Xiaoming Liu

List of Publications by Year
in descending order

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		18482	5120
168	45,567	62	166
papers	citations	h-index	g-index

192	192	192	67300
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	Clinical Whole-Exome Sequencing for the Diagnosis of Mendelian Disorders. New England Journal of Medicine, 2013, 369, 1502-1511.	27.0	1,717
4	Expansion of an unstable trinucleotide CAG repeat in spinocerebellar ataxia type 1. Nature Genetics, 1993, 4, 221-226.	21.4	1,673
5	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	12.6	1,535
6	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	8.1	1,219
7	Molecular Findings Among Patients Referred for Clinical Whole-Exome Sequencing. JAMA - Journal of the American Medical Association, 2014, 312, 1870.	7.4	1,171
8	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
9	High-throughput discovery of novel developmental phenotypes. Nature, 2016, 537, 508-514.	27.8	1,001
10	Comparison and integration of deleteriousness prediction methods for nonsynonymous SNVs in whole exome sequencing studies. Human Molecular Genetics, 2015, 24, 2125-2137.	2.9	892
11	dbNSFP v3.0: A One-Stop Database of Functional Predictions and Annotations for Human Nonsynonymous and Splice-Site SNVs. Human Mutation, 2016, 37, 235-241.	2.5	845
12	De novo truncating mutations in E6-AP ubiquitin-protein ligase gene (UBE3A) in Angelman syndrome. Nature Genetics, 1997, 15, 74-77.	21.4	801
13	dbNSFP: A lightweight database of human nonsynonymous SNPs and their functional predictions. Human Mutation, 2011, 32, 894-899.	2.5	706
14	Genomic DNA transfer with a high-capacity adenovirus vector results in improved in vivo gene expression and decreased toxicity. Nature Genetics, 1998, 18, 180-183.	21.4	641
15	Resolution of Disease Phenotypes Resulting from Multilocus Genomic Variation. New England Journal of Medicine, 2017, 376, 21-31.	27.0	565
16	dbNSFP v2.0: A Database of Human Non-synonymous SNVs and Their Functional Predictions and Annotations. Human Mutation, 2013, 34, E2393-E2402.	2.5	546
17	Imprinted expression of the murine Angelman syndrome gene, Ube3a, in hippocampal and Purkinje neurons. Nature Genetics, 1997, 17, 75-78.	21.4	466
18	Towards a therapy for Angelman syndrome by targeting a long non-coding RNA. Nature, 2015, 518, 409-412.	27.8	423

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19	Deletions of a differentially methylated CpG island at the SNRPN gene define a putative imprinting control region. Nature Genetics, 1994, 8, 52-58.	21.4	418
20	In silico prediction of splice-altering single nucleotide variants in the human genome. Nucleic Acids Research, 2014, 42, 13534-13544.	14.5	396
21	A suggested nomenclature for designating mutations. Human Mutation, 1993, 2, 245-248.	2.5	354
22	Use of Exome Sequencing for Infants in Intensive Care Units. JAMA Pediatrics, 2017, 171, e173438.	6.2	348
23	Exploring population size changes using SNP frequency spectra. Nature Genetics, 2015, 47, 555-559.	21.4	332
24	dbNSFP v4: a comprehensive database of transcript-specific functional predictions and annotations for human nonsynonymous and splice-site SNVs. Genome Medicine, 2020, 12, 103.	8.2	300
25	Genome-wide scan for familial nasopharyngeal carcinoma reveals evidence of linkage to chromosome 4. Nature Genetics, 2002, 31, 395-399.	21.4	217
26	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	21.4	216
27	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. Nature Communications, 2010, 1, 131.	12.8	213
28	Reanalysis of Clinical Exome Sequencing Data. New England Journal of Medicine, 2019, 380, 2478-2480.	27.0	205
29	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	12.8	200
30	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
31	Molecular diagnostic experience of whole-exome sequencing in adult patients. Genetics in Medicine, 2016, 18, 678-685.	2.4	186
32	Lessons learned from additional research analyses of unsolved clinical exome cases. Genome Medicine, 2017, 9, 26.	8.2	184
33	Epigenetics and Human Disease. Cold Spring Harbor Perspectives in Biology, 2016, 8, a019497.	5.5	177
34	Untargeted metabolomic analysis for the clinical screening of inborn errors of metabolism. Journal of Inherited Metabolic Disease, 2015, 38, 1029-1039.	3.6	169
35	A Genome-wide Association Study of Autism Using the Simons Simplex Collection: Does Reducing Phenotypic Heterogeneity in Autism Increase Genetic Homogeneity?. Biological Psychiatry, 2015, 77, 775-784.	1.3	133
36	Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	21.4	132

