Gerton Lunter

List of Publications by Citations

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	The variant call format and VCFtools. *Bioinformatics*, **2011**, 27, 2156-8	7.2	6200
79	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
78	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
77	A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **2012**, 335, 823-8	33.3	880
76	Stampy: a statistical algorithm for sensitive and fast mapping of Illumina sequence reads. *Genome Research*, **2011**, 21, 936-9	9.7	832
75	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. *Nature Genetics*, **2014**, 46, 912-918	36.3	671
74	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. *Genome Research*, **2007**, 17, 556-65	9.7	530
73	Insights into hominid evolution from the gorilla genome sequence. *Nature*, **2012**, 483, 169-75	50.4	517
72	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
71	The bonobo genome compared with the chimpanzee and human genomes. *Nature*, **2012**, 486, 527-31	50.4	350
70	Dindel: accurate indel calls from short-read data. *Genome Research*, **2011**, 21, 961-73	9.7	341
69	The human pancreatic islet transcriptome: expression of candidate genes for type 1 diabetes and the impact of pro-inflammatory cytokines. *PLoS Genetics*, **2012**, 8, e1002552	6	313
68	Genomic and transcriptional co-localization of protein-coding and long non-coding RNA pairs in the developing brain. *PLoS Genetics*, **2009**, 5, e1000617	6	305
67	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. *Nature Genetics*, **2015**, 47, 717-726	36.3	244
66	A fine-scale chimpanzee genetic map from population sequencing. *Science*, **2012**, 336, 193-8	33.3	218
65	Accelerated evolution of the Prdm9 speciation gene across diverse metazoan taxa. *PLoS Genetics*, **2009**, 5, e1000753	6	203
64	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. *Genome Research*, **2013**, 23, 749-61	9.7	150

63	Genome-wide identification of human functional DNA using a neutral indel model. *PLoS Computational Biology*, **2006**, 2, e5	5	141
62	GAT: a simulation framework for testing the association of genomic intervals. *Bioinformatics*, **2013**, 29, 2046-8	7.2	136
61	8.2% of the Human genome is constrained: variation in rates of turnover across functional element classes in the human lineage. *PLoS Genetics*, **2014**, 10, e1004525	6	124
60	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13127-32	11.5	121
59	Bayesian coestimation of phylogeny and sequence alignment. *BMC Bioinformatics*, **2005**, 6, 83	3.6	119
58	Improved workflows for high throughput library preparation using the transposome-based Nextera system. *BMC Biotechnology*, **2013**, 13, 104	3.5	106
57	Novel type IV secretion system involved in propagation of genomic islands. *Journal of Bacteriology*, **2007**, 189, 761-71	3.5	103
56	Uncertainty in homology inferences: assessing and improving genomic sequence alignment. *Genome Research*, **2008**, 18, 298-309	9.7	100
55	A "Long Indel" model for evolutionary sequence alignment. *Molecular Biology and Evolution*, **2004**, 21, 529-40	8.3	91
54	Identification of antigen-specific B cell receptor sequences using public repertoire analysis. *Journal of Immunology*, **2015**, 194, 252-261	5.3	90
53	Sequencing of human genomes with nanopore technology. *Nature Communications*, **2019**, 10, 1869	17.4	89
52	A new isolation with migration model along complete genomes infers very different divergence processes among closely related great ape species. *PLoS Genetics*, **2012**, 8, e1003125	6	83
51	Massive turnover of functional sequence in human and other mammalian genomes. *Genome Research*, **2010**, 20, 1335-43	9.7	76
50	Recessive mutations in SPTBN2 implicate βII spectrin in both cognitive and motor development. *PLoS Genetics*, **2012**, 8, e1003074	6	74
49	scrm: efficiently simulating long sequences using the approximated coalescent with recombination. *Bioinformatics*, **2015**, 31, 1680-2	7.2	72
48	Estimating divergence time and ancestral effective population size of Bornean and Sumatran orangutan subspecies using a coalescent hidden Markov model. *PLoS Genetics*, **2011**, 7, e1001319	6	69
47	BCR repertoire sequencing: different patterns of B-cell activation after two Meningococcal vaccines. *Immunology and Cell Biology*, **2015**, 93, 885-95	5	62
46	Analysis of B Cell Repertoire Dynamics Following Hepatitis B Vaccination in Humans, and Enrichment of Vaccine-specific Antibody Sequences. *EBioMedicine*, **2015**, 2, 2070-9	8.8	61

