Andrew Collins

List of Publications by Citations

181 papers	8,115 citations	45 h-index	85 g-index
191 ext. papers	9,048 ext. citations	6.7 avg, IF	5.48 L-index

#	Paper	IF	Citations
181	An efficient procedure for genotyping single nucleotide polymorphisms. *Nucleic Acids Research*, **2001**, 29, E88-8	20.1	684
180	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. *Nature Genetics*, **2009**, 41, 35-46	36.3	588
179	JAK2 haplotype is a major risk factor for the development of myeloproliferative neoplasms. *Nature Genetics*, **2009**, 41, 446-9	36.3	320
178	Extended tracts of homozygosity in outbred human populations. *Human Molecular Genetics*, **2006**, 15, 789-95	5.6	282
177	A metric map of humans: 23,500 loci in 850 bands. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 14771-5	11.5	233
176	Genetic epidemiology of single-nucleotide polymorphisms. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 15173-7	11.5	231
175	Tests and estimates of allelic association in complex inheritance. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 11389-93	11.5	214
174	Magnitude and distribution of linkage disequilibrium in population isolates and implications for genome-wide association studies. *Nature Genetics*, **2006**, 38, 556-60	36.3	202
173	The impact of SNP density on fine-scale patterns of linkage disequilibrium. *Human Molecular Genetics*, **2004**, 13, 577-88	5.6	171
172	The clinical significance of NOTCH1 and SF3B1 mutations in the UK LRF CLL4 trial. *Blood*, **2013**, 121, 468-75	9.5	167
171	Extent of genome-wide linkage disequilibrium in Australian Holstein-Friesian cattle based on a high-density SNP panel. *BMC Genomics*, **2008**, 9, 187	4.5	155
170	The first linkage disequilibrium (LD) maps: delineation of hot and cold blocks by diplotype analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 2228-33	11.5	155
169	Mapping a disease locus by allelic association. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 1741-5	11.5	144
168	Association between the SERPING1 gene and age-related macular degeneration: a two-stage case-control study. *Lancet, The*, **2008**, 372, 1828-34	40	143
167	Influence of vascular endothelial growth factor single nucleotide polymorphisms on tumour development in cutaneous malignant melanoma. *Genes and Immunity*, **2002**, 3, 229-32	4.4	143
166	The genome-wide patterns of variation expose significant substructure in a founder population. *American Journal of Human Genetics*, **2008**, 83, 787-94	11	116
165	Polymorphisms in a disintegrin and metalloprotease 33 (ADAM33) predict impaired early-life lung function. *American Journal of Respiratory and Critical Care Medicine*, **2005**, 172, 55-60	10.2	116

164	Evidence that genetic susceptibility to Mycobacterium tuberculosis in a Brazilian population is under oligogenic control: linkage study of the candidate genes NRAMP1 and TNFA. *Tubercle and Lung Disease*, **1997**, 78, 35-45		105
163	The optimal measure of allelic association. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 5217-21	11.5	99
162	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. *Clinical Cancer Research*, **2015**, 21, 4174-4183	12.9	96
161	13q deletion anatomy and disease progression in patients with chronic lymphocytic leukemia. *Leukemia*, **2011**, 25, 489-97	10.7	93
160	Next generation exome sequencing of paediatric inflammatory bowel disease patients identifies rare and novel variants in candidate genes. *Gut*, **2013**, 62, 977-84	19.2	92
159	The linkage disequilibrium maps of three human chromosomes across four populations reflect their demographic history and a common underlying recombination pattern. *Genome Research*, **2005**, 15, 454-62	9.7	87
158	Haplotypic analysis of the MMP-9 gene in relation to coronary artery disease. *Journal of Molecular Medicine*, **2003**, 81, 321-6	5.5	83
157	Association and linkage of leprosy phenotypes with HLA class II and tumour necrosis factor genes. *Genes and Immunity*, **2001**, 2, 196-204	4.4	79
156	Non-disjunction of chromosome 18. *Human Molecular Genetics*, **1998**, 7, 661-9	5.6	78
155	Genetic epidemiology of complex phenotypes. *Annals of Human Genetics*, **1991**, 55, 301-14	2.2	75
154	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. *Nature Communications*, **2019**, 10, 260	17.4	75
153	Linkage of asthma to markers on chromosome 12 in a sample of 240 families using quantitative phenotype scores. *Genomics*, **1998**, 53, 251-9	4.3	72
152	A map of the human genome in linkage disequilibrium units. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 11835-9	11.5	71
151	Properties of linkage disequilibrium (LD) maps. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 17004-7	11.5	71
150	Primer1: Primer Design Web Service for Tetra-Primer ARMS-PCR. *Open Bioinformatics Journal*, **2012**, 6, 55-58	0.8	62
149	Machine learning approaches for the discovery of gene-gene interactions in disease data. *Briefings in Bioinformatics*, **2013**, 14, 251-60	13.4	60
148	Error filtration, interference, and the human linkage map. *Proceedings of the National Academy of Sciences of the United States of America*, **1991**, 88, 6501-5	11.5	60
147	ATM mutation rather than BIRC3 deletion and/or mutation predicts reduced survival in 11q-deleted chronic lymphocytic leukemia: data from the UK LRF CLL4 trial. *Haematologica*, **2014**, 99, 736-42	6.6	59

