Ludmila Vodickova

List of Publications by Year
in descending order

66 papers	1,660 citations	304743 22 h-index	330143 37 g-index
67 all docs	67 docs citations	67 times ranked	2807 citing authors

#	Article	IF	Citations
1	HOTAIR long non-coding RNA is a negative prognostic factor not only in primary tumors, but also in the blood of colorectal cancer patients. Carcinogenesis, 2014, 35, 1510-1515.	2.8	227
2	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
3	Cumulative Burden of Colorectal Cancerâ€"Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	1.3	110
4	Circulating Levels of Insulin-like Growth Factor 1 and Insulin-like Growth Factor Binding Protein 3 Associate With Risk of Colorectal Cancer Based on Serologic and Mendelian Randomization Analyses. Gastroenterology, 2020, 158, 1300-1312.e20.	1.3	90
5	<scp>TERT</scp> gene harbors multiple variants associated with pancreatic cancer susceptibility. International Journal of Cancer, 2015, 137, 2175-2183.	5.1	57
6	ABO blood groups and pancreatic cancer risk and survival: Results from the PANcreatic Disease ReseArch (PANDoRA) consortium. Oncology Reports, 2013, 29, 1637-1644.	2.6	55
7	Genetic susceptibility to pancreatic cancer and its functional characterisation: The PANcreatic Disease ReseArch (PANDoRA) consortium. Digestive and Liver Disease, 2013, 45, 95-99.	0.9	45
8	DNA damage and repair measured by comet assay in cancer patients. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2019, 843, 95-110.	1.7	43
9	Functional single nucleotide polymorphisms within the cyclin-dependent kinase inhibitor 2A/2B region affect pancreatic cancer risk. Oncotarget, 2016, 7, 57011-57020.	1.8	41
10	DNA repair and cancer in colon and rectum: Novel players in genetic susceptibility. International Journal of Cancer, 2020, 146, 363-372.	5.1	40
11	Double-strand break repair and colorectal cancer: gene variants within 3â€² UTRs and microRNAs binding as modulators of cancer risk and clinical outcome. Oncotarget, 2016, 7, 23156-23169.	1.8	40
12	Genetic determinants of telomere length and risk of pancreatic cancer: A PANDoRA study. International Journal of Cancer, 2019, 144, 1275-1283.	5.1	36
13	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	1.3	36
14	Structural chromosomal aberrations as potential risk markers in incident cancer patients. Mutagenesis, 2015, 30, 557-563.	2.6	34
15	Fusobacterium nucleatum tumor DNA levels are associated with survival in colorectal cancer patients. European Journal of Clinical Microbiology and Infectious Diseases, 2019, 38, 1891-1899.	2.9	33
16	Polygenic and multifactorial scores for pancreatic ductal adenocarcinoma risk prediction. Journal of Medical Genetics, 2021, 58, 369-377.	3.2	31
17	Single Nucleotide Polymorphisms within Interferon Signaling Pathway Genes Are Associated with Colorectal Cancer Susceptibility and Survival. PLoS ONE, 2014, 9, e111061.	2.5	29
18	Relationship of telomere length in colorectal cancer patients with cancer phenotype and patient prognosis. British Journal of Cancer, 2019, 121, 344-350.	6.4	28

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19	Base excision repair capacity as a determinant of prognosis and therapy response in colon cancer patients. DNA Repair, 2018, 72, 77-85.	2.8	27
20	Interactions of DNA repair gene variants modulate chromosomal aberrations in healthy subjects. Carcinogenesis, 2015, 36, 1299-1306.	2.8	24
21	Polymorphisms in microRNA binding sites of mucin genes as predictors of clinical outcome in colorectal cancer patients. Carcinogenesis, 2017, 38, 28-39.	2.8	23
22	Ganoderma Lucidum induces oxidative DNA damage and enhances the effect of 5-Fluorouracil in colorectal cancer in vitro and in vivo. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2019, 845, 403065.	1.7	23
23	Epigenome-wide analysis of DNA methylation reveals a rectal cancer-specific epigenomic signature. Epigenomics, 2016, 8, 1193-1207.	2.1	22
24	Association between taste receptor (TAS) genes and the perception of wine characteristics. Scientific Reports, 2017, 7, 9239.	3.3	22
25	Association between polymorphisms of TAS2R16 and susceptibility to colorectal cancer. BMC Gastroenterology, 2017, 17, 104.	2.0	21
26	Variations in mismatch repair genes and colorectal cancer risk and clinical outcome. Mutagenesis, 2014, 29, 259-265.	2.6	20
27	Genomeâ€wide association study identifies an early onset pancreatic cancer risk locus. International Journal of Cancer, 2020, 147, 2065-2074.	5.1	20
28	The Interactions of DNA Repair, Telomere Homeostasis, and p53 Mutational Status in Solid Cancers: Risk, Prognosis, and Prediction. Cancers, 2021, 13, 479.	3.7	20
29	Genetic variation of acquired structural chromosomal aberrations. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2018, 836, 13-21.	1.7	19
30	Genotype and Haplotype Analyses of TP53 Gene in Breast Cancer Patients: Association with Risk and Clinical Outcomes. PLoS ONE, 2015, 10, e0134463.	2.5	19
31	Post-treatment recovery of suboptimal DNA repair capacity and gene expression levels in colorectal cancer patients. Molecular Carcinogenesis, 2015, 54, 769-778.	2.7	16
32	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79.	2.2	16
33	DNA and chromosomal damage in medical workers exposed to anaesthetic gases assessed by the lymphocyte cytokinesis-block micronucleus (CBMN) assay. A critical review. Mutation Research - Reviews in Mutation Research, 2016, 770, 26-34.	5.5	15
34	SLC22A3 polymorphisms do not modify pancreatic cancer risk, but may influence overall patient survival. Scientific Reports, 2017, 7, 43812.	3.3	15
35	Single nucleotide polymorphisms within MUC4 are associated with colorectal cancer survival. PLoS ONE, 2019, 14, e0216666.	2.5	15
36	Non-Coding Polymorphisms in Nucleotide Binding Domain 1 in ABCC1 Gene Associate with Transcript Level and Survival of Patients with Breast Cancer. PLoS ONE, 2014, 9, e101740.	2.5	14

