Ludmil B Alexandrov

List of Publications by Year
in descending order

146	40,202	13099	12597
papers	citations	68 h-index	132 g-index

176	176	176	48198
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	27.8	2,104
3	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
4	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
5	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
6	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	12.6	1,431
7	Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. Nature Genetics, 2015, 47, 505-511.	21.4	1,372
8	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
9	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185
10	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	6.4	1,087
11	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
12	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	12.6	842
13	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	21.4	837
14	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	12.8	741
15	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
16	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
17	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	9.4	637
18	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	16.8	534

#	Article	IF	Citations
19	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	21.4	502
20	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. Nature, 2016, 538, 378-382.	27.8	418
21	Intra-tumour diversification in colorectal cancer at the single-cell level. Nature, 2018, 556, 457-462.	27.8	406
22	Mutational signatures: the patterns of somatic mutations hidden in cancer genomes. Current Opinion in Genetics and Development, 2014, 24, 52-60.	3.3	393
23	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	21.4	380
24	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
25	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
26	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	27.8	315
27	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 116-125.	21.4	313
28	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. Nature Communications, 2015, 6, 6605.	12.8	312
29	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. Nature Genetics, 2015, 47, 257-262.	21.4	306
30	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. Cell, 2012, 148, 780-791.	28.9	300
31	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	28.9	298
32	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. Nature Genetics, 2014, 46, 487-491.	21.4	254
33	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. Nature Communications, 2018, 9, 1048.	12.8	254
34	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235
35	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
36	Association of Distinct Mutational Signatures With Correlates of Increased Immune Activity in Pancreatic Ductal Adenocarcinoma. JAMA Oncology, 2017, 3, 774.	7.1	221

#	Article	IF	Citations
37	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	12.8	214
38	The genomic landscape of cutaneous SCC reveals drivers and a novel azathioprine associated mutational signature. Nature Communications, 2018, 9, 3667.	12.8	208
39	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. Nature Genetics, 2018, 50, 682-692.	21.4	182
40	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. Nature Communications, 2017, 8, 15936.	12.8	179
41	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	12.8	177
42	The genome as a record of environmental exposure. Mutagenesis, 2015, 30, gev073.	2.6	174
43	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
44	A Specific Mutational Signature Associated with DNA 8-Oxoguanine Persistence in MUTYH-defective Colorectal Cancer. EBioMedicine, 2017, 20, 39-49.	6.1	170
45	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. Genome Research, 2014, 24, 1624-1636.	5.5	164
46	Genomic patterns of progression in smoldering multiple myeloma. Nature Communications, 2018, 9, 3363.	12.8	163
47	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. BMC Genomics, 2019, 20, 685.	2.8	162
48	Signatures of copy number alterations in human cancer. Nature, 2022, 606, 984-991.	27.8	154
49	SETD2 loss-of-function promotes renal cancer branched evolution through replication stress and impaired DNA repair. Oncogene, 2015, 34, 5699-5708.	5.9	147
50	A mutational signature in gastric cancer suggests therapeutic strategies. Nature Communications, 2015, 6, 8683.	12.8	146
51	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. Science, 2014, 343, 437-440.	12.6	144
52	Mutational signature analysis identifies <scp>MUTYH</scp> deficiency in colorectal cancers and adrenocortical carcinomas. Journal of Pathology, 2017, 242, 10-15.	4.5	130
53	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. Science, 2018, 361, .	12.6	121
54	Precancer Atlas to Drive Precision Prevention Trials. Cancer Research, 2017, 77, 1510-1541.	0.9	116