146	Allelic association between marker loci. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 1621-6	11.5	59
145	Genetic epidemiology of glioma. *British Journal of Cancer*, **2001**, 84, 429-34	8.7	57
144	Whole exome sequencing identifies novel recurrently mutated genes in patients with splenic marginal zone lymphoma. *PLoS ONE*, **2013**, 8, e83244	3.7	56
143	Exome sequence read depth methods for identifying copy number changes. *Briefings in Bioinformatics*, **2015**, 16, 380-92	13.4	55
142	Support for the involvement of complement factor I in age-related macular degeneration. *European Journal of Human Genetics*, **2010**, 18, 15-6	5.3	53
141	Linkage disequilibrium in human populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 6069-74	11.5	52
140	Algorithms for a location database. *Annals of Human Genetics*, **1992**, 56, 223-32	2.2	52
139	Positional cloning by linkage disequilibrium. *American Journal of Human Genetics*, **2004**, 74, 846-55	11	50
138	Maternal sex chromosome non-disjunction: evidence for X chromosome-specific risk factors. *Human Molecular Genetics*, **2001**, 10, 243-50	5.6	50
137	A SNP profiling panel for sample tracking in whole-exome sequencing studies. *Genome Medicine*, **2013**, 5, 89	14.4	45
136	TFG, a target of chromosome translocations in lymphoma and soft tissue tumors, fuses to GPR128 in healthy individuals. *Haematologica*, **2010**, 95, 20-6	6.6	45
135	Standard maps of chromosome 10. *Annals of Human Genetics*, **1990**, 54, 235-51	2.2	45
134	Complex segregation analysis of hypospadias. *Human Genetics*, **2002**, 111, 231-4	6.3	44
133	A reinvestigation of non-disjunction resulting in 47, XXY males of paternal origin. *European Journal of Human Genetics*, **2000**, 8, 805-8	5.3	44
132	Does haplotype diversity predict power for association mapping of disease susceptibility?. *Human Genetics*, **2004**, 115, 157-64	6.3	43
131	Complex segregation analysis of nasopharyngeal carcinoma in Guangdong, China: evidence for a multifactorial mode of inheritance (complex segregation analysis of NPC in China). *European Journal of Human Genetics*, **2005**, 13, 248-52	5.3	43
130	The influence of genetic variation in 30 selected genes on the clinical characteristics of early onset breast cancer. *Breast Cancer Research*, **2008**, 10, R108	8.3	42
129	The optimal measure of linkage disequilibrium reduces error in association mapping of affection status. *Human Molecular Genetics*, **2005**, 14, 145-53	5.6	40