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37	Array-Based DNA Diagnostics: Let the Revolution Begin. Annual Review of Medicine, 2008, 59, 113-129.	12.2	131
38	Spinocerebellar ataxia: Variable age of onset and linkage to human leukocyte antigen in a large kindred. Annals of Neurology, 1988, 23, 580-584.	5.3	126
39	Diagnostic Utility of Genome-wide DNA Methylation Testing in Genetically Unsolved Individuals with Suspected Hereditary Conditions. American Journal of Human Genetics, 2019, 104, 685-700.	6.2	125
40	Stairway Plot 2: demographic history inference with folded SNP frequency spectra. Genome Biology, 2020, 21, 280.	8.8	125
41	Truncation of Ube3a-ATS Unsilences Paternal Ube3a and Ameliorates Behavioral Defects in the Angelman Syndrome Mouse Model. PLoS Genetics, 2013, 9, e1004039.	3.5	124
42	In silico tools for splicing defect prediction: a survey from the viewpoint of end users. Genetics in Medicine, 2014, 16, 497-503.	2.4	124
43	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. Nature Communications, 2017, 8, 886.	12.8	116
44	Combined array CGH plus SNP genome analyses in a single assay for optimized clinical testing. European Journal of Human Genetics, 2014, 22, 79-87.	2.8	112
45	Absence of P-Selectin, but Not Intercellular Adhesion Molecule-1, Attenuates Neointimal Growth After Arterial Injury in Apolipoprotein Eâ€“Deficient Mice. Circulation, 2001, 103, 1000-1005.	1.6	108
46	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
47	The population genomics of rhesus macaques (Macaca mulatta) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	5.5	101
48	Homozygous and hemizygous CNV detection from exome sequencing data in a Mendelian disease cohort. Nucleic Acids Research, 2017, 45, gkw1237.	14.5	98
49	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	3.2	96
50	The SNRPN promoter is not required for genomic imprinting of the Prader-Willi/Angelman domain in mice. Nature Genetics, 2001, 28, 232-240.	21.4	95
51	Climate-driven range shifts of the king penguin in a fragmented ecosystem. Nature Climate Change, 2018, 8, 245-251.	18.8	95
52	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
53	Mutations in PURA Cause Profound Neonatal Hypotonia, Seizures, and Encephalopathy in 5q31.3 Microdeletion Syndrome. American Journal of Human Genetics, 2014, 95, 579-583.	6.2	92
54	Validation studies of SNRPN methylation as a diagnostic test for Prader-Willi syndrome. , 1996, 66, 77-80.		87

