Peter Van Loo

List of Publications by Citations

116 papers	24,629 citations	58 h-index	137 g-index
137 ext. papers	31,829 ext. citations	24.1 avg, IF	6.05 L-index

#	Paper	IF	Citations
116	Genomic Classification and Prognosis in Acute Myeloid Leukemia. *New England Journal of Medicine*, **2016**, 374, 2209-2221	59.2	1999
115	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
114	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
113	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
112	Clinical and biological implications of driver mutations in myelodysplastic syndromes. *Blood*, **2013**, 122, 3616-27; quiz 3699	2.2	1169
111	Tracking the Evolution of Non-Small-Cell Lung Cancer. *New England Journal of Medicine*, **2017**, 376, 2109-2121	59.2	1156
110	Tumor evolution. High burden and pervasive positive selection of somatic mutations in normal human skin. *Science*, **2015**, 348, 880-6	33.3	983
109	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
108	The evolutionary history of lethal metastatic prostate cancer. *Nature*, **2015**, 520, 353-357	50.4	857
107	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. *Nature*, **2017**, 545, 446-451	50.4	796
106	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. *Science*, **2014**, 346, 251-6	33.3	752
105	Allele-specific copy number analysis of tumors. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 16910-5	11.5	699
104	Gene prioritization through genomic data fusion. *Nature Biotechnology*, **2006**, 24, 537-44	44.5	685
103	Universal Patterns of Selection in Cancer and Somatic Tissues. *Cell*, **2017**, 171, 1029-1041.e21	56.2	576
102	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nature Communications*, **2014**, 5, 2997	17.4	564
101	Mutational signatures associated with tobacco smoking in human cancer. *Science*, **2016**, 354, 618-622	33.3	562
100	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. *Cell*, **2017**, 171, 1259-1271.e11	56.2	541

99	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. *Nature Medicine*, **2015**, 21, 751-9	50.5	521
98	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. *Nature Genetics*, **2013**, 45, 1479-82	36.3	482
97	Neoantigen-directed immune escape in lung cancer evolution. *Nature*, **2019**, 567, 479-485	50.4	358
96	Genomic Evolution of Breast Cancer Metastasis and Relapse. *Cancer Cell*, **2017**, 32, 169-184.e7	24.3	346
95	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
94	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. *Nature Genetics*, **2015**, 47, 367-372	36.3	292
93	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. *Cell*, **2018**, 173, 595-610.e11	56.2	268
92	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. *Nature Genetics*, **2015**, 47, 257-62	36.3	253
91	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
90	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. *Nature Communications*, **2015**, 6, 6605	17.4	245
89	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. *Nature Genetics*, **2014**, 46, 116-25	36.3	244
88	ORegAnno: an open-access community-driven resource for regulatory annotation. *Nucleic Acids Research*, **2008**, 36, D107-13	20.1	199
87	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. *Nature Genetics*, **2014**, 46, 376-379	36.3	196
86	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. *Nature*, **2014**, 508, 98-102	50.4	192
85	Whole exome sequencing of adenoid cystic carcinoma. *Journal of Clinical Investigation*, **2013**, 123, 2965-8	15.9	188
84	ENDEAVOUR update: a web resource for gene prioritization in multiple species. *Nucleic Acids Research*, **2008**, 36, W377-84	20.1	182
83	Genomic Characterization of Primary Invasive Lobular Breast Cancer. *Journal of Clinical Oncology*, **2016**, 34, 1872-81	2.2	175
82	Copynumber: Efficient algorithms for single- and multi-track copy number segmentation. *BMC Genomics*, **2012**, 13, 591	4.5	175