128	A novel X-linked dominant condition: X-linked congenital isolated ptosis. *American Journal of Human Genetics*, **2000**, 66, 1455-60	11	40
127	A metric linkage disequilibrium map of a human chromosome. *Annals of Human Genetics*, **2003**, 67, 487-94	2.2	39
126	Linkage map integration. *Genomics*, **1996**, 36, 157-62	4.3	39
125	Kinship bioassay on hypervariable loci in blacks and Caucasians. *Proceedings of the National Academy of Sciences of the United States of America*, **1993**, 90, 1892-6	11.5	39
124	Telomere length predicts progression and overall survival in chronic lymphocytic leukemia: data from the UK LRF CLL4 trial. *Leukemia*, **2015**, 29, 2411-4	10.7	38
123	Identification of inherited genetic variations influencing prognosis in early-onset breast cancer. *Cancer Research*, **2013**, 73, 1883-91	10.1	36
122	Independent effects of the -219 G>T and epsilon 2/ epsilon 3/ epsilon 4 polymorphisms in the apolipoprotein E gene on coronary artery disease: the Southampton Atherosclerosis Study. *European Journal of Human Genetics*, **2003**, 11, 437-43	5.3	36
121	The distinguishing sequence characteristics of mouse imprinted genes. *Mammalian Genome*, **2002**, 13, 639-45	3.2	35
120	Integration of gene maps: chromosome 1. *Proceedings of the National Academy of Sciences of the United States of America*, **1992**, 89, 4598-602	11.5	35
119	CpG islands in human X-inactivation. *Annals of Human Genetics*, **2003**, 67, 242-9	2.2	34
118	Impact of population structure, effective bottleneck time, and allele frequency on linkage disequilibrium maps. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 18075-80	11.5	33
117	Mutations in phospholipase C epsilon 1 are not sufficient to cause diffuse mesangial sclerosis. *Kidney International*, **2009**, 75, 415-9	9.9	32
116	A first-generation metric linkage disequilibrium map of bovine chromosome 6. *Genetics*, **2006**, 174, 79-85	4	32
115	Non-disjunction of chromosome 13. *Human Molecular Genetics*, **2007**, 16, 2004-10	5.6	32
114	Influence of TNFalpha and LTalpha single nucleotide polymorphisms on susceptibility to and prognosis in cutaneous malignant melanoma in the British population. *International Journal of Immunogenetics*, **2002**, 29, 17-23		32
113	An n-allele model for progressive amplification in the FMR1 locus. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 4833-7	11.5	32
112	Longitudinal copy number, whole exome and targeted deep sequencing of ‘good risk’ IGHV-mutated CLL patients with progressive disease. *Leukemia*, **2016**, 30, 1301-10	10.7	32
111	Allelic association under map error and recombinational heterogeneity: a tale of two sites. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 11366-70	11.5	31

