J Brent Richards

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63 130 214 17,359 h-index g-index citations papers 10.6 5.89 246 22,441 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
214	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016 , 48, 1279-83	36.3	1447
213	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. <i>Lancet, The,</i> 2010 , 376, 180-8	40	1183
212	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. <i>Nature Genetics</i> , 2012 , 44, 491-501	36.3	866
211	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776
210	An atlas of genetic influences on human blood metabolites. <i>Nature Genetics</i> , 2014 , 46, 543-550	36.3	695
209	Causal relationship between obesity and vitamin D status: bi-directional Mendelian randomization analysis of multiple cohorts. <i>PLoS Medicine</i> , 2013 , 10, e1001383	11.6	592
208	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2009 , 41, 1199-206	36.3	566
207	Bone mineral density, osteoporosis, and osteoporotic fractures: a genome-wide association study. <i>Lancet, The</i> , 2008 , 371, 1505-12	40	538
206	The association between physical activity in leisure time and leukocyte telomere length. <i>Archives of Internal Medicine</i> , 2008 , 168, 154-8		410
205	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
204	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015 , 526, 112-7	50.4	308
203	Effect of selective serotonin reuptake inhibitors on the risk of fracture. <i>Archives of Internal Medicine</i> , 2007 , 167, 188-94		276
202	Use of genome-wide association studies for drug repositioning. <i>Nature Biotechnology</i> , 2012 , 30, 317-20	44.5	275
201	An atlas of genetic influences on osteoporosis in humans and mice. <i>Nature Genetics</i> , 2019 , 51, 258-266	36.3	270
200	Vitamin D and Risk of Multiple Sclerosis: A Mendelian Randomization Study. <i>PLoS Medicine</i> , 2015 , 12, e1001866	11.6	252
199	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. <i>Nature Genetics</i> , 2017 , 49, 1468-1475	36.3	235
198	Genetic architecture: the shape of the genetic contribution to human traits and disease. <i>Nature Reviews Genetics</i> , 2018 , 19, 110-124	30.1	219

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197	Genetics of osteoporosis from genome-wide association studies: advances and challenges. <i>Nature Reviews Genetics</i> , 2012 , 13, 576-88	30.1	216
196	Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. <i>Annals of Internal Medicine</i> , 2009 , 151, 528-37	8	215
195	Genome-wide association study using extreme truncate selection identifies novel genes affecting bone mineral density and fracture risk. <i>PLoS Genetics</i> , 2011 , 7, e1001372	6	199
194	Meta-analysis of genome-wide scans for human adult stature identifies novel Loci and associations with measures of skeletal frame size. <i>PLoS Genetics</i> , 2009 , 5, e1000445	6	198
193	WNT16 influences bone mineral density, cortical bone thickness, bone strength, and osteoporotic fracture risk. <i>PLoS Genetics</i> , 2012 , 8, e1002745	6	192
192	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. <i>Nature Communications</i> , 2015 , 6, 8111	17.4	186
191	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
190	Serum adiponectin and bone mineral density in women. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2007 , 92, 1517-23	5.6	177
189	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018 , 9, 260	17.4	174
188	Higher serum vitamin D concentrations are associated with longer leukocyte telomere length in women. <i>American Journal of Clinical Nutrition</i> , 2007 , 86, 1420-5	7	169
187	An integration of genome-wide association study and gene expression profiling to prioritize the discovery of novel susceptibility Loci for osteoporosis-related traits. <i>PLoS Genetics</i> , 2010 , 6, e1000977	6	163
186	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021 ,	50.4	162
185	Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies. <i>American Journal of Human Genetics</i> , 2010 , 86, 229-	3 ⁵ 1	156
184	A meta-analysis of thyroid-related traits reveals novel loci and gender-specific differences in the regulation of thyroid function. <i>PLoS Genetics</i> , 2013 , 9, e1003266	6	146
183	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. <i>Nature Genetics</i> , 2015 , 47, 88-91	36.3	140
