

# Ville Mustonen

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

10,532  
citations

159585

30  
h-index

149698

56  
g-index

81  
all docs

81  
docs citations

81  
times ranked

18209  
citing authors

#	ARTICLE	IF	CITATIONS
1	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	27.8	2,104
2	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
3	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. <i>Nature</i> , 2011, 469, 539-542.	27.8	1,127
4	Somatic <i>SF3B1</i> Mutation in Myelodysplasia with Ring Sideroblasts. <i>New England Journal of Medicine</i> , 2011, 365, 1384-1395.	27.0	1,094
5	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	27.8	690
6	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 872-888.	8.9	328
7	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	19.0	297
8	Predicting evolution. <i>Nature Ecology and Evolution</i> , 2017, 1, 77.	7.8	272
9	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	28.9	260
10	From fitness landscapes to seascapes: non-equilibrium dynamics of selection and adaptation. <i>Trends in Genetics</i> , 2009, 25, 111-119.	6.7	202
11	High-Definition Reconstruction of Clonal Composition in Cancer. <i>Cell Reports</i> , 2014, 7, 1740-1752.	6.4	165
12	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <i>Genetics</i> , 2013, 195, 1141-1155.	2.9	164
13	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	19.0	161
14	Fitness flux and ubiquity of adaptive evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4248-4253.	7.1	151
15	Prediction of antibiotic resistance in <i>Escherichia coli</i> from large-scale pan-genome data. <i>PLoS Computational Biology</i> , 2018, 14, e1006258.	3.2	127
16	Emergent Neutrality in Adaptive Asexual Evolution. <i>Genetics</i> , 2011, 189, 1361-1375.	2.9	109
17	Energy-dependent fitness: A quantitative model for the evolution of yeast transcription factor binding sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12376-12381.	7.1	107
18	Evolutionary population genetics of promoters: Predicting binding sites and functional phylogenies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15936-15941.	7.1	106

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19	EMu: probabilistic inference of mutational processes and their localization in the cancer genome. <i>Genome Biology</i> , 2013, 14, R39.	9.6	100
20	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018, 2, 1661-1672.	7.8	99
21	Clonal Heterogeneity Influences the Fate of New Adaptive Mutations. <i>Cell Reports</i> , 2017, 21, 732-744.	6.4	70
22	Adaptations to fluctuating selection in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2277-2282.	7.1	68
23	Molecular Evolution under Fitness Fluctuations. <i>Physical Review Letters</i> , 2008, 100, 108101.	7.8	65
24	Quantifying Selection Acting on a Complex Trait Using Allele Frequency Time Series Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 1187-1197.	8.9	64
25	Neutral tumor evolution?. <i>Nature Genetics</i> , 2018, 50, 1630-1633.	21.4	59
26	The value of monitoring to control evolving populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1007-1012.	7.1	50
27	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. <i>Blood</i> , 2016, 128, e1-e9.	1.4	49
28	Distinguishing Driver and Passenger Mutations in an Evolutionary History Categorized by Interference. <i>Genetics</i> , 2011, 189, 989-1000.	2.9	48
29	Shared Molecular Targets Confer Resistance over Short and Long Evolutionary Timescales. <i>Molecular Biology and Evolution</i> , 2019, 36, 691-708.	8.9	43
30	Identifying Selection in the Within-Host Evolution of Influenza Using Viral Sequence Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003755.	3.2	39
31	Adenoma development in familial adenomatous polyposis and <i>MUTYH</i> -associated polyposis: somatic landscape and driver genes. <i>Journal of Pathology</i> , 2016, 238, 98-108.	4.5	39
32	Components of Selection in the Evolution of the Influenza Virus: Linkage Effects Beat Inherent Selection. <i>PLoS Pathogens</i> , 2012, 8, e1003091.	4.7	36
33	Inferring Genome-Wide Recombination Landscapes from Advanced Intercross Lines: Application to Yeast Crosses. <i>PLoS ONE</i> , 2013, 8, e62266.	2.5	29
34	Contrasting the impact of cytotoxic and cytostatic drug therapies on tumour progression. <i>PLoS Computational Biology</i> , 2019, 15, e1007493.	3.2	26
35	Rapid identification of genes controlling virulence and immunity in malaria parasites. <i>PLoS Pathogens</i> , 2017, 13, e1006447.	4.7	23
36	Numerical estimation of the asymptotic behaviour of solid partitions of an integer. <i>Journal of Physics A</i> , 2003, 36, 6651-6659.	1.6	22

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37	Repeatable ecological dynamics govern the response of experimental communities to antibiotic pulse perturbation. <i>Nature Ecology and Evolution</i> , 2020, 4, 1385-1394.	7.8	22
38	A method to infer positive selection from marker dynamics in an asexual population. <i>Bioinformatics</i> , 2012, 28, 831-837.	4.1	21
39	Genomic Epidemiology and Evolution of <i>Escherichia coli</i> in Wild Animals in Mexico. <i>MSphere</i> , 2021, 6, .	2.9	19
40	Triangular lattice solution for filling in a wedge. <i>Europhysics Letters</i> , 2003, 63, 408-414.	2.0	18
41	Eco-evolutionary control of pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19694-19704.	7.1	16
42	Germline Fitness-Based Scoring of Cancer Mutations. <i>Genetics</i> , 2011, 188, 383-393.	2.9	15
43	Drug-induced resistance evolution necessitates less aggressive treatment. <i>PLoS Computational Biology</i> , 2021, 17, e1009418.	3.2	14
44	Multiobjective optimization identifies cancer-selective combination therapies. <i>PLoS Computational Biology</i> , 2020, 16, e1008538.	3.2	9
45	Wetting Effects at a Grain Boundary. <i>Physical Review Letters</i> , 2004, 93, 076101.	7.8	8
46	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. <i>Genetics</i> , 2018, 210, 733-744.	2.9	8
47	Quantifying selection in evolving populations using time-resolved genetic data. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013, 2013, P01004.	2.3	7
48	GraphAlignment: Bayesian pairwise alignment of biological networks. <i>BMC Systems Biology</i> , 2012, 6, 144.	3.0	6
49	Machine Learning Prediction of Resistance to Subinhibitory Antimicrobial Concentrations from <i>Escherichia coli</i> Genomes. <i>MSystems</i> , 2021, 6, e0034621.	3.8	6
50	Evaluating genetic drift in time-series evolutionary analysis. <i>Journal of Theoretical Biology</i> , 2018, 437, 51-57.	1.7	5
51	MOLECULAR DYNAMIC STUDY OF A SINGLE DISLOCATION IN A TWO-DIMENSIONAL LENNARD-JONES SYSTEM. <i>International Journal of Modern Physics C</i> , 2003, 14, 407-421.	1.7	4
52	Solid on solid model for an interface crossing a grain boundary. <i>Journal of Physics A</i> , 2004, 37, L233-L239.	1.6	4
53	Relaxation dynamics of a system with a grain boundary. <i>Physical Review E</i> , 2004, 70, 066138.	2.1	4
54	Strong selective environments determine evolutionary outcome in time-dependent fitness seascapes. <i>Evolution Letters</i> , 2022, 6, 266-279.	3.3	4

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55	Equilibrium statistical mechanics of a grain boundary. <i>Physical Review E</i> , 2005, 71, 036106.	2.1	2
56	Exact Results for Wetting and Filling on a Triangular Lattice. <i>International Journal of Thermophysics</i> , 2004, 25, 1051-1062.	2.1	0
57	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
58	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
59	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
60	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
61	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
62	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0