110	Linkage disequilibrium analysis of case-control data: an application to generalized aggressive periodontitis. *Genes and Immunity*, **2005**, 6, 44-52	4.4	30
109	Mapping genes for common diseases: the case for genetic (LD) maps. *Human Heredity*, **2004**, 58, 2-9	1.1	29
108	Allelic association with SNPs: metrics, populations, and the linkage disequilibrium map. *Human Mutation*, **2001**, 17, 255-62	4.7	28
107	Integration of gene maps: chromosome X. *Genomics*, **1994**, 22, 590-604	4.3	27
106	The origin of trisomy 13. *American Journal of Medical Genetics, Part A*, **2007**, 143A, 2242-8	2.5	26
105	Exploiting large scale computing to construct high resolution linkage disequilibrium maps of the human genome. *Bioinformatics*, **2007**, 23, 517-9	7.2	26
104	Genetic analysis of multicase families of visceral leishmaniasis in northeastern Brazil: no major role for class II or class III regions of HLA. *Genes and Immunity*, **2002**, 3, 350-8	4.4	25
103	A genome wide meta-analysis study for identification of common variation associated with breast cancer prognosis. *PLoS ONE*, **2014**, 9, e101488	3.7	24
102	Complex segregation analysis in a sample of consecutive newborns with cleft lip with or without cleft palate in Italy. *Human Heredity*, **1995**, 45, 157-64	1.1	24
101	Integration of gene maps: chromosome 21. *Proceedings of the National Academy of Sciences of the United States of America*, **1993**, 90, 7210-4	11.5	24
100	Trials of the beta model for complex inheritance. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 9177-81	11.5	23
99	Exclusion from proximal 11q of a common gene with megaphenic effect on atopy. *Annals of Human Genetics*, **1995**, 59, 403-11	2.2	22
98	Non-coding NOTCH1 mutations in chronic lymphocytic leukemia; their clinical impact in the UK CLL4 trial. *Leukemia*, **2017**, 31, 510-514	10.7	21
97	The genetics of breast cancer: risk factors for disease. *The Application of Clinical Genetics*, **2011**, 4, 11-9	3.1	21
96	Determination of a gene and environment risk model for age-related macular degeneration. *British Journal of Ophthalmology*, **2010**, 94, 1382-7	5.5	21
95	Clinical significance of TP53, BIRC3, ATM and MAPK-ERK genes in chronic lymphocytic leukaemia: data from the randomised UK LRF CLL4 trial. *Leukemia*, **2020**, 34, 1760-1774	10.7	20
94	A novel approach for identifying candidate imprinted genes through sequence analysis of imprinted and control genes. *Human Genetics*, **2002**, 111, 511-20	6.3	20
93	Genetic epidemiology of hereditary non-polyposis colorectal cancer syndromes in Modena, Italy: results of a complex segregation analysis. *Annals of Human Genetics*, **1994**, 58, 275-95	2.2	20

92	Likelihood ratios for DNA identification. *Proceedings of the National Academy of Sciences of the United States of America*, **1994**, 91, 6007-11	11.5	20
91	Nonparametric tests for linkage with dependent sib pairs. *Human Heredity*, **1995**, 45, 311-8	1.1	19
90	CEPH consortium Map of chromosome 9. *Genomics*, **1994**, 19, 203-14	4.3	19
89	Exome sequencing in tracking clonal evolution in multiple myeloma following therapy. *Leukemia*, **2013**, 27, 1188-91	10.7	17
88	The interleukin-1 cluster gene region is associated with multiple sclerosis in an Italian Caucasian population. *European Journal of Neurology*, **2010**, 17, 930-8	6	17
87	Refined association mapping for a quantitative trait: weight in the H19-IGF2-INS-TH region. *Annals of Human Genetics*, **2006**, 70, 848-56	2.2	17
86	Genetic epidemiology of early onset breast cancer. *Journal of Medical Genetics*, **1994**, 31, 944-9	5.8	17
85	Megalencephaly syndromes: exome pipeline strategies for detecting low-level mosaic mutations. *PLoS ONE*, **2014**, 9, e86940	3.7	17
84	Genome scanning by composite likelihood. *American Journal of Human Genetics*, **2007**, 80, 19-28	11	16
83	Combined segregation and linkage analysis of inflammatory bowel disease in the IBD1 region using severity to characterise Crohn disease and ulcerative colitis. On behalf of the GISC. *European Journal of Human Genetics*, **2000**, 8, 846-52	5.3	16
82	Combined segregation and linkage analysis of nonsyndromic orofacial cleft in two candidate regions. *Annals of Human Genetics*, **1999**, 63, 17-25	2.2	16
81	Quantitated transcript haplotypes (QTH) of AGTR1, reduced abundance of mRNA haplotypes containing 1166C (rs5186:A>C), and relevance to metabolic syndrome traits. *Human Mutation*, **2007**, 28, 365-73	4.7	15
80	Effects of single SNPs, haplotypes, and whole-genome LD maps on accuracy of association mapping. *Genetic Epidemiology*, **2007**, 31, 179-88	2.6	15
79	Evaluating phenotype-driven approaches for genetic diagnoses from exomes in a clinical setting. *Scientific Reports*, **2017**, 7, 13509	4.9	14
78	Deleterious coding variants in multi-case families with non-syndromic cleft lip and/or palate phenotypes. *Scientific Reports*, **2016**, 6, 30457	4.9	14
77	Resolving clinical diagnoses for syndromic cleft lip and/or palate phenotypes using whole-exome sequencing. *Clinical Genetics*, **2015**, 88, 441-9	4	14
76	Variation in complement component C1 inhibitor in age-related macular degeneration. *Immunobiology*, **2012**, 217, 251-5	3.4	14
75	A comparative location database (CompLDB): map integration within and between species. *Mammalian Genome*, **2007**, 18, 287-99	3.2	14