182	Genetic evidence for a normal-weight "metabolically obese" phenotype linking insulin resistance, hypertension, coronary artery disease, and type 2 diabetes. <i>Diabetes</i> , 2014 , 63, 4369-77	0.9	131
181	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. <i>PLoS Genetics</i> , 2009 , 5, e1000768	6	129
180	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: results of genome-wide association analyses including 4659 European individuals. <i>Atherosclerosis</i> , 2010 , 208, 412-20	3.1	128

179	Identification of novel genetic Loci associated with thyroid peroxidase antibodies and clinical thyroid disease. <i>PLoS Genetics</i> , 2014 , 10, e1004123	6	122
178	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. <i>American Journal of Human Genetics</i> , 2018 , 102, 88-102	11	119
177	Meta-analysis of genome-wide scans for total body BMD in children and adults reveals allelic heterogeneity and age-specific effects at the WNT16 locus. <i>PLoS Genetics</i> , 2012 , 8, e1002718	6	118
176	Telomere length in leukocytes correlates with bone mineral density and is shorter in women with osteoporosis. <i>Osteoporosis International</i> , 2007 , 18, 1203-10	5.3	118
175	25-Hydroxyvitamin D in Canadian adults: biological, environmental, and behavioral correlates. <i>Osteoporosis International</i> , 2011 , 22, 1389-99	5.3	117
174	Obesity and Multiple Sclerosis: A Mendelian Randomization Study. <i>PLoS Medicine</i> , 2016 , 13, e1002053	11.6	115
173	Assessment of the genetic and clinical determinants of fracture risk: genome wide association and mendelian randomisation study. <i>BMJ, The</i> , 2018 , 362, k3225	5.9	114
172	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016 , 7, 10494	17.4	107
171	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. <i>Human Molecular Genetics</i> , 2009 , 18, 1510-7	5.6	107
170	Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. <i>Diabetes</i> , 2013 , 62, 3589-98	0.9	95
169	Male-pattern baldness susceptibility locus at 20p11. <i>Nature Genetics</i> , 2008 , 40, 1282-4	36.3	93
168	The empirical power of rare variant association methods: results from sanger sequencing in 1,998 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002496	6	89
167	Genetic interactions affecting human gene expression identified by variance association mapping. <i>ELife</i> , 2014 , 3, e01381	8.9	86
166	A Mendelian randomization study of the effect of type-2 diabetes on coronary heart disease. Nature Communications, 2015 , 6, 7060	17.4	84
165	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014 , 112, 317-38	3.7	81
164	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017 , 8, 16015	17.4	80
163	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 3054-68	5.6	78
162	Cohort Profile: The Canadian Longitudinal Study on Aging (CLSA). <i>International Journal of Epidemiology</i> , 2019 , 48, 1752-1753j	7.8	76

(2014-2017)

Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018 , 9, 4455	17.4	75
Meta-analysis of genome-wide studies identifies WNT16 and ESR1 SNPs associated with bone mineral density in premenopausal women. <i>Journal of Bone and Mineral Research</i> , 2013 , 28, 547-58	6.3	74
Heritability of serum TSH, free T4 and free T3 concentrations: a study of a large UK twin cohort. <i>Clinical Endocrinology</i> , 2008 , 68, 652-9	3.4	72
Homocysteine levels and leukocyte telomere length. <i>Atherosclerosis</i> , 2008 , 200, 271-7	3.1	71
Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases. <i>PLoS Genetics</i> , 2012 , 8, e1002746	6	70
A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. <i>Journal of Medical Genetics</i> , 2009 , 46, 451-4	5.8	69
Genetically decreased vitamin D and risk of Alzheimer disease. <i>Neurology</i> , 2016 , 87, 2567-2574	6.5	64
Androgenetic alopecia: identification of four genetic risk loci and evidence for the contribution of WNT signaling to its etiology. <i>Journal of Investigative Dermatology</i> , 2013 , 133, 1489-96	4.3	64
Mendelian Randomization Studies Do Not Support a Role for Vitamin D in Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 349-56		63
Genome-wide association study with 1000 genomes imputation identifies signals for nine sex hormone-related phenotypes. <i>European Journal of Human Genetics</i> , 2016 , 24, 284-90	5.3	61