81	Optimized filtering reduces the error rate in detecting genomic variants by short-read sequencing. *Nature Biotechnology*, **2011**, 30, 61-8	44.5	163
80	Mutational signatures of ionizing radiation in second malignancies. *Nature Communications*, **2016**, 7, 12605	17.4	152
79	Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. *Cell*, **2021**, 184, 596-614.e14	56.2	144
78	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. *Nature Genetics*, **2013**, 45, 923-6	36.3	138
77	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. *Nature Communications*, **2017**, 8, 15936	17.4	125
76	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. *Nucleic Acids Research*, **2013**, 41, 6119-38	20.1	125
75	Integrated molecular profiles of invasive breast tumors and ductal carcinoma in situ (DCIS) reveal differential vascular and interleukin signaling. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 2802-7	11.5	125
74	Polysomy 17 in breast cancer: clinicopathologic significance and impact on HER-2 testing. *Journal of Clinical Oncology*, **2008**, 26, 4869-74	2.2	124
73	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
72	Cleavage of NIK by the API2-MALT1 fusion oncoprotein leads to noncanonical NF-kappaB activation. *Science*, **2011**, 331, 468-72	33.3	122
71	TOUCAN 2: the all-inclusive open source workbench for regulatory sequence analysis. *Nucleic Acids Research*, **2005**, 33, W393-6	20.1	122
70	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. *Nature Genetics*, **2018**, 50, 682-692	36.3	112
69	Single cell analysis of cancer genomes. *Current Opinion in Genetics and Development*, **2014**, 24, 82-91	4.9	99
68	Diagnostic value of H3F3A mutations in giant cell tumour of bone compared to osteoclast-rich mimics. *Journal of Pathology: Clinical Research*, **2015**, 1, 113-23	5.3	98
67	Integrated study of copy number states and genotype calls using high-density SNP arrays. *Nucleic Acids Research*, **2009**, 37, 5365-77	20.1	93
66	Computational detection of cis -regulatory modules. *Bioinformatics*, **2003**, 19 Suppl 2, ii5-14	7.2	83
65	Evidence for co-evolution between human microRNAs and Alu-repeats. *PLoS ONE*, **2009**, 4, e4456	3.7	77
64	Haploinsufficiency of TAB2 causes congenital heart defects in humans. *American Journal of Human Genetics*, **2010**, 86, 839-49	11	75

63	LRP1B deletion in high-grade serous ovarian cancers is associated with acquired chemotherapy resistance to liposomal doxorubicin. *Cancer Research*, **2012**, 72, 4060-73	10.1	73
62	Recurrent rearrangements of FOS and FOSB define osteoblastoma. *Nature Communications*, **2018**, 9, 2150	17.4	69
61	Pervasive chromosomal instability and karyotype order in tumour evolution. *Nature*, **2020**, 587, 126-132	50.4	67
60	Interplay between whole-genome doubling and the accumulation of deleterious alterations in cancer evolution. *Nature Genetics*, **2020**, 52, 283-293	36.3	63
59	ascatNgs: Identifying Somatically Acquired Copy-Number Alterations from Whole-Genome Sequencing Data. *Current Protocols in Bioinformatics*, **2016**, 56, 15.9.1-15.9.17	24.2	60
58	Principles of Reconstructing the Subclonal Architecture of Cancers. *Cold Spring Harbor Perspectives in Medicine*, **2017**, 7,	5.4	58
57	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
56	T-cell/histiocyte-rich large B-cell lymphoma shows transcriptional features suggestive of a tolerogenic host immune response. *Haematologica*, **2010**, 95, 440-8	6.6	48
55	Computational methods for the detection of cis-regulatory modules. *Briefings in Bioinformatics*, **2009**, 10, 509-24	13.4	48
54	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. *Genome Biology*, **2016**, 17, 250	18.3	48
53	On the identification of low allele frequency mosaic mutations in the brains of Alzheimer's disease patients. *Alzheimer's and Dementia*, **2015**, 11, 1265-76	1.2	47
52	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. *Nature Communications*, **2018**, 9, 4181	17.4	45
51	Differential and limited expression of mutant alleles in multiple myeloma. *Blood*, **2014**, 124, 3110-7	2.2	42
50	Timing somatic events in the evolution of cancer. *Genome Biology*, **2018**, 19, 95	18.3	41
49	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. *Nature Communications*, **2017**, 8, 1221	17.4	40
48	A genetic algorithm for the detection of new cis-regulatory modules in sets of coregulated genes. *Bioinformatics*, **2004**, 20, 1974-6	7.2	38
47	Neutral tumor evolution?. *Nature Genetics*, **2018**, 50, 1630-1633	36.3	38
46	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. *Cancer Cell*, **2019**, 35, 441-456.e8	24.3	35