74	A sequence-based integrated map of chromosome 22. *Genome Research*, **2001**, 11, 1290-5	9.7	14
73	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. *Nature Communications*, **2017**, 8, 1632	17.4	13
72	Support Vector Machine classifier for estrogen receptor positive and negative early-onset breast cancer. *PLoS ONE*, **2013**, 8, e68606	3.7	13
71	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. *Blood Advances*, **2019**, 3, 2474-2481	7.8	13
70	Whole genome sequences are required to fully resolve the linkage disequilibrium structure of human populations. *BMC Genomics*, **2015**, 16, 666	4.5	12
69	Studies on locus content mapping. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 11814-8	11.5	12
68	Exome-based linkage disequilibrium maps of individual genes: functional clustering and relationship to disease. *Human Genetics*, **2013**, 132, 233-43	6.3	11
67	CHROMSCAN: genome-wide association using a linkage disequilibrium map. *Journal of Human Genetics*, **2008**, 53, 121-126	4.3	11
66	Fine-scale linkage disequilibrium mapping of age-related macular degeneration in the complement factor H gene region. *British Journal of Ophthalmology*, **2007**, 91, 966-70	5.5	11
65	Evolutionary dynamics of the FMR1 locus. *Annals of Human Genetics*, **1995**, 59, 283-9	2.2	11
64	Exome Sequencing in Classic Hairy Cell Leukaemia Reveals Widespread Variation in Acquired Somatic Mutations between Individual Tumours Apart from the Signature BRAF V(600)E Lesion. *PLoS ONE*, **2016**, 11, e0149162	3.7	11
63	Cosmopolitan linkage disequilibrium maps. *Human Genomics*, **2005**, 2, 20-7	6.8	10
62	An integrated map of chromosome 9. *Annals of Human Genetics*, **1995**, 59, 393-402	2.2	10
61	Statistical and genetic aspects of quality control for DNA identification. *Electrophoresis*, **1995**, 16, 1670-7	3.6	10
60	Commercial chicken breeds exhibit highly divergent patterns of linkage disequilibrium. *Heredity*, **2016**, 117, 375-382	3.6	10
59	Allelic association: linkage disequilibrium structure and gene mapping. *Molecular Biotechnology*, **2009**, 41, 83-9	3	9
58	Recombination, interference and sequence: comparison of chromosomes 21 and 22. *Annals of Human Genetics*, **2002**, 66, 75-86	2.2	9
57	A tournament of linkage tests in complex inheritance. *Human Heredity*, **2001**, 52, 140-8	1.1	9

