Andrew Collins

List of Publications by Year
in descending order

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Version: 2024-02-01

184 papers	9,783 citations	41344 49 h-index	40979 93 g-index

191 all docs	191 docs citations	191 times ranked	13575 citing authors

#	Article	IF	Citations
1	An efficient procedure for genotyping single nucleotide polymorphisms. Nucleic Acids Research, 2001, 29, 88e-88.	14.5	831
2	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. Nature Genetics, 2009, 41, 35-46.	21.4	676
3	Extended tracts of homozygosity in outbred human populations. Human Molecular Genetics, 2006, 15, 789-795.	2.9	401
4	JAK2 haplotype is a major risk factor for the development of myeloproliferative neoplasms. Nature Genetics, 2009, 41, 446-449.	21.4	365
5	Genetic epidemiology of single-nucleotide polymorphisms. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 15173-15177.	7.1	275
6	A metric map of humans: 23,500 loci in 850â€‰bands. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 14771-14775.	7.1	253
7	Tests and estimates of allelic association in complex inheritance. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 11389-11393.	7.1	230
8	Magnitude and distribution of linkage disequilibrium in population isolates and implications for genome-wide association studies. Nature Genetics, 2006, 38, 556-560.	21.4	227
9	Extent of genome-wide linkage disequilibrium in Australian Holstein-Friesian cattle based on a high-density SNP panel. BMC Genomics, 2008, 9, 187.	2.8	203
10	The clinical significance of NOTCH1 and SF3B1 mutations in the UK LRF CLL4 trial. Blood, 2013, 121, 468-475.	1.4	190
11	The impact of SNP density on fine-scale patterns of linkage disequilibrium. Human Molecular Genetics, 2004, 13, 577-588.	2.9	184
12	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, 2228-2233.	7.1	170
13	Mapping a disease locus by allelicâ€‰association. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 1741-1745.	7.1	169
14	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. Nature Communications, 2019, 10, 260.	12.8	161
15	Association between the SERPING1 gene and age-related macular degeneration: a two-stage caseâ€“control study. Lancet, The, 2008, 372, 1828-1834.	13.7	156
16	Influence of vascular endothelial growth factor single nucleotide polymorphisms on tumour development in cutaneous malignant melanoma. Genes and Immunity, 2002, 3, 229-232.	4.1	153
17	The Genome-wide Patterns of Variation Expose Significant Substructure in a Founder Population. American Journal of Human Genetics, 2008, 83, 787-794.	6.2	132
18	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.	5.6	130

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19	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. Clinical Cancer Research, 2015, 21, 4174-4183.	7.0	129
20	Evidence that genetic susceptibility to Mycobacterium tuberculosis in a brazilian population is under oligogenic control: Linkage study of the candidate genes NRAMP1 and TBFA. Tubercle and Lung Disease, 1997, 78, 35-45.	2.1	128
21	Non-disjunction of chromosome 18. Human Molecular Genetics, 1998, 7, 661-669.	2.9	115
22	The optimal measure of allelic association. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 5217-5221.	7.1	113
23	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, 454-462.	5.5	107
24	13q deletion anatomy and disease progression in patients with chronic lymphocytic leukemia. Leukemia, 2011, 25, 489-497.	7.2	104
25	Next generation exome sequencing of paediatric inflammatory bowel disease patients identifies rare and novel variants in candidate genes. Gut, 2013, 62, 977-984.	12.1	104
26	Primer1: Primer Design Web Service for Tetra-Primer ARMS-PCR. Open Bioinformatics Journal, 2012, 6, 55-58.	1.0	103
27	Haplotypic analysis of the MMP-9 gene in relation to coronary artery disease. Journal of Molecular Medicine, 2003, 81, 321-326.	3.9	97
28	Association and linkage of leprosy phenotypes with HLA class II and tumour necrosis factor genes. Genes and Immunity, 2001, 2, 196-204.	4.1	92
29	Properties of linkage disequilibrium (LD) maps. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 17004-17007.	7.1	89
30	Exome sequence read depth methods for identifying copy number changes. Briefings in Bioinformatics, 2015, 16, 380-392.	6.5	84
31	Genetic epidemiology of complex phenotypes. Annals of Human Genetics, 1991, 55, 301-314.	0.8	83
32	Machine learning approaches for the discovery of gene-gene interactions in disease data. Briefings in Bioinformatics, 2013, 14, 251-260.	6.5	81
33	Error filtration, interference, and the human linkage map.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 6501-6505.	7.1	79
34	Genetic epidemiology of glioma. British Journal of Cancer, 2001, 84, 429-434.	6.4	75
35	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, 11835-11839.	7.1	75
36	Linkage of Asthma to Markers on Chromosome 12 in a Sample of 240 Families Using Quantitative Phenotype Scores. Genomics, 1998, 53, 251-259.	2.9	73

