Esa PitkÃ¤nen

List of Publications by Year in descending order

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Version: 2024-02-01

67	2,641	218677	206112
papers	citations	26 h-index	48 g-index

74	74	74	5289
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Spectral decoupling for training transferable neural networks in medical imaging. IScience, 2022, 25, 103767.	4.1	2
3	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
4	Enrichment of cancer-predisposing germline variants in adult and pediatric patients with acute lymphoblastic leukemia. Scientific Reports, 2022, 12, .	3.3	3
5	Comparative analysis of molecular fingerprints in prediction of drug combination effects. Briefings in Bioinformatics, 2021, 22, .	6.5	47
6	Retrotransposon insertions can initiate colorectal cancer and are associated with poor survival. Nature Communications, 2019, 10, 4022.	12.8	53
7	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
8	ERCC6L2 defines a novel entity within inherited acute myeloid leukemia. Blood, 2019, 133, 2724-2728.	1.4	35
9	Germline alterations in a consecutive series of acute myeloid leukemia. Leukemia, 2018, 32, 2282-2285.	7.2	24
10	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
11	Contribution of allelic imbalance to colorectal cancer. Nature Communications, 2018, 9, 3664.	12.8	25
12	Towards pan-genome read alignment to improve variation calling. BMC Genomics, 2018, 19, 87.	2.8	29
13	Comprehensive evaluation of coding region point mutations in microsatelliteâ€unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	6.9	10
14	Exome-wide somatic mutation characterization of small bowel adenocarcinoma. PLoS Genetics, 2018, 14, e1007200.	3.5	62
15	Somatic MED12 Nonsense Mutation Escapes mRNA Decay and Reveals a Motif Required for Nuclear Entry. Human Mutation, 2017, 38, 269-274.	2.5	20
16	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.9	18
17	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
18	Global metabolomic profiling of uterine leiomyomas. British Journal of Cancer, 2017, 117, 1855-1864.	6.4	29

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19	Multiple clinical characteristics separate MED12-mutation-positive and -negative uterine leiomyomas. Scientific Reports, 2017, 7, 1015.	3.3	44
20	Detection of subclonal L1 transductions in colorectal cancer by long-distance inverse-PCR and Nanopore sequencing. Scientific Reports, 2017, 7, 14521.	3.3	24
21	Whole-exome sequencing identifies novel candidate predisposition genes for familial polycythemia vera. Human Genomics, 2017, 11, 6.	2.9	11
22	Abstract 4381: The mobile genome of colorectal cancer: Characterization of retrotransposon insertions in 202 colorectal cancer whole genomes. , 2017, , .		0
23	Abstract 4379: Somatic exomic landscape of small intestinal adenocarcinomas. , 2017, , .		0
24	Abstract 1440: Germline loss-of-function alleles in Finnish colorectal cancer patients. , 2017, , .		0
25	Whole-genome metabolic model of Trichoderma reesei built by comparative reconstruction. Biotechnology for Biofuels, 2016, 9, 252.	6.2	21
26	Identification of candidate predisposing factors in familial polycythemia vera with exome sequencing. European Journal of Cancer, 2016, 61, S12.	2.8	0
27	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
28	MED12 mutations and FH inactivation are mutually exclusive in uterine leiomyomas. British Journal of Cancer, 2016, 114, 1405-1411.	6.4	43
29	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
30	Abstract 5281: Fast and scalable software for comparative variant analysis and visualization of massive next-generation sequencing data. , 2016, , .		0
31	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	21.4	383
32	3â€²-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
33	Clonally related uterine leiomyomas are common and display branched tumor evolution. Human Molecular Genetics, 2015, 24, 4407-4416.	2.9	19
34	Service Outsourcing with Process Views. IEEE Transactions on Services Computing, 2015, 8, 136-154.	4.6	26
35	Systematic search for rare variants in Finnish early-onset colorectal cancer patients. Cancer Genetics, 2015, 208, 35-40.	0.4	24
36	Whole-Genome Sequencing of Growth Hormone (GH)-Secreting Pituitary Adenomas. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 3918-3927.	3.6	96