Temporal trends and determinants of longitudinal change in 25-hydroxyvitamin D and parathyroid hormone levels. <i>Journal of Bone and Mineral Research</i> , 2012 , 27, 1381-9	6.3	59
Genetic regulation of vitamin D levels. Calcified Tissue International, 2013, 92, 106-17	3.9	58
Somatic point mutations occurring early in development: a monozygotic twin study. <i>Journal of Medical Genetics</i> , 2014 , 51, 28-34	5.8	57
Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015 , 6, 5681	17.4	56
Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. <i>American Journal of Human Genetics</i> , 2020 , 106, 327-337	11	54
A genome-wide association study suggests that a locus within the ataxin 2 binding protein 1 gene is associated with hand osteoarthritis: the Treat-OA consortium. <i>Journal of Medical Genetics</i> , 2009 , 46, 614	ı-₹ ⁸	54
The causal effect of vitamin D binding protein (DBP) levels on calcemic and cardiometabolic diseases: a Mendelian randomization study. <i>PLoS Medicine</i> , 2014 , 11, e1001751	11.6	52
	Meta-analysis of genome-wide studies identifies WNT16 and ESR1 SNPs associated with bone mineral density in premenopausal women. Journal of Bone and Mineral Research, 2013, 28, 547-58 Heritability of serum TSH, free T4 and free T3 concentrations: a study of a large UK twin cohort. Clinical Endocrinology, 2008, 68, 652-9 Homocysteine levels and leukocyte telomere length. Atherosclerosis, 2008, 200, 271-7 Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases. PLoS Genetics, 2012, 8, e1002746 A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. Journal of Medical Genetics, 2009, 46, 451-4 Genetically decreased vitamin D and risk of Alzheimer disease. Neurology, 2016, 87, 2567-2574 Androgenetic alopecia: identification of four genetic risk loci and evidence for the contribution of WNT signaling to its etiology. Journal of Investigative Dermatology, 2013, 133, 1489-96 Mendelian Randomization Studies Do Not Support a Role for Vitamin D in Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2016, 9, 349-56 Genome-wide association study with 1000 genomes imputation identifies signals for nine sex hormone-related phenotypes. European Journal of Human Genetics, 2016, 24, 284-90 Temporal trends and determinants of longitudinal change in 25-hydroxyvitamin D and parathyroid hormone levels. Journal of Bone and Mineral Research, 2012, 27, 1381-9 Genetic regulation of vitamin D levels. Calcified Tissue International, 2013, 92, 106-17 Somatic point mutations occurring early in development: a monozygotic twin study. Journal of Medical Genetics, 2014, 51, 28-34 Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681 Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. American Journal of Human Genetics, 2020, 106, 327-337 A genome-wide association Study suggests that a locus within the ataxin 2 binding protei	Meta-analysis of genome-wide studies identifies WNT16 and ESR1 SNPs associated with bone mineral density in premenopausal women. Journal of Bone and Mineral Research, 2013, 28, 547-58 Heritability of serum TSH, free T4 and free T3 concentrations: a study of a large UK twin cohort. Clinical Endocrinology, 2008, 68, 652-9 Homocysteine levels and leukocyte telomere length. Atherosclerosis, 2008, 200, 271-7 3.1 Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases. PLoS Genetics, 2012, 8, e1002746 A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. Journal of Medical Genetics, 2009, 46, 451-4 Genetically decreased vitamin D and risk of Alzheimer disease. Neurology, 2016, 87, 2567-2574 Androgenetic alopecia: identification of four genetic risk loci and evidence for the contribution of WNT signaling to its etiology. Journal of Investigative Dermatology, 2013, 133, 1489-96 Mendelian Randomization Studies Do Not Support a Role for Vitamin D in Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2016, 9, 349-56 Genome-wide association study with 1000 genomes imputation identifies signals for nine sex hormone-related phenotypes. European Journal of Human Genetics, 2016, 24, 284-90 5.3 Temporal trends and determinants of longitudinal change in 25-hydroxyvitamin D and parathyroid hormone levels. Journal of Bone and Mineral Research, 2012, 27, 1381-9 Genetic regulation of vitamin D levels. Calcified Tissue International, 2013, 92, 106-17 3.9 Somatic point mutations occurring early in development: a monozygotic twin study. Journal of Medical Genetics, 2014, 51, 28-34 Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681 7.4 Genome-wide Association Study sugests that a locus within the ataxin 2 binding protein 1 gene is associated with hand osteoarthritis: the Treat-OA consortium. Journal of Medical Genetics, 2009, 46, 614-