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37	Linkage disequilibrium in human populations. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6069-6074.	7.1	69
38	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, 736-742.	3.5	69
39	Allelic association between marker loci. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 1621-1626.	7.1	68
40	Whole Exome Sequencing Identifies Novel Recurrently Mutated Genes in Patients with Splenic Marginal Zone Lymphoma. PLoS ONE, 2013, 8, e83244.	2.5	66
41	Maternal sex chromosome non-disjunction: evidence for X chromosome-specific risk factors. Human Molecular Genetics, 2001, 10, 243-250.	2.9	64
42	TFG, a target of chromosome translocations in lymphoma and soft tissue tumors, fuses to GPR128 in healthy individuals. Haematologica, 2010, 95, 20-26.	3.5	63
43	Algorithms for a location database. Annals of Human Genetics, 1992, 56, 223-232.	0.8	58
44	A SNP profiling panel for sample tracking in whole-exome sequencing studies. Genome Medicine, 2013, 5, 89.	8.2	57
45	Complex segregation analysis of hypospadias. Human Genetics, 2002, 111, 231-234.	3.8	55
46	Support for the involvement of complement factor I in age-related macular degeneration. European Journal of Human Genetics, 2010, 18, 15-16.	2.8	54
47	Positional Cloning by Linkage Disequilibrium. American Journal of Human Genetics, 2004, 74, 846-855.	6.2	53
48	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, 248-252.	2.8	52
49	Standard maps of chromosome 10. Annals of Human Genetics, 1990, 54, 235-251.	0.8	51
50	A reinvestigation of non-disjunction resulting in 47, XXY males of paternal origin. European Journal of Human Genetics, 2000, 8, 805-808.	2.8	51
51	Does haplotype diversity predict power for association mapping of disease susceptibility?. Human Genetics, 2004, 115, 157-64.	3.8	49
52	The influence of genetic variation in 30 selected genes on the clinical characteristics of early onset breast cancer. Breast Cancer Research, 2008, 10, R108.	5.0	49
53	A Novel X-Linked Dominant Condition: X-Linked Congenital Isolated Ptosis. American Journal of Human Genetics, 2000, 66, 1455-1460.	6.2	47
54	Kinship bioassay on hypervariable loci in blacks and Caucasians.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 1892-1896.	7.1	46

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55	Linkage Map Integration. Genomics, 1996, 36, 157-162.	2.9	46
56	A Metric Linkage Disequilibrium Map of a Human Chromosome. Annals of Human Genetics, 2003, 67, 487-494.	0.8	44
57	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, 18075-18080.	7.1	44
58	The optimal measure of linkage disequilibrium reduces error in association mapping of affection status. Human Molecular Genetics, 2005, 14, 145-153.	2.9	42
59	Identification of Inherited Genetic Variations Influencing Prognosis in Early-Onset Breast Cancer. Cancer Research, 2013, 73, 1883-1891.	0.9	42
60	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	2.5	42
61	Telomere length predicts progression and overall survival in chronic lymphocytic leukemia: data from the UK LRF CLL4 trial. Leukemia, 2015, 29, 2411-2414.	7.2	42
62	Independent effects of the â^'219â€‰G>T and Îµ2/Îµ3/Îµ4 polymorphisms in the apolipoprotein E gene on coronary artery disease: The Southampton Atherosclerosis Study. European Journal of Human Genetics, 2003, 11, 437-443.	2.8	39
63	Integration of gene maps: chromosome 1.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 4598-4602.	7.1	38
64	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, 11366-11370.	7.1	38
65	Non-disjunction of chromosome 13. Human Molecular Genetics, 2007, 16, 2004-2010.	2.9	38
66	Integration of gene maps: chromosome 21.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 7210-7214.	7.1	37
67	The distinguishing sequence characteristics of mouse imprinted genes. Mammalian Genome, 2002, 13, 639-645.	2.2	37
68	Longitudinal copy number, whole exome and targeted deep sequencing of 'good risk' IGHV-mutated CLL patients with progressive disease. Leukemia, 2016, 30, 1301-1310.	7.2	37
69	Likelihood ratios for DNA identification.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 6007-6011.	7.1	35
70	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, 4833-4837.	7.1	35
71	Allelic association with SNPs: Metrics, populations, and the linkage disequilibrium map. Human Mutation, 2001, 17, 255-262.	2.5	35
72	CpG Islands in Human X-Inactivation. Annals of Human Genetics, 2003, 67, 242-249.	0.8	35

