The repertoire of mutational signatures in human cance

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Somatic evolution and global expansion of an ancient transmissible cancer lineage. Science, 2019, 365, .	6.0	58
2	Mutational Processes in Hepatocellular Carcinoma: The Story of Aristolochic Acid. Seminars in Liver Disease, 2019, 39, 334-340.	1.8	24
3	Clinicopathological and molecular characterisation of â€˜multipleâ€classifierâ€™ endometrial carcinomas. Journal of Pathology, 2020, 250, 312-322.	2.1	205
4	Modulation of <i>N</i>-Methyl-<i>N</i>-nitrosourea Mutagenesis in Mouse Embryo Fibroblasts Derived from the <i>gpt</i> Delta Mouse by an Inhibitor of the <i>O</i>⁶-Methylguanine Methyltransferase, MGMT. Chemical Research in Toxicology, 2020, 33, 625-633.	1.7	6
5	Defining the mutation signatures of DNA polymerase Î¸ in cancer genomes. NAR Cancer, 2020, 2, zcaa017.	1.6	33
6	Characteristics of mutational signatures of unknown etiology. NAR Cancer, 2020, 2, zcaa026.	1.6	13
7	Macroscopic somatic clonal expansion in morphologically normal human urothelium. Science, 2020, 370, 82-89.	6.0	115
8	Mutational selection in normal urothelium. Science, 2020, 370, 34-35.	6.0	7
9	Origin of Genome Instability and Determinants of Mutational Landscape in Cancer Cells. Genes, 2020, 11, 1101.	1.0	8
10	Clinical assays for assessment of homologous recombination DNA repair deficiency. Gynecologic Oncology, 2020, 159, 887-898.	0.6	70
11	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	5.8	87
12	Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis. Bioinformatics, 2021, 37, 1590-1592.	1.8	26
13	Genomic Instability Signature of Palindromic Non-Coding Somatic Mutations in Bladder Cancer. Cancers, 2020, 12, 2882.	1.7	13
14	Chromothripsis in Human Breast Cancer. Cancer Research, 2020, 80, 4918-4931.	0.4	11
15	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	13.5	141
16	Analysis of mutational signatures in C. elegans: Implications for cancer genome analysis. DNA Repair, 2020, 95, 102957.	1.3	8
17	The mutational signature profile of known and suspected human carcinogens in mice. Nature Genetics, 2020, 52, 1189-1197.	9.4	84
18	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102

#	Article	IF	Citations
19	Clonal Evolution and Timing of Metastatic Colorectal Cancer. Cancers, 2020, 12, 2938.	1.7	9
20	No Impact of Smoking Status on Breast Cancer Tumor Infiltrating Lymphocytes, Response to Neoadjuvant Chemotherapy and Prognosis. Cancers, 2020, 12, 2943.	1.7	3
21	Practical classification of triple-negative breast cancer: intratumoral heterogeneity, mechanisms of drug resistance, and novel therapies. Npj Breast Cancer, 2020, 6, 54.	2.3	181
22	Cancer predictive studies. Biology Direct, 2020, 15, 18.	1.9	37
23	Parallelized Latent Dirichlet Allocation Provides a Novel Interpretability of Mutation Signatures in Cancer Genomes. Genes, 2020, 11, 1127.	1.0	4
24	Generating realistic null hypothesis of cancer mutational landscapes using SigProfilerSimulator. BMC Bioinformatics, 2020, 21, 438.	1.2	27
25	ESMO recommendations on predictive biomarker testing for homologous recombination deficiency and PARP inhibitor benefit in ovarian cancer. Annals of Oncology, 2020, 31, 1606-1622.	0.6	238
27	Trapped topoisomerase II initiates formation of de novo duplications via the nonhomologous end-joining pathway in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26876-26884.	3.3	17
28	Dynamics of genomic and immune responses during primary immunotherapy resistance in mismatch repairâ€“deficient tumors. Journal of Physical Education and Sports Management, 2020, 6, a005678.	0.5	3
29	Genomic, transcriptomic, and viral integration profiles associated with recurrent/metastatic progression in highâ€risk human papillomavirus cervical carcinomas. Cancer Medicine, 2020, 9, 8243-8257.	1.3	4
30	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	9.4	79
31	Genome-Wide Somatic Alterations in Multiple Myeloma Reveal a Superior Outcome Group. Journal of Clinical Oncology, 2020, 38, 3107-3118.	0.8	45
32	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	13.5	122
33	Copy number evolution with weighted aberrations in cancer. Bioinformatics, 2020, 36, i344-i352.	1.8	11
34	Mutational signature learning with supervised negative binomial non-negative matrix factorization. Bioinformatics, 2020, 36, i154-i160.	1.8	6
35	Comprehensive Constitutional Genetic and Epigenetic Characterization of Lynch-Like Individuals. Cancers, 2020, 12, 1799.	1.7	15
36	Tracking hematopoietic stem cells and their progeny using whole-genome sequencing. Experimental Hematology, 2020, 83, 12-24.	0.2	19
37	The DNA damage response pathway as a land of therapeutic opportunities for colorectal cancer. Annals of Oncology, 2020, 31, 1135-1147.	0.6	58

#	ARTICLE	IF	CITATIONS
38	Scientific diligence for oncology drugs: a pharmacology, translational medicine and clinical perspective. Drug Discovery Today, 2020, 25, 1855-1864.	3.2	0
39	Accelerated single cell seeding in relapsed multiple myeloma. Nature Communications, 2020, 11, 3617.	5.8	41
40	Spontaneous Polyploids and Antimutators Compete During the Evolution of <i>Saccharomyces cerevisiae</i> Mutator Cells. Genetics, 2020, 215, 959-974.	1.2	10
41	Exploiting the Microhomology-Mediated End-Joining Pathway in Cancer Therapy. Cancer Research, 2020, 80, 4593-4600.	0.4	47
42	How should molecular findings be integrated in the classification for lung cancer?. Translational Lung Cancer Research, 2020, 9, 2245-2254.	1.3	5
43	The evolution of relapse of adult T cell acute lymphoblastic leukemia. Genome Biology, 2020, 21, 284.	3.8	13
44	Prognostic value of HLA-I homozygosity in patients with non-small cell lung cancer treated with single agent immunotherapy. , 2020, 8, e001620.		30
45	Candidate Gene Discovery in Hereditary Colorectal Cancer and Polyposis Syndromesâ€"Considerations for Future Studies. International Journal of Molecular Sciences, 2020, 21, 8757.	1.8	7
46	Integrated molecular drivers coordinate biological and clinical states in melanoma. Nature Genetics, 2020, 52, 1373-1383.	9.4	36
47	APOBEC3A catalyzes mutation and drives carcinogenesis in vivo. Journal of Experimental Medicine, 2020, 217, .	4.2	87
48	Unique genomic features and prognostic value of COSMIC mutational signature 4 in lung adenocarcinoma and lung squamous cell carcinoma. Annals of Translational Medicine, 2020, 8, 1176-1176.	0.7	8
49	CaMuS: simultaneous fitting and de novo imputation of cancer mutational signature. Scientific Reports, 2020, 10, 19316.	1.6	6
50	John W. (Jan) Drake: A Biochemical View of a Geneticist Par Excellence. Genetics, 2020, 216, 827-836.	1.2	0
51	Formaldehyde Causes Bone Marrow Failure Linked to Transcriptional Reprogramming or Metabolic Deficiency. Molecular Cell, 2020, 80, 935-937.	4.5	3
52	Complete Response to PD-1 Inhibition in an Adolescent With Relapsed Clear Cell Adenocarcinoma of the Cervix Predicted by Neoepitope Burden and APOBEC Signature. JCO Precision Oncology, 2020, 4, 1321-1332.	1.5	5
54	Hotspots of Human Mutation. Trends in Genetics, 2021, 37, 717-729.	2.9	62
55	RNA: a double-edged sword in genome maintenance. Nature Reviews Genetics, 2020, 21, 651-670.	7.7	37
56	Characterization of tumors with ultralow tumor mutational burden in Japanese cancer patients. Cancer Science, 2020, 111, 3893-3901.	1.7	15

#	ARTICLE	IF	CITATIONS
57	A compendium of mutational cancer driver genes. Nature Reviews Cancer, 2020, 20, 555-572.	12.8	605
58	Cancerâ€associated mutations in normal human endometrium: Surprise or expected?. Cancer Science, 2020, 111, 3458-3467.	1.7	23
59	Experimental investigations of carcinogen-induced mutation spectra: Innovation, challenges and future directions. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 853, 503195.	0.9	1
60	Genetics and Epigenetics of Sex Bias: Insights from Human Cancer and Autoimmunity. Trends in Genetics, 2020, 36, 650-663.	2.9	23
61	Using sigLASSO to optimize cancer mutation signatures jointly with sampling likelihood. Nature Communications, 2020, 11, 3575.	5.8	28
62	Distinct Molecular Landscape of Epsteinâ€“Barr Virus Associated Pulmonary Lymphoepithelioma-Like Carcinoma Revealed by Genomic Sequencing. Cancers, 2020, 12, 2065.	1.7	25
63	Defining relative mutational difficulty to understand cancer formation. Cell Discovery, 2020, 6, 48.	3.1	4
64	Mutational signature SBS8 predominantly arises due to late replication errors in cancer. Communications Biology, 2020, 3, 421.	2.0	34
65	The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2020, 15, 1844-1856.	0.5	83
66	Role of POLE and POLD1 in familial cancer. Genetics in Medicine, 2020, 22, 2089-2100.	1.1	76
67	Cell plasticity and genomic instability in cancer evolution. Genome Instability & Disease, 2020, 1, 301-309.	0.5	1
68	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. Nature Cancer, 2020, 1, 1066-1081.	5.7	51
69	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	9.4	367
70	Prediction of genome-wide effects of single nucleotide variants on transcription factor binding. Scientific Reports, 2020, 10, 17632.	1.6	11
71	Multiple neoplasia in a patient with Gitelman syndrome harboring germline monoallelic MUTYH mutation. Npj Genomic Medicine, 2020, 5, 39.	1.7	3
72	Are carcinogens direct mutagens?. Nature Genetics, 2020, 52, 1137-1138.	9.4	13
73	New biomarkers for checkpoint inhibitor therapy. ESMO Open, 2020, 5, e000597.	2.0	16
74	The LL-100 Cell Lines Panel: Tool for Molecular Leukemiaâ€“Lymphoma Research. International Journal of Molecular Sciences, 2020, 21, 5800.	1.8	11

#	ARTICLE	IF	CITATIONS
75	The shared frameshift mutation landscape of microsatellite-unstable cancers suggests immunoediting during tumor evolution. Nature Communications, 2020, 11, 4740.	5.8	78
76	Trajectory and uniqueness of mutational signatures in yeast mutators. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24947-24956.	3.3	29
77	Monoallelic NTHL1 Loss-of-Function Variants and Risk of Polyposis and Colorectal Cancer. Gastroenterology, 2020, 159, 2241-2243.e6.	0.6	20
78	Chemically induced mutations in a MutaMouse reporter gene inform mechanisms underlying human cancer mutational signatures. Communications Biology, 2020, 3, 438.	2.0	16
79	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature Communications, 2020, 11, 4306.	5.8	26
80	Genetic Susceptibility to Endometrial Cancer: Risk Factors and Clinical Management. Cancers, 2020, 12, 2407.	1.7	32
81	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	5.8	60
82	Mutagenicity of acrylamide and glycidamide in human TP53 knock-in (Hupki) mouse embryo fibroblasts. Archives of Toxicology, 2020, 94, 4173-4196.	1.9	21
84	Mosaicism in Human Health and Disease. Annual Review of Genetics, 2020, 54, 487-510.	3.2	48
85	Integrative Analysis of Pleomorphic Dermal Sarcomas Reveals Fibroblastic Differentiation and Susceptibility to Immunotherapy. Clinical Cancer Research, 2020, 26, 5638-5645.	3.2	21
86	A Practical Guide for Structural Variation Detection in the Human Genome. Current Protocols in Human Genetics, 2020, 107, e103.	3.5	12
87	The road ahead in genetics and genomics. Nature Reviews Genetics, 2020, 21, 581-596.	7.7	118
88	Computational methods for detecting cancer hotspots. Computational and Structural Biotechnology Journal, 2020, 18, 3567-3576.	1.9	12
89	The genetic and epigenetic landscape of early-onset colorectal cancer. Colorectal Cancer, 2020, 9, .	0.8	9
90	Tumor Mutational Burden as a Predictive Biomarker in Solid Tumors. Cancer Discovery, 2020, 10, 1808-1825.	7.7	388
92	Two Aldehyde Clearance Systems Are Essential to Prevent Lethal Formaldehyde Accumulation in Mice and Humans. Molecular Cell, 2020, 80, 996-1012.e9.	4.5	92
93	Procarcinogen Activation and Mutational Signatures Model the Initiation of Carcinogenesis in Human Urothelial Tissues In Vitro. European Urology, 2020, 78, 143-147.	0.9	8
94	Impact of mitochondrial DNA mutations in multiple myeloma. Blood Cancer Journal, 2020, 10, 46.	2.8	8

#	ARTICLE	IF	CITATIONS
95	Tumor-Infiltrating CD8 T Cells Predict Clinical Breast Cancer Outcomes in Young Women. Cancers, 2020, 12, 1076.	1.7	31
96	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	5.8	86
97	Extreme differences between human germline and tumor mutation densities are driven by ancestral human-specific deviations. Nature Communications, 2020, 11, 2512.	5.8	9
98	Wnts and the hallmarks of cancer. Cancer and Metastasis Reviews, 2020, 39, 625-645.	2.7	59
99	Why do young people get cancer?. Pediatric Blood and Cancer, 2020, 67, e28335.	0.8	18
100	Colibactin DNA-damage signature indicates mutational impact in colorectal cancer. Nature Medicine, 2020, 26, 1063-1069.	15.2	149
101	Oxidative Stress and Genotoxicity in Melanoma Induction: Impact on Repair Rather Than Formation of DNA Damage?. Photochemistry and Photobiology, 2020, 96, 962-972.	1.3	17
102	Developmental Mutators and Early Onset Cancer. Frontiers in Pediatrics, 2020, 8, 189.	0.9	4
103	Phase and context shape the function of composite oncogenic mutations. Nature, 2020, 582, 100-103.	13.7	31
104	Decoding whole-genome mutational signatures in 37 human pan-cancers by denoising sparse autoencoder neural network. Oncogene, 2020, 39, 5031-5041.	2.6	9
105	Germline ancestry influences the evolutionary disease course in lung adenocarcinomas. Evolutionary Applications, 2020, 13, 1550-1557.	1.5	6
106	Multi-omic analysis reveals significantly mutated genes and DDX3X as a sex-specific tumor suppressor in cutaneous melanoma. Nature Cancer, 2020, 1, 635-652.	5.7	26
107	Sarcoma and the 100,000 Genomes Project: our experience and changes to practice. Journal of Pathology: Clinical Research, 2020, 6, 297-307.	1.3	20
108	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
109	EGFP Reporters for Direct and Sensitive Detection of Mutagenic Bypass of DNA Lesions. Biomolecules, 2020, 10, 902.	1.8	2
110	The role of host environment in cancer evolution. Evolutionary Applications, 2020, 13, 1756-1770.	1.5	15
111	Genomic Instability in Multiple Myeloma. Trends in Cancer, 2020, 6, 858-873.	3.8	18
112	Beyond the Variants: Mutational Patterns in Next-Generation Sequencing Data for Cancer Precision Medicine. Frontiers in Cell and Developmental Biology, 2020, 8, 370.	1.8	6

#	ARTICLE	IF	CITATIONS
113	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	5.8	19
114	Mutation Signatures in Melanocytic Nevi Reveal Characteristics of Defective DNA Repair. Journal of Investigative Dermatology, 2020, 140, 2093-2096.e2.	0.3	7
115	Mutational signature in colorectal cancer caused by genotoxic pks+ E. coli. Nature, 2020, 580, 269-273.	13.7	587
116	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. Genome Research, 2020, 30, 334-346.	2.4	56
117	An organoid biobank for childhood kidney cancers that captures disease and tissue heterogeneity. Nature Communications, 2020, 11, 1310.	5.8	183
119	The mutREAD method detects mutational signatures from low quantities of cancer DNA. Nature Communications, 2020, 11, 3166.	5.8	9
120	Molecular origins of APOBEC-associated mutations in cancer. DNA Repair, 2020, 94, 102905.	1.3	48
121	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	5.8	24
122	Emerging Precision Oncology Applications of Liquid Biopsy using Circulating Tumour DNA and Methylome Profiling. Clinical Oncology, 2020, 32, 626-631.	0.6	1
123	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	0.6	131
124	Human genes differ by their UV sensitivity estimated through analysis of UVâ€induced silent mutations in melanoma. Human Mutation, 2020, 41, 1751-1760.	1.1	0
125	Chromosome Abnormalities: New Insights into Their Clinical Significance in Cancer. Molecular Therapy - Oncolytics, 2020, 17, 562-570.	2.0	36
126	Lung-only melanoma: UV mutational signature supports origin from occult cutaneous primaries and argues against the concept of primary pulmonary melanoma. Modern Pathology, 2020, 33, 2244-2255.	2.9	23
127	Germline de novo mutation rates on exons versus introns in humans. Nature Communications, 2020, 11, 3304.	5.8	18
128	Characterization of colibactin-associated mutational signature in an Asian oral squamous cell carcinoma and in other mucosal tumor types. Genome Research, 2020, 30, 803-813.	2.4	32
129	Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig. Nature Communications, 2020, 11, 731.	5.8	36
130	Not all cancers are created equal: Tissue specificity in cancer genes and pathways. Current Opinion in Cell Biology, 2020, 63, 135-143.	2.6	34
131	BATCAVE: calling somatic mutations with a tumor- and site-specific prior. NAR Genomics and Bioinformatics, 2020, 2, lqaa004.	1.5	1

#	Article	IF	Citations
132	Mutational signatures: experimental design and analytical framework. Genome Biology, 2020, 21, 37.	3.8	27
133	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. Cell, 2020, 180, 915-927.e16.	13.5	98
134	Optimising gene editing for cancer therapy. Nature Cell Biology, 2020, 22, 259-261.	4.6	11
135	The promise of toxicogenomics for genetic toxicology: past, present and future. Mutagenesis, 2020, 35, 153-159.	1.0	12
136	Tobacco smoking and somatic mutations in human bronchial epithelium. Nature, 2020, 578, 266-272.	13.7	336
137	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	2.6	93
138	Reconstructing the evolutionary history of multiple myeloma. Best Practice and Research in Clinical Haematology, 2020, 33, 101145.	0.7	21
139	Global genomics project unravels cancerâ€™s complexity at unprecedented scale. Nature, 2020, 578, 39-40.	13.7	18
140	A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. Nature Communications, 2020, 11, 728.	5.8	140
141	Divergent mutational processes distinguish hypoxic and normoxic tumours. Nature Communications, 2020, 11, 737.	5.8	90
142	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
143	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	13.7	690
144	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
145	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
146	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
147	Mutational signatures are jointly shaped by DNA damage and repair. Nature Communications, 2020, 11, 2169.	5.8	137
148	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	5.7	103
149	Spatial clustersÂof cancer incidence: analyzing 1940 census data linked to 1966â€“2017 cancer records. Cancer Causes and Control, 2020, 31, 609-615.	0.8	4

#	Article	IF	Citations
150	Contribution of Macrophages and T Cells in Skeletal Metastasis. Cancers, 2020, 12, 1014.	1.7	19
151	Oncology in 2050 â€“ A Retrospective?. Oncologist, 2020, 25, e1127-e1130.	1.9	1
152	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	5.8	99
153	Microbiota and colorectal cancer: colibactin makes its mark. Nature Reviews Gastroenterology and Hepatology, 2020, 17, 317-318.	8.2	17
154	The mutational landscape of normal human endometrial epithelium. Nature, 2020, 580, 640-646.	13.7	338
155	Molecular Trajectory of BRCA1 and BRCA2 Mutations. Frontiers in Oncology, 2020, 10, 361.	1.3	31
156	Morphologic and Genomic Heterogeneity in the Evolution and Progression of Breast Cancer. Cancers, 2020, 12, 848.	1.7	14
157	The genomic landscape of advanced cancer. Nature Cancer, 2020, 1, 372-373.	5.7	8
158	Germline <i>MBD4</i> Mutations and Predisposition to Uveal Melanoma. Journal of the National Cancer Institute, 2021, 113, 80-87.	3.0	43
159	Comprehensive analysis reveals distinct mutational signature and its mechanistic insights of alcohol consumption in human cancers. Briefings in Bioinformatics, 2021, 22, .	3.2	14
160	Biologically based models of cancer risk in radiation research. International Journal of Radiation Biology, 2021, 97, 2-11.	1.0	11
161	Developing Drugs for Tissueâ€Agnostic Indications: A Paradigm Shift in Leveraging Cancer Biology for Precision Medicine. Clinical Pharmacology and Therapeutics, 2021, 109, 334-342.	2.3	41
162	Endogenous APOBEC3B overexpression characterizes HPV-positive and HPV-negative oral epithelial dysplasias and head and neck cancers. Modern Pathology, 2021, 34, 280-290.	2.9	22
163	High tumor mutational burden and T-cell activation are associated with long-term response to anti-PD1 therapy in Lynch syndrome recurrent glioblastoma patient. Cancer Immunology, Immunotherapy, 2021, 70, 831-842.	2.0	20
164	Misannotated Multi-Nucleotide Variants in Public Cancer Genomics Datasets Lead to Inaccurate Mutation Calls with Significant Implications. Cancer Research, 2021, 81, 282-288.	0.4	7
165	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. Circulation, 2021, 143, 410-423.	1.6	87
166	Molecular basis of <i>ETV6</i>-mediated predisposition to childhood acute lymphoblastic leukemia. Blood, 2021, 137, 364-373.	0.6	37
167	A versatile system to introduce clusters of genomic doubleâ€strand breaks in large cell populations. Genes Chromosomes and Cancer, 2021, 60, 303-313.	1.5	3

