Brendan J Keating

List of Publications by Year
in descending order

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Version: 2024-02-01

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	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
2	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
3	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
4	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
5	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
6	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
7	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
8	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
9	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
10	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
11	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
12	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
13	Association of Lipid Fractions With Risks for Coronary Artery Disease and Diabetes. JAMA Cardiology, 2016, 1, 692.	3.0	233
14	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
15	In vivo characterization of regulatory polymorphisms by allele-specific quantification of RNA polymerase loading. Nature Genetics, 2003, 33, 469-475.	9.4	231
16	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
17	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	15.2	212
18	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

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19	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
20	Mutations in PDGFRB Cause Autosomal-Dominant Infantile Myofibromatosis. American Journal of Human Genetics, 2013, 92, 1001-1007.	2.6	174
21	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
22	Trans-ethnic genome-wide association studies: advantages and challenges of mapping in diverse populations. Genome Medicine, 2014, 6, 91.	3.6	167
23	Results of Two Cases of Pig-to-Human Kidney Xenotransplantation. New England Journal of Medicine, 2022, 386, 1889-1898.	13.9	166
24	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
25	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
26	Identification of Common Genetic Variation That Modulates Alternative Splicing. PLoS Genetics, 2007, 3, e99.	1.5	139
27	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
28	Leprosy and the Adaptation of Human Toll-Like Receptor 1. PLoS Pathogens, 2010, 6, e1000979.	2.1	139
29	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
30	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
31	Common Variants in HSPB7 and FRMD4B Associated With Advanced Heart Failure. Circulation: Cardiovascular Genetics, 2010, 3, 147-154.	5.1	119
32	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115
33	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
34	Allele-specific repression of lymphotoxin-Î± by activated B cell factor-1. Nature Genetics, 2004, 36, 394-399.	9.4	105
35	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	2.6	99
36	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

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37	Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1. Blood, 2014, 124, 2767-2774.	0.6	97
38	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
39	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298.	1.5	93
40	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
41	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
42	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
43	Whole-genome sequencing in an autism multiplex family. Molecular Autism, 2013, 4, 8.	2.6	76
44	Subclinical atherosclerosis and increased risk of hearing impairment. Atherosclerosis, 2015, 238, 344-349.	0.4	75
45	NPHP1 (Nephrocystin-1) Gene Deletions Cause Adult-Onset ESRD. Journal of the American Society of Nephrology: JASN, 2018, 29, 1772-1779.	3.0	74
46	De NovoHeterozygous Mutations inSMC3Cause a Range of Cornelia de Lange Syndrome-Overlapping Phenotypes. Human Mutation, 2015, 36, 454-462.	1.1	72
47	Dense Genotyping of Candidate Gene Loci Identifies Variants Associated With High-Density Lipoprotein Cholesterol. Circulation: Cardiovascular Genetics, 2011, 4, 145-155.	5.1	71
48	Association of the Vitamin D Metabolism Gene CYP24A1 With Coronary Artery Calcification. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2648-2654.	1.1	65
49	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
50	Genetic association studies in pre-eclampsia: systematic meta-analyses and field synopsis. International Journal of Epidemiology, 2012, 41, 1764-1775.	0.9	62
51	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
52	Genome-Wide Association of Bipolar Disorder Suggests an Enrichment of Replicable Associations in Regions near Genes. PLoS Genetics, 2011, 7, e1002134.	1.5	59
53	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. Nature Communications, 2015, 6, 8442.	5.8	58
54	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

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55	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
56	CSF1Rmosaicism in a family with hereditary diffuse leukoencephalopathy with spheroids. Brain, 2016, 139, 1666-1672.	3.7	53
57	An ectopically expressed serum miRNA signature is prognostic, diagnostic, and biologically related to liver allograft rejection. Hepatology, 2017, 65, 269-280.	3.6	53
58	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
59	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
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	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
62	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
63	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. Nature Communications, 2020, 11, 255.	5.8	48
64	Gene-Centric Analysis of Preeclampsia Identifies Maternal Association at PLEKHG1. Hypertension, 2018, 72, 408-416.	1.3	46
65	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
66	Return of results in the genomic medicine projects of the eMERGE network. Frontiers in Genetics, 2014, 5, 50.	1.1	40
67	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. PLoS ONE, 2012, 7, e50198.	1.1	40
68	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
69	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
70	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
71	Expanding the phenotype of PRPS1 syndromes in females: neuropathy, hearing loss and retinopathy. Orphanet Journal of Rare Diseases, 2014, 9, 190.	1.2	31
72	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