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73	A First-Generation Metric Linkage Disequilibrium Map of Bovine Chromosome 6. Genetics, 2006, 174, 79-85.	2.9	35
74	Mutations in phospholipase C epsilon 1 are not sufficient to cause diffuse mesangial sclerosis. Kidney International, 2009, 75, 415-419.	5.2	35
75	Mapping Genes for Common Diseases: The Case for Genetic (LD) Maps. Human Heredity, 2004, 58, 2-9.	0.8	34
76	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.	7.2	34
77	Influence of TNFÎ± and LTÎ± single nucleotide polymorphisms on susceptibility to and prognosis in cutaneous malignant melanoma in the British population. International Journal of Immunogenetics, 2002, 29, 17-23.	1.2	33
78	Linkage disequilibrium analysis of caseâ€“control data: an application to generalized aggressive periodontitis. Genes and Immunity, 2005, 6, 44-52.	4.1	32
79	The genetics of breast cancer: risk factors for disease. The Application of Clinical Genetics, 2011, 4, 11.	3.0	32
80	Non-coding NOTCH1 mutations in chronic lymphocytic leukemia; their clinical impact in the UK CLL4 trial. Leukemia, 2017, 31, 510-514.	7.2	31
81	Integration of Gene Maps: Chromosome X. Genomics, 1994, 22, 590-604.	2.9	30
82	The origin of trisomy 13. American Journal of Medical Genetics, Part A, 2007, 143A, 2242-2248.	1.2	30
83	Exploiting large scale computing to construct high resolution linkage disequilibrium maps of the human genome. Bioinformatics, 2007, 23, 517-519.	4.1	27
84	Exclusion from proximal 11q of a common gene with megaphenic effect on atopy. Annals of Human Genetics, 1995, 59, 403-411.	0.8	26
85	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, 350-358.	4.1	26
86	Evaluating phenotype-driven approaches for genetic diagnoses from exomes in a clinical setting. Scientific Reports, 2017, 7, 13509.	3.3	26
87	Determination of a gene and environment risk model for age-related macular degeneration. British Journal of Ophthalmology, 2010, 94, 1382-1387.	3.9	25
88	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. Blood Advances, 2019, 3, 2474-2481.	5.2	25
89	CEPH Consortium Map of Chromosome 9. Genomics, 1994, 19, 203-214.	2.9	24
90	Complex Segregation Analysis in a Sample of Consecutive Newborns with Cleft Lip with or without Cleft Palate in Italy. Human Heredity, 1995, 45, 157-164.	0.8	24