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55	Necdin-deficient mice do not show lethality or the obesity and infertility of Prader-Willi syndrome. Nature Genetics, 1999, 22, 15-16.	21.4	81
56	Evidence for feasibility of fetal trophoblastic cellâ€based noninvasive prenatal testing. Prenatal Diagnosis, 2016, 36, 1009-1019.	2.3	78
57	Polygenic Scores for Major Depressive Disorder and Risk of Alcohol Dependence. JAMA Psychiatry, 2017, 74, 1153.	11.0	73
58	Integrating GWASs and Human Protein Interaction Networks Identifies a Gene Subnetwork Underlying Alcohol Dependence. American Journal of Human Genetics, 2013, 93, 1027-1034.	6.2	72
59	The next generation of population-based spinal muscular atrophy carrier screening: comprehensive pan-ethnic SMN1 copy-number and sequence variant analysis by massively parallel sequencing. Genetics in Medicine, 2017, 19, 936-944.	2.4	70
60	Genome-wide copy number analysis on DNA from fetal cells isolated from the blood of pregnant women. Prenatal Diagnosis, 2016, 36, 1127-1134.	2.3	68
61	The Utility of Chromosomal Microarray Analysis in Developmental and Behavioral Pediatrics. Child Development, 2013, 84, 121-132.	3.0	67
62	Loss-of-Function Variants in MYLK Cause Recessive Megacystis Microcolon Intestinal Hypoperistalsis Syndrome. American Journal of Human Genetics, 2017, 101, 123-129.	6.2	67
63	Evidence for Recombination in Mycobacterium tuberculosis. Journal of Bacteriology, 2006, 188, 8169-8177.	2.2	66
64	De Novo GMNN Mutations Cause Autosomal-Dominant Primordial Dwarfism Associated with Meier-Gorlin Syndrome. American Journal of Human Genetics, 2015, 97, 904-913.	6.2	65
65	Allelic loss and gain, but not genomic instability, as the major somatic mutation in primary hepatocellular carcinoma. Genes Chromosomes and Cancer, 2001, 31, 221-227.	2.8	64
66	Comparative analysis of single-stranded DNA donors to generate conditional null mouse alleles. BMC Biology, 2018, 16, 69.	3.8	64
67	Human and mouse essentiality screens as a resource for disease gene discovery. Nature Communications, 2020, 11, 655.	12.8	64
68	A resource of targeted mutant mouse lines for 5,061 genes. Nature Genetics, 2021, 53, 416-419.	21.4	60
69	The Perlman familial nephroblastomatosis syndrome. American Journal of Medical Genetics Part A, 1986, 24, 101-110.	2.4	59
70	A Rheostat Model for a Rapid and Reversible Form of Imprinting-Dependent Evolution. American Journal of Human Genetics, 2002, 70, 1389-1397.	6.2	58
71	Neonatal diabetes, gallbladder agenesis, duodenal atresia, and intestinal malrotation caused by a novel homozygous mutation inRFX6. Pediatric Diabetes, 2014, 15, 67-72.	2.9	57
72	De Novo Truncating Mutations in AHDC1 in Individuals with Syndromic Expressive Language Delay, Hypotonia, and Sleep Apnea. American Journal of Human Genetics, 2014, 94, 784-789.	6.2	57

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73	Arginase deficiency in multiple tissues in argininemia. Clinical Genetics, 1978, 13, 61-67.	2.0	53
74	Practical Approaches for Whole-Genome Sequence Analysis of Heart- and Blood-Related Traits. American Journal of Human Genetics, 2017, 100, 205-215.	6.2	50
75	Identification of novel candidate disease genes from de novo exonic copy number variants. Genome Medicine, 2017, 9, 83.	8.2	50
76	Analysis of loss-of-function variants and 20 risk factor phenotypes in 8,554 individuals identifies loci influencing chronic disease. Nature Genetics, 2015, 47, 640-642.	21.4	49
77	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. Genome Biology, 2019, 20, 143.	8.8	48
78	Validation Studies for Single Circulating Trophoblast Genetic Testing as a Form of Noninvasive Prenatal Diagnosis. American Journal of Human Genetics, 2019, 105, 1262-1273.	6.2	47
79	iCAGES: integrated CAncer GEnome Score for comprehensively prioritizing driver genes in personal cancer genomes. Genome Medicine, 2016, 8, 135.	8.2	45
80	Three-dimensional microCT imaging of mouse development from early post-implantation to early postnatal stages. Developmental Biology, 2016, 419, 229-236.	2.0	43
81	Abnormal mRNA for argininosuccinate synthetase in citrullinaemia. Nature, 1983, 301, 533-534.	27.8	42
82	Copy number variant and runs of homozygosity detection by microarrays enabled more precise molecular diagnoses in 11,020 clinical exome cases. Genome Medicine, 2019, 11, 30.	8.2	42
83	Identification of genes required for eye development by high-throughput screening of mouse knockouts. Communications Biology, 2018, 1, 236.	4.4	37
84	CNVs cause autosomal recessive genetic diseases with or without involvement of SNV/indels. Genetics in Medicine, 2020, 22, 1633-1641.	2.4	36
85	Brain carnitine deficiency causes nonsyndromic autism with an extreme male bias: A hypothesis. BioEssays, 2017, 39, 1700012.	2.5	35
86	Combinatorial requirements for adhesion molecules in mediating neutrophil emigration during bacterial peritonitis in mice. Journal of Leukocyte Biology, 1998, 64, 291-297.	3.3	31
87	The Deep Genome Project. Genome Biology, 2020, 21, 18.	8.8	30
88	Rapid and Integrative Discovery of Retina Regulatory Molecules. Cell Reports, 2018, 24, 2506-2519.	6.4	28
89	Prenatal diagnosis of citrullinaemia: Review of a 10-year experience including recent use of DNA analysis. Prenatal Diagnosis, 1990, 10, 771-779.	2.3	27
90	Role of <scp>WNT</scp>10A in failure of tooth development in humans and zebrafish. Molecular Genetics & Genomic Medicine, 2017, 5, 730-741.	1.2	27

