

Ludmil B Alexandrov

List of Publications by Year in descending order

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Version: 2024-02-01

146
papers

40,202
citations

13099

68
h-index

12597

132
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176
all docs

176
docs citations

176
times ranked

48198
citing authors

#	ARTICLE	IF	CITATIONS
1	Unwinding the mutational signatures of a DNA topoisomerase enzyme. <i>Nature</i> , 2022, 602, 580-581.	27.8	0
2	Somatic mutational profiles and germline polygenic risk scores in human cancer. <i>Genome Medicine</i> , 2022, 14, 14.	8.2	14
3	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. <i>Nature</i> , 2022, 602, 510-517.	27.8	60
4	A phase 2 evaluation of pembrolizumab for recurrent Lynch-like versus sporadic endometrial cancers with microsatellite instability. <i>Cancer</i> , 2022, 128, 1206-1218.	4.1	28
5	An overview of mutational and copy number signatures in human cancer. <i>Journal of Pathology</i> , 2022, 257, 454-465.	4.5	12
6	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. <i>Gynecologic Oncology</i> , 2022, 166, 117-125.	1.4	12
7	Synergistic activity of neratinib in combination with olaparib in uterine serous carcinoma overexpressing HER2/neu. <i>Gynecologic Oncology</i> , 2022, 166, 351-357.	1.4	8
8	Examining clustered somatic mutations with SigProfilerClusters. <i>Bioinformatics</i> , 2022, 38, 3470-3473.	4.1	14
9	TBIO-04. Comprehensive analysis of mutational signatures in pediatric cancers. <i>Neuro-Oncology</i> , 2022, 24, i183-i183.	1.2	0
10	Signatures of copy number alterations in human cancer. <i>Nature</i> , 2022, 606, 984-991.	27.8	154
11	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. <i>American Journal of Epidemiology</i> , 2021, 190, 962-976.	3.4	16
12	Inflammation-driven deaminase deregulation fuels human pre-leukemia stem cell evolution. <i>Cell Reports</i> , 2021, 34, 108670.	6.4	22
13	Unraveling the genomic landscape of colorectal cancer through mutational signatures. <i>Advances in Cancer Research</i> , 2021, 151, 385-424.	5.0	14
14	Synchronous, Yet Genomically Distinct, GIST Offer New Insights Into Precise Targeting of Tumor Driver Mutations. <i>JCO Precision Oncology</i> , 2021, 5, 525-532.	3.0	1
15	Integrated mutational landscape analysis of uterine leiomyosarcomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
16	Immune evasion in HPV⁺ head and neck precancerâ€“cancer transition is driven by an aneuploid switch involving chromosome 9p loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	45
17	A phase II evaluation of pembrolizumab in recurrent microsatellite instability-high (MSI-H) endometrial cancer patients with Lynch-like versus <i>MLH</i>-1 methylated characteristics (NCT02899793).. <i>Journal of Clinical Oncology</i> , 2021, 39, 5523-5523.	1.6	5
18	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. <i>Nature Communications</i> , 2021, 12, 4496.	12.8	28

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19	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	21.4	81
20	Inhibition of mTOR signaling and clinical activity of metformin in oral premalignant lesions. <i>JCI Insight</i> , 2021, 6, .	5.0	29
21	Significance and limitations of the use of next-generation sequencing technologies for detecting mutational signatures. <i>DNA Repair</i> , 2021, 107, 103200.	2.8	18
22	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. <i>Cancer Discovery</i> , 2021, 11, 1082-1099.	9.4	109
23	Bioinformatic Methods to Identify Mutational Signatures in Cancer. <i>Methods in Molecular Biology</i> , 2021, 2185, 447-473.	0.9	7
24	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. <i>Nature Genetics</i> , 2021, 53, 1553-1563.	21.4	71
25	IL-17 signaling in steatotic hepatocytes and macrophages promotes hepatocellular carcinoma in alcohol-related liver disease. <i>Journal of Hepatology</i> , 2020, 72, 946-959.	3.7	113
26	Whole-exome sequencing reveals the impact of UVA light mutagenesis in xeroderma pigmentosum variant human cells. <i>Nucleic Acids Research</i> , 2020, 48, 1941-1953.	14.5	27
27	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 74-83.	21.4	53
28	The mutational signature profile of known and suspected human carcinogens in mice. <i>Nature Genetics</i> , 2020, 52, 1189-1197.	21.4	84
29	Generating realistic null hypothesis of cancer mutational landscapes using SigProfilerSimulator. <i>BMC Bioinformatics</i> , 2020, 21, 438.	2.6	27
30	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	12.8	27
31	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
32	Strength of immune selection in tumors varies with sex and age. <i>Nature Communications</i> , 2020, 11, 4128.	12.8	78
33	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. <i>Nature Communications</i> , 2020, 11, 3096.	12.8	19
34	The Association of Modifiable Breast Cancer Risk Factors and Somatic Genomic Alterations in Breast Tumors: The Cancer Genome Atlas Network. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 599-605.	2.5	7
35	Mutational signatures in tumours induced by high and low energy radiation in Trp53 deficient mice. <i>Nature Communications</i> , 2020, 11, 394.	12.8	61
36	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	27.8	2,104

