Ludmila V Danilova

List of Publications by Year
in descending order

60 papers	**26,890** citations	109321 **35** h-index	133252 **59** g-index
67 all docs	**67** docs citations	**67** times ranked	**39364** citing authors

#	Article	IF	Citations
1	Mismatch repair deficiency predicts response of solid tumors to PD-1 blockade. Science, 2017, 357, 409-413.	12.6	4,945
2	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
3	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
4	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
5	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
6	Detection and localization of surgically resectable cancers with a multi-analyte blood test. Science, 2018, 359, 926-930.	12.6	1,872
7	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
8	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
9	Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. Genome Biology, 2016, 17, 231.	8.8	746
10	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
11	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
12	Comparison of Biomarker Modalities for Predicting Response to PD-1/PD-L1 Checkpoint Blockade. JAMA Oncology, 2019, 5, 1195.	7.1	431
13	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
14	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
15	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
16	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
17	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
18	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.9	236

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19	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	19.0	209
20	Evaluation of liquid from the Papanicolaou test and other liquid biopsies for the detection of endometrial and ovarian cancers. Science Translational Medicine, 2018, 10, .	12.4	178
21	Programmed Cell Death Ligand-1 (PD-L1) and CD8 Expression Profiling Identify an Immunologic Subtype of Pancreatic Ductal Adenocarcinomas with Favorable Survival. Cancer Immunology Research, 2019, 7, 886-895.	3.4	171
22	Diagnostic utility of telomere length testing in a hospital-based setting. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2358-E2365.	7.1	165
23	Neoadjuvant cabozantinib and nivolumab convert locally advanced hepatocellular carcinoma into resectable disease with enhanced antitumor immunity. Nature Cancer, 2021, 2, 891-903.	13.2	147
24	Association of PD-1/PD-L axis expression with cytolytic activity, mutational load, and prognosis in melanoma and other solid tumors. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7769-E7777.	7.1	145
25	Multidimensional, quantitative assessment of PD-1/PD-L1 expression in patients with Merkel cell carcinoma and association with response to pembrolizumab. , 2018, 6, 99.		129
26	Non-invasive detection of urothelial cancer through the analysis of driver gene mutations and aneuploidy. ELife, 2018, 7, .	6.0	118
27	The Mutation-Associated Neoantigen Functional Expansion of Specific T Cells (MANAFEST) Assay: A Sensitive Platform for Monitoring Antitumor Immunity. Cancer Immunology Research, 2018, 6, 888-899.	3.4	118
28	Analysis of multispectral imaging with the AstroPath platform informs efficacy of PD-1 blockade. Science, 2021, 372, .	12.6	114
29	Epigenetic regulation of gene expression in cancer: techniques, resources and analysis. Briefings in Functional Genomics, 2018, 17, 49-63.	2.7	111
30	Novel Insight into Mutational Landscape of Head and Neck Squamous Cell Carcinoma. PLoS ONE, 2014, 9, e93102.	2.5	87
31	Evaluation of Cyclophosphamide/GVAX Pancreas Followed by Listeria-Mesothelin (CRS-207) with or without Nivolumab in Patients with Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 3578-3588.	7.0	76
32	Integrated Genomic and Functional microRNA Analysis Identifies miR-30-5p as a Tumor Suppressor and Potential Therapeutic Nanomedicine in Head and Neck Cancer. Clinical Cancer Research, 2019, 25, 2860-2873.	7.0	68
33	Integrated Analysis of Whole-Genome ChIP-Seq and RNA-Seq Data of Primary Head and Neck Tumor Samples Associates HPV Integration Sites with Open Chromatin Marks. Cancer Research, 2017, 77, 6538-6550.	0.9	50
34	Revisiting the tumorigenesis timeline with a data-driven generative model. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 857-864.	7.1	44
35	A multi-omic analysis of human naÃ¯ve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
36	<i>GPX3</i> promoter methylation predicts platinum sensitivity in colorectal cancer. Epigenetics, 2017, 12, 540-550.	2.7	43

