Kimmo Palin

List of Publications by Year
in descending order

45 papers	6,066 citations	218677 26 h-index	233421 45 g-index
51 all docs	51 docs citations	51 times ranked	14785 citing authors

#	Article	IF	Citations
1	MTG16 regulates colonic epithelial differentiation, colitis, and tumorigenesis by repressing E protein transcription factors. JCI Insight, 2022, 7, .	5.0	9
2	Lack of an association between gallstone disease and bilirubin levels with risk of colorectal cancer: a Mendelian randomisation analysis. British Journal of Cancer, 2021, 124, 1169-1174.	6.4	6
3	No evidence of EMAST in whole genome sequencing data from 248 colorectal cancers. Genes Chromosomes and Cancer, 2021, 60, 463-473.	2.8	5
4	Human cell transformation by combined lineage conversion and oncogene expression. Oncogene, 2021, 40, 5533-5547.	5.9	12
5	Genetic and Epigenetic Characteristics of Inflammatory Bowel Diseaseâ€“Associated Colorectal Cancer. Gastroenterology, 2021, 161, 592-607.	1.3	81
6	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	27.8	53
7	Parity associates with chromosomal damage in uterine leiomyomas. Nature Communications, 2021, 12, 5448.	12.8	2
8	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. The Lancet Gastroenterology and Hepatology, 2020, 5, 55-62.	8.1	79
9	Defining eligible patients for allele-selective chemotherapies targeting NAT2 in colorectal cancer. Scientific Reports, 2020, 10, 22436.	3.3	5
10	Retrotransposon insertions can initiate colorectal cancer and are associated with poor survival. Nature Communications, 2019, 10, 4022.	12.8	53
11	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
12	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
13	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	5.1	26
14	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
15	Contribution of allelic imbalance to colorectal cancer. Nature Communications, 2018, 9, 3664.	12.8	25
16	Comprehensive evaluation of coding region point mutations in microsatelliteâ€unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	6.9	10
17	Exome-wide somatic mutation characterization of small bowel adenocarcinoma. PLoS Genetics, 2018, 14, e1007200.	3.5	62
18	Genetic predisposition to uterine leiomyoma is determined by loci for genitourinary development and genome stability. ELife, 2018, 7, .	6.0	58

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19	Fast motif matching revisited: high-order PWMs, SNPs and indels. Bioinformatics, 2017, 33, 514-521.	4.1	30
20	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.9	18
21	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	5.1	76
22	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	2.8	81
23	Multiple clinical characteristics separate MED12-mutation-positive and -negative uterine leiomyomas. Scientific Reports, 2017, 7, 1015.	3.3	44
24	Detection of subclonal L1 transductions in colorectal cancer by long-distance inverse-PCR and Nanopore sequencing. Scientific Reports, 2017, 7, 14521.	3.3	24
25	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	6.4	57
26	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	6.2	21
27	Variation at 2q35 (PNKDandTMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. Human Molecular Genetics, 2016, 25, 2349-2359.	2.9	37
28	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	21.4	383
29	Systematic search for rare variants in Finnish early-onset colorectal cancer patients. Cancer Genetics, 2015, 208, 35-40.	0.4	24
30	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.	1.3	19
31	Uterine Leiomyoma-Linked MED12 Mutations Disrupt Mediator-Associated CDK Activity. Cell Reports, 2014, 7, 654-660.	6.4	125
32	Frequent L1 retrotranspositions originating fromTTC28in colorectal cancer. Oncotarget, 2014, 5, 853-859.	1.8	60
33	Identification of Candidate Oncogenes in Human Colorectal Cancers With Microsatellite Instability. Gastroenterology, 2013, 145, 540-543.e22.	1.3	65
34	DNA-Binding Specificities of Human Transcription Factors. Cell, 2013, 152, 327-339.	28.9	1,085
35	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	21.4	469
36	Identityâ€byâ€descentâ€based phasing and imputation in founder populations using graphical models. Genetic Epidemiology, 2011, 35, 853-860.	1.3	31

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37	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. EMBO Journal, 2010, 29, 2147-2160.	7.8	497
38	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
39	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. Genome Research, 2010, 20, 861-873.	5.5	382
40	The common colorectal cancer predisposition SNP rs6983267 at chromosome 8q24 confers potential to enhanced Wnt signaling. Nature Genetics, 2009, 41, 885-890.	21.4	463
41	Integrating sequence, evolution and functional genomics in regulatory genomics. Genome Biology, 2009, 10, 202.	9.6	18
42	Genome-wide Prediction of Mammalian Enhancers Based on Analysis of Transcription-Factor Binding Affinity. Cell, 2006, 124, 47-59.	28.9	435
43	Locating potential enhancer elements by comparative genomics using the EEL software. Nature Protocols, 2006, 1, 368-374.	12.0	31
44	From Gene Networks to Gene Function. Genome Research, 2003, 13, 2568-2576.	5.5	142
45	Correlating gene promoters and expression in gene disruption experiments. Bioinformatics, 2002, 18, S172-S180.	4.1	16