

Gerton Lunter

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

80
papers

26,944
citations

41
h-index

91
g-index

91
ext. papers

33,438
ext. citations

12.1
avg, IF

6.7
L-index

#	Paper	IF	Citations
80	A unified haplotype-based method for accurate and comprehensive variant calling. <i>Nature Biotechnology</i> , 2021 , 39, 885-892	44.5	13
79	Demographic inference from multiple whole genomes using a particle filter for continuous Markov jump processes. <i>PLoS ONE</i> , 2021 , 16, e0247647	3.7	1
78	Short and long-read genome sequencing methodologies for somatic variant detection; genomic analysis of a patient with diffuse large B-cell lymphoma. <i>Scientific Reports</i> , 2021 , 11, 6408	4.9	3
77	Multi Locus View: an extensible web-based tool for the analysis of genomic data. <i>Communications Biology</i> , 2021 , 4, 623	6.7	1
76	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	2
75	Inferring B cell specificity for vaccines using a Bayesian mixture model. <i>BMC Genomics</i> , 2020 , 21, 176	4.5	6
74	Efficient inference in state-space models through adaptive learning in online Monte Carlo expectation maximization. <i>Computational Statistics</i> , 2020 , 35, 1319-1344	1	
73	DeepC: predicting 3D genome folding using megabase-scale transfer learning. <i>Nature Methods</i> , 2020 , 17, 1118-1124	21.6	38
72	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019 , 10, 1869	17.4	89
71	Haplotype matching in large cohorts using the Li and Stephens model. <i>Bioinformatics</i> , 2019 , 35, 798-806	7.2	7
70	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 22664-22672	11.5	29
69	An equivariant Bayesian convolutional network predicts recombination hotspots and accurately resolves binding motifs. <i>Bioinformatics</i> , 2019 , 35, 2177-2184	7.2	5
68	A high throughput screen for active human transposable elements. <i>BMC Genomics</i> , 2018 , 19, 115	4.5	12
67	A Phylogenetic Codon Substitution Model for Antibody Lineages. <i>Genetics</i> , 2017 , 206, 417-427	4	36
66	OpEx - a validated, automated pipeline optimised for clinical exome sequence analysis. <i>Scientific Reports</i> , 2016 , 6, 31029	4.9	10
65	B-cell repertoire dynamics after sequential hepatitis B vaccination and evidence for cross-reactive B-cell activation. <i>Genome Medicine</i> , 2016 , 8, 68	14.4	42
64	The Diversity and Molecular Evolution of B-Cell Receptors during Infection. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1147-57	8.3	48

63	Accurate clinical detection of exon copy number variants in a targeted NGS panel using DECoN. <i>Wellcome Open Research</i> , 2016 , 1, 20	4.8	40
62	BCR repertoire sequencing: different patterns of B-cell activation after two Meningococcal vaccines. <i>Immunology and Cell Biology</i> , 2015 , 93, 885-95	5	62
61	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015 , 47, 717-726	36.3	244
60	Identification of antigen-specific B cell receptor sequences using public repertoire analysis. <i>Journal of Immunology</i> , 2015 , 194, 252-261	5.3	90
59	CSN and CAVA: variant annotation tools for rapid, robust next-generation sequencing analysis in the clinical setting. <i>Genome Medicine</i> , 2015 , 7, 76	14.4	41
58	High-throughput DNA Sequencing Identifies Novel Variants in Muscle-invasive Bladder Cancer Patients. <i>Bladder Cancer</i> , 2015 , 1, 31-44	1	1
57	In-Depth Assessment of Within-Individual and Inter-Individual Variation in the B Cell Receptor Repertoire. <i>Frontiers in Immunology</i> , 2015 , 6, 531	8.4	60
56	scrm: efficiently simulating long sequences using the approximated coalescent with recombination. <i>Bioinformatics</i> , 2015 , 31, 1680-2	7.2	72
55	Analysis of B Cell Repertoire Dynamics Following Hepatitis B Vaccination in Humans, and Enrichment of Vaccine-specific Antibody Sequences. <i>EBioMedicine</i> , 2015 , 2, 2070-9	8.8	61
54	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. <i>Nature Genetics</i> , 2014 , 46, 912-918	36.3	671
53	Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. <i>American Journal of Human Genetics</i> , 2014 , 94, 710-20	11	19
52	Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , 2014 , 99, e201-4	6.6	14
51	8.2% of the Human genome is constrained: variation in rates of turnover across functional element classes in the human lineage. <i>PLoS Genetics</i> , 2014 , 10, e1004525	6	124
50	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13127-32	11.5	121
49	Improved workflows for high throughput library preparation using the transposome-based Nextera system. <i>BMC Biotechnology</i> , 2013 , 13, 104	3.5	106
48	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013 , 23, 749-61	9.7	150
47	Unlocking the bottleneck in forward genetics using whole-genome sequencing and identity by descent to isolate causative mutations. <i>PLoS Genetics</i> , 2013 , 9, e1003219	6	37
46	GAT: a simulation framework for testing the association of genomic intervals. <i>Bioinformatics</i> , 2013 , 29, 2046-8	7.2	136