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91	Bi-allelic Variants in TONSL Cause SPONASTRIME Dysplasia and a Spectrum of Skeletal Dysplasia Phenotypes. American Journal of Human Genetics, 2019, 104, 422-438.	6.2	27
92	Recurrent arginine substitutions in the ACTG2 gene are the primary driver of disease burden and severity in visceral myopathy. Human Mutation, 2020, 41, 641-654.	2.5	27
93	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. Human Molecular Genetics, 2017, 26, 3442-3450.	2.9	25
94	FOXP3 mutations causing earlyâ€onset insulinâ€requiring diabetes but without other features of immune dysregulation, polyendocrinopathy, enteropathy, Xâ€linked syndrome. Pediatric Diabetes, 2018, 19, 388-392.	2.9	25
95	Is medical genetics neglecting epigenetics?. Genetics in Medicine, 2002, 4, 399-402.	2.4	24
96	Gene-Specific Function Prediction for Non-Synonymous Mutations in Monogenic Diabetes Genes. PLoS ONE, 2014, 9, e104452.	2.5	23
97	Atypical presentation and neuropathological studies in 3-hydroxy-3-methylglutaryl-CoA lyase deficiency. Annals of Neurology, 1986, 20, 367-369.	5.3	22
98	Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics. BMC Genomics, 2019, 20, 79.	2.8	22
99	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
100	Universal Prenatal Chromosomal Microarray Analysis: Additive Value and Clinical Dilemmas in Fetuses with a Normal Karyotype. American Journal of Perinatology, 2017, 34, 340-348.	1.4	21
101	Detection of Fabry's disease heterozygotes by hair root analysis. Clinical Genetics, 1978, 13, 251-258.	2.0	20
102	Ethical issues raised by common copy number variants and single nucleotide polymorphisms of certain and uncertain significance in general medical practice. Genome Medicine, 2010, 2, 42.	8.2	20
103	Preventable Forms of Autism?. Science, 2012, 338, 342-343.	12.6	20
104	Incorporating predicted functions of nonsynonymous variants into gene-based analysis of exome sequencing data: a comparative study. BMC Proceedings, 2011, 5, S20.	1.6	18
105	Identification of Common Prognostic Gene Expression Signatures with Biological Meanings from Microarray Gene Expression Datasets. PLoS ONE, 2012, 7, e45894.	2.5	18
106	Sequencing of 2 Subclinical Atherosclerosis Candidate Regions in 3669 Individuals. Circulation: Cardiovascular Genetics, 2014, 7, 359-364.	5.1	18
107	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
108	Colorectal Cancer-Associated Genes Are Associated with Tooth Agenesis and May Have a Role in Tooth Development. Scientific Reports, 2018, 8, 2979.	3.3	18

