Eevi Kaasinen

List of Publications by Year
in descending order

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29 papers	3,603 citations	331259 21 h-index	476904 29 g-index
30 all docs	30 docs citations	30 times ranked	7202 citing authors

#	Article	IF	Citations
1	Sequence determinants of human gene regulatory elements. Nature Genetics, 2022, 54, 283-294.	9.4	87
2	WNT2 activation through proximal germline deletion predisposes to small intestinal neuroendocrine tumors and intestinal adenocarcinomas. Human Molecular Genetics, 2021, 30, 2429-2440.	1.4	6
3	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	13.7	53
4	Parity associates with chromosomal damage in uterine leiomyomas. Nature Communications, 2021, 12, 5448.	5.8	2
5	Candidate susceptibility variants in angioimmunoblastic T-cell lymphoma. Familial Cancer, 2019, 18, 113-119.	0.9	8
6	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
7	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. Nature Communications, 2019, 10, 1252.	5.8	67
8	The interaction landscape between transcription factors and the nucleosome. Nature, 2018, 562, 76-81.	13.7	259
9	Discovery of potential causative mutations in human coding and noncoding genome with the interactive software BasePlayer. Nature Protocols, 2018, 13, 2580-2600.	5.5	27
10	Contribution of allelic imbalance to colorectal cancer. Nature Communications, 2018, 9, 3664.	5.8	25
11	Comprehensive evaluation of coding region point mutations in microsatelliteâ€unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	3.3	10
12	Genetic predisposition to uterine leiomyoma is determined by loci for genitourinary development and genome stability. ELife, 2018, 7, .	2.8	58
13	Candidate susceptibility variants for esophageal squamous cell carcinoma. Genes Chromosomes and Cancer, 2017, 56, 453-459.	1.5	23
14	Impact of cytosine methylation on DNA binding specificities of human transcription factors. Science, 2017, 356, .	6.0	912
15	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.4	18
16	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	2.3	76
17	Global metabolomic profiling of uterine leiomyomas. British Journal of Cancer, 2017, 117, 1855-1864.	2.9	29
18	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	1.3	81

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19	Mice deficient of Myc super-enhancer region reveal differential control mechanism between normal and pathological growth. ELife, 2017, 6, .	2.8	52
20	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	2.9	57
21	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.	3.3	166
22	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	9.4	383
23	Whole-Genome Sequencing of Growth Hormone (GH)-Secreting Pituitary Adenomas. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 3918-3927.	1.8	96
24	Clinical characterization, genetic mapping and whole-genome sequence analysis of a novel autosomal recessive intellectual disability syndrome. European Journal of Medical Genetics, 2014, 57, 543-551.	0.7	19
25	Characterization of Uterine Leiomyomas by Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 43-53.	13.9	280
26	Nationwide Registry-Based Analysis of Cancer Clustering Detects Strong Familial Occurrence of Kaposi Sarcoma. PLoS ONE, 2013, 8, e55209.	1.1	18
27	Characterization of the colorectal cancerâ€“associated enhancer MYC-335 at 8q24: the role of rs67491583. Cancer Genetics, 2012, 205, 25-33.	0.2	24
28	MED12 , the Mediator Complex Subunit 12 Gene, Is Mutated at High Frequency in Uterine Leiomyomas. Science, 2011, 334, 252-255.	6.0	547
29	Recessively inherited right atrial isomerism caused by mutations in growth/differentiation factor 1 (GDF1). Human Molecular Genetics, 2010, 19, 2747-2753.	1.4	48