45	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , 2012 , 336, 193-8	33.3	218
44	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
43	The human pancreatic islet transcriptome: expression of candidate genes for type 1 diabetes and the impact of pro-inflammatory cytokines. <i>PLoS Genetics</i> , 2012 , 8, e1002552	6	313
42	A systematic survey of loss-of-function variants in human protein-coding genes. <i>Science</i> , 2012 , 335, 823-833	33.3	880
41	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012 , 486, 527-31	50.4	350
40	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75	50.4	517
39	A new isolation with migration model along complete genomes infers very different divergence processes among closely related great ape species. <i>PLoS Genetics</i> , 2012 , 8, e1003125	6	83
38	Recessive mutations in SPTBN2 implicate β III spectrin in both cognitive and motor development. <i>PLoS Genetics</i> , 2012 , 8, e1003074	6	74
37	Accurate reconstruction of insertion-deletion histories by statistical phylogenetics. <i>PLoS ONE</i> , 2012 , 7, e34572	3.7	23
36	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431
35	Dindel: accurate indel calls from short-read data. <i>Genome Research</i> , 2011 , 21, 961-73	9.7	341
34	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011 , 27, 2156-8	7.2	6200
33	Stampy: a statistical algorithm for sensitive and fast mapping of Illumina sequence reads. <i>Genome Research</i> , 2011 , 21, 936-9	9.7	832
32	Estimating divergence time and ancestral effective population size of Bornean and Sumatran orangutan subspecies using a coalescent hidden Markov model. <i>PLoS Genetics</i> , 2011 , 7, e1001319	6	69
31	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
30	Genome assembly quality: assessment and improvement using the neutral indel model. <i>Genome Research</i> , 2010 , 20, 675-84	9.7	39
29	Massive turnover of functional sequence in human and other mammalian genomes. <i>Genome Research</i> , 2010 , 20, 1335-43	9.7	76
28	Accelerated evolution of the Prdm9 speciation gene across diverse metazoan taxa. <i>PLoS Genetics</i> , 2009 , 5, e1000753	6	203

27	Genomic and transcriptional co-localization of protein-coding and long non-coding RNA pairs in the developing brain. <i>PLoS Genetics</i> , 2009 , 5, e1000617	6	305
26	Investigating selection on viruses: a statistical alignment approach. <i>BMC Bioinformatics</i> , 2008 , 9, 304	3.6	8
25	Uncertainty in homology inferences: assessing and improving genomic sequence alignment. <i>Genome Research</i> , 2008 , 18, 298-309	9.7	100
24	Evolution of primate gene expression: drift and corrective sweeps?. <i>Genetics</i> , 2008 , 180, 1379-89	4	14
23	Novel type IV secretion system involved in propagation of genomic islands. <i>Journal of Bacteriology</i> , 2007 , 189, 761-71	3.5	103
22	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. <i>Genome Research</i> , 2007 , 17, 556-65	9.7	530
21	Probabilistic whole-genome alignments reveal high indel rates in the human and mouse genomes. <i>Bioinformatics</i> , 2007 , 23, i289-96	7.2	49
20	HMMoC—a compiler for hidden Markov models. <i>Bioinformatics</i> , 2007 , 23, 2485-7	7.2	27
19	Dog as an outgroup to human and mouse. <i>PLoS Computational Biology</i> , 2007 , 3, e74	5	24
18	Genome-wide identification of human functional DNA using a neutral indel model. <i>PLoS Computational Biology</i> , 2006 , 2, e5	5	141
17	Signatures of adaptive evolution within human non-coding sequence. <i>Human Molecular Genetics</i> , 2006 , 15 Spec No 2, R170-5	5.6	35
16	Bayesian coestimation of phylogeny and sequence alignment. <i>BMC Bioinformatics</i> , 2005 , 6, 83	3.6	119
15	A nucleotide substitution model with nearest-neighbour interactions. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i216-23	7.2	56
14	A "Long Indel" model for evolutionary sequence alignment. <i>Molecular Biology and Evolution</i> , 2004 , 21, 529-40	8.3	91
13	An efficient algorithm for statistical multiple alignment on arbitrary phylogenetic trees. <i>Journal of Computational Biology</i> , 2003 , 10, 869-89	1.7	38
12	Resonances in a spring-pendulum: algorithms for equivariant singularity theory. <i>Nonlinearity</i> , 1998 , 11, 1569-1605	1.7	20
11	New Proofs and a Generalization of Inequalities of Fan, Taussky, and Todd. <i>Journal of Mathematical Analysis and Applications</i> , 1994 , 185, 464-476	1.1	4
10	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination		2

9	Fast haplotype matching in very large cohorts using the Li and Stephens model	4
8	Short and long-read genome sequencing methodologies for somatic variant detection; genomic analysis of a patient with diffuse large B-cell lymphoma	1
7	Ancient Admixture into Africa from the ancestors of non-Africans	1
6	Demographic inference using a particle filter for continuous Markov Jump processes	3
5	A unified haplotype-based method for accurate and comprehensive variant calling	4
4	Inferring B cell specificity for vaccines using a mixture model	2
3	DeepC: Predicting chromatin interactions using megabase scaled deep neural networks and transfer learning	10
2	An integrated platform to systematically identify causal variants and genes for polygenic human traits	8
1	Benchmarking small-variant genotyping in polyploids	1