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37	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
38	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
39	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
40	Abstract 2318: The association between somatic mutational profiles and germline polygenic risk scores in TCGA. , 2020, , .		0
41	Abstract 1319: Distinct pancancer mutational signatures are determined byAPOBEC/ADARaberrations. , 2020, , .		0
42	Abstract P5-08-07: Tobacco use, alcohol consumption, and breast cancer somatic genomic alterations. , 2020, , .		0
43	Imetelstat Inhibits Telomerase and Prevents Propagation of ADAR1-Activated Myeloproliferative Neoplasm and Leukemia Stem Cells. Blood, 2020, 136, 18-18.	1.4	3
44	Somatic evolution and global expansion of an ancient transmissible cancer lineage. Science, 2019, 365, .	12.6	58
45	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
46	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. BMC Genomics, 2019, 20, 685.	2.8	162
47	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
48	Insights into BRCA Cancer Predisposition from Integrated Germline and Somatic Analyses in 7632 Cancers. JNCI Cancer Spectrum, 2019, 3, pkz028.	2.9	10
49	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	12.8	46
50	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. Cancer Cell, 2019, 35, 441-456.e8.	16.8	82
51	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	28.9	298
52	Timing the initiation of multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e6-e7.	0.4	1
53	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
54	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

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55	Abstract 2506: Exploring the complex etiology of oncogenic fusions in childhood cancer. , 2019, , .		0
56	Inflammatory Cytokine Responsive Enzymatic Mutagenesis Fuels Myeloproliferative Neoplasm Pre-Leukemia Stem Cell Evolution. Blood, 2019, 134, 3780-3780.	1.4	0
57	Timing the Initiation of Multiple Myeloma. Blood, 2019, 134, 573-573.	1.4	0
58	Abstract SY26-02:<i>Sherlock-Lung</i>: Tracing lung cancer mutational processes in never smokers. , 2019, , .		0
59	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
60	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. Nature Genetics, 2018, 50, 682-692.	21.4	182
61	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. Cancer Cell, 2018, 33, 607-619.e15.	16.8	88
62	Intra-tumour diversification in colorectal cancer at the single-cell level. Nature, 2018, 556, 457-462.	27.8	406
63	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
64	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
65	Nonnegative/Binary matrix factorization with a D-Wave quantum annealer. PLoS ONE, 2018, 13, e0206653.	2.5	68
66	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
67	The genomic landscape of cutaneous SCC reveals drivers and a novel azathioprine associated mutational signature. Nature Communications, 2018, 9, 3667.	12.8	208
68	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. Science, 2018, 361, .	12.6	121
69	Genomic patterns of progression in smoldering multiple myeloma. Nature Communications, 2018, 9, 3363.	12.8	163
70	Mutational Signatures and the Etiology of Human Cancers. , 2018, , .		3
71	APOBEC mutation drives early-onset squamous cell carcinomas in recessive dystrophic epidermolysis bullosa. Science Translational Medicine, 2018, 10, .	12.4	91
72	Base changes in tumour DNA have the power to reveal the causes and evolution of cancer. Oncogene, 2017, 36, 158-167.	5.9	58

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73	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017, 49, 341-348.	21.4	75
74	Mutational signature analysis identifies <i>MUTYH</i> deficiency in colorectal cancers and adrenocortical carcinomas. <i>Journal of Pathology</i> , 2017, 242, 10-15.	4.5	130
75	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
76	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017, 8, 15936.	12.8	179
77	A Specific Mutational Signature Associated with DNA 8-Oxoguanine Persistence in <i>MUTYH</i> -defective Colorectal Cancer. <i>EBioMedicine</i> , 2017, 20, 39-49.	6.1	170
78	Precancer Atlas to Drive Precision Prevention Trials. <i>Cancer Research</i> , 2017, 77, 1510-1541.	0.9	116
79	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	27.8	229
80	The driver landscape of sporadic chordoma. <i>Nature Communications</i> , 2017, 8, 890.	12.8	115
81	Evaluating the role of coherent delocalized phonon-like modes in DNA cyclization. <i>Scientific Reports</i> , 2017, 7, 9731.	3.3	13
82	Uracil Accumulation and Mutagenesis Dominated by Cytosine Deamination in CpG Dinucleotides in Mice Lacking <i>UNG</i> and <i>SMUG1</i> . <i>Scientific Reports</i> , 2017, 7, 7199.	3.3	43
83	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	16.8	534
84	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	9.4	637
85	Association of Distinct Mutational Signatures With Correlates of Increased Immune Activity in Pancreatic Ductal Adenocarcinoma. <i>JAMA Oncology</i> , 2017, 3, 774.	7.1	221
86	Revertant mosaicism repairs skin lesions in a patient with keratitis-ichthyosis-deafness syndrome by second-site mutations in connexin 26. <i>Human Molecular Genetics</i> , 2017, 26, 1070-1077.	2.9	25
87	Abstract IA11: Signatures of mutational processes in human cancer. , 2017, , .		1
88	Germline <i>MC1R</i> status influences somatic mutation burden in melanoma. <i>Nature Communications</i> , 2016, 7, 12064.	12.8	103
89	Understanding mutagenesis through delineation of mutational signatures in human cancer. <i>Carcinogenesis</i> , 2016, 37, 531-540.	2.8	90
90	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760