#	Article	IF	Citations
168	Multiple Roles for Hepatitis B and C Viruses and the Host in the Development of Hepatocellular Carcinoma. Hepatology, 2021, 73, 27-37.	3.6	23
169	Designing Evolutionary-based Interception Strategies to Block the Transition from Precursor Phases to Multiple Myeloma. Clinical Cancer Research, 2021, 27, 15-23.	3.2	20
170	The role of genomics in global cancer prevention. Nature Reviews Clinical Oncology, 2021, 18, 116-128.	12.5	22
171	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. Cancer Discovery, 2021, 11, 340-361.	7.7	66
172	A Role for N6-Methyladenine in DNA Damage Repair. Trends in Biochemical Sciences, 2021, 46, 175-183.	3.7	14
173	Analysis of mutational signatures with yet another package for signature analysis. Genes Chromosomes and Cancer, 2021, 60, 314-331.	1.5	40
174	Mutagenicity of 2-hydroxyamino-1-methyl-6-phenylimidazo[4,5-b]pyridine (Nâ€"OH-PhIP) in human TP53 knock-in (Hupki) mouse embryo fibroblasts. Food and Chemical Toxicology, 2021, 147, 111855.	1.8	4
175	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	1.6	16
176	The effect of age on the acquisition and selection of cancer driver mutations in sun-exposed normal skin. Annals of Oncology, 2021, 32, 412-421.	0.6	29
177	Adverse outcome pathways, key events, and radiation risk assessment. International Journal of Radiation Biology, 2021, 97, 804-814.	1.0	17
178	Genomic and transcriptomic correlates of Richter transformation in chronic lymphocytic leukemia. Blood, 2021, 137, 2800-2816.	0.6	51
179	The head and neck cancer genome in the era of immunotherapy. Oral Oncology, 2021, 112, 105040.	0.8	13
180	Identification of a Synthetic Lethal Relationship between Nucleotide Excision Repair Deficiency and Irofulven Sensitivity in Urothelial Cancer. Clinical Cancer Research, 2021, 27, 2011-2022.	3.2	19
181	How wide is the application of genetic big data in biomedicine. Biomedicine and Pharmacotherapy, 2021, 133, 111074.	2.5	5
182	Postâ€treatment hypermutation in a recurrent diffuse glioma with H3.3 p.G34 Mutation. Neuropathology and Applied Neurobiology, 2021, 47, 460-463.	1.8	9
183	Germline variants of DNA repair genes in early onset mantle cell lymphoma. Oncogene, 2021, 40, 551-563.	2.6	9
184	New horizons of DNA adductome for exploring environmental causes of cancer. Cancer Science, 2021, 112, 7-15.	1.7	28
185	Recurrent coâ€alteration of HDGF and SETDB1 on chromosome 1q drives cutaneous melanoma progression and poor prognosis. Pigment Cell and Melanoma Research, 2021, 34, 641-647.	1.5	7

#	ARTICLE	IF	CITATIONS
186	Transient activation of tumoral DNA damage tolerance pathway coupled with immune checkpoint blockade exerts durable tumor regression in mouse melanoma. Pigment Cell and Melanoma Research, 2021, 34, 605-617.	1.5	4
187	Depiction of tumor stemlike features and underlying relationships with hazard immune infiltrations based on large prostate cancer cohorts. Briefings in Bioinformatics, 2021, 22, .	3.2	36
188	The Distinctive Genomic Landscape of Giant Congenital Melanocytic Nevi. Journal of Investigative Dermatology, 2021, 141, 692-695.e2.	0.3	8
189	Integrated Analysis of Mutations and Dysregulated Pathways Unravels Carcinogenic Effect and Clinical Actionability of Mutational Processes. SSRN Electronic Journal, 0, , .	0.4	0
190	Cullin-5 (CUL5) as a potential prognostic marker in a pan-cancer analysis of human tumors. Bioengineered, 2021, 12, 5348-5360.	1.4	8
191	A comparative analysis of the mutagenicity of platinum-containing chemotherapeutic agents reveals direct and indirect mutagenic mechanisms. Mutagenesis, 2021, 36, 75-86.	1.0	19
193	DNA repair | DNA Oxidation. , 2021, , 236-243.		0
194	Preventing Colitis-Associated Colon Cancer With Antioxidants: A Systematic Review. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 1177-1197.	2.3	14
195	Inflammation-driven deaminase deregulation fuels human pre-leukemia stem cell evolution. Cell Reports, 2021, 34, 108670.	2.9	22
196	Unraveling the genomic landscape of colorectal cancer through mutational signatures. Advances in Cancer Research, 2021, 151, 385-424.	1.9	14
197	Tumor heterogeneity-driven individualized therapy. Future Oncology, 2021, 17, 235-240.	1.1	2
198	Evolutionary Mechanisms of Cancer Suggest Rational Therapeutic Approaches. Cytogenetic and Genome Research, 2021, 161, 362-371.	0.6	4
199	Initial Whole-Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. Clinical Cancer Research, 2021, 27, 2111-2118.	3.2	5
200	Cancer Biology, Epidemiology, and Treatment in the 21st Century: Current Status and Future Challenges From a Biomedical Perspective. Cancer Control, 2021, 28, 107327482110387.	0.7	8
201	Precision Radiotherapy: Reduction in Radiation for Oropharyngeal Cancer in the 30 ROC Trial. Journal of the National Cancer Institute, 2021, 113, 742-751.	3.0	98
202	Finding the Number of Latent Topics With Semantic Non-Negative Matrix Factorization. IEEE Access, 2021, 9, 117217-117231.	2.6	15
203	Deep Tumor Profiling for Molecular Tumor Boards. , 2021, , 352-360.		0
204	An automated approach for determining the number of components in non-negative matrix factorization with application to mutational signature learning. Machine Learning: Science and Technology, 2021, 2, 015013.	2.4	2

#	Article	IF	Citations
205	Editorial: Genomic Colocalization and Enrichment Analyses. Frontiers in Genetics, 2020, 11, 617876.	1.1	0
207	High-fidelity DNA ligation enforces accurate Okazaki fragment maturation during DNA replication. Nature Communications, 2021, 12, 482.	5.8	18
208	Evaluating the utility of tumour mutational signatures for identifying hereditary colorectal cancer and polyposis syndrome carriers. Gut, 2021, 70, 2138-2149.	6.1	27
209	Targeting translesion synthesis (TLS) to expose replication gaps, a unique cancer vulnerability. Expert Opinion on Therapeutic Targets, 2021, 25, 27-36.	1.5	16
210	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. Nature Communications, 2021, 12, 293.	5.8	54
211	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. Nature Neuroscience, 2021, 24, 176-185.	7.1	73
212	Molecular correlates of immune cytolytic subgroups in colorectal cancer by integrated genomics analysis. NAR Cancer, 2021, 3, zcab005.	1.6	9
213	Genomic Landscapes of Acral Melanomas in East Asia. Cancer Genomics and Proteomics, 2021, 18, 83-92.	1.0	6
214	Mutational signatures associated with exposure to carcinogenic microplastic compounds bisphenol A and styrene oxide. NAR Cancer, 2021, 3, zcab004.	1.6	13
215	Integrated Genomic and Transcriptomic Analysis reveals key genes for predicting dual-phenotype Hepatocellular Carcinoma Prognosis. Journal of Cancer, 2021, 12, 2993-3010.	1.2	5
216	Meiosis and beyond â€" understanding the mechanistic and evolutionary processes shaping the germline genome. Biological Reviews, 2021, 96, 822-841.	4.7	25
218	Somatic mutation profiles as molecular classifiers of ulcerative colitisâ€associated colorectal cancer. International Journal of Cancer, 2021, 148, 2997-3007.	2.3	10
219	Homologous recombination repair deficiency (HRD): From biology to clinical exploitation. Genes Chromosomes and Cancer, 2021, 60, 299-302.	1.5	16
220	Can integrative biomarker approaches improve prediction of platinum and PARP inhibitor response in ovarian cancer?. Seminars in Cancer Biology, 2021, 77, 67-82.	4.3	12
221	Clonal expansion in non-cancer tissues. Nature Reviews Cancer, 2021, 21, 239-256.	12.8	133
222	Hawk-Seqâ„¢ differentiates between various mutations in Salmonella typhimurium TA100 strain caused by exposure to Ames test-positive mutagens. Mutagenesis, 2021, 36, 245-254.	1.0	5
227	Genetic drivers of nonâ€cutaneous melanomas: Challenges and opportunities in a heterogeneous landscape. Experimental Dermatology, 2022, 31, 13-30.	1.4	14
228	A Semiparametric Kernel Independence Test With Application to Mutational Signatures. Journal of the American Statistical Association, 2021, 116, 1-14.	1.8	0

#	ARTICLE	IF	CITATIONS
229	Recent Advances in Integrative Multi-Omics Research in Breast and Ovarian Cancer. Journal of Personalized Medicine, 2021, 11, 149.	1.1	16
230	Impact of cancer evolution on immune surveillance and checkpoint inhibitor response. Seminars in Cancer Biology, 2022, 84, 89-102.	4.3	21
231	<i>KRAS</i> G12C Mutation Is Associated with Increased Risk of Recurrence in Surgically Resected Lung Adenocarcinoma. Clinical Cancer Research, 2021, 27, 2604-2612.	3.2	20
232	Unravelling the Sequential Interplay of Mutational Mechanisms during Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Genes, 2021, 12, 214.	1.0	6
233	Spectrum of mutational signatures in T-cell lymphoma reveals a key role for UV radiation in cutaneous T-cell lymphoma. Scientific Reports, 2021, 11, 3962.	1.6	33
235	Editorial: Cancer Staging in Squamous Cell Carcinoma of the Vermilion Lip. Annals of Surgical Oncology, 2021, 28, 2944-2945.	0.7	2
236	No evidence of EMAST in whole genome sequencing data from 248 colorectal cancers. Genes Chromosomes and Cancer, 2021, 60, 463-473.	1.5	5
237	Prediction of neo-epitope immunogenicity reveals TCR recognition determinants and provides insight into immunoediting. Cell Reports Medicine, 2021, 2, 100194.	3.3	77
239	Mutational signatures in squamous cell carcinoma of the lung. Journal of Thoracic Disease, 2021, 13, 1075-1082.	0.6	4
240	Sequential filtering for clinically relevant variants as a method for clinical interpretation of whole exome sequencing findings in glioma. BMC Medical Genomics, 2021, 14, 54.	0.7	0
241	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	5.8	31
242	Mutational Landscape of Virus- and UV-Associated Merkel Cell Carcinoma Cell Lines Is Comparable to Tumor Tissue. Cancers, 2021, 13, 649.	1.7	16
243	Identifying key questions in the ecology and evolution of cancer. Evolutionary Applications, 2021, 14, 877-892.	1.5	58
244	Mutational processes in cancer preferentially affect binding of particular transcription factors. Scientific Reports, 2021, 11, 3339.	1.6	2
245	A novel gene selection method for gene expression data for the task of cancer type classification. Biology Direct, 2021, 16, 7.	1.9	9
246	Solving problems is smart, preventing them is wise: Lessons learned from the 2nd International DKFZ Conference on Cancer Prevention. International Journal of Cancer, 2021, 148, 3086-3096.	2.3	1
247	Clinical-grade whole-genome sequencing and 3â€² transcriptome analysis of colorectal cancer patients. Genome Medicine, 2021, 13, 33.	3.6	5
248	DNA Sequence Modulates the Efficiency of NEIL1-Catalyzed Excision of the Aflatoxin B₁-Induced Formamidopyrimidine Guanine Adduct. Chemical Research in Toxicology, 2021, 34, 901-911.	1.7	7

#	ARTICLE	IF	CITATIONS
249	A Functional Taxonomy of Tumor Suppression in Oncogenic KRASâ€"Driven Lung Cancer. Cancer Discovery, 2021, 11, 1754-1773.	7.7	35
250	Homologous recombination deficiency: how genomic signatures are generated. Current Opinion in Genetics and Development, 2021, 66, 93-100.	1.5	13
251	Mutational signatures and heterogeneous host response revealed via large-scale characterization of SARS-CoV-2 genomic diversity. IScience, 2021, 24, 102116.	1.9	64
252	Loss of TGFÎ² signaling increases alternative end-joining DNA repair that sensitizes to genotoxic therapies across cancer types. Science Translational Medicine, 2021, 13, .	5.8	33
253	RRM2B Is Frequently Amplified Across Multiple Tumor Types: Implications for DNA Repair, Cellular Survival, and Cancer Therapy. Frontiers in Genetics, 2021, 12, 628758.	1.1	9
254	Transitioning the Molecular Tumor Board from Proof of Concept to Clinical Routine: A German Single-Center Analysis. Cancers, 2021, 13, 1151.	1.7	27
256	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	5.2	29
257	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. Nature Communications, 2021, 12, 1861.	5.8	68
258	Reconstructing the Lineage Histories and Differentiation Trajectories of Individual Cancer Cells in Myeloproliferative Neoplasms. Cell Stem Cell, 2021, 28, 514-523.e9.	5.2	130
259	Clonal architecture in mesothelioma is prognostic and shapes the tumour microenvironment. Nature Communications, 2021, 12, 1751.	5.8	66
260	Folate Intake Alters Mutation Frequency and Profiles in a Tissue- and Dose-Specific Manner in MutaMouse Male Mice. Journal of Nutrition, 2021, 151, 800-809.	1.3	2
261	Comprehensive Molecular Profiling of Desmoplastic Small Round Cell Tumor. Molecular Cancer Research, 2021, 19, 1146-1155.	1.5	14
262	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. Communications Biology, 2021, 4, 424.	2.0	21
264	Non-IDH1-R132H IDH1/2 mutations are associated with increased DNA methylation and improved survival in astrocytomas, compared to IDH1-R132H mutations. Acta Neuropathologica, 2021, 141, 945-957.	3.9	32
266	Recent Advances in Our Knowledge of mCRC Tumor Biology and Genetics: A Focus on Targeted Therapy Development. OncoTargets and Therapy, 2021, Volume 14, 2121-2130.	1.0	8
267	Translational Research in the Era of Precision Medicine: Where We Are and Where We Will Go. Journal of Personalized Medicine, 2021, 11, 216.	1.1	44
268	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. Nature Communications, 2021, 12, 1434.	5.8	46
269	An Update on the Epidemiology, Molecular Characterization, Diagnosis, and Screening Strategies for Early-Onset Colorectal Cancer. Gastroenterology, 2021, 160, 1041-1049.	0.6	119

#	ARTICLE	IF	CITATIONS
271	The Inherited and Familial Component of Early-Onset Colorectal Cancer. Cells, 2021, 10, 710.	1.8	41
272	Promises and challenges of adoptive T-cell therapies for solid tumours. British Journal of Cancer, 2021, 124, 1759-1776.	2.9	113
273	Inherent mosaicism and extensive mutation of human placentas. Nature, 2021, 592, 80-85.	13.7	126
274	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. Molecular Cancer Research, 2021, 19, 991-1004.	1.5	19
275	Genomic Instability Profiles at the Single Cell Level in Mouse Colorectal Cancers of Defined Genotypes. Cancers, 2021, 13, 1267.	1.7	5
279	Immune-Related Mutational Landscape and Gene Signatures: Prognostic Value and Therapeutic Impact for Head and Neck Cancer. Cancers, 2021, 13, 1162.	1.7	16
280	Comprehensive Genomic Characterization of Fifteen Early-Onset Lynch-Like Syndrome Colorectal Cancers. Cancers, 2021, 13, 1259.	1.7	3
282	Comparison of Structural and Short Variants Detected by Linked-Read and Whole-Exome Sequencing in Multiple Myeloma. Cancers, 2021, 13, 1212.	1.7	5
283	Shaping the BRCAness mutational landscape by alternative double-strand break repair, replication stress and mitotic aberrancies. Nucleic Acids Research, 2021, 49, 4239-4257.	6.5	42
284	A bacterial mutational footprint in colorectal cancer genomes. British Journal of Cancer, 2021, 124, 1751-1753.	2.9	2
285	A selection-based next generation sequencing approach to develop robust, genotype-specific mutation profiles in Saccharomyces cerevisiae. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	4
287	The origins and genetic interactions of KRAS mutations are allele- and tissue-specific. Nature Communications, 2021, 12, 1808.	5.8	90
288	Engaging the Innate and Adaptive Antitumor Immune Response in Lymphoma. International Journal of Molecular Sciences, 2021, 22, 3302.	1.8	9
289	Assessing Novel Therapies Based on Late-Stage Efficacy: A Dangerous Concept?. Trends in Cancer, 2021, 7, 181-185.	3.8	1
290	Aberrant phase separation and cancer. FEBS Journal, 2022, 289, 17-39.	2.2	42
291	Clinical cancer genomic profiling. Nature Reviews Genetics, 2021, 22, 483-501.	7.7	79
292	Moss enables high sensitivity single-nucleotide variant calling from multiple bulk DNA tumor samples. Nature Communications, 2021, 12, 2204.	5.8	1
293	Genomic profiling of multiple tissues in two patients with multiple endocrine neoplasia type 1. Biomedical Research, 2021, 42, 89-94.	0.3	0

#	Article	IF	Citations
295	Measuring nonhomologous end-joining, homologous recombinationÂand alternative end-joining simultaneously at an endogenous locus in any transfectable human cell. Nucleic Acids Research, 2021, 49, e74-e74.	6.5	14
296	Integrated mutational landscape analysis of uterine leiomyosarcomas. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	48
297	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	13.7	254
298	Multidisciplinary management of locally advanced pancreatic adenocarcinoma: Biology is King. Journal of Surgical Oncology, 2021, 123, 1395-1404.	0.8	2
299	Predicting clinical outcomes using cancer progression associated signatures. Oncotarget, 2021, 12, 845-858.	0.8	1
304	Targeted Deep Sequencing of Bladder Tumors Reveals Novel Associations between Cancer Gene Mutations and Mutational Signatures with Major Risk Factors. Clinical Cancer Research, 2021, 27, 3725-3733.	3.2	11
307	Distinct patterns of somatic genomic alterations and mutational signatures in central and peripheral-type small-cell lung cancer. Translational Lung Cancer Research, 2021, 10, 1747-1760.	1.3	5
308	Routine Molecular Pathology Diagnostics in Precision Oncology. Deutsches A&#x0308;rzteblatt International, 2021, 118, .	0.6	2
310	MutVizÂ2.0: visual analysis of somatic mutations and the impact of mutational signatures on selected genomic regions. NAR Cancer, 2021, 3, zcab012.	1.6	0
311	Discovering the Mutational Profile of Early Colorectal Lesions: A Translational Impact. Cancers, 2021, 13, 2081.	1.7	2
312	Sex disparities matter in cancer development and therapy. Nature Reviews Cancer, 2021, 21, 393-407.	12.8	136
313	A systematic CRISPR screen defines mutational mechanisms underpinning signatures caused by replication errors and endogenous DNA damage. Nature Cancer, 2021, 2, 643-657.	5.7	94
314	Evolutionary Trajectories and Genomic Divergence in Localized Breast Cancers after Ipsilateral Breast Tumor Recurrence. Cancers, 2021, 13, 1821.	1.7	3
315	Genomic landscape of extraordinary responses in metastatic breast cancer. Communications Biology, 2021, 4, 449.	2.0	3
318	Reconstructing tumor history in breast cancer: signatures of mutational processes and response to neoadjuvant chemotherapyâ‹†. Annals of Oncology, 2021, 32, 500-511.	0.6	9
319	TERT promoter hotspot mutations and gene amplification in metaplastic breast cancer. Npj Breast Cancer, 2021, 7, 43.	2.3	16
320	Preferential CEBP binding to T:G mismatches and increased C-to-T human somatic mutations. Nucleic Acids Research, 2021, 49, 5084-5094.	6.5	8
321	Stepwise generation of AID knock-in and conditional knockout mice from a single gene-targeting event. International Immunology, 2021, 33, 387-398.	1.8	0

