transplantation, 2022, 106, 1548-1557.	0.5	2
4	FC033: Genome-Wide Association Meta-Analysis Identifies Novel Loci for Kidney Failure. Nephrology Dialysis Transplantation, 2022, 37, .	0.4	0
5	Results of Two Cases of Pig-to-Human Kidney Xenotransplantation. New England Journal of Medicine, 2022, 386, 1889-1898.	13.9	166
6	Risk of preâ€eclampsia in patients with a maternal genetic predisposition to common medical conditions: a caseâ€“control study. BJOG: an International Journal of Obstetrics and Gynaecology, 2021, 128, 55-65.	1.1	19
7	Noninvasive biomarkers for prediction and diagnosis of heart transplantation rejection. Transplantation Reviews, 2021, 35, 100590.	1.2	11
8	Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. European Heart Journal, 2021, 42, 2000-2011.	1.0	49
9	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18
10	Exome sequencing in high and low fetal haemoglobin Arabâ€“Indian haplotype sickle cell disease. British Journal of Haematology, 2021, 194, e61-e64.	1.2	2
11	Early detection of SARSâ€CoVâ€2 and other infections in solid organ transplant recipients and household members using wearable devices. Transplant International, 2021, 34, 1019-1031.	0.8	6
12	Design and Methods of the Validating Injury to the Renal Transplant Using Urinary Signatures (VIRTUUS) Study in Children. Transplantation Direct, 2021, 7, e791.	0.8	3
13	Pharmacogenomics in kidney transplant recipients and potential for integration into practice. Journal of Clinical Pharmacy and Therapeutics, 2020, 45, 1457-1465.	0.7	3
14	Joint testing of donor and recipient genetic matching scores and recipient genotype has robust power for finding genes associated with transplant outcomes. Genetic Epidemiology, 2020, 44, 893-907.	0.6	7
15	Polygenic risk score of nonâ€melanoma skin cancer predicts postâ€transplant skin cancer across multiple organ types. Clinical Transplantation, 2020, 34, e13904.	0.8	11
16	Genomics and Liver Transplantation: Genomic Biomarkers for the Diagnosis of Acute Cellular Rejection. Liver Transplantation, 2020, 26, 1337-1350.	1.3	13
17	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. Nature Communications, 2020, 11, 255.	5.8	48
18	Genome-wide non-HLA donor-recipient genetic differences influence renal allograft survival via early allograft fibrosis. Kidney International, 2020, 98, 758-768.	2.6	25

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19	Polygenic risk score as a determinant of risk of non-melanoma skin cancer in a European-descent renal transplant cohort. American Journal of Transplantation, 2019, 19, 801-810.	2.6	26
20	Exome sequencing of Saudi Arabian patients with ADPKD. Renal Failure, 2019, 41, 842-849.	0.8	6
21	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	2.6	99
22	The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. American Journal of Transplantation, 2019, 19, 2262-2273.	2.6	13
23	Tacrolimus troughs and genetic determinants of metabolism in kidney transplant recipients: A comparison of four ancestry groups. American Journal of Transplantation, 2019, 19, 2795-2804.	2.6	35
24	Contribution of non-HLA incompatibility between donor and recipient to kidney allograft survival: genome-wide analysis in a prospective cohort. Lancet, The, 2019, 393, 910-917.	6.3	99
25	Genome-Wide Study Updates in the International Genetics and Translational Research in Transplantation Network (iGeneTRAiN). Frontiers in Genetics, 2019, 10, 1084.	1.1	13
26	Genetic Variants Associated With Immunosuppressant Pharmacokinetics and Adverse Effects in the DeKAF Genomics Genome-wide Association Studies. Transplantation, 2019, 103, 1131-1139.	0.5	17
27	Non-HLA Genetic Factors and Their Influence on Heart Transplant Outcomes: A Systematic Review. Transplantation Direct, 2019, 5, e422.	0.8	3
28	Current and Future Approaches for Monitoring Responses to Anti-complement Therapeutics. Frontiers in Immunology, 2019, 10, 2539.	2.2	13
29	Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion, 2019, 59, 101-111.	0.8	30
30	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.3	7
31	NPHP1 (Nephrocystin-1) Gene Deletions Cause Adult-Onset ESRD. Journal of the American Society of Nephrology: JASN, 2018, 29, 1772-1779.	3.0	74
32	Applying genomics in heart transplantation. Transplant International, 2018, 31, 278-290.	0.8	8
33	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. Journal of Human Genetics, 2018, 63, 327-337.	1.1	7
34	Assessing known chronic kidney disease associated genetic variants in Saudi Arabian populations. BMC Nephrology, 2018, 19, 88.	0.8	10
35	Immunologic Monitoring to Personalize Immunosuppression After Liver Transplant. Gastroenterology Clinics of North America, 2018, 47, 281-296.	1.0	3
36	Gene-Centric Analysis of Preeclampsia Identifies Maternal Association at <i>PLEKHG1</i>. Hypertension, 2018, 72, 408-416.	1.3	46