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91	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. Nature, 2016, 538, 378-382.	27.8	418
92	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	12.8	177
93	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235
94	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	12.8	214
95	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	12.6	842
96	The role of structural parameters in DNA cyclization. BMC Bioinformatics, 2016, 17, 68.	2.6	7
97	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	21.4	502
98	Abstract A009: Benchmarking the foreign antigen space of human malignancies. , 2016, , .		0
99	SETD2 loss-of-function promotes renal cancer branched evolution through replication stress and impaired DNA repair. Oncogene, 2015, 34, 5699-5708.	5.9	147
100	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	12.6	1,431
101	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. Nature Communications, 2015, 6, 6605.	12.8	312
102	Understanding the origins of human cancer. Science, 2015, 350, 1175-1177.	12.6	32
103	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
104	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
105	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
106	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
107	Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. Nature Genetics, 2015, 47, 505-511.	21.4	1,372
108	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185

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109	A mutational signature in gastric cancer suggests therapeutic strategies. Nature Communications, 2015, 6, 8683.	12.8	146
110	The genome as a record of environmental exposure. Mutagenesis, 2015, 30, gev073.	2.6	174
111	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	21.4	837
112	Tracking clonal diversity in metastatic prostate cancer progression.. Journal of Clinical Oncology, 2015, 33, 193-193.	1.6	0
113	Abstract 2973: Exome sequencing of 243 liver tumors identifies new mutational signatures and potential therapeutic targets. , 2015, , .		0
114	Abstract 956: The evolutionary history of lethal metastatic prostate cancer. , 2015, , .		0
115	Abstract B09: DNA polymerase mutations trigger rapid onset of ultra-hypermutant malignant brain tumors in children with biallelic mismatch repair deficiency. , 2015, , .		0
116	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
117	<i>C. elegans</i> whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. Genome Research, 2014, 24, 1624-1636.	5.5	164
118	Fast randomization of large genomic datasets while preserving alteration counts. Bioinformatics, 2014, 30, i617-i623.	4.1	36
119	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
120	Mutational signatures: the patterns of somatic mutations hidden in cancer genomes. Current Opinion in Genetics and Development, 2014, 24, 52-60.	3.3	393
121	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	12.8	741
122	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. Science, 2014, 343, 437-440.	12.6	144
123	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
124	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	21.4	111
125	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
126	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

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127	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	27.8	315
128	Abstract 4322: The landscape of mitochondrial DNA mutations in human cancer. Cancer Research, 2014, 74, 4322-4322.	0.9	3
129	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
130	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	6.4	1,087
131	Specificity and Heterogeneity of Terahertz Radiation Effect on Gene Expression in Mouse Mesenchymal Stem Cells. Scientific Reports, 2013, 3, 1184.	3.3	78
132	Binding of Nucleoid-Associated Protein Fis to DNA Is Regulated by DNA Breathing Dynamics. PLoS Computational Biology, 2013, 9, e1002881.	3.2	23
133	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. Blood, 2013, 122, 399-399.	1.4	0
134	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. Cell, 2012, 148, 780-791.	28.9	300
135	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
136	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
137	Non-thermal effects of terahertz radiation on gene expression in mouse stem cells. Biomedical Optics Express, 2011, 2, 2679.	2.9	73
138	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
139	Mammalian Stem Cells Reprogramming in Response to Terahertz Radiation. PLoS ONE, 2010, 5, e15806.	2.5	109
140	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
141	A nonlinear dynamic model of DNA with a sequence-dependent stacking term. Nucleic Acids Research, 2009, 37, 2405-2410.	14.5	61
142	Computer Modeling Describes Gravity-Related Adaptation in Cell Cultures. PLoS ONE, 2009, 4, e8332.	2.5	1
143	Modelling the magnetic signature of neuronal tissue. Neurolmage, 2007, 37, 137-148.	4.2	55
144	Benchmarking the Foreign Antigen Space of Human Malignancies. SSRN Electronic Journal, 0, , .	0.4	0

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145	Undifferentiated Sarcomas Develop Through Distinct Evolutionary Pathways. SSRN Electronic Journal, 0, , .	0.4	0
146	Clonal Diaspora in Metastatic Esophageal Adenocarcinoma Describes a New Model of Cancer Progression. SSRN Electronic Journal, 0, , .	0.4	0