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109	Pharmacogenomics of statin-related myopathy: Meta-analysis of rare variants from whole-exome sequencing. PLoS ONE, 2019, 14, e0218115.	2.5	18
110	Whole genome sequence analysis of serum amino acid levels. Genome Biology, 2016, 17, 237.	8.8	17
111	In Silico Prediction of Deleteriousness for Nonsynonymous and Splice-Altering Single Nucleotide Variants in the Human Genome. Methods in Molecular Biology, 2017, 1498, 191-197.	0.9	17
112	SARS-COV-2 as potential microRNA sponge in COVID-19 patients. BMC Medical Genomics, 2022, 15, 94.	1.5	17
113	Estimating population genetic parameters and comparing model goodness-of-fit using DNA sequences with error. Genome Research, 2010, 20, 101-109.	5.5	16
114	The performance of deleteriousness prediction scores for rare non-protein-changing single nucleotide variants in human genes. Journal of Medical Genetics, 2017, 54, 134-144.	3.2	16
115	Simulating Sequences of the Human Genome with Rare Variants. Human Heredity, 2010, 70, 287-291.	0.8	15
116	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	6.1	14
117	Simultaneous analysis of mutant and normal alleles for multiple cystic fibrosis mutations by the ligase chain reaction. Human Mutation, 1995, 6, 144-151.	2.5	13
118	Genome annotation of disease-causing microorganisms. Briefings in Bioinformatics, 2021, 22, 845-854.	6.5	13
119	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644.	2.5	13
120	Cholesteryl Lignocerate Hydrolysis in Adrenoleukodystrophy. Pediatric Research, 1980, 14, 21-23.	2.3	12
121	Side Effects and Behavioral Outcomes Following High-Dose Carnitine Supplementation Among Young Males With Autism Spectrum Disorder: A Pilot Study. Global Pediatric Health, 2019, 6, 2333794X1983069.	0.7	12
122	Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes. BMC Medical Genomics, 2019, 12, 22.	1.5	12
123	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. BMC Biology, 2021, 19, 32.	3.8	12
124	FLAGS: A Flexible and Adaptive Association Test for Gene Sets Using Summary Statistics. Genetics, 2016, 202, 919-929.	2.9	11
125	dbMTS: A comprehensive database of putative human microRNA target site SNVs and their functional predictions. Human Mutation, 2020, 41, 1123-1130.	2.5	11
126	Iron Hack - A symposium/hackathon focused on porphyrias, Friedreichâ€™s ataxia, and other rare iron-related diseases. F1000Research, 2019, 8, 1135.	1.6	11

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127	Associations of NINJ2 Sequence Variants with Incident Ischemic Stroke in the Cohorts for Heart and Aging in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2014, 9, e99798.	2.5	11
128	Inferring Population Mutation Rate and Sequencing Error Rate Using the SNP Frequency Spectrum in a Sample of DNA Sequences. Molecular Biology and Evolution, 2009, 26, 1479-1490.	8.9	10
129	Identification of Rare Variants in Metabolites of the Carnitine Pathway by Whole Genome Sequencing Analysis. Genetic Epidemiology, 2016, 40, 486-491.	1.3	10
130	Glycogen storage disease: long-term follow-up of nocturnal intragastric feeding. Clinical Genetics, 2008, 21, 136-140.	2.0	9
131	Genetic variants in microRNA genes and targets associated with cardiovascular disease risk factors in the African-American population. Human Genetics, 2018, 137, 85-94.	3.8	9
132	Phenotypic association of 15q11.2 CNVs of the region of breakpoints 1â€“2 (BP1â€“BP2) in a large cohort of samples referred for genetic diagnosis. Journal of Human Genetics, 2019, 64, 253-255.	2.3	9
133	Epigenetics and Complex Human Disease: Is There a Role in IBD?. Journal of Pediatric Gastroenterology and Nutrition, 2008, 46, E2.	1.8	8
134	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics, 2018, 209, 607-616.	2.9	8
135	Human Prehistoric Demography Revealed by the Polymorphic Pattern of CpG Transitions. Molecular Biology and Evolution, 2020, 37, 2691-2698.	8.9	8
136	Repair of bleomycin-damaged DNA by human fibroblasts. Journal of Supramolecular Structure and Cellular Biochemistry, 1981, 16, 303-309.	1.4	7
137	A population genetics model of linkage disequilibrium in admixed populations. Science Bulletin, 2001, 46, 193-197.	1.7	7
138	Reduced meiotic recombination in rhesus macaques and the origin of the human recombination landscape. PLoS ONE, 2020, 15, e0236285.	2.5	7
139	Dynamics of Plasmodium vivax populations in border areas of the Greater Mekong sub-region during malaria elimination. Malaria Journal, 2020, 19, 145.	2.3	7
140	Identifying Putative Causal Links between MicroRNAs and Severe COVID-19 Using Mendelian Randomization. Cells, 2021, 10, 3504.	4.1	7
141	Translational signatures and mRNA levels are highly correlated in human stably expressed genes. BMC Genomics, 2013, 14, 268.	2.8	6
142	Chromosomal microarray analysis, or comparative genomic hybridization: A high throughput approach. MethodsX, 2016, 3, 8-18.	1.6	6
143	Structure of the murine E-selectin ligand 1 (ESL-1) gene and assignment to Chromosome 8. Mammalian Genome, 1999, 10, 1085-1088.	2.2	5
144	Allan Award Lecture: Rare Patients Leading to Epigenetics and Back to Genetics. American Journal of Human Genetics, 2008, 82, 1034-1038.	6.2	5