#	Article	IF	Citations
55	The driver landscape of sporadic chordoma. Nature Communications, 2017, 8, 890.	12.8	115
56	IL-17 signaling in steatotic hepatocytes and macrophages promotes hepatocellular carcinoma in alcohol-related liver disease. Journal of Hepatology, 2020, 72, 946-959.	3.7	113
57	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	21.4	111
58	Mammalian Stem Cells Reprogramming in Response to Terahertz Radiation. PLoS ONE, 2010, 5, e15806.	2.5	109
59	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	9.4	109
60	Germline MC1R status influences somatic mutation burden in melanoma. Nature Communications, 2016, 7, 12064.	12.8	103
61	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
62	Syngeneic animal models of tobacco-associated oral cancer reveal the activity of in situ anti-CTLA-4. Nature Communications, 2019, 10, 5546.	12.8	98
63	APOBEC mutation drives early-onset squamous cell carcinomas in recessive dystrophic epidermolysis bullosa. Science Translational Medicine, 2018, 10, .	12.4	91
64	Understanding mutagenesis through delineation of mutational signatures in human cancer. Carcinogenesis, 2016, 37, 531-540.	2.8	90
65	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. Cancer Cell, 2018, 33, 607-619.e15.	16.8	88
66	Biological and prognostic impact of APOBEC-induced mutations in the spectrum of plasma cell dyscrasias and multiple myeloma cell lines. Leukemia, 2018, 32, 1043-1047.	7.2	87
67	The mutational signature profile of known and suspected human carcinogens in mice. Nature Genetics, 2020, 52, 1189-1197.	21.4	84
68	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. Cancer Cell, 2019, 35, 441-456.e8.	16.8	82
69	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81
70	Specificity and Heterogeneity of Terahertz Radiation Effect on Gene Expression in Mouse Mesenchymal Stem Cells. Scientific Reports, 2013, 3, 1184.	3.3	78
71	Strength of immune selection in tumors varies with sex and age. Nature Communications, 2020, 11, 4128.	12.8	78
72	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	21.4	75

#	Article	IF	Citations
73	Non-thermal effects of terahertz radiation on gene expression in mouse stem cells. Biomedical Optics Express, 2011, 2, 2679.	2.9	73
74	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. Nature Genetics, 2021, 53, 1553-1563.	21.4	71
75	Nonnegative/Binary matrix factorization with a D-Wave quantum annealer. PLoS ONE, 2018, 13, e0206653.	2.5	68
76	Integrative genomic analysis of mouse and human hepatocellular carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9879-E9888.	7.1	67
77	A nonlinear dynamic model of DNA with a sequence-dependent stacking term. Nucleic Acids Research, 2009, 37, 2405-2410.	14.5	61
78	Mutational signatures in tumours induced by high and low energy radiation in Trp53 deficient mice. Nature Communications, 2020, 11, 394.	12.8	61
79	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	12.8	60
80	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	27.8	60
81	DNA dynamics play a role as a basal transcription factor in the positioning and regulation of gene transcription initiation. Nucleic Acids Research, 2010, 38, 1790-1795.	14.5	59
82	Base changes in tumour DNA have the power to reveal the causes and evolution of cancer. Oncogene, 2017, 36, 158-167.	5.9	58
83	Somatic evolution and global expansion of an ancient transmissible cancer lineage. Science, 2019, 365, .	12.6	58
84	Modelling the magnetic signature of neuronal tissue. NeuroImage, 2007, 37, 137-148.	4.2	55
85	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. Nature Genetics, 2020, 52, 74-83.	21.4	53
86	Whole-exome sequencing of cervical carcinomas identifies activating ERBB2 and PIK3CA mutations as targets for combination therapy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22730-22736.	7.1	52
87	Integrated mutational landscape analysis of uterine leiomyosarcomas. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	48
88	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	12.8	46
89	Immune evasion in HPV^{â^'}head and neck precancerâ€“cancer transition is driven by an aneuploid switch involving chromosome 9p loss. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	45
90	Uracil Accumulation and Mutagenesis Dominated by Cytosine Deamination in CpG Dinucleotides in Mice Lacking UNG and SMUG1. Scientific Reports, 2017, 7, 7199.	3.3	43

