

Gerton Lunter

List of Publications by Year in descending order

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74
papers

36,976
citations

57631

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79541

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docs citations

91
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60638
citing authors

#	ARTICLE	IF	CITATIONS
1	Respiratory Syncytial Virus, Human Metapneumovirus, and Parainfluenza Virus Infections in Lung Transplant Recipients: A Systematic Review of Outcomes and Treatment Strategies. <i>Clinical Infectious Diseases</i> , 2022, 74, 2252-2260.	2.9	14
2	Recurrence and survival after laparoscopy versus laparotomy without lymphadenectomy in early-stage endometrial cancer: Long-term outcomes of a randomised trial. <i>Gynecologic Oncology</i> , 2022, 164, 265-270.	0.6	18
3	Benchmarking small-variant genotyping in polyploids. <i>Genome Research</i> , 2022, 32, 403-408.	2.4	4
4	A unified haplotype-based method for accurate and comprehensive variant calling. <i>Nature Biotechnology</i> , 2021, 39, 885-892.	9.4	56
5	Demographic inference from multiple whole genomes using a particle filter for continuous Markov jump processes. <i>PLoS ONE</i> , 2021, 16, e0247647.	1.1	2
6	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.	1.6	14
7	Multi Locus View: an extensible web-based tool for the analysis of genomic data.. <i>Communications Biology</i> , 2021, 4, 623.	2.0	4
8	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	23
9	Efficient inference in state-space models through adaptive learning in online Monte Carlo expectation maximization. <i>Computational Statistics</i> , 2020, 35, 1319-1344.	0.8	0
10	DeepC: predicting 3D genome folding using megabase-scale transfer learning. <i>Nature Methods</i> , 2020, 17, 1118-1124.	9.0	109
11	Inferring B cell specificity for vaccines using a Bayesian mixture model. <i>BMC Genomics</i> , 2020, 21, 176.	1.2	8
12	Haplotype matching in large cohorts using the Li and Stephens model. <i>Bioinformatics</i> , 2019, 35, 798-806.	1.8	17
13	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019, 10, 1869.	5.8	140
14	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.	3.3	71
15	An equivariant Bayesian convolutional network predicts recombination hotspots and accurately resolves binding motifs. <i>Bioinformatics</i> , 2019, 35, 2177-2184.	1.8	10
16	A high throughput screen for active human transposable elements. <i>BMC Genomics</i> , 2018, 19, 115.	1.2	14
17	A Phylogenetic Codon Substitution Model for Antibody Lineages. <i>Genetics</i> , 2017, 206, 417-427.	1.2	56
18	Accurate clinical detection of exon copy number variants in a targeted NGS panel using DECoN. <i>Wellcome Open Research</i> , 2016, 1, 20.	0.9	79

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19	OpEx - a validated, automated pipeline optimised for clinical exome sequence analysis. <i>Scientific Reports</i> , 2016, 6, 31029.	1.6	10
20	B-cell repertoire dynamics after sequential hepatitis B vaccination and evidence for cross-reactive B-cell activation. <i>Genome Medicine</i> , 2016, 8, 68.	3.6	64
21	The Diversity and Molecular Evolution of B-Cell Receptors during Infection. <i>Molecular Biology and Evolution</i> , 2016, 33, 1147-1157.	3.5	72
22	CSN and CAVA: variant annotation tools for rapid, robust next-generation sequencing analysis in the clinical setting. <i>Genome Medicine</i> , 2015, 7, 76.	3.6	54
23	High-throughput DNA Sequencing Identifies Novel CtIP (RBBP8) Variants in Muscle-invasive Bladder Cancer Patients. <i>Bladder Cancer</i> , 2015, 1, 31-44.	0.2	2
24	In-Depth Assessment of Within-Individual and Inter-Individual Variation in the B Cell Receptor Repertoire. <i>Frontiers in Immunology</i> , 2015, 6, 531.	2.2	92
25	scrm: efficiently simulating long sequences using the approximated coalescent with recombination. <i>Bioinformatics</i> , 2015, 31, 1680-1682.	1.8	112
26	Analysis of B Cell Repertoire Dynamics Following Hepatitis B Vaccination in Humans, and Enrichment of Vaccine-specific Antibody Sequences. <i>EBioMedicine</i> , 2015, 2, 2070-2079.	2.7	92
27	BCR repertoire sequencing: different patterns of B-cell activation after two Meningococcal vaccines. <i>Immunology and Cell Biology</i> , 2015, 93, 885-895.	1.0	83
28	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.	9.4	310
29	Identification of Antigen-Specific B Cell Receptor Sequences Using Public Repertoire Analysis. <i>Journal of Immunology</i> , 2015, 194, 252-261.	0.4	115
30	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.	1.5	213
31	Rare variants in <i>PPARG</i> 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, 13127-13132.	3.3	152
32	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. <i>Nature Genetics</i> , 2014, 46, 912-918.	9.4	937
33	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, 710-720.	2.6	24
34	Erythrocytosis associated with a novel missense mutation in the <i>BPGM</i> gene. <i>Haematologica</i> , 2014, 99, e201-e204.	1.7	35
35	Improved workflows for high throughput library preparation using the transposome-based nextera system. <i>BMC Biotechnology</i> , 2013, 13, 104.	1.7	141
36	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013, 23, 749-761.	2.4	206