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91	A novel approach for identifying candidate imprinted genes through sequence analysis of imprinted and control genes. Human Genetics, 2002, 111, 511-520.	3.8	24
92	Predicting Pancreatic Cancer in the UK Biobank Cohort Using Polygenic Risk Scores and Diabetes Mellitus. Gastroenterology, 2022, 162, 1665-1674.e2.	1.3	24
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, 275-295.	0.8	23
94	Trials of the beta model for complex inheritance.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 9177-9181.	7.1	23
95	Nonparametric Tests for Linkage with Dependent Sib Pairs. Human Heredity, 1995, 45, 311-318.	0.8	22
96	Commercial chicken breeds exhibit highly divergent patterns of linkage disequilibrium. Heredity, 2016, 117, 375-382.	2.6	21
97	Megalencephaly Syndromes: Exome Pipeline Strategies for Detecting Low-Level Mosaic Mutations. PLoS ONE, 2014, 9, e86940.	2.5	20
98	Genetic epidemiology of early onset breast cancer.. Journal of Medical Genetics, 1994, 31, 944-949.	3.2	19
99	Allelic Association: Linkage Disequilibrium Structure and Gene Mapping. Molecular Biotechnology, 2009, 41, 83-89.	2.4	19
100	The interleukinâ€1 cluster gene region is associated with multiple sclerosis in an Italian Caucasian population. European Journal of Neurology, 2010, 17, 930-938.	3.3	19
101	Exome sequencing in tracking clonal evolution in multiple myeloma following therapy. Leukemia, 2013, 27, 1188-1191.	7.2	19
102	Deleterious coding variants in multi-case families with non-syndromic cleft lip and/or palate phenotypes. Scientific Reports, 2016, 6, 30457.	3.3	19
103	Combined segregation and linkage analysis of nonsyndromic orofacial cleft in two candidate regions. Annals of Human Genetics, 1999, 63, 17-25.	0.8	18
104	Combined segregation and linkage analysis of inflammatory bowel disease in the IBD1 region using severity to characterise Crohn's disease and ulcerative colitis. European Journal of Human Genetics, 2000, 8, 846-852.	2.8	18
105	Fine-scale linkage disequilibrium mapping of age-related macular degeneration in the complement factor H gene region. British Journal of Ophthalmology, 2007, 91, 966-970.	3.9	18
106	Quantitated transcript haplotypes (QTH) ofAGTR1, reduced abundance of mRNA haplotypes containing 1166C (rs5186:A>C), and relevance to metabolic syndrome traits. Human Mutation, 2007, 28, 365-373.	2.5	18
107	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	12.8	18
108	Sequencing era methods for identifying signatures of selection in the genome. Briefings in Bioinformatics, 2019, 20, 1997-2008.	6.5	18

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109	A Sequence-Based Integrated Map of Chromosome 22. Genome Research, 2001, 11, 1290-1295.	5.5	17
110	Refined Association Mapping for a Quantitative Trait: Weight in the H19-IGF2-INS-TH Region. Annals of Human Genetics, 2006, 70, 848-856.	0.8	17
111	Genome Scanning by Composite Likelihood. American Journal of Human Genetics, 2007, 80, 19-28.	6.2	17
112	Effects of single SNPs, haplotypes, and whole-genome LD maps on accuracy of association mapping. Genetic Epidemiology, 2007, 31, 179-188.	1.3	17
113	A comparative location database (CompLDB): map integration within and between species. Mammalian Genome, 2007, 18, 287-299.	2.2	17
114	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.	2.5	17
115	Machine Learning Approaches: Data Integration for Disease Prediction and Prognosis. Translational Bioinformatics, 2018, , 137-141.	0.0	16
116	Studies on locus content mapping.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 11814-11818.	7.1	15
117	Variation in complement component C1 inhibitor in age-related macular degeneration. Immunobiology, 2012, 217, 251-255.	1.9	15
118	Exome-based linkage disequilibrium maps of individual genes: functional clustering and relationship to disease. Human Genetics, 2013, 132, 233-243.	3.8	15
119	Whole genome sequences are required to fully resolve the linkage disequilibrium structure of human populations. BMC Genomics, 2015, 16, 666.	2.8	14
120	Resolving clinical diagnoses for syndromic cleft lip and/or palate phenotypes using wholeâ€exome sequencing. Clinical Genetics, 2015, 88, 441-449.	2.0	14
121	Support Vector Machine Classifier for Estrogen Receptor Positive and Negative Early-Onset Breast Cancer. PLoS ONE, 2013, 8, e68606.	2.5	13
122	Statistical and genetic aspects of quality control for DNA identification. Electrophoresis, 1995, 16, 1670-1677.	2.4	12
123	Evolutionary dynamics of the FMR1 locus. Annals of Human Genetics, 1995, 59, 283-289.	0.8	12
124	An integrated map of chromosome 9. Annals of Human Genetics, 1995, 59, 393-402.	0.8	11
125	CHROMSCAN: genome-wide association using a linkage disequilibrium map. Journal of Human Genetics, 2008, 53, 121-126.	2.3	11
126	Linkage disequilibrium maps for European and African populations constructed from whole genome sequence data. Scientific Data, 2019, 6, 208.	5.3	11