#	ARTICLE	IF	CITATIONS
322	Genome instability and loss of protein homeostasis: converging paths to neurodegeneration?. Open Biology, 2021, 11, 200296.	1.5	26
323	The Quandary of DNA-Based Treatment Assessment in De Novo Metastatic Prostate Cancer in the Era of Precision Oncology. Journal of Personalized Medicine, 2021, 11, 330.	1.1	1
324	Mutational pressure by host APOBEC3s more strongly affects genes expressed early in the lytic phase of herpes simplex virus-1 (HSV-1) and human polyomavirus (HPyV) infection. PLoS Pathogens, 2021, 17, e1009560.	2.1	9
325	Integrated approaches for precision oncology in colorectal cancer: The more you know, the better. Seminars in Cancer Biology, 2022, 84, 199-213.	4.3	35
326	Genetic interactions among Brca1, Brca2, Palb2, and Trp53 in mammary tumor development. Npj Breast Cancer, 2021, 7, 45.	2.3	7
328	Protection of the C. elegans germ cell genome depends on diverse DNA repair pathways during normal proliferation. PLoS ONE, 2021, 16, e0250291.	1.1	18
329	Characteristics of Pan-Cancer Patients With Ultrahigh Tumor Mutation Burden. Frontiers in Oncology, 2021, 11, 682017.	1.3	4
330	Identification of combinations of somatic mutations that predict cancer survival and immunotherapy benefit. NAR Cancer, 2021, 3, zcab017.	1.6	2
331	Interpretation of allele-specific chromatin accessibility using cell stateâ€“aware deep learning. Genome Research, 2021, 31, 1082-1096.	2.4	34
332	Recurrent deletions in clonal hematopoiesis are driven by microhomology-mediated end joining. Nature Communications, 2021, 12, 2455.	5.8	23
333	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	6.0	85
334	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
335	p53 Expression, Programmed Death Ligand 1, and Risk Factors in Urinary Tract Small Cell Carcinoma. Frontiers in Oncology, 2021, 11, 651754.	1.3	0
338	Drug Repurposing in Oncology, an Attractive Opportunity for Novel Combinatorial Regimens. Current Medicinal Chemistry, 2021, 28, 2114-2136.	1.2	6
339	Ppp6c haploinsufficiency accelerates UVâ€induced BRAF(V600E)â€initiated melanomagenesis. Cancer Science, 2021, 112, 2233-2244.	1.7	3
340	Integrated Genomic Analysis Identifies Driver Genes and Cisplatin-Resistant Progenitor Phenotype in Pediatric Liver Cancer. Cancer Discovery, 2021, 11, 2524-2543.	7.7	41
341	Virus-Driven Carcinogenesis. Cancers, 2021, 13, 2625.	1.7	31
342	Cell-free DNA captures tumor heterogeneity and driver alterations in rapid autopsies with pre-treated metastatic cancer. Nature Communications, 2021, 12, 3199.	5.8	33

#	ARTICLE	IF	CITATIONS
343	High tumor mutation burden fails to predict immune checkpoint blockade response across all cancer types. Annals of Oncology, 2021, 32, 661-672.	0.6	586
344	Comparative genomic signatures in young and old Chinese patients with colorectal cancer. Cancer Medicine, 2021, 10, 4375-4386.	1.3	1
345	Mutational signatures impact the evolution of anti-EGFR antibody resistance in colorectal cancer. Nature Ecology and Evolution, 2021, 5, 1024-1032.	3.4	16
346	Mining mutation contexts across the cancer genome to map tumor site of origin. Nature Communications, 2021, 12, 3051.	5.8	8
347	Copy number signature analysis tool and its application in prostate cancer reveals distinct mutational processes and clinical outcomes. PLoS Genetics, 2021, 17, e1009557.	1.5	65
348	Common DNA methylation dynamics in endometriod adenocarcinoma and glioblastoma suggest universal epigenomic alterations in tumorigenesis. Communications Biology, 2021, 4, 607.	2.0	9
350	Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. Cancer Gene Therapy, 2022, 29, 697-708.	2.2	10
351	Radiotherapy is associated with a deletion signature that contributes to poor outcomes in patients with cancer. Nature Genetics, 2021, 53, 1088-1096.	9.4	94
352	Selective multiplexed enrichment for the detection and quantitation of low-fraction DNA variants via low-depth sequencing. Nature Biomedical Engineering, 2021, 5, 690-701.	11.6	27
353	Cytidine Deaminase APOBEC3A Regulates PD-L1 Expression in Cancer Cells in a JNK/c-JUN-Dependent Manner. Molecular Cancer Research, 2021, 19, 1571-1582.	1.5	8
354	Functional and genetic determinants of mutation rate variability in regulatory elements of cancer genomes. Genome Biology, 2021, 22, 133.	3.8	12
355	DNA Methylation, Deamination, and Translesion Synthesis Combine to Generate Footprint Mutations in Cancer Driver Genes in B-Cell Derived Lymphomas and Other Cancers. Frontiers in Genetics, 2021, 12, 671866.	1.1	4
356	Molecular characterization of high-grade serous ovarian cancers occurring in younger and older women. Gynecologic Oncology, 2021, 161, 545-552.	0.6	8
357	The prevalence of cancer in Britain before industrialization. Cancer, 2021, 127, 3054-3059.	2.0	12
359	Genomic landscape of hepatocarcinogenesis. Journal of Human Genetics, 2021, 66, 845-851.	1.1	20
361	Prognostic Immune-Related Genes of Patients With Ewingâ€™s Sarcoma. Frontiers in Genetics, 2021, 12, 669549.	1.1	6
362	The mutagenic impact of melphalan in multiple myeloma. Leukemia, 2021, 35, 2145-2150.	3.3	32
363	Clonal hematopoiesis and therapy-related myeloid neoplasms following neuroblastoma treatment. Blood, 2021, 137, 2992-2997.	0.6	19

#	ARTICLE	IF	CITATIONS
364	It takes a village: microbiota, parainflammation, paligenosis and bystander effects in colorectal cancer initiation. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	12
365	Indolent feature ofÂHelicobacter pylori-uninfected intramucosal signet ring cell carcinomas withÂCDH1Âmutations. Gastric Cancer, 2021, 24, 1102-1114.	2.7	13
366	Prognostic Genetic Biomarkers Based on Oncogenic Signaling Pathways for Outcome Prediction in Patients with Oral Cavity Squamous Cell Carcinoma. Cancers, 2021, 13, 2709.	1.7	12
367	Arsenic co-carcinogenesis: Inhibition of DNA repair and interaction with zinc finger proteins. Seminars in Cancer Biology, 2021, 76, 86-98.	4.3	32
368	Carbon ion radiotherapy eradicates medulloblastomas with chromothripsis in an orthotopic Li-Fraumeni patient-derived mouse model. Neuro-Oncology, 2021, 23, 2028-2041.	0.6	7
369	Detection of Molecular Signatures of Homologous Recombination Deficiency in Bladder Cancer. Clinical Cancer Research, 2021, 27, 3734-3743.	3.2	17
370	Mechanisms of Immune Escape and Resistance to Checkpoint Inhibitor Therapies in Mismatch Repair Deficient Metastatic Colorectal Cancers. Cancers, 2021, 13, 2638.	1.7	32
371	The landscape and driver potential of site-specific hotspots across cancer genomes. Npj Genomic Medicine, 2021, 6, 33.	1.7	8
372	Induction of APOBEC3 Exacerbates DNA Replication Stress and Chromosomal Instability in Early Breast and Lung Cancer Evolution. Cancer Discovery, 2021, 11, 2456-2473.	7.7	74
373	Epigenetic Regulation of Genomic Stability by Vitamin C. Frontiers in Genetics, 2021, 12, 675780.	1.1	45
375	Environmental and sex-specific molecular signatures of glioma causation. Neuro-Oncology, 2022, 24, 29-36.	0.6	12
376	Genomic Features and Classification of Homologous Recombination Deficient Pancreatic Ductal Adenocarcinoma. Gastroenterology, 2021, 160, 2119-2132.e9.	0.6	83
380	Shining a Light on Colibactin Biology. Toxins, 2021, 13, 346.	1.5	38
381	Development of a system combining comprehensive genotyping and organoid cultures for identifying and testing genotype-oriented personalised medicine for pancreatobiliary cancers. European Journal of Cancer, 2021, 148, 239-250.	1.3	10
384	Identification of a Genome Instability-Associated LncRNA Signature for Prognosis Prediction in Colon Cancer. Frontiers in Genetics, 2021, 12, 679150.	1.1	12
385	Infection of Bronchial Epithelial Cells by the Human Adenoviruses A12, B3, and C2 Differently Regulates the Innate Antiviral Effector APOBEC3B. Journal of Virology, 2021, 95, e0241320.	1.5	3
386	COSMIC Cancer Gene Census 3D database: understanding the impacts of mutations on cancer targets. Briefings in Bioinformatics, 2021, 22, .	3.2	8
388	A subset of lung cancer cases shows robust signs of homologous recombination deficiency associated genomic mutational signatures. Npj Precision Oncology, 2021, 5, 55.	2.3	16

#	Article	IF	Citations
389	Upregulation of FGF9 in Lung Adenocarcinoma Transdifferentiation to Small Cell Lung Cancer. Cancer Research, 2021, 81, 3916-3929.	0.4	13
390	The pancreatic cancer genome revisited. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 469-481.	8.2	100
391	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	7.7	65
392	Comparison of Genomic Characterization in Upper Tract Urothelial Carcinoma and Urothelial Carcinoma of the Bladder. Oncologist, 2021, 26, e1395-e1405.	1.9	27
394	Rhabdomyosarcoma: How Advanced Molecular Methods Are Shaping the Diagnostic and Therapeutic Paradigm. Pediatric and Developmental Pathology, 2021, 24, 395-404.	0.5	6
396	Confirming putative variants atâ€‰â‰â€‰5% allele frequency using allele enrichment and Sanger sequencing. Scientific Reports, 2021, 11, 11640.	1.6	20
398	Regulating Twisted Skeleton to Construct Organâ€Specific Perylene for Intensive Cancer Chemotherapy. Angewandte Chemie, 2021, 133, 16351-16359.	1.6	2
399	The challenge and promise of estimating the de novo mutation rate from wholeâ€genome comparisons among closely related individuals. Molecular Ecology, 2021, 30, 6087-6100.	2.0	26
400	DIVIS: Integrated and Customizable Pipeline for Cancer Genome Sequencing Analysis and Interpretation. Frontiers in Oncology, 2021, 11, 672597.	1.3	0
401	Clinical utility of whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 32-39.	4.3	35
402	Regulating Twisted Skeleton to Construct Organâ€Specific Perylene for Intensive Cancer Chemotherapy. Angewandte Chemie - International Edition, 2021, 60, 16215-16223.	7.2	25
403	Learning mutational signatures and their multidimensional genomic properties with TensorSignatures. Nature Communications, 2021, 12, 3628.	5.8	30
404	Helicobacter pylori CagA elicits BRCAness to induce genome instability that may underlie bacterial gastric carcinogenesis. Cell Host and Microbe, 2021, 29, 941-958.e10.	5.1	66
405	Coupling between Sequence-Mediated Nucleosome Organization and Genome Evolution. Genes, 2021, 12, 851.	1.0	5
406	Aggressive early-stage lung adenocarcinoma is characterized by epithelial cell plasticity with acquirement of stem-like traits and immune evasion phenotype. Oncogene, 2021, 40, 4980-4991.	2.6	8
407	Evolution and genomic signatures of spontaneous somatic mutation in <i>Drosophila</i> intestinal stem cells. Genome Research, 2021, 31, 1419-1432.	2.4	7
408	Mutational Signature Analysis Reveals Widespread Contribution of Pyrrolizidine Alkaloid Exposure to Human Liver Cancer. Hepatology, 2021, 74, 264-280.	3.6	27
409	Discovery and Features of an Alkylating Signature in Colorectal Cancer. Cancer Discovery, 2021, 11, 2446-2455.	7.7	42

#	Article	IF	Citations
410	Enhanced C/EBP binding to GÂ·T mismatches facilitates fixation of CpG mutations in cancer and adult stem cells. Cell Reports, 2021, 35, 109221.	2.9	5
412	Decoding human cancer with whole genome sequencing: a review of PCAWG Project studies published in February 2020. Cancer and Metastasis Reviews, 2021, 40, 909-924.	2.7	10
414	From RNA World to SARS-CoV-2: The Edited Story of RNA Viral Evolution. Cells, 2021, 10, 1557.	1.8	18
415	An integrated DNA and RNA variant detector identifies a highly conserved three base exon in the <i>MAP4K5</i> kinase locus. RNA Biology, 2021, 18, 2556-2575.	1.5	1
416	The Roles of DNA Demethylases in Triple-Negative Breast Cancer. Pharmaceuticals, 2021, 14, 628.	1.7	4
417	De novo mutational signature discovery in tumor genomes using SparseSignatures. PLoS Computational Biology, 2021, 17, e1009119.	1.5	20
418	The origin of human mutation in light of genomic data. Nature Reviews Genetics, 2021, 22, 672-686.	7.7	26
419	Functional annotation of noncoding mutations in cancer. Life Science Alliance, 2021, 4, e201900523.	1.3	3
421	Geospatial Assessments of DNA Adducts in the Human Stomach: A Model of Field Cancerization. Cancers, 2021, 13, 3728.	1.7	3
422	Genomics of Smoldering Multiple Myeloma: Time for Clinical Translation of Findings?. Cancers, 2021, 13, 3319.	1.7	2
424	Proteins from the DNA Damage Response: Regulation, Dysfunction, and Anticancer Strategies. Cancers, 2021, 13, 3819.	1.7	23
425	EXO5-DNA structure and BLM interactions direct DNA resection critical for ATR-dependent replication restart. Molecular Cell, 2021, 81, 2989-3006.e9.	4.5	26
426	The landscape of driver mutations in cutaneous squamous cell carcinoma. Npj Genomic Medicine, 2021, 6, 61.	1.7	54
427	Genomic instability signals offer diagnostic possibility in early cancer detection. Trends in Genetics, 2021, 37, 966-972.	2.9	11
428	Reexamining the role of tissue inflammation in radiation carcinogenesis: a hypothesis to explain an earlier onset of cancer. International Journal of Radiation Biology, 2021, 97, 1341-1351.	1.0	5
429	MutVis: Automated framework for analysis and visualization of mutational signatures in pathogenic bacterial strains. Infection, Genetics and Evolution, 2021, 91, 104805.	1.0	1
430	Pan-Cancer Survey of Tumor Mass Dormancy and Underlying Mutational Processes. Frontiers in Cell and Developmental Biology, 2021, 9, 698659.	1.8	3
431	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. Cancer Discovery, 2021, 11, 3008-3027.	7.7	88

#	ARTICLE	IF	CITATIONS
432	Cancer Whole-Genome Sequencing. Journal of Molecular Diagnostics, 2021, 23, 784-787.	1.2	4
433	Pegylation of phenothiazine â€“ A synthetic route towards potent anticancer drugs. Journal of Advanced Research, 2022, 37, 279-290.	4.4	12
435	Genetic Determinants of Somatic Selection of Mutational Processes in 3,566 Human Cancers. Cancer Research, 2021, 81, 4205-4217.	0.4	6
436	A pan-cancer landscape of somatic mutations in non-unique regions of the human genome. Nature Biotechnology, 2021, 39, 1589-1596.	9.4	6
437	Structure-Based Design of First-Generation Small Molecule Inhibitors Targeting the Catalytic Pockets of AID, APOBEC3A, and APOBEC3B. ACS Pharmacology and Translational Science, 2021, 4, 1390-1407.	2.5	11
438	The genomic landscape of 85 advanced neuroendocrine neoplasms reveals subtype-heterogeneity and potential therapeutic targets. Nature Communications, 2021, 12, 4612.	5.8	55
439	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. Nature Communications, 2021, 12, 4496.	5.8	28
440	Expression of the cancer-associated DNA polymerase Îµ P286R in fission yeast leads to translesion synthesis polymerase dependent hypermutation and defective DNA replication. PLoS Genetics, 2021, 17, e1009526.	1.5	8
441	From <i>APC</i> to the genetics of hereditary and familial colon cancer syndromes. Human Molecular Genetics, 2021, 30, R206-R224.	1.4	15
442	Mutational Signatures: From Methods to Mechanisms. Annual Review of Biomedical Data Science, 2021, 4, 189-206.	2.8	19
444	Human APOBEC3 Variations and Viral Infection. Viruses, 2021, 13, 1366.	1.5	31
446	Comparison of the oncogenomic landscape of canine and feline hemangiosarcoma shows novel parallels with human angiosarcoma. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	18
447	Ethanol-Induced Cell Damage Can Result in the Development of Oral Tumors. Cancers, 2021, 13, 3846.	1.7	7
448	Comparative analysis of clonal evolution among patients with right- and left-sided colon and rectal cancer. IScience, 2021, 24, 102718.	1.9	9
449	Targeting Metastatic Colorectal Cancer with Immune Oncological Therapies. Cancers, 2021, 13, 3566.	1.7	6
450	UVB mutagenesis differs in <i>Nras</i>- and <i>Braf</i>-mutant mouse models of melanoma. Life Science Alliance, 2021, 4, e202101135.	1.3	8
451	Preoperative clinical and tumor genomic features associated with pathologic lymph node metastasis in clinical stage I and II lung adenocarcinoma. Npj Precision Oncology, 2021, 5, 70.	2.3	8
452	Transcription-coupled nucleotide excision repair: New insights revealed by genomic approaches. DNA Repair, 2021, 103, 103126.	1.3	22

#	ARTICLE	IF	CITATIONS
454	Enhanced Antitumor Response to Immune Checkpoint Blockade Exerted by Cisplatin-Induced Mutagenesis in a Murine Melanoma Model. Frontiers in Oncology, 2021, 11, 701968.	1.3	6
455	Multi-Gene Testing Overview with a Clinical Perspective in Metastatic Triple-Negative Breast Cancer. International Journal of Molecular Sciences, 2021, 22, 7154.	1.8	5
456	Somatic Tumor Profile Analysis in a Patient with Germline PMS2 Mutation and Synchronous Ovarian and Uterine Carcinomas. Journal of Personalized Medicine, 2021, 11, 634.	1.1	1
457	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. Cell Reports, 2021, 36, 109394.	2.9	41
458	Patient-derived organoids reflect the genetic profile of endometrial tumors and predict patient prognosis. Communications Medicine, 2021, 1, .	1.9	20
459	Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA. Nature Biotechnology, 2021, 39, 1537-1547.	9.4	151
460	Solving the enigma of POLD1 p.V295M as a potential cause of increased cancer risk. European Journal of Human Genetics, 2022, 30, 485-489.	1.4	2
461	The Genomic Landscape of Actinic Keratosis. Journal of Investigative Dermatology, 2021, 141, 1664-1674.e7.	0.3	34
462	Mutation Signatures of Pediatric Acute Myeloid Leukemia and Normal Blood Progenitors Associated with Differential Patient Outcomes. Blood Cancer Discovery, 2021, 2, 484-499.	2.6	13
463	Biochemical and photochemical mechanisms that produce different UV-induced mutation spectra. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2021, 823, 111762.	0.4	6
464	In silico saturation mutagenesis of cancer genes. Nature, 2021, 596, 428-432.	13.7	61
465	Genomic Analysis of Response to Neoadjuvant Chemotherapy in Esophageal Adenocarcinoma. Cancers, 2021, 13, 3394.	1.7	9
466	Global mapping of cancers: The Cancer Genome Atlas and beyond. Molecular Oncology, 2021, 15, 2823-2840.	2.1	55
467	Metabolism and biomarkers of heterocyclic aromatic amines in humans. Genes and Environment, 2021, 43, 29.	0.9	22
468	Validation of a Targeted Next-Generation Sequencing Panel for Tumor Mutation Burden Analysis. Journal of Molecular Diagnostics, 2021, 23, 882-893.	1.2	2
469	Mutational signatures: emerging concepts, caveats and clinical applications. Nature Reviews Cancer, 2021, 21, 619-637.	12.8	128
471	Physiological mediators of prenatal environmental influences in autism spectrum disorder. BioEssays, 2021, 43, e2000307.	1.2	12
472	The genomic architectures of tumour-adjacent tissues, plasma and saliva reveal evolutionary underpinnings of relapse in head and neck squamous cell carcinoma. British Journal of Cancer, 2021, 125, 854-864.	2.9	11

#	ARTICLE	IF	CITATIONS
473	Genomic landscape of a mouse model of diffuse-type gastric adenocarcinoma. Gastric Cancer, 2022, 25, 83-95.	2.7	3
474	Multi-omic profiling of peritoneal metastases in gastric cancer identifies molecular subtypes and therapeutic vulnerabilities. Nature Cancer, 2021, 2, 962-977.	5.7	41
476	Cutaneous T cell lymphoma. Nature Reviews Disease Primers, 2021, 7, 61.	18.1	70
477	Homologous Recombination Deficiency in Pancreatic Cancer: A Systematic Review and Prevalence Meta-Analysis. Journal of Clinical Oncology, 2021, 39, 2617-2631.	0.8	63
478	Tumor BRCA testing can reveal a high tumor mutational burden related to POLE pathogenic variants. Gynecologic Oncology Reports, 2021, 37, 100855.	0.3	0
479	Nature or Nurture? Role of the Bone Marrow Microenvironment in the Genesis and Maintenance of Myelodysplastic Syndromes. Cancers, 2021, 13, 4116.	1.7	11
480	Guardians of the Genome: BRCA2 and Its Partners. Genes, 2021, 12, 1229.	1.0	17
481	Genome-Derived Classification Signature for Ampullary Adenocarcinoma to Improve Clinical Cancer Care. Clinical Cancer Research, 2021, 27, 5891-5899.	3.2	9
482	A body map of somatic mutagenesis in morphologically normal human tissues. Nature, 2021, 597, 398-403.	13.7	107
483	The Identification of the Metabolism Subtypes of Skin Cutaneous Melanoma Associated With the Tumor Microenvironment and the Immunotherapy. Frontiers in Cell and Developmental Biology, 2021, 9, 707677.	1.8	9
484	Comparative Assessment of Diagnostic Homologous Recombination Deficiencyâ€"Associated Mutational Signatures in Ovarian Cancer. Clinical Cancer Research, 2021, 27, 5681-5687.	3.2	18
485	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. Cell Systems, 2021, 12, 994-1003.e4.	2.9	6
486	Targeting the DNA damage response in immuno-oncology: developments and opportunities. Nature Reviews Cancer, 2021, 21, 701-717.	12.8	150
487	Whole-Genome Analysis of De Novo Somatic Point Mutations Reveals Novel Mutational Biomarkers in Pancreatic Cancer. Cancers, 2021, 13, 4376.	1.7	9
489	Identification and Targeting of Mutant Peptide Neoantigens in Cancer Immunotherapy. Cancers, 2021, 13, 4245.	1.7	13
491	Mutational burden and immune recognition of gliomas. Current Opinion in Oncology, 2021, 33, 626-634.	1.1	5
492	The evolution of hematopoietic cells under cancer therapy. Nature Communications, 2021, 12, 4803.	5.8	28
493	CENP-A Subnuclear Localization Pattern as Marker Predicting Curability by Chemoradiation Therapy for Locally Advanced Head and Neck Cancer Patients. Cancers, 2021, 13, 3928.	1.7	10