45	In-Depth Assessment of Within-Individual and Inter-Individual Variation in the B Cell Receptor Repertoire. *Frontiers in Immunology*, **2015**, 6, 531	8.4	60
44	A nucleotide substitution model with nearest-neighbour interactions. *Bioinformatics*, **2004**, 20 Suppl 1, i216-23	7.2	56
43	Probabilistic whole-genome alignments reveal high indel rates in the human and mouse genomes. *Bioinformatics*, **2007**, 23, i289-96	7.2	49
42	The Diversity and Molecular Evolution of B-Cell Receptors during Infection. *Molecular Biology and Evolution*, **2016**, 33, 1147-57	8.3	48
41	B-cell repertoire dynamics after sequential hepatitis B vaccination and evidence for cross-reactive B-cell activation. *Genome Medicine*, **2016**, 8, 68	14.4	42
40	CSN and CAVA: variant annotation tools for rapid, robust next-generation sequencing analysis in the clinical setting. *Genome Medicine*, **2015**, 7, 76	14.4	41
39	Accurate clinical detection of exon copy number variants in a targeted NGS panel using DECoN. *Wellcome Open Research*, **2016**, 1, 20	4.8	40
38	Genome assembly quality: assessment and improvement using the neutral indel model. *Genome Research*, **2010**, 20, 675-84	9.7	39
37	An efficient algorithm for statistical multiple alignment on arbitrary phylogenetic trees. *Journal of Computational Biology*, **2003**, 10, 869-89	1.7	38
36	DeepC: predicting 3D genome folding using megabase-scale transfer learning. *Nature Methods*, **2020**, 17, 1118-1124	21.6	38
35	Unlocking the bottleneck in forward genetics using whole-genome sequencing and identity by descent to isolate causative mutations. *PLoS Genetics*, **2013**, 9, e1003219	6	37
34	A Phylogenetic Codon Substitution Model for Antibody Lineages. *Genetics*, **2017**, 206, 417-427	4	36
33	Signatures of adaptive evolution within human non-coding sequence. *Human Molecular Genetics*, **2006**, 15 Spec No 2, R170-5	5.6	35
32	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 22664-22672	11.5	29
31	HMMoC--a compiler for hidden Markov models. *Bioinformatics*, **2007**, 23, 2485-7	7.2	27
30	Dog as an outgroup to human and mouse. *PLoS Computational Biology*, **2007**, 3, e74	5	24
29	Accurate reconstruction of insertion-deletion histories by statistical phylogenetics. *PLoS ONE*, **2012**, 7, e34572	3.7	23
28	Resonances in a spring-pendulum: algorithms for equivariant singularity theory. *Nonlinearity*, **1998**, 11, 1569-1605	1.7	20

27	Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. *American Journal of Human Genetics*, **2014**, 94, 710-20	11	19
26	Erythrocytosis associated with a novel missense mutation in the BPGM gene. *Haematologica*, **2014**, 99, e201-4	6.6	14
25	Evolution of primate gene expression: drift and corrective sweeps?. *Genetics*, **2008**, 180, 1379-89	4	14
24	A unified haplotype-based method for accurate and comprehensive variant calling. *Nature Biotechnology*, **2021**, 39, 885-892	44.5	13
23	A high throughput screen for active human transposable elements. *BMC Genomics*, **2018**, 19, 115	4.5	12
22	OpEx - a validated, automated pipeline optimised for clinical exome sequence analysis. *Scientific Reports*, **2016**, 6, 31029	4.9	10
21	DeepC: Predicting chromatin interactions using megabase scaled deep neural networks and transfer learning		10
20	Investigating selection on viruses: a statistical alignment approach. *BMC Bioinformatics*, **2008**, 9, 304	3.6	8
19	An integrated platform to systematically identify causal variants and genes for polygenic human traits		8
18	Haplotype matching in large cohorts using the Li and Stephens model. *Bioinformatics*, **2019**, 35, 798-806	7.2	7
17	Inferring B cell specificity for vaccines using a Bayesian mixture model. *BMC Genomics*, **2020**, 21, 176	4.5	6
16	An equivariant Bayesian convolutional network predicts recombination hotspots and accurately resolves binding motifs. *Bioinformatics*, **2019**, 35, 2177-2184	7.2	5
15	New Proofs and a Generalization of Inequalities of Fan, Taussky, and Todd. *Journal of Mathematical Analysis and Applications*, **1994**, 185, 464-476	1.1	4
14	Fast haplotype matching in very large cohorts using the Li and Stephens model		4
13	A unified haplotype-based method for accurate and comprehensive variant calling		4
12	Demographic inference using a particle filter for continuous Markov Jump processes		3
11	Short and long-read genome sequencing methodologies for somatic variant detection; genomic analysis of a patient with diffuse large B-cell lymphoma. *Scientific Reports*, **2021**, 11, 6408	4.9	3
10	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination		2

9	Inferring B cell specificity for vaccines using a mixture model		2
8	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. *Science Translational Medicine*, **2021**, 13,	17.5	2
7	High-throughput DNA Sequencing Identifies Novel Variants in Muscle-invasive Bladder Cancer Patients. *Bladder Cancer*, **2015**, 1, 31-44	1	1
6	Short and long-read genome sequencing methodologies for somatic variant detection; genomic analysis of a patient with diffuse large B-cell lymphoma		1
5	Ancient Admixture into Africa from the ancestors of non-Africans		1
4	Benchmarking small-variant genotyping in polyploids		1
3	Demographic inference from multiple whole genomes using a particle filter for continuous Markov jump processes. *PLoS ONE*, **2021**, 16, e0247647	3.7	1
2	Multi Locus View: an extensible web-based tool for the analysis of genomic data. *Communications Biology*, **2021**, 4, 623	6.7	1
1	Efficient inference in state-space models through adaptive learning in online Monte Carlo expectation maximization. *Computational Statistics*, **2020**, 35, 1319-1344	1	