Esa Pitkänen

List of Publications by Year
in descending order

67 papers	**2,641** citations	218677 **26** h-index	206112 **48** g-index
74 all docs	**74** docs citations	**74** times ranked	**5289** citing authors

#	Article	IF	Citations
1	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	21.4	383
2	Characterization of Uterine Leiomyomas by Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 43-53.	27.0	280
3	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	12.8	196
4	Integrated data analysis reveals uterine leiomyoma subtypes with distinct driver pathways and biomarkers. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1315-1320.	7.1	166
5	Exome sequencing reveals frequent inactivating mutations in *ARID1A, ARID1B, ARID2* and *ARID4A* in microsatellite unstable colorectal cancer. International Journal of Cancer, 2014, 135, 611-623.	5.1	107
6	Whole-Genome Sequencing of Growth Hormone (GH)-Secreting Pituitary Adenomas. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 3918-3927.	3.6	96
7	Comparative Genome-Scale Reconstruction of Gapless Metabolic Networks for Present and Ancestral Species. PLoS Computational Biology, 2014, 10, e1003465.	3.2	84
8	Eleven Candidate Susceptibility Genes for Common Familial Colorectal Cancer. PLoS Genetics, 2013, 9, e1003876.	3.5	69
9	Identification of Candidate Oncogenes in Human Colorectal Cancers With Microsatellite Instability. Gastroenterology, 2013, 145, 540-543.e22.	1.3	65
10	MED12 mutation frequency in unselected sporadic uterine leiomyomas. Fertility and Sterility, 2014, 102, 1137-1142.	1.0	62
11	Exome-wide somatic mutation characterization of small bowel adenocarcinoma. PLoS Genetics, 2018, 14, e1007200.	3.5	62
12	Frequent L1 retrotranspositions originating from *TTC28* in colorectal cancer. Oncotarget, 2014, 5, 853-859.	1.8	60
13	Inferring branching pathways in genome-scale metabolic networks. BMC Systems Biology, 2009, 3, 103.	3.0	59
14	Retrotransposon insertions can initiate colorectal cancer and are associated with poor survival. Nature Communications, 2019, 10, 4022.	12.8	53
15	Comparative analysis of molecular fingerprints in prediction of drug combination effects. Briefings in Bioinformatics, 2021, 22, .	6.5	47
16	Computational methods for metabolic reconstruction. Current Opinion in Biotechnology, 2010, 21, 70-77.	6.6	46
17	Multiple clinical characteristics separate MED12-mutation-positive and -negative uterine leiomyomas. Scientific Reports, 2017, 7, 1015.	3.3	44
18	Digestive Tract in Collagen Diseases. Acta Medica Scandinavica, 1965, 178, 13-25.	0.0	43

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19	MED12 mutations and FH inactivation are mutually exclusive in uterine leiomyomas. British Journal of Cancer, 2016, 114, 1405-1411.	6.4	43
20	Molecular features encoded in the ctDNA reveal heterogeneity and predict outcome in high-risk aggressiveÂB-cell lymphoma. Blood, 2022, 139, 1863-1877.	1.4	43
21	Determination of mannose and fructose in human plasma using deuterium labelling and gas chromatography/mass spectrometry. Biological Mass Spectrometry, 1994, 23, 590-595.	0.5	35
22	ERCC6L2 defines a novel entity within inherited acute myeloid leukemia. Blood, 2019, 133, 2724-2728.	1.4	35
23	Towards structured output prediction of enzyme function. BMC Proceedings, 2008, 2, S2.	1.6	32
24	Identification of 33 candidate oncogenes by screening for base-specific mutations. British Journal of Cancer, 2014, 111, 1657-1662.	6.4	30
25	Global metabolomic profiling of uterine leiomyomas. British Journal of Cancer, 2017, 117, 1855-1864.	6.4	29
26	Towards pan-genome read alignment to improve variation calling. BMC Genomics, 2018, 19, 87.	2.8	29
27	Discovery of potential causative mutations in human coding and noncoding genome with the interactive software BasePlayer. Nature Protocols, 2018, 13, 2580-2600.	12.0	27
28	Unusual Electrocardiographic Changes in Pheochromocytoma. Acta Medica Scandinavica, 1963, 173, 41-44.	0.0	26
29	Service Outsourcing with Process Views. IEEE Transactions on Services Computing, 2015, 8, 136-154.	4.6	26
30	Contribution of allelic imbalance to colorectal cancer. Nature Communications, 2018, 9, 3664.	12.8	25
31	Systematic search for rare variants in Finnish early-onset colorectal cancer patients. Cancer Genetics, 2015, 208, 35-40.	0.4	24
32	Impact of AIP and inhibitory G protein alpha 2 proteins on clinical features of sporadic GH-secreting pituitary adenomas. European Journal of Endocrinology, 2017, 176, 243-252.	3.7	24
33	Detection of subclonal L1 transductions in colorectal cancer by long-distance inverse-PCR and Nanopore sequencing. Scientific Reports, 2017, 7, 14521.	3.3	24
34	Germline alterations in a consecutive series of acute myeloid leukemia. Leukemia, 2018, 32, 2282-2285.	7.2	24
35	Whole-genome metabolic model of Trichoderma reesei built by comparative reconstruction. Biotechnology for Biofuels, 2016, 9, 252.	6.2	21
36	13C-metabolic flux ratio and novel carbon path analyses confirmed that Trichoderma reesei uses primarily the respirative pathway also on the preferred carbon source glucose. BMC Systems Biology, 2009, 3, 104.	3.0	20