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37	Abstract 2176: Joint structural variant analysis of colorectal cancer whole genome sequencing data. , 2015, , .		0
38	Abstract 1079: Transcriptional profiling reveals uterine leiomyoma subtypes with distinct pathways and biomarkers of tumorigenesis. , 2015, , .		0
39	Comparative Genome-Scale Reconstruction of Gapless Metabolic Networks for Present and Ancestral Species. PLoS Computational Biology, 2014, 10, e1003465.	3.2	84
40	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	12.8	196
41	Exome sequencing reveals frequent inactivating mutations inARID1A, ARID1B, ARID2andARID4Ain microsatellite unstable colorectal cancer. International Journal of Cancer, 2014, 135, 611-623.	5.1	107
42	MED12 mutation frequency in unselected sporadic uterine leiomyomas. Fertility and Sterility, 2014, 102, 1137-1142.	1.0	62
43	Identification of 33 candidate oncogenes by screening for base-specific mutations. British Journal of Cancer, 2014, 111, 1657-1662.	6.4	30
44	Frequent L1 retrotranspositions originating fromTTC28in colorectal cancer. Oncotarget, 2014, 5, 853-859.	1.8	60
45	Abstract 2401: Identification of new target genes in microsatellite unstable colorectal cancer by exome sequencing. , 2014, , .		0
46	Abstract 5193: Novel candidate oncogenes with mutation hot spots in microsatellite unstable colorectal cancer. , 2014, , .		1
47	Characterization of Uterine Leiomyomas by Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 43-53.	27.0	280
48	Reconstructing Gapless Ancestral Metabolic Networks. Communications in Computer and Information Science, 2013, , 126-140.	0.5	1
49	Identification of Candidate Oncogenes in Human Colorectal Cancers With Microsatellite Instability. Gastroenterology, 2013, 145, 540-543.e22.	1.3	65
50	Eleven Candidate Susceptibility Genes for Common Familial Colorectal Cancer. PLoS Genetics, 2013, 9, e1003876.	3.5	69
51	Nationwide Registry-Based Analysis of Cancer Clustering Detects Strong Familial Occurrence of Kaposi Sarcoma. PLoS ONE, 2013, 8, e55209.	2.5	18
52	Structured Output Prediction of Novel Enzyme Function with Reaction Kernels. Communications in Computer and Information Science, 2011, , 367-379.	0.5	3
53	Computational methods for metabolic reconstruction. Current Opinion in Biotechnology, 2010, 21, 70-77.	6.6	46
54	Inferring branching pathways in genome-scale metabolic networks. BMC Systems Biology, 2009, 3, 103.	3.0	59

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55	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
56	Towards structured output prediction of enzyme function. BMC Proceedings, 2008, 2, S2.	1.6	32
57	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
58	A Computational Method for Reconstructing Gapless Metabolic Networks. Communications in Computer and Information Science, 2008, , 288-302.	0.5	4
59	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
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	Finding Feasible Pathways in Metabolic Networks. Lecture Notes in Computer Science, 2005, , 123-133.	1.3	6
62	Proteinuria and plasma hexosugars in early-stage glomerulonephritis. Clinical Nephrology, 1996, 45, 226-9.	0.7	5
63	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
64	Digestive Tract in Collagen Diseases. Acta Medica Scandinavica, 1965, 178, 13-25.	0.0	43
65	Collagen Disease Associated with Intestinal Malabsorption and Sprueâ€like Changes in the Intestinal Mucosa. Acta Medica Scandinavica, 1964, 175, 91-95.	0.0	11
66	Unusual Electrocardiographic Changes in Pheochromocytoma. Acta Medica Scandinavica, 1963, 173, 41-44.	0.0	26
67	Single-Cell Mononucleotide Microsatellite Analysis Reveals Differential Insertion-Deletion Dynamics in Mouse T Cells. Frontiers in Genetics, 0, 13, .	2.3	1