#	ARTICLE	IF	CITATIONS
495	Capturing cancer evolution using genetically engineered mouse models (GEMMs). Trends in Cell Biology, 2021, 31, 1007-1018.	3.6	20
498	Mutational spectrum of SARS-CoV-2 during the global pandemic. Experimental and Molecular Medicine, 2021, 53, 1229-1237.	3.2	30
500	GATA2 deficiency syndrome: A decade of discovery. Human Mutation, 2021, 42, 1399-1421.	1.1	30
501	Interaction with the CCT chaperonin complex limits APOBEC3A cytidine deaminase cytotoxicity. EMBO Reports, 2021, 22, e52145.	2.0	7
502	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. Cancer Research, 2021, 81, 4926-4938.	0.4	20
503	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	6.0	43
504	Mutational patterns and clonal evolution from diagnosis to relapse in pediatric acute lymphoblastic leukemia. Scientific Reports, 2021, 11, 15988.	1.6	6
505	Identification of Key Genes Mutations Associated With the Radiosensitivity by Whole Exome Sequencing in Pancreatic Cancer. Frontiers in Oncology, 2021, 11, 697308.	1.3	4
507	Upfront Adjuvant Immunotherapy of Replication Repairâ€"Deficient Pediatric Glioblastoma With Chemoradiation-Sparing Approach. JCO Precision Oncology, 2021, 5, 1426-1431.	1.5	6
508	Genomic and Transcriptomic Characteristics of Esophageal Adenocarcinoma. Cancers, 2021, 13, 4300.	1.7	4
511	APOBECs orchestrate genomic and epigenomic editing across health and disease. Trends in Genetics, 2021, 37, 1028-1043.	2.9	30
512	Genotoxic stress and viral infection induce transient expression of APOBEC3A and pro-inflammatory genes through two distinct pathways. Nature Communications, 2021, 12, 4917.	5.8	28
513	High tumour mutational burden and EGFR/MAPK pathway activation are therapeutic targets in metastatic porocarcinoma. British Journal of Dermatology, 2021, , .	1.4	6
514	Clonal Hematopoiesis Is Associated With Low CD4 Nadir and Increased Residual HIV Transcriptional Activity in Virally Suppressed Individuals With HIV. Journal of Infectious Diseases, 2022, 225, 1339-1347.	1.9	17
515	Clonal dynamics in early human embryogenesis inferred from somatic mutation. Nature, 2021, 597, 393-397.	13.7	70
516	TCR Clonality and Genomic Instability Signatures as Prognostic Biomarkers in High Grade Serous Ovarian Cancer. Cancers, 2021, 13, 4394.	1.7	6
517	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	2.8	110
518	Canine tumor mutational burden is correlated with TP53 mutation across tumor types and breeds. Nature Communications, 2021, 12, 4670.	5.8	31

#	ARTICLE	IF	CITATIONS
520	Copy number signatures predict chromothripsis and clinical outcomes in newly diagnosed multiple myeloma. Nature Communications, 2021, 12, 5172.	5.8	27
521	Data-driven approaches to advance research and clinical care for pediatric cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188571.	3.3	5
522	Linking Immunity with Genomics in Sarcomas: Is Genomic Complexity an Immunogenic Trigger?. Biomedicines, 2021, 9, 1048.	1.4	6
523	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	13.7	180
524	Histological and Somatic Mutational Profiles of Mismatch Repair Deficient Endometrial Tumours of Different Aetiologies. Cancers, 2021, 13, 4538.	1.7	8
525	The Genomic Processes of Biological Invasions: From Invasive Species to Cancer Metastases and Back Again. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	9
527	Therapeutic and prognostic insights from the analysis of cancer mutational signatures. Trends in Genetics, 2022, 38, 194-208.	2.9	39
528	Comprehensive Molecular Analysis of Inflammatory Myofibroblastic Tumors Reveals Diverse Genomic Landscape and Potential Predictive Markers for Response to Crizotinib. Clinical Cancer Research, 2021, 27, 6737-6748.	3.2	12
529	Evolution and progression of Barrettâ€™s oesophagus to oesophageal cancer. Nature Reviews Cancer, 2021, 21, 731-741.	12.8	32
530	Determinants of Homologous Recombination Deficiency in Pancreatic Cancer. Cancers, 2021, 13, 4716.	1.7	9
531	Genetic and epigenetic insights into cutaneous T-cell lymphoma. Blood, 2022, 139, 15-33.	0.6	28
532	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	9.4	85
533	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. Nature Genetics, 2021, 53, 1456-1468.	9.4	111
534	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	9.4	81
535	CloneSig can jointly infer intra-tumor heterogeneity and mutational signature activity in bulk tumor sequencing data. Nature Communications, 2021, 12, 5352.	5.8	8
536	Moving pan-cancer studies from basic research toward the clinic. Nature Cancer, 2021, 2, 879-890.	5.7	40
537	Immunological exhaustion: How to make a disparate concept operational?. PLoS Pathogens, 2021, 17, e1009892.	2.1	11
539	Mutagenicity of carcinogenic heterocyclic amines in Salmonella typhimurium YG strains and transgenic rodents including gpt delta. Genes and Environment, 2021, 43, 38.	0.9	9

#	ARTICLE	IF	CITATIONS
540	Mechanism, cellular functions and cancer roles of polymerase-theta-mediated DNA end joining. Nature Reviews Molecular Cell Biology, 2022, 23, 125-140.	16.1	84
541	Clonal Architecture and Evolutionary Dynamics in Acute Myeloid Leukemias. Cancers, 2021, 13, 4887.	1.7	11
542	POLE/POLD1 mutation in nonâ€exonuclease domain matters for predicting efficacy of immuneâ€checkpointâ€inhibitor therapy. Clinical and Translational Medicine, 2021, 11, e524.	1.7	6
543	Ovarian Cancerâ€"Specific <i>BRCA</i>-like Copy-Number Aberration Classifiers Detect Mutations Associated with Homologous Recombination Deficiency in the AGO-TR1 Trial. Clinical Cancer Research, 2021, 27, 6559-6569.	3.2	9
545	Genomic and epigenomic evolution of acquired resistance to combination therapy in esophageal squamous cell carcinoma. JCI Insight, 2021, 6, .	2.3	7
546	Bacterial Genotoxin Accelerates Transient Infectionâ€"Driven Murine Colon Tumorigenesis. Cancer Discovery, 2022, 12, 236-249.	7.7	23
547	Effector TÂcell responses unleashed by regulatory TÂcell ablation exacerbate oral squamous cell carcinoma. Cell Reports Medicine, 2021, 2, 100399.	3.3	11
548	The Sound of Silence: How Silenced Chromatin Orchestrates the Repair of Double-Strand Breaks. Genes, 2021, 12, 1415.	1.0	6
549	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. Journal of Clinical Oncology, 2021, 39, 3747-3758.	0.8	38
551	Differential whole-genome doubling and homologous recombination deficiencies across breast cancer subtypes from the Taiwanese population. Communications Biology, 2021, 4, 1052.	2.0	2
552	Defining the Role of Immunotherapy in the Curative Treatment of Locoregionally Advanced Head and Neck Cancer: Promises, Challenges, and Opportunities. Frontiers in Oncology, 2021, 11, 738626.	1.3	9
553	Cell reprogramming shapes the mitochondrial DNA landscape. Nature Communications, 2021, 12, 5241.	5.8	21
554	The promise and perils of immunotherapy. Blood Advances, 2021, 5, 3709-3725.	2.5	23
555	Homologous recombination deficiency and glycolysisâ€related pathway in adjuvant chemotherapy for tripleâ€negative breast cancer: A genomic landscape and biomarker assessment of the PATTERN trial. Clinical and Translational Medicine, 2021, 11, e513.	1.7	0
556	Defects in 8-oxo-guanine repair pathway cause high frequency of C > A substitutions in neuroblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	16
557	Mutagenicity Profile Induced by UVB Light in Human Xeroderma Pigmentosum Group C Cells^{â€}. Photochemistry and Photobiology, 2022, 98, 713-731.	1.3	3
559	Clonal hematopoiesis in sickle cell disease. Blood, 2021, 138, 2148-2152.	0.6	29
560	Skin lesion classification in dermoscopic images using stacked Convolutional Neural Network. Journal of Ambient Intelligence and Humanized Computing, 2023, 14, 3551-3565.	3.3	11

#	Article	IF	Citations
561	Bromodomain proteins: protectors against endogenous DNA damage and facilitators of genome integrity. Experimental and Molecular Medicine, 2021, 53, 1268-1277.	3.2	8
562	Prospects and challenges of cancer systems medicine: from genes to disease networks. Briefings in Bioinformatics, 2022, 23, .	3.2	7
563	Oncogene Concatenated Enriched Amplicon Nanopore Sequencing for rapid, accurate, and affordable somatic mutation detection. Genome Biology, 2021, 22, 227.	3.8	13
566	Molecular features of exceptional response to neoadjuvant anti-androgen therapy in high-risk localized prostate cancer. Cell Reports, 2021, 36, 109665.	2.9	24
567	Integrated exome and RNA sequencing of TFE3-translocation renal cell carcinoma. Nature Communications, 2021, 12, 5262.	5.8	40
568	Targeting DNA Homologous Repair Proficiency With Concomitant Topoisomerase II and c-Abl Inhibition. Frontiers in Oncology, 2021, 11, 733700.	1.3	4
569	The developmental origin of cancers defines basic principles of cisplatin resistance. Cancer Letters, 2021, 519, 199-210.	3.2	17
570	Indication-specific tumor evolution and its impact on neoantigen targeting and biomarkers for individualized cancer immunotherapies. , 2021, 9, e003001.		8
571	Interpretation of cancer mutations using a multiscale map of protein systems. Science, 2021, 374, eabf3067.	6.0	29
572	Host-specific asymmetric accumulation of mutation types reveals that the origin of SARS-CoV-2 is consistent with a natural process. Innovation(China), 2021, 2, 100159.	5.2	15
573	Significance and limitations of the use of next-generation sequencing technologies for detecting mutational signatures. DNA Repair, 2021, 107, 103200.	1.3	18
575	UV-exposure, endogenous DNA damage, and DNA replication errors shape the spectra of genome changes in human skin. PLoS Genetics, 2021, 17, e1009302.	1.5	26
576	Use of signals of positive and negative selection to distinguish cancer genes and passenger genes. ELife, 2021, 10, .	2.8	12
577	Relationships among smoking, oxidative stress, inflammation, macromolecular damage, and cancer. Mutation Research - Reviews in Mutation Research, 2021, 787, 108365.	2.4	181
578	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	7.7	109
579	SomaMutDB: a database of somatic mutations in normal human tissues. Nucleic Acids Research, 2022, 50, D1100-D1108.	6.5	21
580	Somatic data usage for classification of germ line variants. , 2021, , 169-192.		0
581	Increased risk of leukaemia in children with Down syndrome: a somatic evolutionary view. Expert Reviews in Molecular Medicine, 2021, 23, e5.	1.6	3

#	ARTICLE	IF	CITATIONS
583	Exons and introns exhibit transcriptional strand asymmetry of dinucleotide distribution, damage formation and DNA repair. NAR Genomics and Bioinformatics, 2021, 3, lqab020.	1.5	3
584	Bioinformatics workflows for clinical applications in precision oncology. Seminars in Cancer Biology, 2022, 84, 103-112.	4.3	8
585	Genomic Adaption and Mutational Patterns in a HaCaT Subline Resistant to Alkylating Agents and Ionizing Radiation. International Journal of Molecular Sciences, 2021, 22, 1146.	1.8	2
586	Improved Protein Decoy Selection via Non-Negative Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	1
588	Profiling of host genetic alterations and intra-tumor microbiomes in colorectal cancer. Computational and Structural Biotechnology Journal, 2021, 19, 3330-3338.	1.9	15
589	Molecular Subtyping and Precision Medicine for Pancreatic Cancer. Journal of Clinical Medicine, 2021, 10, 149.	1.0	34
590	Validation of the American Joint Committee on Cancer Staging in Squamous Cell Carcinoma of the Vermilion Lip. Annals of Surgical Oncology, 2021, 28, 3092-3099.	0.7	4
591	Identification of New Genes Involved in Germline Predisposition to Early-Onset Gastric Cancer. International Journal of Molecular Sciences, 2021, 22, 1310.	1.8	8
592	Comprehensive molecular profiling to predict clinical outcomes in pancreatic cancer. Therapeutic Advances in Medical Oncology, 2021, 13, 175883592110384.	1.4	10
593	Reactive oxygen species and DNA damage response in cancer. International Review of Cell and Molecular Biology, 2021, 364, 139-161.	1.6	67
594	DiaDeL: An Accurate Deep Learning-Based Model With Mutational Signatures for Predicting Metastasis Stage and Cancer Types. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1336-1343.	1.9	3
595	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. Nature Communications, 2021, 12, 574.	5.8	39
596	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	7.7	151
597	Hypermutation in single-stranded DNA. DNA Repair, 2020, 91-92, 102868.	1.3	28
598	Epigenetic plasticity, selection, and tumorigenesis. Biochemical Society Transactions, 2020, 48, 1609-1621.	1.6	11
599	Genome-wide mutational signatures revealed distinct developmental paths for human B cell lymphomas. Journal of Experimental Medicine, 2021, 218, .	4.2	29
600	Variable interplay of UV-induced DNA damage and repair at transcription factor binding sites. Nucleic Acids Research, 2021, 49, 891-901.	6.5	23
601	A Journey Through Myeloma Evolution: From the Normal Plasma Cell to Disease Complexity. HemaSphere, 2020, 4, e502.	1.2	10

#	Article	IF	Citations
602	POLE, MMR, and MSI Testing in Endometrial Cancer: Proceedings of the ISGyP Companion Society Session at the USCAP 2020 Annual Meeting. International Journal of Gynecological Pathology, 2021, 40, 5-16.	0.9	37
603	The interesting relationship between APOBEC3 deoxycytidine deaminases and cancer: a long road ahead. Open Biology, 2020, 10, 200188.	1.5	27
638	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	6.0	195
639	TrackSigFreq: subclonal reconstructions based on mutation signatures and allele frequencies. , 2019, , .		5
640	The Genetic Evolution of Treatment-Resistant Cutaneous, Acral, and Uveal Melanomas. Clinical Cancer Research, 2021, 27, 1516-1525.	3.2	6
641	DNA Polymerase and Mismatch Repair Exert Distinct Microsatellite Instability Signatures in Normal and Malignant Human Cells. Cancer Discovery, 2021, 11, 1176-1191.	7.7	46
642	A PoleP286R mouse model of endometrial cancer recapitulates high mutational burden and immunotherapy response. JCI Insight, 2020, 5, .	2.3	25
643	Germline biallelic Mcm8 variants are associated with early-onset Lynch-like syndrome. JCI Insight, 2020, 5, .	2.3	18
644	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. Journal of Clinical Investigation, 2020, 130, 5833-5846.	3.9	58
645	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic. PLoS ONE, 2020, 15, e0237689.	1.1	53
646	A xenograft and cell line model of SDH-deficient pheochromocytoma derived from Sdhb+/âˆ' rats. Endocrine-Related Cancer, 2020, 27, 337-354.	1.6	16
647	<i>CDKN2A</i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). Haematologica, 2021, 106, 2918-2926.	1.7	18
648	The Impact of Whole Genome Data on Therapeutic Decision-Making in Metastatic Prostate Cancer: A Retrospective Analysis. Cancers, 2020, 12, 1178.	1.7	10
649	Recurrent Glioblastoma: From Molecular Landscape to New Treatment Perspectives. Cancers, 2021, 13, 47.	1.7	106
650	The Molecular Pathogenesis of Multiple Myeloma. Hematology Reports, 2020, 12, 9054.	0.3	9
651	Characterization of the mechanism by which the RB/E2F pathway controls expression of the cancer genomic DNA deaminase APOBEC3B. ELife, 2020, 9, .	2.8	25
652	Identification of a Somatic Mutation-Derived Long Non-Coding RNA Signatures of Genomic Instability in Renal Cell Carcinoma. Frontiers in Oncology, 2021, 11, 728181.	1.3	6
653	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. Nature Genetics, 2021, 53, 1553-1563.	9.4	71

#	ARTICLE	IF	CITATIONS
654	Precision diagnostics: Integration of tissue pathology and genomics in cancer. Pathology, 2021, 53, 809-817.	0.3	2
655	The Mutational Signature Comprehensive Analysis Toolkit (musicatk) for the Discovery, Prediction, and Exploration of Mutational Signatures. Cancer Research, 2021, 81, 5813-5817.	0.4	11
656	The role of patient-derived ovarian cancer organoids in the study of PARP inhibitors sensitivity and resistance: from genomic analysis to functional testing. Journal of Experimental and Clinical Cancer Research, 2021, 40, 338.	3.5	12
657	Single-stranded DNA binding proteins influence APOBEC3A substrate preference. Scientific Reports, 2021, 11, 21008.	1.6	18
658	<i>BRCA1/Trp53</i> heterozygosity and replication stress drive esophageal cancer development in a mouse model. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	5
659	Molecular and genomic characterisation of a panel of human anal cancer cell lines. Cell Death and Disease, 2021, 12, 959.	2.7	3
660	Genomic characterization of rare molecular subclasses of hepatocellular carcinoma. Communications Biology, 2021, 4, 1150.	2.0	6
661	FOXOs: masters of the equilibrium. FEBS Journal, 2022, 289, 7918-7939.	2.2	39
662	Esophageal cancer mutational signatures around the world. Nature Genetics, 2021, 53, 1522-1523.	9.4	2
664	Genomic alterations associated with mutational signatures, DNA damage repair and chromatin remodeling pathways in cervical carcinoma. Npj Genomic Medicine, 2021, 6, 82.	1.7	9
665	Somatic Mosaicism in Biology and Disease. Annual Review of Physiology, 2022, 84, 113-133.	5.6	5
666	Signatures Beyond Oncogenic Mutations in Cell-Free DNA Sequencing for Non-Invasive, Early Detection of Cancer. Frontiers in Genetics, 2021, 12, 759832.	1.1	1
667	Homologous Recombination Deficiency Assays in Epithelial Ovarian Cancer: Current Status and Future Direction. Frontiers in Oncology, 2021, 11, 675972.	1.3	21
668	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. Nature, 2021, 598, 510-514.	13.7	95
670	Whole-genome landscape of adult T-cell leukemia/lymphoma. Blood, 2022, 139, 967-982.	0.6	44
673	A DNA Damage Response Gene Panel for Different Histologic Types of Epithelial Ovarian Carcinomas and Their Outcomes. Biomedicines, 2021, 9, 1384.	1.4	4
674	In-depth cell-free DNA sequencing reveals genomic landscape of Hodgkinâ€™s lymphoma and facilitates ultrasensitive residual disease detection. Med, 2021, 2, 1171-1193.e11.	2.2	24
677	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	13.7	87

#	ARTICLE	IF	CITATIONS
678	Dissecting single-cell genomes through the clonal organoid technique. Experimental and Molecular Medicine, 2021, 53, 1503-1511.	3.2	9
679	Structural and functional analysis of somatic coding and UTR indels in breast and lung cancer genomes. Scientific Reports, 2021, 11, 21178.	1.6	1
680	Mapping the genomic diaspora of gastric cancer. Nature Reviews Cancer, 2022, 22, 71-84.	12.8	72
681	Genomic Signatures in HPV-Associated Tumors. Viruses, 2021, 13, 1998.	1.5	9
682	Genomic and Transcriptomic Analysis of Relapsed and Refractory Childhood Solid Tumors Reveals a Diverse Molecular Landscape and Mechanisms of Immune Evasion. Cancer Research, 2021, 81, 5818-5832.	0.4	10
683	Unravelling roles of error-prone DNA polymerases in shaping cancer genomes. Oncogene, 2021, 40, 6549-6565.	2.6	14
686	A data-driven approach for constructing mutation categories for mutational signature analysis. PLoS Computational Biology, 2021, 17, e1009542.	1.5	1
687	Caught in the antiviral crossfire: Ganciclovir-associated mutagenesis in HSC transplant recipients. Cell Stem Cell, 2021, 28, 1683-1685.	5.2	1
688	Transcriptional Response of Mycobacterium tuberculosis to Cigarette Smoke Condensate. Frontiers in Microbiology, 2021, 12, 744800.	1.5	2
689	C. elegans genome-wide analysis reveals DNA repair pathways that act cooperatively to preserve genome integrity upon ionizing radiation. PLoS ONE, 2021, 16, e0258269.	1.1	0
690	UNMASC: tumor-only variant calling with unmatched normal controls. NAR Cancer, 2021, 3, zcab040.	1.6	4
691	Cancer Mutational Processes Vary in Their Association with Replication Timing and Chromatin Accessibility. Cancer Research, 2021, 81, 6106-6116.	0.4	12
695	Understanding cancer breakpoint determinants with omics data. Integrative Cancer Science and Therapeutics, 2020, 7, .	0.1	1
704	iMutSig: a web application to identify the most similar mutational signature using shiny. F1000Research, 2020, 9, 586.	0.8	0
715	Tumor-Agnostic Biomarkers: Heed Caution, and Why Cell of Origin Still Matters. Onco, 2021, 1, 95-100.	0.2	0
716	Application of third-generation sequencing in cancer research. Medical Review, 2021, 1, 150-171.	0.3	6
717	Clone decomposition based on mutation signatures provides novel insights into mutational processes. NAR Genomics and Bioinformatics, 2021, 3, lqab093.	1.5	0
718	Heavy mutagenesis by tobacco leads to lung adenocarcinoma tumors with KRAS G12 mutations other than G12D, leading KRAS G12D tumorsâ€"on averageâ€"to exhibit a lower mutation burden. Lung Cancer, 2022, 166, 265-269.	0.9	3