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73	Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion, 2019, 59, 101-111.	0.8	30
74	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
75	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
76	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
77	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
78	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
79	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
80	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
81	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
82	Novel Genetic Approach to Investigate the Role of Plasma Secretory Phospholipase A2 (sPLA) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 144-150.	5.1	22
83	Elevated Fibroblast Growth Factor 23 Concentration: Prediction of Mortality among Chronic Kidney Disease Patients. CardioRenal Medicine, 2016, 6, 73-82.	0.7	21
84	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
85	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
86	Genetic Predisposition to Dyslipidemia and Risk of Preeclampsia. American Journal of Hypertension, 2015, 28, 915-923.	1.0	19
87	Genetic Risk Score for Essential Hypertension and Risk of Preeclampsia. American Journal of Hypertension, 2016, 29, 17-24.	1.0	19
88	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
89	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
90	Machine learning derived risk prediction of anorexia nervosa. BMC Medical Genomics, 2015, 9, 4.	0.7	18

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91	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
92	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
93	Ultraconserved Elements in the Human Genome: Association and Transmission Analyses of Highly Constrained Single-Nucleotide Polymorphisms. Genetics, 2012, 192, 253-266.	1.2	17
94	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
95	Advances in Risk Prediction of Type 2 Diabetes: Integrating Genetic Scores With Framingham Risk Models. Diabetes, 2015, 64, 1495-1497.	0.3	17
96	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
97	Delayed diagnosis of congenital myasthenia due to associated mitochondrial enzyme defect. Neuromuscular Disorders, 2015, 25, 257-261.	0.3	16
98	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
99	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
100	Donor and recipient polygenic risk scores influence the risk of post-transplant diabetes. Nature Medicine, 2022, 28, 999-1005.	15.2	15
101	Copy Number Variations in Alternative Splicing Gene Networks Impact Lifespan. PLoS ONE, 2013, 8, e53846.	1.1	13
102	Imputation of TPMT defective alleles for the identification of patients with high-risk phenotypes. Frontiers in Genetics, 2014, 5, 96.	1.1	13
103	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
104	Genome-Wide Study Updates in the International Genetics and Translational Research in Transplantation Network (iGeneTRAiN). Frontiers in Genetics, 2019, 10, 1084.	1.1	13
105	Current and Future Approaches for Monitoring Responses to Anti-complement Therapeutics. Frontiers in Immunology, 2019, 10, 2539.	2.2	13
106	Genomics and Liver Transplantation: Genomic Biomarkers for the Diagnosis of Acute Cellular Rejection. Liver Transplantation, 2020, 26, 1337-1350.	1.3	13
107	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
108	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

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109	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
110	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
111	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
112	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
113	Noninvasive biomarkers for prediction and diagnosis of heart transplantation rejection. Transplantation Reviews, 2021, 35, 100590.	1.2	11
114	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
115	Assessing known chronic kidney disease associated genetic variants in Saudi Arabian populations. BMC Nephrology, 2018, 19, 88.	0.8	10
116	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. Human Genomics, 2015, 9, 31.	1.4	9
117	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. Pharmacogenomics, 2016, 17, 583-591.	0.6	9
118	Genetic analysis of impaired trimethylamine metabolism using whole exome sequencing. BMC Medical Genetics, 2017, 18, 11.	2.1	9
119	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
120	Applying genomics in heart transplantation. Transplant International, 2018, 31, 278-290.	0.8	8
121	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
122	Value of whole exome sequencing for syndromic retinal dystrophy diagnosis in young patients. Clinical and Experimental Ophthalmology, 2015, 43, 132-138.	1.3	7
123	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
124	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
125	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.3	7
126	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

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127	Exome sequencing of Saudi Arabian patients with ADPKD. Renal Failure, 2019, 41, 842-849.	0.8	6
128	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
129	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
130	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
131	Examination of genetic variants influencing lipid traits in pediatric populations. Journal of Pediatric Genetics, 2012, 1, 85-98.	0.3	4
132	Immunologic Monitoring to Personalize Immunosuppression After Liver Transplant. Gastroenterology Clinics of North America, 2018, 47, 281-296.	1.0	3
133	Non-HLA Genetic Factors and Their Influence on Heart Transplant Outcomes: A Systematic Review. Transplantation Direct, 2019, 5, e422.	0.8	3
134	Pharmacogenomics in kidney transplant recipients and potential for integration into practice. Journal of Clinical Pharmacy and Therapeutics, 2020, 45, 1457-1465.	0.7	3
135	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
136	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
137	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
138	IBC CARe Microarray Allelic Population Prevalences in an American Indian Population. PLoS ONE, 2013, 8, e75080.	1.1	0
139	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
140	FC033: Genome-Wide Association Meta-Analysis Identifies Novel Loci for Kidney Failure. Nephrology Dialysis Transplantation, 2022, 37, .	0.4	0