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37	Persistent mutant oncogene specific T cells in two patients benefitting from anti-PD-1. , 2019, 7, 40.		42
38	A Novel Functional Splice Variant of <i>AKT3</i> Defined by Analysis of Alternative Splice Expression in HPV-Positive Oropharyngeal Cancers. Cancer Research, 2017, 77, 5248-5258.	0.9	41
39	Preferential Activation of the Hedgehog Pathway by Epigenetic Modulations in HPV Negative HNSCC Identified with Meta-Pathway Analysis. PLoS ONE, 2013, 8, e78127.	2.5	39
40	Viral status, immune microenvironment and immunological response to checkpoint inhibitors in hepatocellular carcinoma. , 2020, 8, e000394.		39
41	Discovery and development of differentially methylated regions in human papillomavirusâ€related oropharyngeal squamous cell carcinoma. International Journal of Cancer, 2018, 143, 2425-2436.	5.1	35
42	Multi-omic profiling of lung and liver tumor microenvironments of metastatic pancreatic cancer reveals site-specific immune regulatory pathways. Genome Biology, 2021, 22, 154.	8.8	30
43	Integrated time course omics analysis distinguishes immediate therapeutic response from acquired resistance. Genome Medicine, 2018, 10, 37.	8.2	25
44	Systemic inhibition of PTPN22 augments anticancer immunity. Journal of Clinical Investigation, 2021, 131, .	8.2	24
45	DNA methylation regulates TMEM16A/ANO1 expression through multiple CpG islands in head and neck squamous cell carcinoma. Scientific Reports, 2017, 7, 15173.	3.3	20
46	Extracellular Vesicles Released by Tumor Endothelial Cells Spread Immunosuppressive and Transforming Signals Through Various Recipient Cells. Frontiers in Cell and Developmental Biology, 2020, 8, 698.	3.7	18
47	Mechanistically detailed systems biology modeling of the HGF/Met pathway in hepatocellular carcinoma. Npj Systems Biology and Applications, 2019, 5, 29.	3.0	17
48	Cytokines secreted by stromal cells in TNBC microenvironment as potential targets for cancer therapy. Cancer Biology and Therapy, 2020, 21, 560-569.	3.4	17
49	Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. Epigenetics, 2020, 15, 959-971.	2.7	17
50	Transfer learning between preclinical models and human tumors identifies a conserved NK cell activation signature in anti-CTLA-4 responsive tumors. Genome Medicine, 2021, 13, 129.	8.2	17
51	Multipanel mass cytometry reveals antiâ€"PD-1 therapyâ€"mediated B and T cell compartment remodeling in tumor-draining lymph nodes. JCI Insight, 2020, 5, .	5.0	17
52	Integrative computational analysis of transcriptional and epigenetic alterations implicates <i>DTX1</i> as a putative tumor suppressor gene in HNSCC. Oncotarget, 2017, 8, 15349-15363.	1.8	16
53	Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. Translational Research, 2018, 202, 109-119.	5.0	15
54	PTPRT epigenetic silencing defines lung cancer with STAT3 activation and can direct STAT3 targeted therapies. Epigenetics, 2020, 15, 604-617.	2.7	15

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55	Supervised mutational signatures for obesity and other tissue-specific etiological factors in cancer. ELife, 2021, 10, .	6.0	12
56	Genome-wide DNA methylation profiling identifies epigenetic changes in CD4+ and CD14+ cells of multiple sclerosis patients. Multiple Sclerosis and Related Disorders, 2022, 60, 103714.	2.0	10
57	Differentially Methylated Super-Enhancers Regulate Target Gene Expression in Human Cancer. Scientific Reports, 2019, 9, 15034.	3.3	9
58	Spatial UMAP and Image Cytometry for Topographic Immuno-oncology Biomarker Discovery. Cancer Immunology Research, 2021, 9, 1262-1269.	3.4	8
59	DNA-methylation for the detection and distinction of 19 human malignancies. Epigenetics, 2022, 17, 191-201.	2.7	7
60	MVisAGe Identifies Concordant and Discordant Genomic Alterations of Driver Genes in Squamous Tumors. Cancer Research, 2018, 78, 3375-3385.	0.9	5