#	ARTICLE	IF	CITATIONS
721	Maintenance of genome sequence integrity in long- and short-lived rodent species. Science Advances, 2021, 7, eabj3284.	4.7	29
724	Integrating Toxicogenomics Data into Risk Assessment. , 2020, , 23-51.		0
728	Systems biology approaches in solid organ transplantation. Current Opinion in Organ Transplantation, 2021, 26, 37-42.	0.8	1
729	In-situ preparation of palygorskite-montmorillonite materials from palygorskite mineral via hydrothermal process for high-efficient adsorption of aflatoxin B1. Separation and Purification Technology, 2022, 280, 119960.	3.9	9
730	Comparison of Benign and Malignant Pilomatricomas Using Whole-exome Sequencing. Cancer Genomics and Proteomics, 2020, 17, 795-802.	1.0	6
731	ROS-Induced DNA Damage as an Underlying Cause of Aging. Advances in Geriatric Medicine and Research, 2020, , .	0.6	2
735	The Mutagenic Impact of Environmental Exposures in Human Cells and Cancer: Imprints Through Time. Frontiers in Genetics, 2021, 12, 760039.	1.1	12
736	High-Throughput Nucleotide Resolution Predictions of Assay Limitations Increase the Reliability and Concordance of Clinical Tests. JCO Clinical Cancer Informatics, 2021, 5, 1085-1095.	1.0	4
737	MutScape: an analytical toolkit for probing the mutational landscape in cancer genomics. NAR Genomics and Bioinformatics, 2021, 3, lqab099.	1.5	0
738	Independent somatic evolution underlies clustered neuroendocrine tumors in the human small intestine. Nature Communications, 2021, 12, 6367.	5.8	11
739	MSA: reproducible mutational signature attribution with confidence based on simulations. BMC Bioinformatics, 2021, 22, 540.	1.2	6
741	Thyroid cancer under the scope of emerging technologies. Molecular and Cellular Endocrinology, 2022, 541, 111491.	1.6	9
742	Deficiency of replication-independent DNA mismatch repair drives a 5-methylcytosine deamination mutational signature in cancer. Science Advances, 2021, 7, eabg4398.	4.7	11
745	Identifying Novel Causes of Cancers to Enhance Cancer Prevention: New Strategies Are Needed. Journal of the National Cancer Institute, 2022, 114, 353-360.	3.0	25
751	Whole-exome Sequencing Reveals Genetic Underpinnings of Tongue Carcinoma in Chinese Population. Asia-Pacific Journal of Oncology, 2020, , 1-9.	0.2	0
755	Low dose radiation risk: comment on the opinion article â€˜Interpretation of risk for low dose radiation exposures: inconsistences, philosophical problems and fallaciesâ€™ by Walsh (2020). Journal of Radiological Protection, 2020, 40, 1534-1538.	0.6	1
759	iMutSig: a web application to identify the most similar mutational signature using shiny. F1000Research, 0, 9, 586.	0.8	0
761	Single cell sequencing reveals cell populations that predict primary resistance to imatinib in chronic myeloid leukemia. Aging, 2020, 12, 25337-25355.	1.4	8

#	Article	IF	Citations
762	Inhibition of P53-mediated cell cycle control as the determinant in dedifferentiated liposarcomas development. American Journal of Cancer Research, 2021, 11, 3271-3284.	1.4	0
763	A mapping platform for mitotic crossover by single-cell multi-omics. Methods in Enzymology, 2021, 661, 183-204.	0.4	0
764	Recent advances in lung cancer genomics: Application in targeted therapy. Advances in Genetics, 2021, 108, 201-275.	0.8	5
765	Toxicogenomics: A Primer for Toxicologic Pathologists. , 2022, , 491-543.		0
766	Endometrial cancer may be part of the MUTYH-associated polyposis cancer spectrum. European Journal of Medical Genetics, 2022, 65, 104385.	0.7	6
767	The Epidemiology of Central Nervous System Tumors. Hematology/Oncology Clinics of North America, 2022, 36, 23-42.	0.9	15
768	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. Nature Communications, 2021, 12, 6946.	5.8	22
770	Dietary Patterns and Associated Microbiome Changes that Promote Oncogenesis. Frontiers in Cell and Developmental Biology, 2021, 9, 725821.	1.8	8
771	Genomic and Transcriptomic Profiling of Brain Metastases. Cancers, 2021, 13, 5598.	1.7	0
772	Landscape of Driver Gene Events, Biomarkers and Druggable Targets Identified by Whole Genome Sequencing of Glioblastomas. Neuro-Oncology Advances, 2022, 4, vdab177.	0.4	3
773	APOBEC3A drives deaminase domain-independent chromosomal instability to promote pancreatic cancer metastasis. Nature Cancer, 2021, 2, 1338-1356.	5.7	35
774	Oral Squamous Cell Carcinoma in Young Patients Show Higher Rates of EGFR Amplification: Implications for Novel Personalized Therapy. Frontiers in Oncology, 2021, 11, 750852.	1.3	6
775	Genomic Sequencing for Bladder Urothelial Carcinoma and Its Clinical Implications for Immunotherapy. Cancer Research and Treatment, 2022, 54, 894-906.	1.3	6
776	Evolution under Spatially Heterogeneous Selection in Solid Tumors. Molecular Biology and Evolution, 2022, 39, .	3.5	5
777	TP53 Mutation Infers a Poor Prognosis and Is Correlated to Immunocytes Infiltration in Breast Cancer. Frontiers in Cell and Developmental Biology, 2021, 9, 759154.	1.8	19
778	Mutational signature analysis in non-small cell lung cancer patients with a high tumor mutational burden. Respiratory Research, 2021, 22, 302.	1.4	5
779	Genomic Instability and Cancer Risk Associated with Erroneous DNA Repair. International Journal of Molecular Sciences, 2021, 22, 12254.	1.8	21
780	Translesion polymerase eta both facilitates DNA replication and promotes increased human genetic variation at common fragile sites. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	20

#	Article	IF	Citations
781	Cancer drivers and clonal dynamics in acute lymphoblastic leukaemia subtypes. Blood Cancer Journal, 2021, 11, 177.	2.8	9
782	Variant profiling of colorectal adenomas from three patients of two families with MSH3-related adenomatous polyposis. PLoS ONE, 2021, 16, e0259185.	1.1	5
783	Chromothripsis followed by circular recombination drives oncogene amplification in human cancer. Nature Genetics, 2021, 53, 1673-1685.	9.4	61
784	APOBEC Mutagenesis Inhibits Breast Cancer Growth through Induction of T cellâ€"Mediated Antitumor Immune Responses. Cancer Immunology Research, 2022, 10, 70-86.	1.6	20
785	Profile of Basal Cell Carcinoma Mutations and Copy Number Alterations - Focus on Gene-Associated Noncoding Variants. Frontiers in Oncology, 2021, 11, 752579.	1.3	1
786	Genome Instability in Multiple Myeloma: Facts and Factors. Cancers, 2021, 13, 5949.	1.7	17
788	Analysis of Mutations and Dysregulated Pathways Unravels Carcinogenic Effect and Clinical Actionability of Mutational Processes. Frontiers in Cell and Developmental Biology, 2021, 9, 768981.	1.8	1
789	Precancerous liver diseases do not cause increased mutagenesis in liver stem cells. Communications Biology, 2021, 4, 1301.	2.0	9
790	RAB42 Promotes Glioma Pathogenesis via the VEGF Signaling Pathway. Frontiers in Oncology, 2021, 11, 657029.	1.3	3
793	Monoallelic deleterious <scp><i>MUTYH</i></scp> germline variants as a driver for tumorigenesis. Journal of Pathology, 2022, 256, 214-222.	2.1	12
794	Advanced Omics and Radiobiological Tissue Archives: The Future in the Past. Applied Sciences (Switzerland), 2021, 11, 11108.	1.3	5
795	Molecular characterization of Barrettâ€™s esophagus at single-cell resolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
797	Nature of spontaneously arising single base substitutions in normal cells. Genome Instability & Disease, 2021, 2, 339.	0.5	0
798	Constitutional <i>POLE</i> variants causing a phenotype reminiscent of constitutional mismatch repair deficiency. Human Mutation, 2022, 43, 85-96.	1.1	8
799	Integration of Mutational Signature Analysis with 3D Chromatin Data Unveils Differential AID-Related Mutagenesis in Indolent Lymphomas. International Journal of Molecular Sciences, 2021, 22, 13015.	1.8	1
800	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.0	3
801	Therapeutic vulnerability to PARP1,2 inhibition in RB1-mutant osteosarcoma. Nature Communications, 2021, 12, 7064.	5.8	19
802	Robust deep learning model for prognostic stratification of pancreatic ductal adenocarcinoma patients. IScience, 2021, 24, 103415.	1.9	6

#	ARTICLE	IF	CITATIONS
803	Genomic Landscape and Clinical Utility in Korean Advanced Pan-Cancer Patients from Prospective Clinical Sequencing: K-MASTER Program. Cancer Discovery, 2022, 12, 938-948.	7.7	19
804	The Genomic Landscape of Pediatric Renal Cell Carcinomas. SSRN Electronic Journal, 0, , .	0.4	0
805	Onkogenese: Komplette Genomanalysen versprechen neue Einblicke. , 0, , .		0
806	Proteogenomic Characterization of Korean Never-Smoker Lung Adenocarcinoma Harboring Rare or Unknown Driver Oncogenes. SSRN Electronic Journal, 0, , .	0.4	0
807	Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency. Nature Medicine, 2022, 28, 125-135.	15.2	53
808	<scp>ScalpelSig</scp> Designs Targeted Genomic Panels from Data to Detect Activity of Mutational Signatures. Journal of Computational Biology, 2022, 29, 56-73.	0.8	1
809	When breaks get hot: inflammatory signaling in BRCA1/2-mutant cancers. Trends in Cancer, 2022, 8, 174-189.	3.8	27
810	Age influences on the molecular presentation of tumours. Nature Communications, 2022, 13, 208.	5.8	26
811	Accuracy of mutational signature software on correlated signatures. Scientific Reports, 2022, 12, 390.	1.6	6
813	Integrative molecular analysis of combined small-cell lung carcinomas identifies major subtypes with different therapeutic opportunities. ESMO Open, 2022, 7, 100308.	2.0	5
817	Germline predisposition to glial neoplasms in children and young adults: A narrative review. Glioma (Mumbai, India), 2021, 4, 68.	0.0	1
818	Sex-Biased<i>ZRSR2</i>Mutations in Myeloid Malignancies Impair Plasmacytoid Dendritic Cell Activation and Apoptosis. Cancer Discovery, 2022, 12, 522-541.	7.7	44
819	PARP Inhibitors in Pancreatic Cancer. Cancer Journal (Sudbury, Mass), 2021, 27, 465-475.	1.0	18
820	Arginine Depletion in Human Cancers. Cancers, 2021, 13, 6274.	1.7	2
822	Whole genome deep sequencing analysis of cell-free DNA in samples with low tumour content. BMC Cancer, 2022, 22, 85.	1.1	9
825	Integrative Genomic Analyses of 1,145 Patient Samples Reveal New Biomarkers in Esophageal Squamous Cell Carcinoma. Frontiers in Molecular Biosciences, 2021, 8, 792779.	1.6	4
827	Barrett's esophagus stages: their correlation with SBS17-associated DNA mutations and the identification of histological marker genes. Molecular and Cellular Oncology, 2022, 9, 2026559.	0.3	0
828	Human genetic risk of treatment with antiviral nucleoside analog drugs that induce lethal mutagenesis: the special case of molnupiravir. Environmental and Molecular Mutagenesis, 2022, 63, 37-63.	0.9	39

#	ARTICLE	IF	CITATIONS
830	A framework for mutational signature analysis based on DNA shape parameters. PLoS ONE, 2022, 17, e0262495.	1.1	4
831	High Level of Aristolochic Acid Detected With a Unique Genomic Landscape Predicts Early UTUC Onset After Renal Transplantation in Taiwan. Frontiers in Oncology, 2021, 11, 828314.	1.3	4
832	Evaluation of an integrative Bayesian peptide detection approach on a combinatorial peptide library. European Journal of Mass Spectrometry, 2021, 27, 217-234.	0.5	0
833	Single-cell analysis of somatic mutation burden in mammary epithelial cells of pathogenic BRCA1/2 mutation carriers. Journal of Clinical Investigation, 2022, 132, .	3.9	7
835	Genomic characterization of functional high-risk multiple myeloma patients. Blood Cancer Journal, 2022, 12, 24.	2.8	16
836	Defining genomic events involved in the evolutionary trajectories of myeloma and its precursor conditions. Seminars in Oncology, 2022, , .	0.8	1
837	Identification of Somatic Mutations From Bulk and Single-Cell Sequencing Data. Frontiers in Aging, 2022, 2, .	1.2	3
838	Natural Barcodes for Longitudinal Single Cell Tracking of Leukemic and Immune Cell Dynamics. Frontiers in Immunology, 2021, 12, 788891.	2.2	12
839	Preneoplastic somatic mutations including <i>MYD88</i> ^{L265P} in lymphoplasmacytic lymphoma. Science Advances, 2022, 8, eabl4644.	4.7	21
841	BRCA1 deficiency specific base substitution mutagenesis is dependent on translesion synthesis and regulated by 53BP1. Nature Communications, 2022, 13, 226.	5.8	11
842	Association of mutation signature effectuating processes with mutation hotspots in driver genes and non-coding regions. Nature Communications, 2022, 13, 178.	5.8	12
843	Molecular Mechanisms of lncRNAs in the Dependent Regulation of Cancer and Their Potential Therapeutic Use. International Journal of Molecular Sciences, 2022, 23, 764.	1.8	16
844	Somatic and Germline Genomic Alterations in Very Young Women with Breast Cancer. Clinical Cancer Research, 2022, 28, 2339-2348.	3.2	20
845	Lasting Complete Clinical Response of a Recurring Cutaneous Squamous Cell Carcinoma With MEK Mutation and PIK3CA Amplification Achieved by Dual Trametinib and Metformin Therapy. JCO Precision Oncology, 2022, 6, e2100344.	1.5	1
846	Computational methods and translational applications for targeted nextâ€generation sequencing platforms. Genes Chromosomes and Cancer, 2022, 61, 322-331.	1.5	3
847	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	7.7	64
848	Multilocus Inherited Neoplasia Allele Syndrome (MINAS): an update. European Journal of Human Genetics, 2022, 30, 265-270.	1.4	12
849	Identifying Transcripts with Tandem Duplications from RNA-Sequencing Data to Predict BRCA1-Type Primary Breast Cancer. Cancers, 2022, 14, 753.	1.7	1

#	Article	IF	Citations
850	Pathogenesis of Triple-Negative Breast Cancer. Annual Review of Pathology: Mechanisms of Disease, 2022, 17, 181-204.	9.6	132
851	Deep Unfolding for Non-Negative Matrix Factorization with Application to Mutational Signature Analysis. Journal of Computational Biology, 2022, 29, 45-55.	0.8	1
852	The breast pre-cancer atlas illustrates the molecular and micro-environmental diversity of ductal carcinoma in situ. Npj Breast Cancer, 2022, 8, 6.	2.3	13
853	Therapeutic Opportunities of Disrupting Genome Integrity in Adult Diffuse Glioma. Biomedicines, 2022, 10, 332.	1.4	0
854	APOBEC mediated mutagenesis drives genomic heterogeneity in endometriosis. Journal of Human Genetics, 2022, 67, 323-329.	1.1	3
855	Assessing chemical carcinogenicity: hazard identification, classification, and risk assessment. Insight from a Toxicology Forum state-of-the-science workshop. Critical Reviews in Toxicology, 2021, 51, 653-694.	1.9	10
856	The simplest explanation does not have to be preferred: co-occurrence of pathogenic variants in cancer-predisposing genes. European Journal of Human Genetics, 2022, , .	1.4	0
857	Tandem Substitutions in Somatic Hypermutation. Frontiers in Immunology, 2021, 12, 807015.	2.2	2
858	Rare Occurrence of Aristolochic Acid Mutational Signatures in Oro-Gastrointestinal Tract Cancers. Cancers, 2022, 14, 576.	1.7	6
860	Recurrent mutations in topoisomerase IIÎ± cause a previously undescribed mutator phenotype in human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	22
861	A gradient tree boosting and network propagation derived pan-cancer survival network of the tumor microenvironment. IScience, 2022, 25, 103617.	1.9	4
862	Human induced pluripotent stem cells display a similar mutation burden as embryonic pluripotent cells inÂvivo. IScience, 2022, 25, 103736.	1.9	5
863	Distinct Genomic Landscapes in Early-Onset and Late-Onset Endometrial Cancer. JCO Precision Oncology, 2022, 6, e2100401.	1.5	3
864	The radiobiology of TGFÎ². Seminars in Cancer Biology, 2022, 86, 857-867.	4.3	15
867	Immune subtypes and neoantigen-related immune evasion in advanced colorectal cancer. IScience, 2022, 25, 103740.	1.9	4
869	Mutational signatures reveal ternary relationships between homologous recombination repair, APOBEC, and mismatch repair in gynecological cancers. Journal of Translational Medicine, 2022, 20, 65.	1.8	6
871	MetaMutationalSigs: comparison of mutational signature refitting results made easy. Bioinformatics, 2022, 38, 2344-2347.	1.8	0
873	Multiregion sequencing of sarcomatoid renal cell carcinoma arising from autosomal dominant polycystic kidney disease. Molecular Genetics & Genomic Medicine, 2022, , e1853.	0.6	1

#	Article	IF	Citations
874	Refining risk stratification in HR-positive/HER2-negative early breast cancer: how to select patients for treatment escalation?. Breast Cancer Research and Treatment, 2022, 192, 465-484.	1.1	6
875	The threat of programmed DNA damage to neuronal genome integrity and plasticity. Nature Genetics, 2022, 54, 115-120.	9.4	35
876	Genotoxic aldehydes in the hematopoietic system. Blood, 2022, 139, 2119-2129.	0.6	18
877	Characterisation of the spectrum and genetic dependence of collateral mutations induced by translesion DNA synthesis. PLoS Genetics, 2022, 18, e1010051.	1.5	7
878	Unwinding the mutational signatures of a DNA topoisomerase enzyme. Nature, 2022, 602, 580-581.	13.7	0
879	A platform for oncogenomic reporting and interpretation. Nature Communications, 2022, 13, 756.	5.8	7
881	Wholeâ€exome sequencing of transforming oral lichen planus reveals mutations in DNA damage repair and apoptosis pathway genes. Journal of Oral Pathology and Medicine, 2022, 51, 395-404.	1.4	5
882	Biallelic mutations in cancer genomes reveal local mutational determinants. Nature Genetics, 2022, 54, 128-133.	9.4	16
883	Intratumor genetic heterogeneity and clonal evolution to decode endometrial cancer progression. Oncogene, 2022, 41, 1835-1850.	2.6	9
884	Somatic mutation analyses of stem-like cells in gingivobuccal oral squamous cell carcinoma reveals DNA damage response genes. Genomics, 2022, 114, 110308.	1.3	1
885	Somatic mutational profiles and germline polygenic risk scores in human cancer. Genome Medicine, 2022, 14, 14.	3.6	14
886	Myeloid cell interferon responses correlate with clearance of SARS-CoV-2. Nature Communications, 2022, 13, 679.	5.8	30
887	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	13.7	60
888	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. Nature, 2022, 602, 623-631.	13.7	38
889	Gut Microbiota in Colorectal Cancer: Associations, Mechanisms, and Clinical Approaches. Annual Review of Cancer Biology, 2022, 6, 65-84.	2.3	7
890	A phase 2 evaluation of pembrolizumab for recurrent Lynchâ€like versus sporadic endometrial cancers with microsatellite instability. Cancer, 2022, 128, 1206-1218.	2.0	28
891	Genomic Features of Muscle-invasive Bladder Cancer Arising After Prostate Radiotherapy. European Urology, 2022, 81, 466-473.	0.9	12
892	Avelumab maintenance in advanced urothelial carcinoma: biomarker analysis of the phase 3 JAVELIN Bladder 100 trial. Nature Medicine, 2021, 27, 2200-2211.	15.2	65