143	A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity. <i>Nature Medicine</i> , 2021 , 27, 659-667	50.5	52
142	Vitamin D levels and susceptibility to asthma, elevated immunoglobulin E levels, and atopic dermatitis: A Mendelian randomization study. <i>PLoS Medicine</i> , 2017 , 14, e1002294	11.6	47
141	Adjusted sequence kernel association test for rare variants controlling for cryptic and family relatedness. <i>Genetic Epidemiology</i> , 2013 , 37, 366-76	2.6	47
140	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014 , 5, 4871	17.4	46
139	Blood lipids and prostate cancer: a Mendelian randomization analysis. <i>Cancer Medicine</i> , 2016 , 5, 1125-30	54.8	45
138	Imputation of variants from the 1000 Genomes Project modestly improves known associations and can identify low-frequency variant-phenotype associations undetected by HapMap based imputation. <i>PLoS ONE</i> , 2013 , 8, e64343	3.7	42
137	The effect of cyclooxygenase-2 inhibitors on bone mineral density: results from the Canadian Multicentre Osteoporosis Study. <i>Osteoporosis International</i> , 2006 , 17, 1410-9	5.3	38
136	The influence of obesity-related factors in the etiology of renal cell carcinoma-A mendelian randomization study. <i>PLoS Medicine</i> , 2019 , 16, e1002724	11.6	38
135	Mendelian randomisation applied to drug development in cardiovascular disease: a review. <i>Journal of Medical Genetics</i> , 2015 , 52, 71-9	5.8	37
134	In healthy adults, biological activity of vitamin D, as assessed by serum PTH, is largely independent of DBP concentrations. <i>Journal of Bone and Mineral Research</i> , 2014 , 29, 494-9	6.3	37
133	Assessment of gene-by-sex interaction effect on bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2012 , 27, 2051-64	6.3	37
132	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. <i>Nature Communications</i> , 2017 , 8, 14694	17.4	36
131	The use of genome-wide eQTL associations in lymphoblastoid cell lines to identify novel genetic pathways involved in complex traits. <i>PLoS ONE</i> , 2011 , 6, e22070	3.7	35
130	Performance of genotype imputation for low frequency and rare variants from the 1000 genomes. <i>PLoS ONE</i> , 2015 , 10, e0116487	3.7	34
129	A locus on chromosome 1p36 is associated with thyrotropin and thyroid function as identified by genome-wide association study. <i>American Journal of Human Genetics</i> , 2010 , 87, 430-5	11	34
128	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. Journal of Bone and Mineral Research, 2017 , 32, 1644-1650	6.3	33
127	A genome-wide copy number association study of osteoporotic fractures points to the 6p25.1 locus. <i>Journal of Medical Genetics</i> , 2014 , 51, 122-31	5.8	32
126	Strengthening the Reporting of Observational Studies in Epidemiology Using Mendelian Randomization: The STROBE-MR Statement. <i>JAMA - Journal of the American Medical Association</i> , 2021 , 326, 1614-1621	27.4	32

125	Vitamin D and COVID-19 susceptibility and severity in the COVID-19 Host Genetics Initiative: A Mendelian randomization study. <i>PLoS Medicine</i> , 2021 , 18, e1003605	11.6	32
124	Identification of Novel Loci Associated With Hip Shape: A Meta-Analysis of Genomewide Association Studies. <i>Journal of Bone and Mineral Research</i> , 2019 , 34, 241-251	6.3	32
123	A Mendelian Randomization Study of the Effect of Type-2 Diabetes and Glycemic Traits on Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2017 , 32, 1072-1081	6.3	31
122	Changes to osteoporosis prevalence according to method of risk assessment. <i>Journal of Bone and Mineral Research</i> , 2007 , 22, 228-34	6.3	31
121	The health effects of vitamin D supplementation: evidence from human studies. <i>Nature Reviews Endocrinology</i> , 2021 ,	15.2	30
120	Investigating causality in the association between 25(OH)D and schizophrenia. <i>Scientific Reports</i> , 2016 , 6, 26496	4.9	29