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37	Genotoxic and Cytotoxic Effects in Exfoliated Buccal and Nasal Cells of Chromium and Cobalt Exposed Electroplaters. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2017, 80, 651-660.	2.3	14
38	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821.	7.2	14
39	Associations between pancreatic expression quantitative traits and risk of pancreatic ductal adenocarcinoma. Carcinogenesis, 2021, 42, 1037-1045.	2.8	14
40	Eight novel loci implicate shared genetic etiology in multiple myeloma, AL amyloidosis, and monoclonal gammopathy of unknown significance. Leukemia, 2020, 34, 1187-1191.	7.2	13
41	Genetic variation in the major mitotic checkpoint genes associated with chromosomal aberrations in healthy humans. Cancer Letters, 2016, 380, 442-446.	7.2	12
42	Bleomycinâ€induced chromosomal damage and shortening of telomeres in peripheral blood lymphocytes of incident cancer patients. Genes Chromosomes and Cancer, 2018, 57, 61-69.	2.8	12
43	Truncated PPM1D impairs stem cell response to genotoxic stress and promotes growth of APC-deficient tumors in the mouse colon. Cell Death and Disease, 2019, 10, 818.	6.3	12
44	DNA repair capacity and response to treatment of colon cancer. Pharmacogenomics, 2019, 20, 1225-1233.	1.3	11
45	Telomere maintenance in interplay with DNA repair in pathogenesis and treatment of colorectal cancer. Mutagenesis, 2020, 35, 261-271.	2.6	11
46	Telomere length in peripheral blood lymphocytes related to genetic variation in telomerase, prognosis and clinicopathological features in breast cancer patients. Mutagenesis, 2020, 35, 491-497.	2.6	11
47	Epistatic effect of TLR3 and cGASâ€STINGâ€IKKÎµâ€TBK1â€IFN signaling variants on colorectal cancer risk. Cancer Medicine, 2020, 9, 1473-1484.	2.8	10
48	Genetic variation associated with chromosomal aberration frequency: A genomeâ€wide association study. Environmental and Molecular Mutagenesis, 2019, 60, 17-28.	2.2	9
49	Association between CASP8 â€“652 6N Del Polymorphism (rs3834129) and Colorectal Cancer Risk: Results from a Multi-Centric Study. PLoS ONE, 2014, 9, e85538.	2.5	8
50	Histopathological aspects of liver under variable food restriction: Has the intense one-week food restriction a protective effect on non-alcoholic-fatty-liver-disease (NAFLD) development?. Pathology Research and Practice, 2014, 210, 855-862.	2.3	7
51	The focus on sample quality: Influence of colon tissue collection on reliability of qPCR data. Scientific Reports, 2016, 6, 29023.	3.3	7
52	Coding variants in NOD-like receptors: An association study on risk and survival of colorectal cancer. PLoS ONE, 2018, 13, e0199350.	2.5	6
53	Distinct pathways associated with chromosomal aberration frequency in a cohort exposed to genotoxic compounds compared to general population. Mutagenesis, 2019, 34, 323-330.	2.6	6
54	Genetic variations in microRNA-binding sites of solute carrier transporter genes as predictors of clinical outcome in colorectal cancer. Carcinogenesis, 2021, 42, 378-394.	2.8	6

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55	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	6.2	5
56	Mutational analysis of driver genes defines the colorectal adenoma: in situ carcinoma transition. Scientific Reports, 2022, 12, 2570.	3.3	5
57	Polymorphisms within Autophagy-Related Genes Influence the Risk of Developing Colorectal Cancer: A Meta-Analysis of Four Large Cohorts. Cancers, 2021, 13, 1258.	3.7	3
58	DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. DNA Repair, 2021, 101, 103079.	2.8	3
59	DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. Frontiers in Genetics, 2021, 12, 691947.	2.3	3
60	A novel c. 204 Ile68Met germline variant in exon 2 of the mutL homolog 1 gene in a colorectal cancer patient. Oncology Letters, 2015, 9, 183-186.	1.8	2
61	Expression quantitative trait loci in ABC transporters are associated with survival in 5-FU treated colorectal cancer patients. Mutagenesis, 2020, 35, 273-281.	2.6	2
62	Impact of genetic polymorphisms in kinetochore and spindle assembly genes on chromosomal aberration frequency in healthy humans. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 858-860, 503253.	1.7	2
63	Genome-wide meta-analysis of monoclonal gammopathy of undetermined significance (MGUS) identifies risk loci impacting IRF-6. Blood Cancer Journal, 2022, 12, 60.	6.2	2
64	Single nucleotide polymorphisms within Mucin-type O-glycan genes are associated with colorectal cancer survival.. Journal of Clinical Oncology, 2018, 36, e15607-e15607.	1.6	0
65	Genetic Susceptibility in Understanding of Pancreatic Ductal Adenocarcinoma Risk: A Decade-Long Effort of the PANDORA Consortium. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 942-948.	2.5	0
66	Abstract 2316: Malignant potential of colorectal adenoma based on the telomere length. Cancer Research, 2022, 82, 2316-2316.	0.9	0