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145	Test of Genetical Isochronism for Longitudinal Samples of DNA Sequences. Genetics, 2007, 176, 327-342.	2.9	4
146	Algorithms to estimate the lower bounds of recombination with or without recurrent mutations. BMC Genomics, 2008, 9, S24.	2.8	4
147	Significantly fewer protein functional changing variants for lipid metabolism in Africans than in Europeans. Journal of Translational Medicine, 2013, 11, 67.	4.4	4
148	Global genetic carrier testing: a vision for the future. Genome Medicine, 2015, 7, 79.	8.2	4
149	Rate of decay in admixture linkage disequilibrium and its implication in gene mapping. Science Bulletin, 2001, 46, 358-363.	1.7	3
150	Age-of-onset of hypertension vs. a single measurement of systolic blood pressure in a combined linkage and segregation analysis. BMC Genetics, 2003, 4, S80.	2.7	3
151	jPopGen Suite: population genetic analysis of DNA polymorphism from nucleotide sequences with errors. Methods in Ecology and Evolution, 2012, 3, 624-627.	5.2	3
152	Darwin Comes to Clinic. Trends in Genetics, 2017, 33, 1-2.	6.7	3
153	Identification of MicroRNA-Related Tumorigenesis Variants and Genes in the Cancer Genome Atlas (TCGA) Data. Genes, 2020, 11, 953.	2.4	3
154	Smaller Genetic Risk in Catabolic Process Explains Lower Energy Expenditure, More Athletic Capability and Higher Prevalence of Obesity in Africans. PLoS ONE, 2011, 6, e26027.	2.5	3
155	Summary statistics of neutral mutations in longitudinal DNA samples. Theoretical Population Biology, 2008, 74, 56-67.	1.1	2
156	Ornithine transcarbamylase deficiency: longâ€term survival. Clinical Genetics, 1982, 22, 211-214.	2.0	2
157	Progress toward Noninvasive Prenatal Diagnosis. Clinical Chemistry, 2011, 57, 802-804.	3.2	2
158	MMiRNA-Viewer2, a bioinformatics tool for visualizing functional annotation for MiRNA and MRNA pairs in a network. BMC Bioinformatics, 2020, 21, 247.	2.6	2
159	Advantages of RT-PCR and denaturing gradient gel electrophoresis for analysis of genomic imprinting: Detection of new mouse and human expressed polymorphisms. , 1996, 7, 144-148.		1
160	The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications. BMC Bioinformatics, 2018, 19, 492.	2.6	1
161	False Alarms in Consumer Genomics Add to Public Fear and Potential Health Care Burden. Journal of Personalized Medicine, 2020, 10, 187.	2.5	1
162	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. Human Heredity, 2018, 83, 105-106.	0.8	0

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163	2017 Victor A. McKusick Leadership Award. American Journal of Human Genetics, 2018, 102, 361-363.	6.2	0
164	A Deep Learning Model for Ancestry Estimation with Craniometric Measurements. , 2021, , .		0
165	Title is missing!. , 2020, 15, e0236285.		0
166	Title is missing!. , 2020, 15, e0236285.		0
167	Title is missing!. , 2020, 15, e0236285.		0
168	Title is missing!. , 2020, 15, e0236285.		0