#	ARTICLE	IF	CITATIONS
893	DNA repair, recombination, and damage signaling. Genetics, 2022, 220, .	1.2	26
894	Mouse model and human patient data reveal critical roles for Pten and p53 in suppressing POLE mutant tumor development. NAR Cancer, 2022, 4, zcac004.	1.6	5
895	The role of DNA mismatch repair in immunotherapy of human cancer. International Journal of Biological Sciences, 2022, 18, 2821-2832.	2.6	20
897	Toward More Comprehensive Homologous Recombination Deficiency Assays in Ovarian Cancer, Part 1: Technical Considerations. Cancers, 2022, 14, 1132.	1.7	8
898	Visualization of the Effect of Assay Size on the Error Profile of Tumor Mutational Burden Measurement. Genes, 2022, 13, 432.	1.0	0
899	DNA Hydroxymethylation in Smoking-Associated Cancers. International Journal of Molecular Sciences, 2022, 23, 2657.	1.8	7
900	Spatiotemporal dynamics of clonal selection and diversification in normal endometrial epithelium. Nature Communications, 2022, 13, 943.	5.8	24
901	<i>PTEN</i> Loss and <i>BRCA1</i> Promoter Hypermethylation Negatively Predict for Immunogenicity in BRCA-Deficient Ovarian Cancer. JCO Precision Oncology, 2022, 6, e2100159.	1.5	4
902	Human topoisomerases and their roles in genome stability and organization. Nature Reviews Molecular Cell Biology, 2022, 23, 407-427.	16.1	125
903	Induction of APOBEC3-mediated genomic damage in urothelium implicates BK polyomavirus (BKPyV) as a hit-and-run driver for bladder cancer. Oncogene, 2022, 41, 2139-2151.	2.6	21
905	Differential Selection on Caste-Associated Genes in a Subterranean Termite. Insects, 2022, 13, 224.	1.0	2
906	Case Report Series: Aggressive HR Deficient Colorectal Cancers Related to BRCA1 Pathogenic Germline Variants. Frontiers in Oncology, 2022, 12, 835581.	1.3	3
907	Discovery of an unusually high number of de novo mutations in sperm of older men using duplex sequencing. Genome Research, 2022, 32, 499-511.	2.4	9
908	Mutational signature profiling classifies subtypes of clinically different mismatch-repair-deficient tumours with a differential immunogenic response potential. British Journal of Cancer, 2022, , .	2.9	2
909	MutationalPatterns: the one stop shop for the analysis of mutational processes. BMC Genomics, 2022, 23, 134.	1.2	66
910	Toward More Comprehensive Homologous Recombination Deficiency Assays in Ovarian Cancer Part 2: Medical Perspectives. Cancers, 2022, 14, 1098.	1.7	8
911	Comparison of sampling methods for next generation sequencing for patients with lung cancer. Cancer Medicine, 2022, 11, 2744-2754.	1.3	13
913	Functions and consequences of AID/APOBEC-mediated DNA and RNA deamination. Nature Reviews Genetics, 2022, 23, 505-518.	7.7	103

#	ARTICLE	IF	CITATIONS
914	Benefit and toxicity of programmed death-1 blockade vary by ethnicity in patients with advanced melanoma: an international multicentre observational study. British Journal of Dermatology, 2022, 187, 401-410.	1.4	21
915	High Mutation Burden in ER-Positive/HER2-Negative/Luminal Breast Cancers. Journal of Clinical Medicine, 2022, 11, 1605.	1.0	2
916	Prospectively defined patterns of APOBEC3A mutagenesis are prevalent in human cancers. Cell Reports, 2022, 38, 110555.	2.9	25
917	The Current State of Treatment and Future Directions in Cutaneous Malignant Melanoma. Biomedicines, 2022, 10, 822.	1.4	18
919	Identification of genetic mutations of cutaneous squamous cell carcinoma using whole exome sequencing in non-Caucasian population. Journal of Dermatological Science, 2022, 106, 70-77.	1.0	4
921	SomaticSiMu: a mutational signature simulator. Bioinformatics, 2022, 38, 2619-2620.	1.8	0
922	Temozolomide Followed by Combination With Low-Dose Ipilimumab and Nivolumab in Patients With Microsatellite-Stable, O⁶-Methylguanineâ€“DNA Methyltransferaseâ€“Silenced Metastatic Colorectal Cancer: The MAYA Trial. Journal of Clinical Oncology, 2022, 40, 1562-1573.	0.8	52
923	Epidemiology, risk factors, and prognostic factors of gliomas. Clinical and Translational Imaging, 2022, 10, 467-475.	1.1	16
924	Comprehensive characterization of m6A methylation and its impact on prognosis, genome instability, and tumor microenvironment in hepatocellular carcinoma. BMC Medical Genomics, 2022, 15, 53.	0.7	8
925	Unique molecular characteristics of NAFLD-associated liver cancer accentuate Î²-catenin/TNFRSF19-mediated immune evasion. Journal of Hepatology, 2022, 77, 410-423.	1.8	13
926	Spectrum of DNA mismatch repair failures viewed through the lens of cancer genomics and implications for therapy. Clinical Science, 2022, 136, 383-404.	1.8	8
927	Comprehensive Genomic Profiling of Neuroendocrine Carcinomas of the Gastrointestinal System. Cancer Discovery, 2022, 12, 692-711.	7.7	58
928	Who ever thought genetic mutations were random?. Trends in Plant Science, 2022, , .	4.3	1
929	Prevalence of UV Mutational Signatures Among Cutaneous Primary Tumors. JAMA Network Open, 2022, 5, e223833.	2.8	11
930	Universal encoding of pan-cancer histology by deep texture representations. Cell Reports, 2022, 38, 110424.	2.9	19
931	Unravelling the tumour genome: The evolutionary and clinical impacts of structural variants in tumourigenesis. Journal of Pathology, 2022, 257, 479-493.	2.1	6
933	<i>Helicobacter pylori</i>â€induced DNA doubleâ€stranded break in the development of gastric cancer. Cancer Science, 2022, 113, 1909-1918.	1.7	15
935	Distinct Genomic Profiles Are Associated with Treatment Response and Survival in Ovarian Cancer. Cancers, 2022, 14, 1511.	1.7	5

#	Article	IF	Citations
936	A general calculus of fitness landscapes finds genes under selection in cancers. Genome Research, 2022, , gr.275811.121.	2.4	7
937	Ultrasensitive profiling of UV-induced mutations identifies thousands of subclinical facial tumors in tuberous sclerosis complex. Journal of Clinical Investigation, 2022, 132, .	3.9	6
938	Polymerase Epsilon-Associated Ultramutagenesis in Cancer. Cancers, 2022, 14, 1467.	1.7	9
939	Single-cell landscapes of primary glioblastomas and matched explants and cell lines show variable retention of inter- and intratumor heterogeneity. Cancer Cell, 2022, 40, 379-392.e9.	7.7	54
940	Immune Checkpoint Inhibition as Single Therapy for Synchronous Cancers Exhibiting Hypermutation: An IRRDC Study. JCO Precision Oncology, 2022, 6, e2100286.	1.5	8
941	Exome and Tissue-Associated Microbiota as Predictive Markers of Response to Neoadjuvant Treatment in Locally Advanced Rectal Cancer. Frontiers in Oncology, 2022, 12, 809441.	1.3	2
942	Mutational signatures and processes in hepatobiliary cancers. Nature Reviews Gastroenterology and Hepatology, 2022, 19, 367-382.	8.2	2
943	Comparative Analysis of Differentially Mutated Genes in Non-Muscle and Muscle-Invasive Bladder Cancer in the Chinese Population by Whole Exome Sequencing. Frontiers in Genetics, 2022, 13, 831146.	1.1	5
945	APOBEC SBS13 Mutational Signatureâ€"A Novel Predictor of Radioactive Iodine Refractory Papillary Thyroid Carcinoma. Cancers, 2022, 14, 1584.	1.7	4
946	Local Ablative Therapy Associated with Immunotherapy in Locally Advanced Pancreatic Cancer: A Solution to Overcome the Double Trouble?â€"A Comprehensive Review. Journal of Clinical Medicine, 2022, 11, 1948.	1.0	7
947	Technologies to Assess Drug Response and Heterogeneity in Patient-Derived Cancer Organoids. Annual Review of Biomedical Engineering, 2022, 24, 157-177.	5.7	10
948	Single-cell transcriptomics reveals a distinct developmental state of KMT2A-rearranged infant B-cell acute lymphoblastic leukemia. Nature Medicine, 2022, 28, 743-751.	15.2	35
950	Comprehensive characterization of PTEN mutational profile in a series of 34,129 colorectal cancers. Nature Communications, 2022, 13, 1618.	5.8	23
952	Toward Targeted Therapies in Oesophageal Cancers: An Overview. Cancers, 2022, 14, 1522.	1.7	3
953	Emerging Trends in the Pathological Research of Human Papillomavirus-positive Oropharyngeal Squamous Cell Carcinoma. , 2022, 000, 000-000.		0
954	Integrative Genomic Profiling Uncovers Therapeutic Targets of Acral Melanoma in Asian Populations. Clinical Cancer Research, 2022, 28, 2690-2703.	3.2	10
956	The genotypes and phenotypes of missense mutations in the proline domain of the p53 protein. Cell Death and Differentiation, 2022, 29, 938-945.	5.0	18
957	Accurate detection of subclonal variants in paired diagnosis-relapse acute myeloid leukemia samples by next generation Duplex Sequencing. Leukemia Research, 2022, 115, 106822.	0.4	2

#	ARTICLE	IF	CITATIONS
958	Templated Insertions Are Associated Specifically with <i>BRCA2</i> Deficiency and Overall Survival in Advanced Ovarian Cancer. Molecular Cancer Research, 2022, 20, 1061-1070.	1.5	1
959	SUITOR: Selecting the number of mutational signatures through cross-validation. PLoS Computational Biology, 2022, 18, e1009309.	1.5	1
960	Genome-wide analysis of somatic noncoding mutation patterns in cancer. Science, 2022, 376, eabg5601.	6.0	33
961	The genomic landscape of pediatric renal cell carcinomas. IScience, 2022, 25, 104167.	1.9	3
962	Origins and Timing of Emerging Lesions in Advanced Renal Cell Carcinoma. Molecular Cancer Research, 2022, 20, 909-922.	1.5	0
963	Rearrangement processes and structural variations show evidence of selection in oesophageal adenocarcinomas. Communications Biology, 2022, 5, 335.	2.0	8
964	Genomic and Single-Cell Landscape Reveals Novel Drivers and Therapeutic Vulnerabilities of Transformed Cutaneous T-cell Lymphoma. Cancer Discovery, 2022, 12, 1294-1313.	7.7	18
965	Clinical, genomic, and transcriptomic correlates of response to immune checkpoint blockade-based therapy in a cohort of patients with angiosarcoma treated at a single center. , 2022, 10, e004149.		20
966	Copy number alteration signatures as biomarkers in cancer: a review. Biomarkers in Medicine, 2022, 16, 371-386.	0.6	6
967	Integrated, Integral, and Exploratory Biomarkers in the Development of Poly(ADP-Ribose) Polymerase Inhibitors. Cancer Journal (Sudbury, Mass), 2021, 27, 482-490.	1.0	0
968	Do We Need a New Approach to Cancer Biology Education for Radiation Oncology Residents?. Cureus, 2021, 13, e20662.	0.2	0
969	Clonal Evolution of High-Risk Chronic Lymphocytic Leukemia: A Contemporary Perspective. Frontiers in Oncology, 2021, 11, 790004.	1.3	11
970	Early Tumorâ€"Immune Microenvironmental Remodeling and Response to First-Line Fluoropyrimidine and Platinum Chemotherapy in Advanced Gastric Cancer. Cancer Discovery, 2022, 12, 984-1001.	7.7	52
971	TMBleR: a bioinformatic tool to optimize TMB estimation and predictive power. Bioinformatics, 2022, 38, 1724-1726.	1.8	1
972	Genomic attributes of homology-directed DNA repair deficiency in metastatic prostate cancer. JCI Insight, 2021, 6, .	2.3	15
973	Computational analysis of cancer genome sequencing data. Nature Reviews Genetics, 2022, 23, 298-314.	7.7	38
974	Somatic Features of Response and Relapse in Nonâ€"muscle-invasive Bladder Cancer Treated with Bacillus Calmette-GuÃ©rin Immunotherapy. European Urology Oncology, 2022, 5, 677-686.	2.6	6
975	Decoding Cancer Variants of Unknown Significance for Helicaseâ€"Nucleaseâ€"RPA Complexes Orchestrating DNA Repair During Transcription and Replication. Frontiers in Molecular Biosciences, 2021, 8, 791792.	1.6	4

#	ARTICLE	IF	CITATIONS
976	Clonal architecture predicts clinical outcomes and drug sensitivity in acute myeloid leukemia. Nature Communications, 2021, 12, 7244.	5.8	29
977	Clinical feature-related single-base substitution sequence signatures identified with an unsupervised machine learning approach. BMC Medical Genomics, 2021, 14, 298.	0.7	0
978	Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. Cell Reports Medicine, 2021, 2, 100472.	3.3	13
979	Anti-recombination function of MutSÎ± restricts telomere extension by ALT-associated homology-directed repair. Cell Reports, 2021, 37, 110088.	2.9	15
981	Cancer-Causative Mutations Occurring in Early Embryogenesis. Cancer Discovery, 2022, 12, 949-957.	7.7	21
985	PARP1 Inhibitor and Trabectedin Combination Does Not Increase Tumor Mutational Burden in Advanced Sarcomasâ€"A Preclinical and Translational Study. Cancers, 2021, 13, 6295.	1.7	0
986	The dominant TP53 hotspot mutation in <i>IDH</i> -mutant astrocytoma, R273C, has distinctive pathologic features and sex-specific prognostic implications. Neuro-Oncology Advances, 2022, 4, vdab182.	0.4	5
987	Molecular damage in aging. Nature Aging, 2021, 1, 1096-1106.	5.3	51
988	Attribution of Cancer Origins to Endogenous, Exogenous, and Preventable Mutational Processes. Molecular Biology and Evolution, 2022, 39, .	3.5	14
990	PD-1 Blockade in Solid Tumors with Defects in Polymerase Epsilon. Cancer Discovery, 2022, 12, 1435-1448.	7.7	28
991	Challenges of proving a causal role of somatic mutations in the aging process. Aging Cell, 2022, 21, e13613.	3.0	7
992	Heterogeneity of neuroendocrine transcriptional states in metastatic small cell lung cancers and patient-derived models. Nature Communications, 2022, 13, 2023.	5.8	36
993	Somatic Mutation: What Shapes the Mutational Landscape of Normal Epithelia?. Cancer Discovery, 2022, 12, 1642-1655.	7.7	8
994	Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking. Nature Genetics, 2022, 54, 492-498.	9.4	47
995	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	13.7	211
996	Panâ€cancer analysis of mutations in open chromatin regions and their possible association with cancer pathogenesis. Cancer Medicine, 2022, , .	1.3	3
998	Beyond the snapshot: optimizing prognostication and prediction by moving from fixed to functional multidimensional cancer pathology. Journal of Pathology, 2022, , .	2.1	1
1000	An overview of mutational and copy number signatures in human cancer. Journal of Pathology, 2022, 257, 454-465.	2.1	12

#	ARTICLE	IF	CITATIONS
1001	Somatic genomic changes in single Alzheimerâ€™s disease neurons. Nature, 2022, 604, 714-722.	13.7	92
1002	The Cooked Meat Carcinogen 2-Amino-1-methyl-6-phenylimidazo[4,5-<i>b</i>]pyridine Hair Dosimeter, DNA Adductomics Discovery, and Associations with Prostate Cancer Pathology Biomarkers. Chemical Research in Toxicology, 2022, 35, 703-730.	1.7	4
1003	Trove of tumour genomes offers clues to cancer origins. Nature, 2022, 604, 609-609.	13.7	1
1004	A stop-gain mutation in GXYLT1 promotes metastasis of colorectal cancer via the MAPK pathway. Cell Death and Disease, 2022, 13, 395.	2.7	5
1005	A fresh look at somatic mutations in cancer. Science, 2022, 376, 351-352.	6.0	4
1006	Distinct clinical and genetic features of hepatitis B virusâ€“associated follicular lymphoma in Chinese patients. Blood Advances, 2022, 6, 2731-2744.	2.5	8
1007	Somatic Mutation Profiling in Head and Neck Paragangliomas. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1833-1842.	1.8	6
1008	Esophageal Cancer Genomics in Africa: Recommendations for Future Research. Frontiers in Genetics, 2022, 13, 864575.	1.1	3
1009	APOBEC3F expression in triple-negative breast cancer is associated with tumor microenvironment infiltration and activation of cancer immunity and improved survival.. American Journal of Cancer Research, 2022, 12, 744-762.	1.4	0
1012	The Significance of Tumor Microenvironment Score for Breast Cancer Patients. BioMed Research International, 2022, 2022, 1-27.	0.9	3
1013	Somatic Mutations Detected in Parkinson Disease Could Affect Genes With a Role in Synaptic and Neuronal Processes. Frontiers in Aging, 2022, 3, .	1.2	7
1014	Whole-genome sequencing reveals complex genomic features underlying anti-CD19 CAR T-cell treatment failures in lymphoma. Blood, 2022, 140, 491-503.	0.6	32
1015	Heteroplasmic mitochondrial DNA mutations in frontotemporal lobar degeneration. Acta Neuropathologica, 2022, 143, 687-695.	3.9	22
1016	Breakage of cytoplasmic chromosomes by pathological DNA base excision repair. Nature, 2022, 606, 930-936.	13.7	41
1017	Substitution mutational signatures in whole-genomeâ€“sequenced cancers in the UK population. Science, 2022, 376, .	6.0	104
1018	Inferring Potential Cancer Driving Synonymous Variants. Genes, 2022, 13, 778.	1.0	1
1020	Somatic whole genome dynamics of precancer in Barrettâ€™s esophagus reveals features associated with disease progression. Nature Communications, 2022, 13, 2300.	5.8	13
1022	Pan-Cancer Analyses Reveal Oncogenic and Immunological Role of PLOD2. Frontiers in Genetics, 2022, 13, 864655.	1.1	6

#	ARTICLE	IF	CITATIONS
1023	Detection of oncogenic and clinically actionable mutations in cancer genomes critically depends on variant calling tools. Bioinformatics, 2022, 38, 3181-3191.	1.8	9
1024	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	5.8	52
1025	Alterations in homologous recombination repair genes in prostate cancer brain metastases. Nature Communications, 2022, 13, 2400.	5.8	13
1026	Genetic and chemotherapeutic influences on germline hypermutation. Nature, 2022, 605, 503-508.	13.7	43
1028	The landscape of genetic aberrations in myxofibrosarcoma. International Journal of Cancer, 2022, 151, 565-577.	2.3	13
1030	The translational challenges of precision oncology. Cancer Cell, 2022, 40, 458-478.	7.7	38
1031	An integrative in-silico analysis discloses a novel molecular subset of colorectal cancer possibly eligible for immune checkpoint immunotherapy. Biology Direct, 2022, 17, 10.	1.9	0
1033	An Update to Hallmarks of Cancer. Cureus, 2022, , .	0.2	4
1034	Temozolomide Treatment Alters Mismatch Repair and Boosts Mutational Burden in Tumor and Blood of Colorectal Cancer Patients. Cancer Discovery, 2022, 12, 1656-1675.	7.7	48
1035	Lost by Transcription: Fork Failures, Elevated Expression, and Clinical Consequences Related to Deletions in Metastatic Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 5080.	1.8	2
1036	A natural mutator allele shapes mutation spectrum variation in mice. Nature, 2022, 605, 497-502.	13.7	38
1037	Early embryonic mutations reveal dynamics of somatic and germ cell lineages in mice. Genome Research, 2022, 32, 945-955.	2.4	2
1038	Assessment of the genotoxicity of acrylamide. EFSA Journal, 2022, 20, e07293.	0.9	13
1039	Computational Identification of Preneoplastic Cells Displaying High Stemness and Risk of Cancer Progression. Cancer Research, 2022, 82, 2520-2537.	0.4	9
1040	Non-canonical genomic driver mutations of urethane carcinogenesis. PLoS ONE, 2022, 17, e0267147.	1.1	0
1041	Genomic landscape of chemical-induced lung tumors under Nrf2 different expression levels. Carcinogenesis, 2022, , .	1.3	0
1042	Construction of an immune-related lncRNA signature pair for predicting oncologic outcomes and the sensitivity of immunosuppressor in treatment of lung adenocarcinoma. Respiratory Research, 2022, 23, 123.	1.4	9
1043	Cancer evolution: special focus on the immune aspect of cancer. Seminars in Cancer Biology, 2022, , .	4.3	4

#	ARTICLE	IF	CITATIONS
1044	Cancer-Associated Microbiota: From Mechanisms of Disease Causation to Microbiota-Centric Anti-Cancer Approaches. Biology, 2022, 11, 757.	1.3	12
1045	A practical framework <scp>RNMF</scp> for exploring the association between mutational signatures and genes using gene cumulative contribution abundance. Cancer Medicine, 2022, 11, 4053-4069.	1.3	4
1046	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature Communications, 2022, 13, 2710.	5.8	19
1047	Feasibility of whole genome and transcriptome profiling in pediatric and young adult cancers. Nature Communications, 2022, 13, 2485.	5.8	31
1048	Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways.. Cold Spring Harbor Molecular Case Studies, 2022, 8, .	0.7	2
1049	Colon Tumors in Enterotoxigenic Bacteroides fragilis (ETBF)-Colonized Mice Do Not Display a Unique Mutational Signature but Instead Possess Host-Dependent Alterations in the APC Gene. Microbiology Spectrum, 2022, 10, e0105522.	1.2	18
1050	Clustered 8-Oxo-Guanine Mutations and Oncogenic Gene Fusions in Microsatellite-Unstable Colorectal Cancer. JCO Precision Oncology, 2022, 6, e2100477.	1.5	2
1051	Characterizing the mutational landscape of MM and its precursor MGUS.. American Journal of Cancer Research, 2022, 12, 1919-1933.	1.4	0
1058	Personalised selection of experimental treatment in patients with advanced solid cancer is feasible using whole-genome sequencing. British Journal of Cancer, 0, , .	2.9	2
1059	APOBEC3 mutational signatures are associated with extensive and diverse genomic instability across multiple tumour types. BMC Biology, 2022, 20, .	1.7	12
1060	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.	0.6	12
1063	Alterations in transcriptional networks in cancer: the role of noncoding somatic driver mutations. Current Opinion in Genetics and Development, 2022, 75, 101919.	1.5	2
1064	Multiomics analysis of male infertility. Biology of Reproduction, 2022, 107, 118-134.	1.2	11
1066	Synergistic activity of neratinib in combination with olaparib in uterine serous carcinoma overexpressing HER2/neu. Gynecologic Oncology, 2022, 166, 351-357.	0.6	8
1067	Mutational signatures are markers of drug sensitivity of cancer cells. Nature Communications, 2022, 13, .	5.8	29
1068	Examining clustered somatic mutations with SigProfilerClusters. Bioinformatics, 2022, 38, 3470-3473.	1.8	14
1069	Bone Microenvironment-Suppressed T Cells Increase Osteoclast Formation and Osteolytic Bone Metastases in Mice. Journal of Bone and Mineral Research, 2020, 37, 1446-1463.	3.1	11
1071	Whole-Exome Sequencing Reveals Clinical Potential of Circulating Tumor DNA from Peritoneal Fluid and Plasma in Endometrial Cancer. Cancers, 2022, 14, 2506.	1.7	3