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37	Somatic *MED12* Nonsense Mutation Escapes mRNA Decay and Reveals a Motif Required for Nuclear Entry. Human Mutation, 2017, 38, 269-274.	2.5	20
38	Clonally related uterine leiomyomas are common and display branched tumor evolution. Human Molecular Genetics, 2015, 24, 4407-4416.	2.9	19
39	Nationwide Registry-Based Analysis of Cancer Clustering Detects Strong Familial Occurrence of Kaposi Sarcoma. PLoS ONE, 2013, 8, e55209.	2.5	18
40	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.9	18
41	sPLINK: a hybrid federated tool as a robust alternative to meta-analysis in genome-wide association studies. Genome Biology, 2022, 23, 32.	8.8	18
42	Collagen Disease Associated with Intestinal Malabsorption and Sprue-like Changes in the Intestinal Mucosa. Acta Medica Scandinavica, 1964, 175, 91-95.	0.0	11
43	Whole-exome sequencing identifies novel candidate predisposition genes for familial polycythemia vera. Human Genomics, 2017, 11, 6.	2.9	11
44	Comprehensive evaluation of coding region point mutations in microsatellite-unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	6.9	10
45	ReMatch: a web-based tool to construct, store and share stoichiometric metabolic models with carbon maps for metabolic flux analysis. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	9
46	Finding Feasible Pathways in Metabolic Networks. Lecture Notes in Computer Science, 2005, , 123-133.	1.3	6
47	ReMatch: a web-based tool to construct, store and share stoichiometric metabolic models with carbon maps for metabolic flux analysis. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	5
48	Proteinuria and plasma hexosugars in early-stage glomerulonephritis. Clinical Nephrology, 1996, 45, 226-9.	0.7	5
49	Exome and immune cell score analyses reveal great variation within synchronous primary colorectal cancers. British Journal of Cancer, 2019, 120, 922-930.	6.4	4
50	A Computational Method for Reconstructing Gapless Metabolic Networks. Communications in Computer and Information Science, 2008, , 288-302.	0.5	4
51	Structured Output Prediction of Novel Enzyme Function with Reaction Kernels. Communications in Computer and Information Science, 2011, , 367-379.	0.5	3
52	Enrichment of cancer-predisposing germline variants in adult and pediatric patients with acute lymphoblastic leukemia. Scientific Reports, 2022, 12, .	3.3	3
53	3′-UTR poly(T/U) repeat of EWSR1 is altered in microsatellite unstable colorectal cancer with nearly perfect sensitivity. Familial Cancer, 2015, 14, 449-453.	1.9	2
54	Spectral decoupling for training transferable neural networks in medical imaging. IScience, 2022, 25, 103767.	4.1	2

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55	Reconstructing Gapless Ancestral Metabolic Networks. Communications in Computer and Information Science, 2013, , 126-140.	0.5	1
56	Abstract 5193: Novel candidate oncogenes with mutation hot spots in microsatellite unstable colorectal cancer. , 2014, , .		1
57	Single-Cell Mononucleotide Microsatellite Analysis Reveals Differential Insertion-Deletion Dynamics in Mouse T Cells. Frontiers in Genetics, 0, 13, .	2.3	1
58	Identification of candidate predisposing factors in familial polycythemia vera with exome sequencing. European Journal of Cancer, 2016, 61, S12.	2.8	0
59	Somatic MED12 exon 1 nonsense mutation in T-cell acute lymphoblastic leukemia escapes nonsense-mediated mRNA decay and prevents protein nuclear localization. European Journal of Cancer, 2016, 61, S88.	2.8	0
60	Equivalence of Metabolite Fragments and Flow Analysis of Isotopomer Distributions for Flux Estimation. Lecture Notes in Computer Science, 2006, , 198-220.	1.3	0
61	Abstract 2401: Identification of new target genes in microsatellite unstable colorectal cancer by exome sequencing. , 2014, , .		0
62	Abstract 2176: Joint structural variant analysis of colorectal cancer whole genome sequencing data. , 2015, , .		0
63	Abstract 1079: Transcriptional profiling reveals uterine leiomyoma subtypes with distinct pathways and biomarkers of tumorigenesis. , 2015, , .		0
64	Abstract 5281: Fast and scalable software for comparative variant analysis and visualization of massive next-generation sequencing data. , 2016, , .		0
65	Abstract 4381: The mobile genome of colorectal cancer: Characterization of retrotransposon insertions in 202 colorectal cancer whole genomes. , 2017, , .		0
66	Abstract 4379: Somatic exomic landscape of small intestinal adenocarcinomas. , 2017, , .		0
67	Abstract 1440: Germline loss-of-function alleles in Finnish colorectal cancer patients. , 2017, , .		0