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37	Genetic analysis of impaired trimethylamine metabolism using whole exome sequencing. BMC Medical Genetics, 2017, 18, 11.	2.1	9
38	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
39	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	2.6	45
40	Correcting the Standard Errors of 2-Stage Residual Inclusion Estimators for Mendelian Randomization Studies. American Journal of Epidemiology, 2017, 186, 1104-1114.	1.6	15
41	Identifying geneâ€"gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	1.8	11
42	An ectopically expressed serum miRNA signature is prognostic, diagnostic, and biologically related to liver allograft rejection. Hepatology, 2017, 65, 269-280.	3.6	53
43	Genetic predisposition to elevated levels of C-reactive protein is associated with a decreased risk for preeclampsia. Hypertension in Pregnancy, 2017, 36, 30-35.	0.5	4
44	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
45	Intronic Polymorphisms in the CDKN2B-AS1 Gene Are Strongly Associated with the Risk of Myocardial Infarction and Coronary Artery Disease in the Saudi Population. International Journal of Molecular Sciences, 2016, 17, 395.	1.8	32
46	Elevated Fibroblast Growth Factor 23 Concentration: Prediction of Mortality among Chronic Kidney Disease Patients. CardioRenal Medicine, 2016, 6, 73-82.	0.7	21
47	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. Pharmacogenomics, 2016, 17, 583-591.	0.6	9
48	Harnessing publicly available genetic data to prioritize lipid modifying therapeutic targets for prevention of coronary heart disease based on dysglycemic risk. Human Genetics, 2016, 135, 453-467.	1.8	15
49	<i>CSF1R</i>mosaicism in a family with hereditary diffuse leukoencephalopathy with spheroids. Brain, 2016, 139, 1666-1672.	3.7	53
50	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
51	Association of Lipid Fractions With Risks for Coronary Artery Disease and Diabetes. JAMA Cardiology, 2016, 1, 692.	3.0	233
52	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
53	The impact of common polymorphisms in CETP and ABCA1 genes with the risk of coronary artery disease in Saudi Arabians. Human Genomics, 2016, 10, 8.	1.4	18
54	Whole Exome Sequencing Identifies the Genetic Basis of Late-Onset Leigh Syndrome in a Patient with MRI but Little Biochemical Evidence of a Mitochondrial Disorder. JIMD Reports, 2016, 32, 117-124.	0.7	11

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55	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	0.9	94
56	Lipids, obesity and gallbladder disease in women: insights from genetic studies using the cardiovascular gene-centric 50K SNP array. European Journal of Human Genetics, 2016, 24, 106-112.	1.4	23
57	Genetic Risk Score for Essential Hypertension and Risk of Preeclampsia. American Journal of Hypertension, 2016, 29, 17-24.	1.0	19
58	Machine learning derived risk prediction of anorexia nervosa. BMC Medical Genomics, 2015, 9, 4.	0.7	18
59	Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). BioData Mining, 2015, 8, 41.	2.2	17
60	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	3.6	49
61	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. Human Genomics, 2015, 9, 31.	1.4	9
62	Genetic Predisposition to Dyslipidemia and Risk of Preeclampsia. American Journal of Hypertension, 2015, 28, 915-923.	1.0	19
63	<i>De Novo</i>Heterozygous Mutations in<i>SMC3</i>Cause a Range of Cornelia de Lange Syndrome-Overlapping Phenotypes. Human Mutation, 2015, 36, 454-462.	1.1	72
64	Value of whole exome sequencing for syndromic retinal dystrophy diagnosis in young patients. Clinical and Experimental Ophthalmology, 2015, 43, 132-138.	1.3	7
65	Delayed diagnosis of congenital myasthenia due to associated mitochondrial enzyme defect. Neuromuscular Disorders, 2015, 25, 257-261.	0.3	16
66	Advantage of Whole Exome Sequencing over Allele-Specific and Targeted Segment Sequencing in Detection of NovelTULP1Mutation in Leber Congenital Amaurosis. Ophthalmic Genetics, 2015, 36, 333-338.	0.5	12
67	Mutation in mitochondrial ribosomal protein S7 (MRPS7) causes congenital sensorineural deafness, progressive hepatic and renal failure and lactic acidemia. Human Molecular Genetics, 2015, 24, 2297-2307.	1.4	64
68	Advances in Risk Prediction of Type 2 Diabetes: Integrating Genetic Scores With Framingham Risk Models. Diabetes, 2015, 64, 1495-1497.	0.3	17
69	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
70	Geneâ€centric approach identifies new and known loci for <scp>F</scp>VIII activity and <scp>VWF</scp> antigen levels in <scp>E</scp>uropean <scp>A</scp>mericans and <scp>A</scp>frican <scp>A</scp>mericans. American Journal of Hematology, 2015, 90, 534-540.	2.0	20
71	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. Nature Communications, 2015, 6, 8442.	5.8	58
72	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	15.2	212