45	A community effort to create standards for evaluating tumor subclonal reconstruction. *Nature Biotechnology*, **2020**, 38, 97-107	44.5	35
44	Translating insights into tumor evolution to clinical practice: promises and challenges. *Genome Medicine*, **2019**, 11, 20	14.4	34
43	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. *Genome Biology*, **2013**, 14, R113	18.3	33
42	Breast tumours maintain a reservoir of subclonal diversity during expansion. *Nature*, **2021**, 592, 302-308	50.4	33
41	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-46	8.6	30
40	Next-generation sequencing of disseminated tumor cells. *Frontiers in Oncology*, **2013**, 3, 320	5.3	29
39	ModuleMiner - improved computational detection of cis-regulatory modules: are there different modes of gene regulation in embryonic development and adult tissues?. *Genome Biology*, **2008**, 9, R66	18.3	29
38	The evolutionary history of 2,658 cancers		28
37	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. *Cancer Research*, **2016**, 76, 5092-102	10.1	27
36	How Subclonal Modeling Is Changing the Metastatic Paradigm. *Clinical Cancer Research*, **2017**, 23, 630-635	12.9	26
35	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
34	A practical guide to cancer subclonal reconstruction from DNA sequencing. *Nature Methods*, **2021**, 18, 144-155	21.6	25
33	Mitotic recombination of chromosome arm 17q as a cause of loss of heterozygosity of NF1 in neurofibromatosis type 1-associated glomus tumors. *Genes Chromosomes and Cancer*, **2012**, 51, 429-37	5	23
32	Collaboratively charting the gene-to-phenotype network of human congenital heart defects. *Genome Medicine*, **2010**, 2, 16	14.4	23
31	The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogen-receptor positive tumors. *Molecular Oncology*, **2014**, 8, 273-84	7.9	21
30	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. *PLoS Genetics*, **2017**, 13, e1007001	6	20
29	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. *Cell Reports*, **2020**, 31, 107550	10.6	19
28	Promises and challenges of adoptive T-cell therapies for solid tumours. *British Journal of Cancer*, **2021**, 124, 1759-1776	8.7	19

27	Canine Mammary Tumours Are Affected by Frequent Copy Number Aberrations, including Amplification of MYC and Loss of PTEN. *PLoS ONE*, **2015**, 10, e0126371	3.7	18
26	Copy number variations alter methylation and parallel IGF2 overexpression in adrenal tumors. *Endocrine-Related Cancer*, **2015**, 22, 953-67	5.7	16
25	EGFR gene variants are associated with specific somatic aberrations in glioma. *PLoS ONE*, **2012**, 7, e47929	3.7	10
24	Ethanol exposure increases mutation rate through error-prone polymerases. *Nature Communications*, **2020**, 11, 3664	17.4	9
23	An integrative analysis of the age-associated multi-omic landscape across cancers. *Nature Communications*, **2021**, 12, 2345	17.4	9
22	Universal patterns of selection in cancer and somatic tissues		7
21	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. *Nature Communications*, **2021**, 12, 6910	17.4	6
20	Comparative expressed sequence hybridization studies of t(11;18)(q21;q21)-positive and -negative gastric MALT lymphomas reveal both unique and overlapping gene programs. *Modern Pathology*, **2010**, 23, 458-69	9.8	5
19	Drivers underpinning the malignant transformation of giant cell tumour of bone. *Journal of Pathology*, **2020**, 252, 433-440	9.4	5
18	Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. *Nature Cancer*, **2021**, 2, 835-852	15.4	5
17	Using DNA sequencing data to quantify T cell fraction and therapy response. *Nature*, **2021**, 597, 555-560	50.4	5
16	DNA copy number motifs are strong and independent predictors of survival in breast cancer. *Communications Biology*, **2020**, 3, 153	6.7	4
15	Rapid parallel acquisition of somatic mutations after NPM1 in acute myeloid leukaemia evolution. *British Journal of Haematology*, **2017**, 176, 825-829	4.5	3
14	Recurrent breakpoints in 14q32.13/TCL1A region in mature B-cell neoplasms with villous lymphocytes. *Leukemia and Lymphoma*, **2012**, 53, 2449-55	1.9	3
13	Creating Standards for Evaluating Tumour Subclonal Reconstruction		3
12	Signatures of copy number alterations in human cancer		3
11	SNES makes sense? Single-cell exome sequencing evolves. *Genome Biology*, **2015**, 16, 86	18.3	2
10	Tumor cell total mRNA expression shapes the molecular and clinical phenotype of cancer		2

9	Biallelic mutations in cancer genomes reveal local mutational determinants		2
8	MEDICC2: whole-genome doubling aware copy-number phylogenies for cancer evolution		2
7	Biallelic mutations in cancer genomes reveal local mutational determinants.. *Nature Genetics*, **2022**, 54, 128-133	36.3	1
6	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. *Nature Communications*, **2021**, 12, 6946	17.4	1
5	Drivers underpinning the malignant transformation of giant cell tumour of bone		1
4	An Integrative Analysis of the Age-Associated Genomic, Transcriptomic and Epigenetic Landscape across Cancers		1
3	A pan-cancer landscape of somatic mutations in non-unique regions of the human genome. *Nature Biotechnology*, **2021**,	44.5	1
2	E3 ubiquitin ligase HECTD2 mediates melanoma progression and immune evasion. *Oncogene*, **2021**, 40, 5567-5578	9.2	0
1	DeCiFering the subclonal composition of tumors. *Cell Systems*, **2021**, 12, 955-957	10.6	