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127	Understanding the disease genome: gene essentiality and the interplay of selection, recombination and mutation. Briefings in Bioinformatics, 2019, 20, 267-273.	6.5	11
128	LDMAP. Methods in Molecular Biology, 2007, 376, 47-57.	0.9	11
129	A Tournament of Linkage Tests in Complex Inheritance. Human Heredity, 2001, 52, 140-148.	0.8	10
130	Recombination, interference and sequence: comparison of chromosomes 21 and 22. Annals of Human Genetics, 2002, 66, 75-86.	0.8	10
131	MaGIC: a program to generate targeted marker sets for genome-wide association studies. BioTechniques, 2004, 37, 996-999.	1.8	10
132	Cosmopolitan linkage disequilibrium maps. Human Genomics, 2005, 2, 20.	2.9	10
133	Segregation Analysis of Colorectal Cancer in Northern Ireland. Human Heredity, 1995, 45, 41-48.	0.8	9
134	Mapping in the Sequencing Era. Human Heredity, 2000, 50, 76-84.	0.8	9
135	Counting algorithms for linkage. Annals of Human Genetics, 1990, 54, 103-106.	0.8	8
136	Integration of gene maps: updating chromosome 1. Annals of Human Genetics, 1995, 59, 291-305.	0.8	8
137	PCR designer for restriction analysis of various types of sequence mutation. Bioinformatics, 2002, 18, 1688-1689.	4.1	8
138	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.	2.7	8
139	Approaches to the identification of susceptibility genes. Parasite Immunology, 2009, 31, 225-233.	1.5	8
140	The genomic and functional characteristics of disease genes. Briefings in Bioinformatics, 2015, 16, 16-23.	6.5	8
141	Significance of maximal lods. Annals of Human Genetics, 1991, 55, 39-41.	0.8	7
142	Limb Girdle Muscular Dystrophy Type 2A (CAPN3): Mapping Using Allelic Association. Human Heredity, 1998, 48, 333-337.	0.8	7
143	Combined segregation and linkage analysis of 59ÂHodgkin's disease families indicates the role of HLA determinants. European Journal of Human Genetics, 2000, 8, 460-463.	2.8	7
144	Allelic association and disease mapping. Briefings in Bioinformatics, 2001, 2, 375-387.	6.5	7

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145	A Comparison of Methods to Detect Recombination Hotspots. Human Heredity, 2008, 66, 157-169.	0.8	7
146	Mapping a gene for rheumatoid arthritis on chromosome 18q21. BMC Proceedings, 2007, 1, S18.	1.6	6
147	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, 2592-2597.	7.1	6
148	Genome-wide association of breast cancer: composite likelihood with imputed genotypes. European Journal of Human Genetics, 2011, 19, 194-199.	2.8	6
149	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.	2.7	6
150	Linkage Disequilibrium and Association Mapping. Methods in Molecular Biology, 2007, 376, 1-15.	0.9	6
151	Integrated genetic map of human chromosome 2. Annals of Human Genetics, 1995, 59, 413-434.	0.8	5
152	Composite likelihood-based meta-analysis of breast cancer association studies. Journal of Human Genetics, 2011, 56, 377-382.	2.3	5
153	Linkage disequilibrium maps to guide contig ordering for genome assembly. Bioinformatics, 2019, 35, 541-545.	4.1	5
154	Clinical and Descriptive Study of Orofacial Clefts in Colombia: 2069 Patients From Operation Smile Foundation. Cleft Palate-Craniofacial Journal, 2022, 59, 200-208.	0.9	5
155	Combination of Linkage Evidence in Complex Inheritance. Human Heredity, 2001, 52, 132-135.	0.8	4
156	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.	0.8	4
157	EFFECT OF THE PEROXISOME PROLIFERATORS-ACTIVATED RECEPTOR (PPAR) GAMMA 3 GENE ON BMI IN 1,210 SCHOOL STUDENTS FROM MORELOS, MEXICO. , 2005, , .		4
158	The Challenge of Genome Sequence Assembly. Open Bioinformatics Journal, 2018, 11, 231-239.	1.0	4
159	Aarskog-Scott syndrome: phenotypic and genetic heterogeneity. AIMS Genetics, 2016, 03, 049-059.	1.9	4
160	Coding of pointers in the segregation analysis program POINTER. Genetic Epidemiology, 1994, 11, 385-387.	1.3	3
161	The impact of redefining affection status for alcoholism on affectedâ€sibâ€pair analysis. Genetic Epidemiology, 1999, 17, S151-6.	1.3	3
162	Individual disease risk and multimetric analysis of Crohn disease. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15843-15847.	7.1	3