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73	Genetic meta-analysis of 15,901 African Americans identifies variation in EXOC3L1 is associated with HDL concentration. Journal of Lipid Research, 2015, 56, 1781-1786.	2.0	11
74	Subclinical atherosclerosis and increased risk of hearing impairment. Atherosclerosis, 2015, 238, 344-349.	0.4	75
75	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
76	Application of Whole Exome Sequencing in Six Families with an Initial Diagnosis of Autosomal Dominant Retinitis Pigmentosa: Lessons Learned. PLoS ONE, 2015, 10, e0133624.	1.1	19
77	Return of results in the genomic medicine projects of the eMERGE network. Frontiers in Genetics, 2014, 5, 50.	1.1	40
78	Making the genomic leap in HCT: application of second-generation sequencing to clinical advances in hematopoietic cell transplantation. European Journal of Human Genetics, 2014, 22, 715-723.	1.4	5
79	Imputation of TPMT defective alleles for the identification of patients with high-risk phenotypes. Frontiers in Genetics, 2014, 5, 96.	1.1	13
80	Testing for non-linear causal effects using a binary genotype in a Mendelian randomization study: application to alcohol and cardiovascular traits. International Journal of Epidemiology, 2014, 43, 1781-1790.	0.9	57
81	Trans-ethnic genome-wide association studies: advantages and challenges of mapping in diverse populations. Genome Medicine, 2014, 6, 91.	3.6	167
82	Expanding the phenotype of PRPS1 syndromes in females: neuropathy, hearing loss and retinopathy. Orphanet Journal of Rare Diseases, 2014, 9, 190.	1.2	31
83	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
84	Return of Genomic Results to Research Participants: The Floor, the Ceiling, and the Choices In Between. American Journal of Human Genetics, 2014, 94, 818-826.	2.6	342
85	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	1.4	28
86	A systematic review and meta-analysis of 130,000 individuals shows smoking does not modify the association of APOE genotype on risk of coronary heart disease. Atherosclerosis, 2014, 237, 5-12.	0.4	27
87	Novel Genetic Approach to Investigate the Role of Plasma Secretory Phospholipase A2 (sPLA) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 144-150.	5.1	22
88	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. Human Genetics, 2014, 133, 985-995.	1.8	31
89	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
90	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60

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91	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. American Journal of Human Genetics, 2014, 94, 198-208.	2.6	199
92	Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1. Blood, 2014, 124, 2767-2774.	0.6	97
93	SESSION INTRODUCTION: CHARACTERIZING THE IMPORTANCE OF ENVIRONMENTAL EXPOSURES, INTERACTIONS BETWEEN THE ENVIRONMENT AND GENETIC ARCHITECTURE, AND GENETIC INTERACTIONS: NEW METHODS FOR UNDERSTANDING THE ETIOLOGY OF COMPLEX TRAITS AND DISEASE. , 2014, , .		0
94	Whole-genome sequencing in an autism multiplex family. Molecular Autism, 2013, 4, 8.	2.6	76
95	First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip. International Journal of Legal Medicine, 2013, 127, 559-572.	1.2	51
96	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	2.6	189
97	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115
98	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
99	Mutations in PDGFRB Cause Autosomal-Dominant Infantile Myofibromatosis. American Journal of Human Genetics, 2013, 92, 1001-1007.	2.6	174
100	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
101	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. Human Molecular Genetics, 2013, 22, 184-201.	1.4	82
102	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. Human Molecular Genetics, 2013, 22, 2529-2538.	1.4	57
103	Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. Human Molecular Genetics, 2013, 22, 3381-3393.	1.4	22
104	Copy Number Variations in Alternative Splicing Gene Networks Impact Lifespan. PLoS ONE, 2013, 8, e53846.	1.1	13
105	Two Variants of the C-Reactive Protein Gene Are Associated with Risk of Pre-Eclampsia in an American Indian Population. PLoS ONE, 2013, 8, e71231.	1.1	22
106	IBC CARe Microarray Allelic Population Prevalences in an American Indian Population. PLoS ONE, 2013, 8, e75080.	1.1	0
107	Genetic association studies in pre-eclampsia: systematic meta-analyses and field synopsis. International Journal of Epidemiology, 2012, 41, 1764-1775.	0.9	62
108	Novel Loci Associated With PR Interval in a Genome-Wide Association Study of 10 African American Cohorts. Circulation: Cardiovascular Genetics, 2012, 5, 639-646.	5.1	48