119	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. <i>Bone</i> , 2014 , 59, 20-27	4.7	29
118	Natural history and risk factors for bone loss in postmenopausal Caucasian women: a 15-year follow-up population-based study. <i>Osteoporosis International</i> , 2008 , 19, 1211-7	5.3	29
117	No clear support for a role for vitamin D in Parkinson® disease: A Mendelian randomization study. <i>Movement Disorders</i> , 2017 , 32, 1249-1252	7	28
116	Mendelian randomization in multiple sclerosis: A causal role for vitamin D and obesity?. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 80-85	5	28
115	Genome-wide association study using family-based cohorts identifies the WLS and CCDC170/ESR1 loci as associated with bone mineral density. <i>BMC Genomics</i> , 2016 , 17, 136	4.5	28
114	Effect of genome-wide genotyping and reference panels on rare variants imputation. <i>Journal of Genetics and Genomics</i> , 2012 , 39, 545-50	4	28
113	Genetic loci linked to pituitary-thyroid axis set points: a genome-wide scan of a large twin cohort. Journal of Clinical Endocrinology and Metabolism, 2008 , 93, 3519-23	5.6	28
112	STROBE-MR: Guidelines for strengthening the reporting of Mendelian randomization studies		28
111	Depressive symptomatology and fracture risk in community-dwelling older men and women. <i>Aging Clinical and Experimental Research</i> , 2008 , 20, 585-92	4.8	27
110	Common variants in genes encoding adiponectin (ADIPOQ) and its receptors (ADIPOR1/2), adiponectin concentrations, and diabetes incidence in the Diabetes Prevention Program. <i>Diabetic Medicine</i> , 2012 , 29, 1579-88	3.5	26
109	An obesogenic postnatal environment is more important than the fetal environment for the development of adult adiposity: a study of female twins. <i>American Journal of Clinical Nutrition</i> , 2009 , 90, 401-6	7	26
108	Metabolomic Pathways to Osteoporosis in Middle-Aged Women: A Genome-Metabolome-Wide Mendelian Randomization Study. <i>Journal of Bone and Mineral Research</i> , 2018 , 33, 643-650	6.3	26

107	Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. <i>Diabetes</i> , 2014 , 63, 1154-65	0.9	25
106	The shared allelic architecture of adiponectin levels and coronary artery disease. <i>Atherosclerosis</i> , 2013 , 229, 145-8	3.1	25
105	Insights into the genetics of osteoporosis from recent genome-wide association studies. <i>Expert Reviews in Molecular Medicine</i> , 2011 , 13, e28	6.7	25
104	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021 , 27, 1876-1884	50.5	25
103	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. <i>American Journal of Human Genetics</i> , 2021 , 108, 1350-1355	11	25
102	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	25
101	Strengthening the reporting of observational studies in epidemiology using mendelian randomisation (STROBE-MR): explanation and elaboration. <i>BMJ, The</i> , 2021 , 375, n2233	5.9	24
100	FAM210A is a novel determinant of bone and muscle structure and strength. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E3759-E3768	11.5	23
99	Genetic predisposition to increased serum calcium, bone mineral density, and fracture risk in individuals with normal calcium levels: mendelian randomisation study. <i>BMJ, The</i> , 2019 , 366, l4410	5.9	23
98	Toward Precision Medicine: TBC1D4 Disruption Is Common Among the Inuit and Leads to Underdiagnosis of Type 2 Diabetes. <i>Diabetes Care</i> , 2016 , 39, 1889-1895	14.6	22
97	Plasma adiponectin concentrations are associated with body composition and plant-based dietary factors in female twins. <i>Journal of Nutrition</i> , 2009 , 139, 353-8	4.1	21
96	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. <i>Human Molecular Genetics</i> , 2017 , 26, 2791-2802	5.6	20
95	Proton pump inhibitors: balancing the benefits and potential fracture risks. <i>Cmaj</i> , 2008 , 179, 306-7	3.5	20
94	Whole-exome sequencing identifies rare variants in STAB2 associated with venous thromboembolic disease. <i>Blood</i> , 2020 , 136, 533-541	2.2	18
93	A method for analyzing multiple continuous phenotypes in rare variant association studies allowing for flexible correlations in variant effects. <i>European Journal of Human Genetics</i> , 2016 , 24, 1344-51	5.3	17
