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	DNA-Binding Specificities of Human Transcription Factors. Cell, 2013, 152, 327-339.	28.9	1,085
2	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
3	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. EMBO Journal, 2010, 29, 2147-2160.	7.8	497
4	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	21.4	469
5	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
6	Genome-wide Prediction of Mammalian Enhancers Based on Analysis of Transcription-Factor Binding Affinity. Cell, 2006, 124, 47-59.	28.9	435
7	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	21.4	383
8	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. Genome Research, 2010, 20, 861-873.	5.5	382
9	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
10	From Gene Networks to Gene Function. Genome Research, 2003, 13, 2568-2576.	5.5	142
11	Uterine Leiomyoma-Linked MED12 Mutations Disrupt Mediator-Associated CDK Activity. Cell Reports, 2014, 7, 654-660.	6.4	125
12	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	2.8	81
13	Genetic and Epigenetic Characteristics of Inflammatory Bowel Diseaseâ€“Associated Colorectal Cancer. Gastroenterology, 2021, 161, 592-607.	1.3	81
14	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. The Lancet Gastroenterology and Hepatology, 2020, 5, 55-62.	8.1	79
15	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	5.1	76
16	Identification of Candidate Oncogenes in Human Colorectal Cancers With Microsatellite Instability. Gastroenterology, 2013, 145, 540-543.e22.	1.3	65
17	Exome-wide somatic mutation characterization of small bowel adenocarcinoma. PLoS Genetics, 2018, 14, e1007200.	3.5	62
18	Frequent L1 retrotranspositions originating fromTTC28in colorectal cancer. Oncotarget, 2014, 5, 853-859.	1.8	60

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19	Genetic predisposition to uterine leiomyoma is determined by loci for genitourinary development and genome stability. ELife, 2018, 7, .	6.0	58
20	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	6.4	57
21	Retrotransposon insertions can initiate colorectal cancer and are associated with poor survival. Nature Communications, 2019, 10, 4022.	12.8	53
22	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	27.8	53
23	Multiple clinical characteristics separate MED12-mutation-positive and -negative uterine leiomyomas. Scientific Reports, 2017, 7, 1015.	3.3	44
24	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
25	Locating potential enhancer elements by comparative genomics using the EEL software. Nature Protocols, 2006, 1, 368-374.	12.0	31
26	Identityâ€byâ€descentâ€based phasing and imputation in founder populations using graphical models. Genetic Epidemiology, 2011, 35, 853-860.	1.3	31
27	Fast motif matching revisited: high-order PWMs, SNPs and indels. Bioinformatics, 2017, 33, 514-521.	4.1	30
28	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
29	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
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	Detection of subclonal L1 transductions in colorectal cancer by long-distance inverse-PCR and Nanopore sequencing. Scientific Reports, 2017, 7, 14521.	3.3	24
33	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
34	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
35	Integrating sequence, evolution and functional genomics in regulatory genomics. Genome Biology, 2009, 10, 202.	9.6	18
36	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.9	18

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37	Correlating gene promoters and expression in gene disruption experiments. Bioinformatics, 2002, 18, S172-S180.	4.1	16
38	Human cell transformation by combined lineage conversion and oncogene expression. Oncogene, 2021, 40, 5533-5547.	5.9	12
39	Comprehensive evaluation of coding region point mutations in microsatelliteâ€unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	6.9	10
40	MTG16 regulates colonic epithelial differentiation, colitis, and tumorigenesis by repressing E protein transcription factors. JCI Insight, 2022, 7, .	5.0	9
41	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
42	No evidence of EMAST in whole genome sequencing data from 248 colorectal cancers. Genes Chromosomes and Cancer, 2021, 60, 463-473.	2.8	5
43	Defining eligible patients for allele-selective chemotherapies targeting NAT2 in colorectal cancer. Scientific Reports, 2020, 10, 22436.	3.3	5
44	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
45	Parity associates with chromosomal damage in uterine leiomyomas. Nature Communications, 2021, 12, 5448.	12.8	2