56	Segregation analysis of colorectal cancer in Northern Ireland. *Human Heredity*, **1995**, 45, 41-8	1.1	9
55	Sequencing era methods for identifying signatures of selection in the genome. *Briefings in Bioinformatics*, **2019**, 20, 1997-2008	13.4	8
54	Approaches to the identification of susceptibility genes. *Parasite Immunology*, **2009**, 31, 225-33	2.2	8
53	MaGIC: a program to generate targeted marker sets for genome-wide association studies. *BioTechniques*, **2004**, 37, 996-9	2.5	8
52	Integration of gene maps: updating chromosome 1. *Annals of Human Genetics*, **1995**, 59, 291-305	2.2	8
51	The genomic and functional characteristics of disease genes. *Briefings in Bioinformatics*, **2015**, 16, 16-23	13.4	7
50	A comparison of methods to detect recombination hotspots. *Human Heredity*, **2008**, 66, 157-69	1.1	7
49	The BRCA1 Ashkenazi founder mutations occur on common haplotypes and are not highly correlated with anonymous single nucleotide polymorphisms likely to be used in genome-wide case-control association studies. *BMC Genetics*, **2007**, 8, 68	2.6	7
48	PCR designer for restriction analysis of various types of sequence mutation. *Bioinformatics*, **2002**, 18, 1688-9	7.2	7
47	Mapping in the sequencing era. *Human Heredity*, **2000**, 50, 76-84	1.1	7
46	Counting algorithms for linkage. *Annals of Human Genetics*, **1990**, 54, 103-6	2.2	7
45	LDMAP: the construction of high-resolution linkage disequilibrium maps of the human genome. *Methods in Molecular Biology*, **2007**, 376, 47-57	1.4	7
44	A multimetric approach to analysis of genome-wide association by single markers and composite likelihood. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 2592-7	11.5	6
43	Allelic association and disease mapping. *Briefings in Bioinformatics*, **2001**, 2, 375-87	13.4	6
42	Combined segregation and linkage analysis of 59 Hodgkin disease families indicates the role of HLA determinants. *European Journal of Human Genetics*, **2000**, 8, 460-3	5.3	6
41	Limb girdle muscular dystrophy type 2A (CAPN3): mapping using allelic association. *Human Heredity* , **1998**, 48, 333-7	1.1	6
40	Significance of maximal lods. *Annals of Human Genetics*, **1991**, 55, 39-41	2.2	6
39	Understanding the disease genome: gene essentiality and the interplay of selection, recombination and mutation. *Briefings in Bioinformatics*, **2019**, 20, 267-273	13.4	6

38	Machine Learning Approaches: Data Integration for Disease Prediction and Prognosis. *Translational Bioinformatics*, **2018**, 137-141		6
37	Linkage disequilibrium maps to guide contig ordering for genome assembly. *Bioinformatics*, **2019**, 35, 541-545	7.2	5
36	Genome-wide association of breast cancer: composite likelihood with imputed genotypes. *European Journal of Human Genetics*, **2011**, 19, 194-9	5.3	5
35	Composite likelihood-based meta-analysis of breast cancer association studies. *Journal of Human Genetics*, **2011**, 56, 377-82	4.3	5
34	Mapping a gene for rheumatoid arthritis on chromosome 18q21. *BMC Proceedings*, **2007**, 1 Suppl 1, S18	2.3	5
33	Integrated genetic map of human chromosome 2. *Annals of Human Genetics*, **1995**, 59, 413-34	2.2	5
32	A linkage tournament: affection status, parametric analysis, multivariate traits, and enhancements to variance components and relative pairs. *Annals of Human Genetics*, **2002**, 66, 87-98	2.2	4
31	Linkage disequilibrium and association mapping: an introduction. *Methods in Molecular Biology*, **2007**, 376, 1-15	1.4	4
30	Linkage disequilibrium maps for European and African populations constructed from whole genome sequence data. *Scientific Data*, **2019**, 6, 208	8.2	3
29	Individual disease risk and multimetric analysis of Crohn disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 15843-7	11.5	3
28	Combination of linkage evidence in complex inheritance. *Human Heredity*, **2001**, 52, 132-5	1.1	3
27	Coding of pointers in the segregation analysis program POINTER. *Genetic Epidemiology*, **1994**, 11, 385-7	2.6	3
26	Clinical and Descriptive Study of Orofacial Clefts in Colombia: 2069 Patients From Operation Smile Foundation. *Cleft Palate-Craniofacial Journal*, **2021**, 10556656211000551	1.9	3
25	Gene-specific metrics to facilitate identification of disease genes for molecular diagnosis in patient genomes: a systematic review. *Briefings in Functional Genomics*, **2019**, 18, 23-29	4.9	3
24	Mapping quantitative effects of oligogenes by allelic association. *Annals of Human Genetics*, **2002**, 66, 211-21	2.2	3
23	Gene-dense autosomal chromosomes show evidence for increased selection. *Heredity*, **2019**, 123, 774-783	3.6	2
22	Heterogeneity in the extent of linkage disequilibrium among exonic, intronic, non-coding RNA and intergenic chromosome regions. *European Journal of Human Genetics*, **2019**, 27, 1436-1444	5.3	2
21	Genome variation: a review of Web resources. *Methods in Molecular Biology*, **2011**, 713, 129-39	1.4	2