92	Common sequence variation in FLNB regulates bone structure in women in the general population and FLNB mRNA expression in osteoblasts in vitro. <i>Journal of Bone and Mineral Research</i> , 2009 , 24, 1989	9- 63	17
91	A combined reference panel from the 1000 Genomes and UK10K projects improved rare variant imputation in European and Chinese samples. <i>Scientific Reports</i> , 2016 , 6, 39313	4.9	17
90	Meta-Analysis of Genomewide Association Studies Reveals Genetic Variants for Hip Bone Geometry. <i>Journal of Bone and Mineral Research</i> , 2019 , 34, 1284-1296	6.3	16

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89	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study. <i>PLoS Medicine</i> , 2020 , 17, e1003152	11.6	16	
88	Genome-wide association study for radiographic vertebral fractures: a potential role for the 16q24 BMD locus. <i>Bone</i> , 2014 , 59, 20-7	4.7	16	
87	Multiple regression methods show great potential for rare variant association tests. <i>PLoS ONE</i> , 2012 , 7, e41694	3.7	15	
86	A reference panel of 64,976 haplotypes for genotype imputation		15	
85	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	15	
84	Meta-analysis of genome-wide studies identifies MEF2C SNPs associated with bone mineral density at forearm. <i>Journal of Medical Genetics</i> , 2013 , 50, 473-8	5.8	14	
83	Relation of birth weight, body mass index, and change in size from birth to adulthood to insulin resistance in a female twin cohort. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2008 , 93, 516-20	5.6	14	
82	Rare Genetic Variants of Large Effect Influence Risk of Type 1 Diabetes. <i>Diabetes</i> , 2020 , 69, 784-795	0.9	14	
81	Effect of age at puberty on risk of multiple sclerosis: A mendelian randomization study. <i>Neurology</i> , 2019 , 92, e1803-e1810	6.5	13	
80	Genotype imputation and reference panel: a systematic evaluation on haplotype size and diversity. <i>Briefings in Bioinformatics</i> , 2019 ,	13.4	12	
79	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. <i>Nature Communications</i> , 2021 , 12, 2444	17.4	12	
78	Interleukin-18 as a drug repositioning opportunity for inflammatory bowel disease: A Mendelian randomization study. <i>Scientific Reports</i> , 2019 , 9, 9386	4.9	11	
77	Empirical power of very rare variants for common traits and disease: results from sanger sequencing 1998 individuals. <i>European Journal of Human Genetics</i> , 2013 , 21, 1027-30	5.3	11	
76	Effectiveness of antiresorptives for the prevention of nonvertebral low-trauma fractures in a population-based cohort of women. <i>Osteoporosis International</i> , 2009 , 20, 283-90	5-3	11	
75	An analysis of which anti-osteoporosis therapeutic regimen would improve compliance in a population of elderly adults. <i>Current Medical Research and Opinion</i> , 2007 , 23, 293-9	2.5	11	
74	Constrained instruments and their application to Mendelian randomization with pleiotropy. <i>Genetic Epidemiology</i> , 2019 , 43, 373-401	2.6	11	
73	Copy number variation of the APC gene is associated with regulation of bone mineral density. <i>Bone</i> , 2012 , 51, 939-43	4.7	10	
72	The undiagnosed disease burden associated with alpha-1 antitrypsin deficiency genotypes. <i>European Respiratory Journal</i> , 2020 , 56,	13.6	10	

71	Individuals with common diseases but with a low polygenic risk score could be prioritized for rare variant screening. <i>Genetics in Medicine</i> , 2021 , 23, 508-515	8.1	10
70	Polygenic risk for coronary heart disease acts through atherosclerosis in type 2 diabetes. <i>Cardiovascular Diabetology</i> , 2020 , 19, 12	8.7	9
69	STROBE-MR: Guidelines for strengthening the reporting of Mendelian randomization studies		9
68	Dnmt3a-mutated clonal hematopoiesis promotes osteoporosis. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	9
67	An efficient paradigm for genetic epidemiology cohort creation. <i>PLoS ONE</i> , 2010 , 5, e14045	3.7	8
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7	Little evidence for an effect of smoking on multiple sclerosis risk: A Mendelian Randomization study 2020 , 18, e3000973		
6	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study 2020 , 17, e1003152		
5	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study 2020 , 17, e1003152		
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