#	Article	IF	Citations
91	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
92	Fast randomization of large genomic datasets while preserving alteration counts. Bioinformatics, 2014, 30, i617-i623.	4.1	36
93	Understanding the origins of human cancer. Science, 2015, 350, 1175-1177.	12.6	32
94	Inhibition of mTOR signaling and clinical activity of metformin in oral premalignant lesions. JCI Insight, 2021, 6, .	5.0	29
95	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. Nature Communications, 2021, 12, 4496.	12.8	28
96	A phase 2 evaluation of pembrolizumab for recurrent Lynchâ€like versus sporadic endometrial cancers with microsatellite instability. Cancer, 2022, 128, 1206-1218.	4.1	28
97	Whole-exome sequencing reveals the impact of UVA light mutagenesis in xeroderma pigmentosum variant human cells. Nucleic Acids Research, 2020, 48, 1941-1953.	14.5	27
98	Generating realistic null hypothesis of cancer mutational landscapes using SigProfilerSimulator. BMC Bioinformatics, 2020, 21, 438.	2.6	27
99	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
100	Analysis of mutational signatures in exomes from B-cell lymphoma cell lines suggest APOBEC3 family members to be involved in the pathogenesis of primary effusion lymphoma. Leukemia, 2015, 29, 1612-1615.	7.2	26
101	Revertant mosaicism repairs skin lesions in a patient with keratitis-ichthyosis-deafness syndrome by second-site mutations in connexin 26. Human Molecular Genetics, 2017, 26, 1070-1077.	2.9	25
102	Binding of Nucleoid-Associated Protein Fis to DNA Is Regulated by DNA Breathing Dynamics. PLoS Computational Biology, 2013, 9, e1002881.	3.2	23
103	Inflammation-driven deaminase deregulation fuels human pre-leukemia stem cell evolution. Cell Reports, 2021, 34, 108670.	6.4	22
104	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
105	Significance and limitations of the use of next-generation sequencing technologies for detecting mutational signatures. DNA Repair, 2021, 107, 103200.	2.8	18
106	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
107	Unraveling the genomic landscape of colorectal cancer through mutational signatures. Advances in Cancer Research, 2021, 151, 385-424.	5.0	14
108	Somatic mutational profiles and germline polygenic risk scores in human cancer. Genome Medicine, 2022, 14, 14.	8.2	14

#	Article	IF	Citations
109	Examining clustered somatic mutations with SigProfilerClusters. Bioinformatics, 2022, 38, 3470-3473.	4.1	14
110	Evaluating the role of coherent delocalized phonon-like modes in DNA cyclization. Scientific Reports, 2017, 7, 9731.	3.3	13
111	An overview of mutational and copy number signatures in human cancer. Journal of Pathology, 2022, 257, 454-465.	4.5	12
112	Homologous recombination deficiency (HRD) signature-3 in ovarian and uterine carcinosarcomas correlates with preclinical sensitivity to Olaparib, a poly (adenosine diphosphate [ADP]- ribose) polymerase (PARP) inhibitor. Gynecologic Oncology, 2022, 166, 117-125.	1.4	12
113	Insights into BRCA Cancer Predisposition from Integrated Germline and Somatic Analyses in 7632 Cancers. JNCI Cancer Spectrum, 2019, 3, pkz028.	2.9	10
114	Stem cell replication, somatic mutations and role of randomness in the development of cancer. European Journal of Epidemiology, 2019, 34, 439-445.	5.7	9
115	DNA Dynamics Is Likely to Be a Factor in the Genomic Nucleotide Repeats Expansions Related to Diseases. PLoS ONE, 2011, 6, e19800.	2.5	8
116	Synergistic activity of neratinib in combination with olaparib in uterine serous carcinoma overexpressing HER2/neu. Gynecologic Oncology, 2022, 166, 351-357.	1.4	8
117	The role of structural parameters in DNA cyclization. BMC Bioinformatics, 2016, 17, 68.	2.6	7
118	The Association of Modifiable Breast Cancer Risk Factors and Somatic Genomic Alterations in Breast Tumors: The Cancer Genome Atlas Network. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 599-605.	2.5	7
119	Bioinformatic Methods to Identify Mutational Signatures in Cancer. Methods in Molecular Biology, 2021, 2185, 447-473.	0.9	7
120	A phase II evaluation of pembrolizumab in recurrent microsatellite instability-high (MSI-H) endometrial cancer patients with Lynch-like versus MLH-1 methylated characteristics (NCT02899793).. Journal of Clinical Oncology, 2021, 39, 5523-5523.	1.6	5
121	Mutational Signatures and the Etiology of Human Cancers. , 2018, , .		3
122	Abstract 4322: The landscape of mitochondrial DNA mutations in human cancer. Cancer Research, 2014, 74, 4322-4322.	0.9	3
123	Imetelstat Inhibits Telomerase and Prevents Propagation of ADAR1-Activated Myeloproliferative Neoplasm and Leukemia Stem Cells. Blood, 2020, 136, 18-18.	1.4	3
124	Timing the initiation of multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e6-e7.	0.4	1
125	Synchronous, Yet Genomically Distinct, GIST Offer New Insights Into Precise Targeting of Tumor Driver Mutations. JCO Precision Oncology, 2021, 5, 525-532.	3.0	1
126	Computer Modeling Describes Gravity-Related Adaptation in Cell Cultures. PLoS ONE, 2009, 4, e8332.	2.5	1