#	Article	IF	Citations
1072	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	3.6	24
1075	Structural Variation in Cancer: Role, Prevalence, and Mechanisms. Annual Review of Genomics and Human Genetics, 2022, 23, 123-152.	2.5	23
1076	Clonal dynamics of haematopoiesis across the human lifespan. Nature, 2022, 606, 343-350.	13.7	160
1077	Estimating tumor mutational burden from RNA-sequencing without a matched-normal sample. Nature Communications, 2022, 13, .	5.8	4
1078	Concordance of hydrogen peroxideâ€“induced 8-oxo-guanine patterns with two cancer mutation signatures of upper GI tract tumors. Science Advances, 2022, 8, .	4.7	10
1081	Genome instability is associated with ethnic differences between Asians and Europeans in hepatocellular carcinoma. Theranostics, 2022, 12, 4703-4717.	4.6	2
1082	Gene Mutational Clusters in the Tumors of Colorectal Cancer Patients With a Family History of Cancer. Frontiers in Oncology, 0, 12, .	1.3	2
1083	Genomic characterization of lymphomas in patients with inborn errors of immunity. Blood Advances, 2022, 6, 5403-5414.	2.5	12
1084	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. Nature Communications, 2022, 13, .	5.8	63
1085	Identification of Prognostic and Tumor Microenvironment by Shelterin Complex-Related Signatures in Oral Squamous Cell Carcinoma. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-35.	1.9	1
1086	Integrated genomic analyses of acral and mucosal melanomas nominate novel driver genes. Genome Medicine, 2022, 14, .	3.6	13
1087	Complex mutation profiles in mismatch repair and ribonucleotide reductase mutants reveal novel repair substrate specificity of MutS homolog (MSH) complexes. Genetics, 2022, 221, .	1.2	7
1088	Whole-genome and transcriptome analysis enhances precision cancer treatment options. Annals of Oncology, 2022, 33, 939-949.	0.6	36
1089	APOBEC3: Friend or Foe in Human Papillomavirus Infection and Oncogenesis?. Annual Review of Virology, 2022, 9, 375-395.	3.0	11
1090	Comprehensive genomic analysis of primary malignant melanoma of the esophagus reveals similar genetic patterns compared with epithelium-associated melanomas. Modern Pathology, 0, , .	2.9	2
1091	The tumor mutational landscape of BRCA2-deficient primary and metastatic prostate cancer. Npj Precision Oncology, 2022, 6, .	2.3	4
1092	Cross Analysis of Genomic-Pathologic Features on Multiple Primary Hepatocellular Carcinoma. Frontiers in Genetics, 0, 13, .	1.1	1
1093	Pan-cancer analysis of genomic scar patterns caused by homologous repair deficiency (HRD). Npj Precision Oncology, 2022, 6, .	2.3	23

#	ARTICLE	IF	CITATIONS
1094	The genomic landscape of canine diffuse large B-cell lymphoma identifies distinct subtypes with clinical and therapeutic implications. Lab Animal, 2022, 51, 191-202.	0.2	6
1095	Somatic point mutations are enriched in non-coding RNAs with possible regulatory function in breast cancer. Communications Biology, 2022, 5, .	2.0	5
1097	Characterization of rare histological subtypes of ovarian cancer based on molecular profiling. Cancer Medicine, 0, , .	1.3	2
1098	Acetyl-CoA metabolism drives epigenome change and contributes to carcinogenesis risk in fatty liver disease. Genome Medicine, 2022, 14, .	3.6	12
1099	Signatures of copy number alterations in human cancer. Nature, 2022, 606, 984-991.	13.7	154
1100	A phylogenetic approach to study the evolution of somatic mutational processes in cancer. Communications Biology, 2022, 5, .	2.0	3
1101	Identifying colorectal cancer caused by biallelic MUTYH pathogenic variants using tumor mutational signatures. Nature Communications, 2022, 13, .	5.8	15
1102	Genome-wide mapping of somatic mutation rates uncovers drivers of cancer. Nature Biotechnology, 2022, 40, 1634-1643.	9.4	23
1103	The impact of genetic modifiers on variation in germline mutation rates within and among human populations. Genetics, 2022, 221, .	1.2	6
1104	A Renalâ€Clearable Activatable Molecular Probe for Fluoroâ€Photacoustic and Radioactive Imaging of Cancer Biomarkers. Small, 2022, 18, .	5.2	18
1105	A Pan-Cancer Analysis Revealing the Dual Roles of Lysine (K)-Specific Demethylase 6B in Tumorigenesis and Immunity. Frontiers in Genetics, 0, 13, .	1.1	1
1106	Genetic subtypes of smoldering multiple myeloma are associated with distinct pathogenic phenotypes and clinical outcomes. Nature Communications, 2022, 13, .	5.8	11
1107	Phasing analysis of lung cancer genomes using a long read sequencer. Nature Communications, 2022, 13, .	5.8	8
1108	A pan-cancer compendium of chromosomal instability. Nature, 2022, 606, 976-983.	13.7	111
1109	Treatment Represents a Key Driver of Metastatic Cancer Evolution. Cancer Research, 2022, 82, 2918-2927.	0.4	11
1111	A new deep learning technique reveals the exclusive functional contributions of individual cancer mutations. Journal of Biological Chemistry, 2022, 298, 102177.	1.6	3
1113	Therapeutic significance of ARID1A mutation in bladder cancer. Neoplasia, 2022, 31, 100814.	2.3	7
1114	Genomic Landscape and Immunological Profile of Glioblastoma in East Asians. SSRN Electronic Journal, 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
1115	Epidemiology beyond its limits. Science Advances, 2022, 8, .	4.7	2
1116	Multimodal data integration using machine learning improves risk stratification of high-grade serous ovarian cancer. Nature Cancer, 2022, 3, 723-733.	5.7	82
1117	The impact of rare germline variants on human somatic mutation processes. Nature Communications, 2022, 13, .	5.8	13
1118	Cancer Risk and Mutational Patterns Following Organ Transplantation. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
1119	Cell-Free DNA as Biomarker for Sepsis by Integration of Microbial and Host Information. Clinical Chemistry, 2022, 68, 1184-1195.	1.5	19
1120	Widespread redundancy in -omics profiles of cancer mutation states. Genome Biology, 2022, 23, .	3.8	5
1121	Pan-Cancer Analysis for Immune Cell Infiltration and Mutational Signatures Using Non-Negative Canonical Correlation Analysis. Applied Sciences (Switzerland), 2022, 12, 6596.	1.3	0
1122	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. Nature Communications, 2022, 13, .	5.8	30
1123	Postmortem Human Dura Mater Cells Exhibit Phenotypic, Transcriptomic and Genetic Abnormalities that Impact their Use for Disease Modeling. Stem Cell Reviews and Reports, 2022, 18, 3050-3065.	1.7	3
1124	Bioinformatics roadmap for therapy selection in cancer genomics. Molecular Oncology, 2022, 16, 3881-3908.	2.1	6
1126	Genomic instability in early systemic sclerosis. Journal of Autoimmunity, 2022, 131, 102847.	3.0	9
1127	Machine learning-based tissue of origin classification for cancer of unknown primary diagnostics using genome-wide mutation features. Nature Communications, 2022, 13, .	5.8	28
1128	Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. Nature Cancer, 2022, 3, 994-1011.	5.7	20
1129	No evidence of increased mutations in the germline of a group of British nuclear test veterans. Scientific Reports, 2022, 12, .	1.6	6
1130	The landscape of genetic alterations of <scp>UVB</scp> â€induced skin tumors in <scp>DNA</scp> repairâ€deficient mice. Experimental Dermatology, 0, , .	1.4	0
1131	MAFDash: An easy-to-use dashboard builder for mutation data. F1000Research, 0, 11, 748.	0.8	0
1132	Resolving mutational signatures in cancer development. Cancer Cell, 2022, 40, 711-713.	7.7	2
1133	J-SPACE: a Julia package for the simulation of spatial models of cancer evolution and of sequencing experiments. BMC Bioinformatics, 2022, 23, .	1.2	2

#	Article	IF	Citations
1134	Moving the Needle on Precision Medicine in Pancreatic Cancer. Journal of Clinical Oncology, 2022, 40, 2693-2705.	0.8	18
1135	The Multi-Dimensional Biomarker Landscape in Cancer Immunotherapy. International Journal of Molecular Sciences, 2022, 23, 7839.	1.8	13
1137	Acetaldehyde makes a distinct mutation signature in single-stranded DNA. Nucleic Acids Research, 2022, 50, 7451-7464.	6.5	10
1138	Inducing Hypermutability to Promote Antiâ€“PD-1 Therapy Response. Cancer Discovery, 2022, 12, 1612-1614.	7.7	1
1139	Single-Cell Mononucleotide Microsatellite Analysis Reveals Differential Insertion-Deletion Dynamics in Mouse T Cells. Frontiers in Genetics, 0, 13, .	1.1	1
1140	Elevated Mutational Age in Blood of Children Treated for Cancer Contributes to Therapy-Related Myeloid Neoplasms. Cancer Discovery, 0, , OF1-OF14.	7.7	5
1141	Mutational landscape of primary breast angiosarcoma with repeated resection and recurrence over a 15â€year period: A case report. Pathology International, 0, , .	0.6	2
1142	Considerations of Biomarker Application for Cancer Continuum in the Era of Precision Medicine. Current Epidemiology Reports, 2022, 9, 200-211.	1.1	2
1144	APOBEC mutagenesis and selection for NFE2L2 contribute to the origin of lung squamous-cell carcinoma. Lung Cancer, 2022, , .	0.9	1
1145	Functional landscapes of POLE and POLD1 mutations in checkpoint blockade-dependent antitumor immunity. Nature Genetics, 2022, 54, 996-1012.	9.4	30
1146	Case Report: Malignant Brain Tumors in Siblings With MSH6 Mutations. Frontiers in Oncology, 0, 12, .	1.3	0
1153	KMT2C-deficient tumors have elevated APOBEC mutagenesis and genomic instability in multiple cancers. NAR Cancer, 2022, 4, .	1.6	2
1155	DNA Damage and Oxidative Stress of Tobacco Smoke Condensate in Human Bladder Epithelial Cells. Chemical Research in Toxicology, 2022, 35, 1863-1880.	1.7	12
1156	Mutation burden-orthogonal tumor genomic subtypes delineate responses to immune checkpoint therapy. , 2022, 10, e004831.		4
1157	Human Variation in DNA Repair, Immune Function, and Cancer Risk. Frontiers in Immunology, 0, 13, .	2.2	4
1158	Somatic mutations in DCC are associated with genomic instability and favourable outcomes in melanoma patients treated with immune checkpoint inhibitors. British Journal of Cancer, 0, , .	2.9	0
1159	Super-enhancer hypermutation alters oncogene expression in B cell lymphoma. Nature, 2022, 607, 808-815.	13.7	55
1160	Whole-exome sequencing identified mutational profiles of urothelial carcinoma post kidney transplantation. Journal of Translational Medicine, 2022, 20, .	1.8	2

#	ARTICLE	IF	CITATIONS
1161	Mechanisms of APOBEC3 mutagenesis in human cancer cells. Nature, 2022, 607, 799-807.	13.7	93
1162	Deep whole-genome ctDNA chronology of treatment-resistant prostate cancer. Nature, 2022, 608, 199-208.	13.7	63
1163	Duplex sequencing identifies genomic features that determine susceptibility to benzo(a)pyrene-induced in vivo mutations. BMC Genomics, 2022, 23, .	1.2	19
1164	Genomic and epigenomic profiles distinguish pulmonary enteric adenocarcinoma from lung metastatic colorectal cancer. EBioMedicine, 2022, 82, 104165.	2.7	7
1165	Mutational Signatures Associate With Survival in Gastrointestinal Carcinomas. Cancer Genomics and Proteomics, 2022, 19, 556-569.	1.0	0
1166	Boosting Antitumor Immunity with an Expanded Neoepitope Landscape. Cancer Research, 2022, 82, 3637-3649.	0.4	4
1168	The molecular landscape of pancreatic ductal adenocarcinoma. Pancreatology, 2022, 22, 925-936.	0.5	5
1169	The shaping of cancer genomes with the regional impact of mutation processes. Experimental and Molecular Medicine, 2022, 54, 1049-1060.	3.2	3
1170	Targeting the DNA Damage Response Pathways and Replication Stress in Colorectal Cancer. Clinical Cancer Research, 2022, 28, 3874-3889.	3.2	13
1171	Discovering the drivers of clonal hematopoiesis. Nature Communications, 2022, 13, .	5.8	33
1173	Mutational Signature and Integrative Genomic Analysis of Human Papillomavirus-Associated Penile Squamous Cell Carcinomas from Latin American Patients. Cancers, 2022, 14, 3514.	1.7	3
1174	Aristolochic acid-associated cancers: a public health risk in need of global action. Nature Reviews Cancer, 2022, 22, 576-591.	12.8	23
1175	Overcoming resistance to Î±PD-1 of MMR-deficient tumors with high tumor-induced neutrophils levels by combination of Î±CTLA-4 and Î±PD-1 blockers. , 2022, 10, e005059.		5
1176	Biased distribution of action-at-a-distance mutations by 8-oxo-7,8-dihydroguanine. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2022, 825, 111794.	0.4	2
1179	An integrated somatic and germline approach to aid interpretation of germline variants of uncertain significance in cancer susceptibility genes. Frontiers in Oncology, 0, 12, .	1.3	3
1180	Whole genome analysis reveals the genomic complexity in metastatic cutaneous squamous cell carcinoma. Frontiers in Oncology, 0, 12, .	1.3	7
1181	Diverse mutational landscapes in human lymphocytes. Nature, 2022, 608, 724-732.	13.7	32
1182	Unifying Different Cancer Theories in a Unique Tumour Model: Chronic Inflammation and Deaminases as Meeting Points. International Journal of Molecular Sciences, 2022, 23, 8720.	1.8	1

#	ARTICLE	IF	CITATIONS
1184	Clonal diversification and histogenesis of malignant germ cell tumours. Nature Communications, 2022, 13, .	5.8	6
1185	Hepatocellular Carcinoma in Mongolia Delineates Unique Molecular Traits and a Mutational Signature Associated with Environmental Agents. Clinical Cancer Research, 2022, 28, 4509-4520.	3.2	3
1186	Genome Protection by DNA Polymerase Î¸. Annual Review of Genetics, 2022, 56, 207-228.	3.2	11
1187	APOBEC-Induced Mutagenesis in Cancer. Annual Review of Genetics, 2022, 56, 229-252.	3.2	21
1188	Re: Matthew Mossanena, Filipe L.F. Carvalhoa, Vinayak Muralidhar, et al. Genomic Features of Muscle-invasive Bladder Cancer Arising After Prostate Radiotherapy. Eur Urol 2022;81:466â€“73. European Urology, 2022, , .	0.9	0
1189	Genomic and transcriptomic determinants of response to neoadjuvant therapy in rectal cancer. Nature Medicine, 2022, 28, 1646-1655.	15.2	42
1190	Cutting-Edge AI Technologies Meet Precision Medicine to Improve Cancer Care. Biomolecules, 2022, 12, 1133.	1.8	1
1192	Comprehensive Analysis of Genomic Alterations in Hepatoid Adenocarcinoma of the Stomach and Identification of Clinically Actionable Alterations. Cancers, 2022, 14, 3849.	1.7	3
1194	Patterns of structural variation define prostate cancer across disease states. JCI Insight, 2022, 7, .	2.3	3
1195	Rapid evolution of mutation rate and spectrum in response to environmental and population-genetic challenges. Nature Communications, 2022, 13, .	5.8	19
1197	A paternal bias in germline mutation is widespread in amniotes and can arise independently of cell division numbers. ELife, 0, 11, .	2.8	20
1198	BRCA Mutations in Ovarian and Prostate Cancer: Bench to Bedside. Cancers, 2022, 14, 3888.	1.7	56
1199	Distinct non-clock-like signatures of the basal cell carcinomas from three sisters with a lethal Gorlin-Goltz syndrome. BMC Medical Genomics, 2022, 15, .	0.7	1
1201	Chromatin accessibility of primary human cancers ties regional mutational processes and signatures with tissues of origin. PLoS Computational Biology, 2022, 18, e1010393.	1.5	4
1202	DBFE: distribution-based feature extraction from structural variants in whole-genome data. Bioinformatics, 2022, 38, 4466-4473.	1.8	0
1203	Understanding precancerous lesions of the oral cavity^{â€}. Journal of Pathology, 2022, 258, 103-105.	2.1	2
1206	Resistance of mitochondrial DNA to cadmium and Aflatoxin B1 damage-induced germline mutation accumulation in<i>C. elegans</i>. Nucleic Acids Research, 2022, 50, 8626-8642.	6.5	5
1207	Exome sequencing reveals a distinct somatic genomic landscape in breast cancer from women with germline PTEN variants. American Journal of Human Genetics, 2022, 109, 1520-1533.	2.6	2

#	Article	IF	Citations
1208	Genomic features of renal cell carcinoma developed during end-stage renal disease and dialysis. Human Molecular Genetics, 2023, 32, 290-303.	1.4	4
1210	Mutational signatures representative transcriptomic perturbations in hepatocellular carcinoma. Frontiers in Genetics, 0, 13, .	1.1	1
1211	Genome-wide mutational signatures in low-coverage whole genome sequencing of cell-free DNA. Nature Communications, 2022, 13, .	5.8	13
1212	Unblinding the watchmaker: cancer treatment and drug design in the face of evolutionary pressure. Expert Opinion on Drug Discovery, 2022, 17, 1081-1094.	2.5	1
1213	Unique Growth Pattern Presentation of a Papillary Renal Cell Carcinoma. Diagnostics, 2022, 12, 1904.	1.3	0
1214	Mesenchymal tumor organoid models recapitulate rhabdomyosarcoma subtypes. EMBO Molecular Medicine, 2022, 14, .	3.3	19
1215	Effects of Wee1 inhibitor adavosertib on patient-derived high-grade serous ovarian cancer cells are multiple and independent of homologous recombination status. Frontiers in Oncology, 0, 12, .	1.3	2
1216	Genomic features of <i>Helicobacter pylori</i>â€naÃ¯ve diffuseâ€type gastric cancer. Journal of Pathology, 2022, 258, 300-311.	2.1	4
1217	Somatic mutations in single human cardiomyocytes reveal age-associated DNA damage and widespread oxidative genotoxicity. Nature Aging, 2022, 2, 714-725.	5.3	28
1218	Detection of early seeding of Richter transformation in chronic lymphocytic leukemia. Nature Medicine, 2022, 28, 1662-1671.	15.2	53
1219	Whole genome sequencing reveals the independent clonal origin of multifocal ileal neuroendocrine tumors. Genome Medicine, 2022, 14, .	3.6	8
1221	Novel insights into RB1 mutation. Cancer Letters, 2022, 547, 215870.	3.2	13
1222	Expanded targeting scope of LbCas12a variants allows editing of multiple oncogenic mutations. Molecular Therapy - Nucleic Acids, 2022, 30, 131-142.	2.3	5
1223	S1-END-seq reveals DNA secondary structures in human cells. Molecular Cell, 2022, 82, 3538-3552.e5.	4.5	16
1224	RESISTOR: A New OSPREY Module to Predict Resistance Mutations. Journal of Computational Biology, 2022, 29, 1346-1352.	0.8	4
1225	The development of therapy related myeloid neoplasms in childhood cancer survivors. Trends in Cancer, 2022, 8, 790-791.	3.8	0
1226	Mutation or not, what directly establishes a neoplastic state, namely cellular immortality and autonomy, still remains unknown and should be prioritized in our research. Journal of Cancer, 2022, 13, 2810-2843.	1.2	5
1227	The metabolic genomic atlas reveals potential drivers and clinically relevant insights into the etiology of esophageal squamous cell carcinoma. Theranostics, 2022, 12, 6160-6178.	4.6	2