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109	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	6.3	886
110	Ultraconserved Elements in the Human Genome: Association and Transmission Analyses of Highly Constrained Single-Nucleotide Polymorphisms. Genetics, 2012, 192, 253-266.	1.2	17
111	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
112	Intensity of Salt Taste and Prevalence of Hypertension Are Not Related in the Beaver Dam Offspring Study. Chemosensory Perception, 2012, 5, 139-145.	0.7	11
113	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239
114	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. PLoS ONE, 2012, 7, e50198.	1.1	40
115	Examination of genetic variants influencing lipid traits in pediatric populations. Journal of Pediatric Genetics, 2012, 1, 85-98.	0.3	4
116	Fatty-acid binding protein 4 gene polymorphisms and plasma levels in children with obstructive sleep apnea. Sleep Medicine, 2011, 12, 666-671.	0.8	50
117	Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate Gene Association Resource (CARe). Blood, 2011, 117, 268-275.	0.6	36
118	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
119	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. Human Genetics, 2011, 129, 307-317.	1.8	81
120	Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARe consortium. Human Molecular Genetics, 2011, 20, 2285-2295.	1.4	77
121	Dense Genotyping of Candidate Gene Loci Identifies Variants Associated With High-Density Lipoprotein Cholesterol. Circulation: Cardiovascular Genetics, 2011, 4, 145-155.	5.1	71
122	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
123	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
124	Genome-Wide Association Study of White Blood Cell Count in 16,388 African Americans: the Continental Origins and Genetic Epidemiology Network (COGENT). PLoS Genetics, 2011, 7, e1002108.	1.5	133
125	A gene-centric association scan for Coagulation Factor VII levels in European and African Americans: the Candidate Gene Association Resource (CARe) Consortium. Human Molecular Genetics, 2011, 20, 3525-3534.	1.4	19
126	Genome-Wide Association of Bipolar Disorder Suggests an Enrichment of Replicable Associations in Regions near Genes. PLoS Genetics, 2011, 7, e1002134.	1.5	59

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127	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298.	1.5	93
128	Genome-Wide Association Study of Coronary Heart Disease and Its Risk Factors in 8,090 African Americans: The NHLBI CARe Project. PLoS Genetics, 2011, 7, e1001300.	1.5	290
129	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
130	An integrated expression phenotype mapping approach defines common variants in LEP, ALOX15 and CAPNS1 associated with induction of IL-6. Human Molecular Genetics, 2010, 19, 720-730.	1.4	23
131	Association of the Vitamin D Metabolism Gene <i>CYP24A1</i> With Coronary Artery Calcification. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2648-2654.	1.1	65
132	Common Variants in <i>HSPB7</i> and <i>FRMD4B</i> Associated With Advanced Heart Failure. Circulation: Cardiovascular Genetics, 2010, 3, 147-154.	5.1	119
133	Leprosy and the Adaptation of Human Toll-Like Receptor 1. PLoS Pathogens, 2010, 6, e1000979.	2.1	139
134	Gene-Centric Approach Identifies New and Known Loci for Factor VIII Activity and Von Willebrand Factor Antigen In the Candidate Gene Association Resource (CARe) Consortium. Blood, 2010, 116, 806-806.	0.6	8
135	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	1.1	339
136	Identification of Common Genetic Variation That Modulates Alternative Splicing. PLoS Genetics, 2007, 3, e99.	1.5	139
137	Implications of inter-population linkage disequilibrium patterns on the approach to a disease association study in the human MHC class III. Immunogenetics, 2006, 58, 465-470.	1.2	10
138	The chromosome 6p22 haplotype associated with dyslexia reduces the expression of KIAA0319 , a novel gene involved in neuronal migration. Human Molecular Genetics, 2006, 15, 1659-1666.	1.4	240
139	Allele-specific repression of lymphotoxin-Î± by activated B cell factor-1. Nature Genetics, 2004, 36, 394-399.	9.4	105
140	In vivo characterization of regulatory polymorphisms by allele-specific quantification of RNA polymerase loading. Nature Genetics, 2003, 33, 469-475.	9.4	231