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	Impact of cytosine methylation on DNA binding specificities of human transcription factors. Science, 2017, 356, .	6.0	912
2	MED12 , the Mediator Complex Subunit 12 Gene, Is Mutated at High Frequency in Uterine Leiomyomas. Science, 2011, 334, 252-255.	6.0	547
3	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	9.4	383
4	Characterization of Uterine Leiomyomas by Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 43-53.	13.9	280
5	The interaction landscape between transcription factors and the nucleosome. Nature, 2018, 562, 76-81.	13.7	259
6	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
7	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
8	Whole-Genome Sequencing of Growth Hormone (GH)-Secreting Pituitary Adenomas. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 3918-3927.	1.8	96
9	Sequence determinants of human gene regulatory elements. Nature Genetics, 2022, 54, 283-294.	9.4	87
10	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	1.3	81
11	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	2.3	76
12	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. Nature Communications, 2019, 10, 1252.	5.8	67
13	Genetic predisposition to uterine leiomyoma is determined by loci for genitourinary development and genome stability. ELife, 2018, 7, .	2.8	58
14	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	2.9	57
15	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	13.7	53
16	Mice deficient of Myc super-enhancer region reveal differential control mechanism between normal and pathological growth. ELife, 2017, 6, .	2.8	52
17	Recessively inherited right atrial isomerism caused by mutations in growth/differentiation factor 1 (GDF1). Human Molecular Genetics, 2010, 19, 2747-2753.	1.4	48
18	Global metabolomic profiling of uterine leiomyomas. British Journal of Cancer, 2017, 117, 1855-1864.	2.9	29

#	Article	IF	Citations
19	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
20	Contribution of allelic imbalance to colorectal cancer. Nature Communications, 2018, 9, 3664.	5.8	25
21	Characterization of the colorectal cancerâ€“associated enhancer MYC-335 at 8q24: the role of rs67491583. Cancer Genetics, 2012, 205, 25-33.	0.2	24
22	Candidate susceptibility variants for esophageal squamous cell carcinoma. Genes Chromosomes and Cancer, 2017, 56, 453-459.	1.5	23
23	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
24	Nationwide Registry-Based Analysis of Cancer Clustering Detects Strong Familial Occurrence of Kaposi Sarcoma. PLoS ONE, 2013, 8, e55209.	1.1	18
25	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.4	18
26	Comprehensive evaluation of coding region point mutations in microsatelliteâ€unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	3.3	10
27	Candidate susceptibility variants in angioimmunoblastic T-cell lymphoma. Familial Cancer, 2019, 18, 113-119.	0.9	8
28	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
29	Parity associates with chromosomal damage in uterine leiomyomas. Nature Communications, 2021, 12, 5448.	5.8	2