20	The power and statistical behaviour of allele-sharing statistics when applied to models with two disease loci. *Journal of Genetics*, **2002**, 81, 99-103	1.2	2
19	EFFECT OF THE PEROXISOME PROLIFERATORS-ACTIVATED RECEPTOR (PPAR) GAMMA 3 GENE ON BMI IN 1,210 SCHOOL STUDENTS FROM MORELOS, MEXICO **2005**,		2
18	The impact of redefining affection status for alcoholism on affected-sib-pair analysis. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S151-6	2.6	2
17	The Challenge of Genome Sequence Assembly. *Open Bioinformatics Journal*, **2018**, 11, 231-239	0.8	2
16	Quantifying the cumulative effect of low-penetrance genetic variants on breast cancer risk. *Molecular Genetics & Genomic Medicine*, **2015**, 3, 182-8	2.3	1
15	The future of gene mapping. *Genetic Analysis, Techniques and Applications*, **1997**, 14, 25-7		1
14	A two-locus model for hereditary non-polyposis colorectal cancer in Modena, Italy. *Annals of Human Genetics*, **1997**, 61, 109-19	2.2	1
13	Deletion Size Influences Clinical Outcome In Patients with Chronic Lymphocytic Leukemia; 13q Deletion Anatomy, Cooperating Lesions and Cancer Pathogenesis. *Blood*, **2010**, 116, 757-757	2.2	1
12	Aarskog-Scott syndrome: phenotypic and genetic heterogeneity. *AIMS Genetics*, **2016**, 03, 049-059	2.1	1
11	Deep-Sequencing Reveals the Molecular Landscape of Splenic Marginal Zone Lymphoma: Biological and Clinical Implications. *Blood*, **2014**, 124, 76-76	2.2	1
10	The Correlation Between Deletion Architecture, ATM Mutational Status and BIRC3 Disruption in 11q-Deleted CLL. *Blood*, **2012**, 120, 658-658	2.2	1
9	Single-cell exomes in an index case of amp1q21 multiple myeloma reveal more diverse mutanomes than the whole population. *Blood*, **2018**, 132, 232-235	2.2	1
8	Essentiality-specific pathogenicity prioritization gene score to improve filtering of disease sequence data. *Briefings in Bioinformatics*, **2021**, 22, 1782-1789	13.4	0
7	Genetic variants within chromosome 4q28.3 are not reproducibly associated with age-related macular degeneration (AMD). *Acta Ophthalmologica*, **2011**, 89, e603-4	3.7	
6	Linkage disequilibrium in maps of SNPs and other markers. *GeneScreen*, **2008**, 1, 59-61		
5	An evaluation of affected-sib-pair methods and transmission/disequilibrium tests for detecting genes underlying a complex trait. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S727-30	2.6	
4	zalpha: an R package for the identification of regions of the genome under selection. *Journal of Open Source Software*, **2020**, 5, 2638	5.2	
3	Single Cell Whole Exome Sequencing in an Index Case of Amp1q21 Multiple Myeloma to Define Intraclonal Variation. *Blood*, **2016**, 128, 5651-5651	2.2	

2 Development of V617F JAK2 Associated Myeloproliferative Neoplasms Is a Non-Random Event That Is Strongly Dependent on JAK2 Haplotype. *Blood*, **2008**, 112, 173-173 2.2

1 Analytical Approaches for Exome Sequence Data. *Translational Bioinformatics*, **2018**, 121-136