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37	Unlocking the Bottleneck in Forward Genetics Using Whole-Genome Sequencing and Identity by Descent to Isolate Causative Mutations. PLoS Genetics, 2013, 9, e1003219.	1.5	44
38	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	1.8	221
39	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.	1.5	102
40	Recessive Mutations in SPTBN2 Implicate β -III Spectrin in Both Cognitive and Motor Development. PLoS Genetics, 2012, 8, e1003074.	1.5	94
41	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	6.0	273
42	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
43	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.	1.5	398
44	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
45	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
46	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
47	Accurate Reconstruction of Insertion-Deletion Histories by Statistical Phylogenetics. PLoS ONE, 2012, 7, e34572.	1.1	28
48	Dindel: Accurate indel calls from short-read data. Genome Research, 2011, 21, 961-973.	2.4	383
49	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	1.8	11,326
50	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
51	Stampy: A statistical algorithm for sensitive and fast mapping of Illumina sequence reads. Genome Research, 2011, 21, 936-939.	2.4	1,044
52	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.	1.5	79
53	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
54	Genome assembly quality: Assessment and improvement using the neutral indel model. Genome Research, 2010, 20, 675-684.	2.4	44

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55	Massive turnover of functional sequence in human and other mammalian genomes. <i>Genome Research</i> , 2010, 20, 1335-1343.	2.4	86
56	Accelerated Evolution of the Prdm9 Speciation Gene across Diverse Metazoan Taxa. <i>PLoS Genetics</i> , 2009, 5, e1000753.	1.5	256
57	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.	1.5	354
58	Investigating selection on viruses: a statistical alignment approach. <i>BMC Bioinformatics</i> , 2008, 9, 304.	1.2	8
59	Uncertainty in homology inferences: Assessing and improving genomic sequence alignment. <i>Genome Research</i> , 2008, 18, 298-309.	2.4	128
60	Evolution of Primate Gene Expression: Drift and Corrective Sweeps?. <i>Genetics</i> , 2008, 180, 1379-1389.	1.2	17
61	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. <i>Genome Research</i> , 2007, 17, 556-565.	2.4	632
62	Probabilistic whole-genome alignments reveal high indel rates in the human and mouse genomes. <i>Bioinformatics</i> , 2007, 23, i289-i296.	1.8	52
63	HMMoCâ€”a compiler for hidden Markov models. <i>Bioinformatics</i> , 2007, 23, 2485-2487.	1.8	28
64	Novel Type IV Secretion System Involved in Propagation of Genomic Islands. <i>Journal of Bacteriology</i> , 2007, 189, 761-771.	1.0	138
65	Dog as an Outgroup to Human and Mouse. <i>PLoS Computational Biology</i> , 2007, 3, e74.	1.5	27
66	Signatures of adaptive evolution within human non-coding sequence. <i>Human Molecular Genetics</i> , 2006, 15, R170-R175.	1.4	45
67	Human brain gene wins genome race. <i>Nature</i> , 2006, 443, 149-150.	13.7	9
68	Genome-Wide Identification of Human Functional DNA Using a Neutral Indel Model. <i>PLoS Computational Biology</i> , 2006, 2, e5.	1.5	157
69	Bayesian coestimation of phylogeny and sequence alignment. <i>BMC Bioinformatics</i> , 2005, 6, 83.	1.2	169
70	A nucleotide substitution model with nearest-neighbour interactions. <i>Bioinformatics</i> , 2004, 20, i216-i223.	1.8	72
71	A "Long Indel" Model For Evolutionary Sequence Alignment. <i>Molecular Biology and Evolution</i> , 2003, 21, 529-540.	3.5	106
72	An Efficient Algorithm for Statistical Multiple Alignment on Arbitrary Phylogenetic Trees. <i>Journal of Computational Biology</i> , 2003, 10, 869-889.	0.8	67

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73	Resonances in a spring-pendulum: algorithms for equivariant singularity theory. <i>Nonlinearity</i> , 1998, 11, 1569-1605.	0.6	24
74	New Proofs and a Generalization of Inequalities of Fan, Taussky, and Todd. <i>Journal of Mathematical Analysis and Applications</i> , 1994, 185, 464-476.	0.5	6