#	Article	IF	Citations
127	Abstract IA11: Signatures of mutational processes in human cancer. , 2017, , .		1
128	MP49-01 SUBCLONAL ORIGIN OF PROSTATE CANCER METASTASIS WITH MUTATOR PHENOTYPE FROM A NOVEL MSH2 GENE FUSION. Journal of Urology, 2014, 191, .	0.4	0
129	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. Blood, 2013, 122, 399-399.	1.4	0
130	Tracking clonal diversity in metastatic prostate cancer progression.. Journal of Clinical Oncology, 2015, 33, 193-193.	1.6	0
131	Abstract 2973: Exome sequencing of 243 liver tumors identifies new mutational signatures and potential therapeutic targets. , 2015, , .		0
132	Abstract 956: The evolutionary history of lethal metastatic prostate cancer. , 2015, , .		0
133	Abstract B09: DNA polymerase mutations trigger rapid onset of ultra-hypermutant malignant brain tumors in children with biallelic mismatch repair deficiency. , 2015, , .		0
134	Abstract A009: Benchmarking the foreign antigen space of human malignancies. , 2016, , .		0
135	Benchmarking the Foreign Antigen Space of Human Malignancies. SSRN Electronic Journal, 0, , .	0.4	0
136	Undifferentiated Sarcomas Develop Through Distinct Evolutionary Pathways. SSRN Electronic Journal, 0, , .	0.4	0
137	Clonal Diaspora in Metastatic Esophageal Adenocarcinoma Describes a New Model of Cancer Progression. SSRN Electronic Journal, 0, , .	0.4	0
138	Abstract 2506: Exploring the complex etiology of oncogenic fusions in childhood cancer. , 2019, , .		0
139	Inflammatory Cytokine Responsive Enzymatic Mutagenesis Fuels Myeloproliferative Neoplasm Pre-Leukemia Stem Cell Evolution. Blood, 2019, 134, 3780-3780.	1.4	0
140	Timing the Initiation of Multiple Myeloma. Blood, 2019, 134, 573-573.	1.4	0
141	Abstract 2318: The association between somatic mutational profiles and germline polygenic risk scores in TCGA. , 2020, , .		0
142	Abstract 1319: Distinct pancancer mutational signatures are determined byAPOBEC/ADARaberrations. , 2020, , .		0
143	Abstract P5-08-07: Tobacco use, alcohol consumption, and breast cancer somatic genomic alterations. , 2020, , .		0
144	Unwinding the mutational signatures of a DNA topoisomerase enzyme. Nature, 2022, 602, 580-581.	27.8	0

#	Article	IF	Citations
145	Abstract SY26-02:Sherlock-Lung: Tracing lung cancer mutational processes in never smokers. , 2019, , .		0
146	TBIO-04. Comprehensive analysis of mutational signatures in pediatric cancers. Neuro-Oncology, 2022, 24, i183-i183.	1.2	0