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163	Gene-dense autosomal chromosomes show evidence for increased selection. Heredity, 2019, 123, 774-783.	2.6	3
164	Essentiality-specific pathogenicity prioritization gene score to improve filtering of disease sequence data. Briefings in Bioinformatics, 2021, 22, 1782-1789.	6.5	3
165	Mapping quantitative effects of oligogenes by allelic association. Annals of Human Genetics, 2002, 66, 211-21.	0.8	3
166	The future of gene mapping. Genetic Analysis, Techniques and Applications, 1997, 14, 25-27.	1.5	2
167	A two-locus model for hereditary non-polyposis colorectal cancer in Modena, Italy. Annals of Human Genetics, 1997, 61, 109-119.	0.8	2
168	The power and statistical behaviour of allele-sharing statistics when applied to models with two disease loci. Journal of Genetics, 2002, 81, 99-103.	0.7	2
169	Genome Variation: A Review of Web Resources. Methods in Molecular Biology, 2011, 713, 129-139.	0.9	2
170	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.	2.8	2
171	Quantifying the cumulative effect of lowâ€penetrance genetic variants on breast cancer risk. Molecular Genetics & Genomic Medicine, 2015, 3, 182-188.	1.2	1
172	Single-cell exomes in an index case of amp1q21 multiple myeloma reveal more diverse mutanomes than the whole population. Blood, 2018, 132, 232-235.	1.4	1
173	Deletion Size Influences Clinical Outcome In Patients with Chronic Lymphocytic Leukemia; 13q Deletion Anatomy, Cooperating Lesions and Cancer Pathogenesis. Blood, 2010, 116, 757-757.	1.4	1
174	The Correlation Between Deletion Architecture, ATM Mutational Status and BIRC3 Disruption in 11q-Deleted CLL. Blood, 2012, 120, 658-658.	1.4	1
175	Deep-Sequencing Reveals the Molecular Landscape of Splenic Marginal Zone Lymphoma: Biological and Clinical Implications. Blood, 2014, 124, 76-76.	1.4	1
176	An evaluation of affectedâ€sibâ€pair methods and transmission/disequilibrium tests for detecting genes underlying a complex trait. Genetic Epidemiology, 1999, 17, S727-30.	1.3	0
177	Creating LD maps of the genome. , 2005, , .		0
178	Linkage disequilibrium in maps of SNPs and other markers. GeneScreen, 2008, 1, 59-61.	0.6	0
179	Genetic variants within chromosome 4q28.3 are not reproducibly associated with Age-related Macular Degeneration (AMD). Acta Ophthalmologica, 2011, 89, e603-e604.	1.1	0
180	Analytical Approaches for Exome Sequence Data. Translational Bioinformatics, 2018, , 121-136.	0.0	0

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181	Development of V617F JAK2 Associated Myeloproliferative Neoplasms Is a Non-Random Event That Is Strongly Dependent on JAK2 Haplotype. Blood, 2008, 112, 173-173.	1.4	0
182	Single Cell Whole Exome Sequencing in an Index Case of Amp1q21 Multiple Myeloma to Define Intraclonal Variation. Blood, 2016, 128, 5651-5651.	1.4	0
183	Abstract 3306: The clinical importance of DNA methylation signatures in chronic lymphocytic leukemia patients treated with chemo-immunotherapy. , 2018, , .		0
184	zalpha: an R package for the identification of regions of the genome under selection. Journal of Open Source Software, 2020, 5, 2638.	4.6	0