#	ARTICLE	IF	CITATIONS
1228	A computational workflow for predicting cancer neo-antigens. Bioinformation, 2022, 18, 214-218.	0.2	0
1229	Mutations somatiques et longÃ©vitÃ©. Medecine/Sciences, 2022, 38, 723-725.	0.0	1
1230	A genetic model for central chondrosarcoma evolution correlates with patient outcome. Genome Medicine, 2022, 14, .	3.6	9
1232	Homologous Recombination Deficiency Scar: Mutations and Beyondâ€"Implications for Precision Oncology. Cancers, 2022, 14, 4157.	1.7	5
1233	CLONAL HEMATOPOIESIS: ROLE IN HEMATOLOGIC NON-HEMATOLOGIC. Mediterranean Journal of Hematology and Infectious Diseases, 2022, 14, e2022069.	0.5	1
1234	Integrative genomic and transcriptomic analyses illuminate the ontology of HER2-low breast carcinomas. Genome Medicine, 2022, 14, .	3.6	17
1235	Nitroreduction: A Critical Metabolic Pathway for Drugs, Environmental Pollutants, and Explosives. Chemical Research in Toxicology, 2022, 35, 1747-1765.	1.7	18
1236	African-specific molecular taxonomy of prostate cancer. Nature, 2022, 609, 552-559.	13.7	26
1238	Analysis of low-level somatic mosaicism reveals stage and tissue-specific mutational features in human development. PLoS Genetics, 2022, 18, e1010404.	1.5	1
1239	Mutational Signature 3 Detected from Clinical Panel Sequencing is Associated with Responses to Olaparib in Breast and Ovarian Cancers. Clinical Cancer Research, 2022, 28, 4714-4723.	3.2	15
1240	Topoisomerase 1-dependent R-loop deficiency drives accelerated replication and genomic instability. Cell Reports, 2022, 40, 111397.	2.9	5
1242	The mutational signatures of formalin fixation on the human genome. Nature Communications, 2022, 13, .	5.8	20
1243	Integrated longitudinal analysis of adult grade 4 diffuse gliomas with long-term relapse interval revealed upregulation of TGF-Î² signaling in recurrent tumors. Neuro-Oncology, 2023, 25, 662-673.	0.6	9
1246	Heterogeneity of triple negative breast cancer: Current advances in subtyping and treatment implications. Journal of Experimental and Clinical Cancer Research, 2022, 41, .	3.5	35
1248	Identification of neoantigens in oesophageal adenocarcinoma. Immunology, 2023, 168, 420-431.	2.0	6
1249	Surveying mutation density patterns around specific genomic features. Genome Research, 0, , .	2.4	1
1250	DETexT: An SNV detection enhancement for low read depth by integrating mutational signatures into TextCNN. Frontiers in Genetics, 0, 13, .	1.1	1
1251	HRD-MILN: Accurately estimate tumor homologous recombination deficiency status from targeted panel sequencing data. Frontiers in Genetics, 0, 13, .	1.1	1

#	ARTICLE	IF	CITATIONS
1252	UVA Radiation, DNA Damage, and Melanoma. ACS Omega, 2022, 7, 32936-32948.	1.6	17
1253	Integrated cohort of esophageal squamous cell cancer reveals genomic features underlying clinical characteristics. Nature Communications, 2022, 13, .	5.8	12
1254	Duplex Sequencing Uncovers Recurrent Low-frequency Cancer-associated Mutations in Infant and Childhood KMT2A-rearranged Acute Leukemia. HemaSphere, 2022, 6, e785.	1.2	1
1255	Mutated processes predict immune checkpoint inhibitor therapy benefit in metastatic melanoma. Nature Communications, 2022, 13, .	5.8	16
1256	Cancer as an infective disease: the role of <scp>EVs</scp> in tumorigenesis. Molecular Oncology, 2023, 17, 390-406.	2.1	4
1257	Mutational Signatures as Sensors of Environmental Exposures: Analysis of Smoking-Induced Lung Tissue Remodeling. Biomolecules, 2022, 12, 1384.	1.8	2
1258	The Drivers, Mechanisms, and Consequences of Genome Instability in HPV-Driven Cancers. Cancers, 2022, 14, 4623.	1.7	8
1259	Molecular Monitoring of Lymphomas. Annual Review of Pathology: Mechanisms of Disease, 2023, 18, .	9.6	3
1261	Uncovering novel mutational signatures by de novo extraction with SigProfilerExtractor. Cell Genomics, 2022, 2, 100179.	3.0	74
1262	Deciphering the expression patterns of homologous recombination-related lncRNAs identifies new molecular subtypes and emerging therapeutic opportunities in epithelial ovarian cancer. Frontiers in Genetics, 0, 13, .	1.1	2
1263	RNA-Based Classification of Homologous Recombination Deficiency in Racially Diverse Patients with Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 2136-2147.	1.1	7
1264	The architecture of clonal expansions in morphologically normal tissue from cancerous and non-cancerous prostates. Molecular Cancer, 2022, 21, .	7.9	4
1265	Therapeutic targeting of DNA damage repair pathways guided by homologous recombination deficiency scoring in ovarian cancers. Fundamental and Clinical Pharmacology, 2023, 37, 194-214.	1.0	1
1266	Comparative Genomics Provides Etiologic and Biological Insight into Melanoma Subtypes. Cancer Discovery, 2022, 12, 2856-2879.	7.7	22
1267	A recurrent somatic missense mutation in GNAS gene identified in familial thyroid follicular cell carcinomas in German longhaired pointer dogs. BMC Genomics, 2022, 23, .	1.2	2
1269	Editorial: The application of sequencing technologies and bioinformatics methods in cancer biology. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
1270	Analyses of mutational patterns induced by formaldehyde and acetaldehyde reveal similarity to a common mutational signature. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	5
1271	Quantification of APOBEC3 Mutation Rates Affecting the VP1 Gene of BK Polyomavirus In Vivo. Viruses, 2022, 14, 2077.	1.5	2

#	Article	IF	Citations
1273	The genomic landscape of pediatric acute lymphoblastic leukemia. Nature Genetics, 2022, 54, 1376-1389.	9.4	104
1274	Comprehensive analyses of genomic features and mutational signatures in adenosquamous carcinoma of the lung. Frontiers in Oncology, 0, 12, .	1.3	3
1275	A Genomically and Clinically Annotated Patient-Derived Xenograft Resource for Preclinical Research in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2022, 82, 4126-4138.	0.4	7
1276	APOBEC mutagenesis, kataegis, chromothripsis in EGFR-mutant osimertinib-resistant lung adenocarcinomas. Annals of Oncology, 2022, 33, 1284-1295.	0.6	22
1279	Two subtypes of cutaneous melanoma with distinct mutational signatures and clinico-genomic characteristics. Frontiers in Genetics, 0, 13, .	1.1	5
1280	Intrinsic base substitution patterns in diverse species reveal links to cancer and metabolism. Genetics, 2022, 222, .	1.2	9
1284	Nuclear-embedded mitochondrial DNA sequences in 66,083 human genomes. Nature, 2022, 611, 105-114.	13.7	69
1285	Genomic profiling with wholeâ€exome sequencing revealed distinct mutations and novel pathways in Asian melanoma. Journal of Dermatology, 2022, 49, 1299-1309.	0.6	3
1286	System-wide identification of myeloid markers of TB disease and HIV-induced reactivation in the macaque model of Mtb infection and Mtb/SIV co-infection. Frontiers in Immunology, 0, 13, .	2.2	4
1290	Ovarian Cancer Therapy: Homologous Recombination Deficiency as a Predictive Biomarker of Response to PARP Inhibitors. OncoTargets and Therapy, 0, Volume 15, 1105-1117.	1.0	7
1291	Common anti-cancer therapies induce somatic mutations in stem cells of healthy tissue. Nature Communications, 2022, 13, .	5.8	5
1292	Comparative analysis of capture methods for genomic profiling of circulating tumor cells in colorectal cancer. Genomics, 2022, 114, 110500.	1.3	2
1295	Excerno: Filtering Mutations Caused by the Clinical Archival Process in Sequencing Data. Lecture Notes in Computer Science, 2022, , 29-37.	1.0	0
1296	Modulation of DNA Methylation/Demethylation Reactions Induced by Nutraceuticals and Pollutants of Exposome Can Promote a C > T Mutation in the Breast Cancer Predisposing Gene PALB2. Epigenomes, 2022, 6, 32.	0.8	0
1297	The multiple de novo copy number variant (MdnCNV) phenomenon presents with peri-zygotic DNA mutational signatures and multilocus pathogenic variation. Genome Medicine, 2022, 14, .	3.6	5
1298	Genomic Microsatellite Signatures Identify Germline Mismatch Repair Deficiency and Risk of Cancer Onset. Journal of Clinical Oncology, 2023, 41, 766-777.	0.8	10
1299	Whole-genome analysis identifies novel drivers and high-risk double-hit events in relapsed/refractory myeloma. Blood, 2023, 141, 620-633.	0.6	8
1300	Sensitization of Patient-Derived Colorectal Cancer Organoids to Photon and Proton Radiation by Targeting DNA Damage Response Mechanisms. Cancers, 2022, 14, 4984.	1.7	0

#	ARTICLE	IF	CITATIONS
1301	The genomic landscape across 474 surgically accessible epileptogenic human brain lesions. Brain, 2023, 146, 1342-1356.	3.7	21
1303	Development of a versatile high-throughput mutagenesis assay with multiplexed short-read NGS using DNA-barcoded supF shuttle vector library amplified in E. coli. ELife, 0, 11, .	2.8	3
1304	Ganciclovir-induced mutations are present in a diverse spectrum of post-transplant malignancies. Genome Medicine, 2022, 14, .	3.6	5
1306	Whole-exome sequencing of epithelial ovarian carcinomas differing in resistance to platinum therapy. Life Science Alliance, 2022, 5, e202201551.	1.3	3
1307	Shared Cancer Dataset Analysis Identifies and Predicts the Quantitative Effects of Pan-Cancer Somatic Driver Variants. Cancer Research, 2023, 83, 74-88.	0.4	2
1308	Replicative Instability Drives Cancer Progression. Biomolecules, 2022, 12, 1570.	1.8	3
1310	A phase II study of talazoparib monotherapy in patients with wild-type BRCA1 and BRCA2 with a mutation in other homologous recombination genes. Nature Cancer, 2022, 3, 1181-1191.	5.7	42
1311	Hyperdiploidy: the longest known, most prevalent, and most enigmatic form of acute lymphoblastic leukemia in children. Leukemia, 2022, 36, 2769-2783.	3.3	11
1312	Mono- and biallelic germline variants of DNA glycosylase genes in colon adenomatous polyposis families from two continents. Frontiers in Oncology, 0, 12, .	1.3	0
1314	Genomic characterization reveals distinct mutation landscapes and therapeutic implications in neuroendocrine carcinomas of the gastrointestinal tract. Cancer Communications, 2022, 42, 1367-1386.	3.7	8
1315	Single-cell genomic variation induced by mutational processes in cancer. Nature, 2022, 612, 106-115.	13.7	40
1316	Site-directed RNA editing by harnessing ADARs: advances and challenges. Functional and Integrative Genomics, 2022, 22, 1089-1103.	1.4	6
1317	Resistor: An algorithm for predicting resistance mutations via Pareto optimization over multistate protein design and mutational signatures. Cell Systems, 2022, 13, 830-843.e3.	2.9	5
1318	Gallbladder cancer. Nature Reviews Disease Primers, 2022, 8, .	18.1	68
1319	Microbial metabolites damage DNA. Science, 2022, 378, 358-359.	6.0	2
1320	Molecular Characterization Reveals Subclasses of 1q Gain in Intermediate Risk Wilms Tumors. Cancers, 2022, 14, 4872.	1.7	2
1322	<scp>Cdt1</scp> overexpression drives colorectal carcinogenesis through origin overlicensing and <scp>DNA</scp> damage. Journal of Pathology, 2023, 259, 10-20.	2.1	3
1323	The two faces of DNA oxidation in genomic and functional mosaicism during aging in human neurons. Frontiers in Aging, 0, 3, .	1.2	4

#	ARTICLE	IF	CITATIONS
1324	Whole-exome sequencing analysis identifies distinct mutational profile and novel prognostic biomarkers in primary gastrointestinal diffuse large B-cell lymphoma. Experimental Hematology and Oncology, 2022, 11, .	2.0	6
1325	CancÃ©rogenÃ¨se et variants faux sens pathogÃ¨nes duÂdomaine exonuclÃ©asique des ADN polymÃ©rases Îµ et Î´. Medecine/Sciences, 2022, 38, 763-765.	0.0	0
1327	Genomic landscape of the immunogenicity regulation in skin melanomas with diverse tumor mutation burden. Frontiers in Immunology, 0, 13, .	2.2	3
1328	Addressing the benefits of inhibiting APOBEC3-dependent mutagenesis in cancer. Nature Genetics, 2022, 54, 1599-1608.	9.4	19
1329	8-Oxoguanine: from oxidative damage to epigenetic and epitranscriptional modification. Experimental and Molecular Medicine, 2022, 54, 1626-1642.	3.2	52
1330	The co-evolution of the genome and epigenome in colorectal cancer. Nature, 2022, 611, 733-743.	13.7	39
1331	Fusion gene recurrence in non-small cell lung cancers and its association with cigarette smoke exposure. Translational Lung Cancer Research, 2022, 11, 2022-2039.	1.3	1
1333	Viral Integration Plays a Minor Role in the Development and Prognostication of Oral Squamous Cell Carcinoma. Cancers, 2022, 14, 5213.	1.7	0
1334	Hereditary cancer variants and homologous recombination deficiency in biliary tract cancer. Journal of Hepatology, 2023, 78, 333-342.	1.8	5
1335	Excerno: Using Mutational Signatures in Sequencing Data to Filter False Variants Caused by Clinical Archival. Journal of Computational Biology, 0, , .	0.8	0
1336	Untangling the roles of TOP2A and TOP2B in transcription and cancer. Science Advances, 2022, 8, .	4.7	41
1337	Demystifying the black box: from ignorance to observation to mechanism in cancer research. European Journal of Epidemiology, 2023, 38, 1265-1267.	2.5	1
1339	Ancestry-defined molecular taxonomy of prostate cancer. Trends in Cancer, 2022, 8, 973-975.	3.8	0
1340	Cytidine analogs are synthetic lethal with base excision repair default due to MBD4 deficiency. Npj Precision Oncology, 2022, 6, .	2.3	0
1341	Leveraging the replication stress response to optimize cancer therapy. Nature Reviews Cancer, 2023, 23, 6-24.	12.8	33
1342	Identification of natural product 3, 5-diiodotyrosine as APOBEC3B inhibitor to prevent somatic mutation accumulation and cancer progression. , 2022, 10, e005503.		3
1343	Thymic Carcinoma Versus Lung Squamous Cell Carcinoma. , 2022, , 113-118.		0
1344	Profiling the immune landscape in mucinous ovarian carcinoma. Gynecologic Oncology, 2023, 168, 23-31.	0.6	6

#	ARTICLE	IF	CITATIONS
1347	<i> <scp>APOBEC3A</scp> /B </i> deletion polymorphism and endometrial cancer risk. Cancer Medicine, 0, , .	1.3	0
1348	Genetic basis and molecular profiling in myeloproliferative neoplasms. Blood, 2023, 141, 1909-1921.	0.6	31
1349	Non-viral precision Tâ€‰cell receptor replacement for personalized cell therapy. Nature, 2023, 615, 687-696.	13.7	85
1350	Evaluating Multiple Next-Generation Sequencingâ€"Derived Tumor Features to Accurately Predict DNA Mismatch Repair Status. Journal of Molecular Diagnostics, 2023, 25, 94-109.	1.2	5
1351	Characterization of genomic alterations and neoantigens and analysis of immune infiltration identified therapeutic and prognostic biomarkers in adenocarcinoma at the gastroesophageal junction. Frontiers in Oncology, 0, 12, .	1.3	1
1353	Recurrent posterior fossa group A (PFA) ependymoma in a young child with constitutional mismatch repair deficiency (CMMRD). Neuropathology and Applied Neurobiology, 2023, 49, .	1.8	2
1354	WaldenstrÃ¶m Macroglobulinemia Whole Genome Reveals Prolonged Germinal Center Activity and Late Copy Number Aberrations. Blood Advances, 0, , .	2.5	1
1355	Not only mutations but also tumorigenesis can be substantially attributed to DNA damage from reactive oxygen species in RUNX1::RUNX1T1-fusion-positive acute myeloid leukemia. Leukemia, 2022, 36, 2931-2933.	3.3	1
1356	Genomic Profiling Identifies Putative Pathogenic Alterations in NSCLC Brain Metastases. JTO Clinical and Research Reports, 2022, 3, 100435.	0.6	2
1357	A CRISPR Path to Finding Vulnerabilities and Solving Drug Resistance: Targeting the Diverse Cancer Landscape and Its Ecosystem. Genetics & Genomics Next, 2022, 3, .	0.8	3
1358	Inferring parameters of cancer evolution in chronic lymphocytic leukemia. PLoS Computational Biology, 2022, 18, e1010677.	1.5	3
1359	Mutation accumulation in mtDNA of cancers resembles mutagenesis in normal stem cells. IScience, 2022, 25, 105610.	1.9	1
1361	Ancestral APOBEC3B Nuclear Localization Is Maintained in Humans and Apes and Altered in Most Other Old World Primate Species. MSphere, 2022, 7, .	1.3	6
1362	Proteogenomic analysis of lung adenocarcinoma reveals tumor heterogeneity, survival determinants, and therapeutically relevant pathways. Cell Reports Medicine, 2022, 3, 100819.	3.3	15
1363	Whole-genome sequencing of chronic lymphocytic leukemia identifies subgroups with distinct biological and clinical features. Nature Genetics, 2022, 54, 1675-1689.	9.4	21
1364	Characterization of HCI-EC-23 a novel estrogen- and progesterone-responsive endometrial cancer cell line. Scientific Reports, 2022, 12, .	1.6	0
1365	Collaborative study from the Bladder Cancer Advocacy Network for the genomic analysis of metastatic urothelial cancer. Nature Communications, 2022, 13, .	5.8	14
1366	DNA replication initiation shapes the mutational landscape and expression of the human genome. Science Advances, 2022, 8, .	4.7	4

#	ARTICLE	IF	CITATIONS
1367	Monitoring APOBEC3A protein levels in human cancer cells. Methods in Cell Biology, 2024, , 313-327.	0.5	0
1368	Structure of the catalytically active APOBEC3G bound to a DNA oligonucleotide inhibitor reveals tetrahedral geometry of the transition state. Nature Communications, 2022, 13, .	5.8	5
1370	Future Role of Molecular Profiling in Small Breast Samples and Personalised Medicine. , 2022, , 895-915.		0
1371	A potential treatment option for transformed small-cell lung cancer on PD-L1 inhibitor-based combination therapy improved survival. Lung Cancer, 2023, 175, 68-78.	0.9	7
1372	The mutational impact of Illudin S on human cells. DNA Repair, 2023, 122, 103433.	1.3	3
1373	Ovarian and uterine carcinosarcomas are sensitive in vitro and in vivo to elimusertib, a novel ataxia-telangiectasia and Rad3-related (ATR) kinase inhibitor. Gynecologic Oncology, 2023, 169, 98-105.	0.6	2
1374	Statistical Challenges in Mutational Signature Analyses of Cancer Sequencing Data. Springer Proceedings in Mathematics and Statistics, 2022, , 241-258.	0.1	0
1375	TGFÎ² pathway is required for viable gestation of Fanconi anemia embryos. PLoS Genetics, 2022, 18, e1010459.	1.5	1
1377	CCAR2 functions downstream of the Shieldin complex to promote double-strand break end-joining. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	3
1378	Competition for DNA binding between the genome protector replication protein A and the genome modifying APOBEC3 single-stranded DNA deaminases. Nucleic Acids Research, 2022, 50, 12039-12057.	6.5	8
1380	Evaluating cancer etiology and risk with a mathematical model of tumor evolution. Nature Communications, 2022, 13, .	5.8	1
1381	T-Cell Infiltration and Clonality May Identify Distinct Survival Groups in Colorectal Cancer: Development and Validation of a Prognostic Model Based on The Cancer Genome Atlas (TCGA) and Clinical Proteomic Tumor Analysis Consortium (CPTAC). Cancers, 2022, 14, 5883.	1.7	1
1382	Immunological and Genomic Analysis Reveals Clinically Relevant Distinctions between Angiosarcoma Subgroups. Cancers, 2022, 14, 5938.	1.7	4
1383	Highly aneuploid non-small cell lung cancer shows enhanced responsiveness to concurrent radiation and immune checkpoint blockade. Nature Cancer, 2022, 3, 1498-1512.	5.7	27
1385	Regional mutational signature activities in cancer genomes. PLoS Computational Biology, 2022, 18, e1010733.	1.5	0
1387	Clinical Implications of APOBEC3-Mediated Mutagenesis in Breast Cancer. Clinical Cancer Research, 2023, 29, 1658-1669.	3.2	4
1388	Echoed induction of nucleotide variants and chromosomal structural variants in cancer cells. Scientific Reports, 2022, 12, .	1.6	2
1389	Greater expectations: meeting clinical needs through broad and rapid genomic testing. Clinical Chemistry and Laboratory Medicine, 2022, .	1.4	1

#	ARTICLE	IF	CITATIONS
1390	Primary mucosal melanomas of the head and neck are characterised by overexpression of the <scp>DNA</scp> mutating enzyme <scp>APOBEC3B</scp>. Histopathology, 2023, 82, 608-621.	1.6	5
1391	Identification of multiplicatively acting modulatory mutational signatures in cancer. BMC Bioinformatics, 2022, 23, .	1.2	0
1392	Recurrent germline variant in ATM associated with familial myeloproliferative neoplasms. Leukemia, 0, , .	3.3	0
1393	Multiscale reorganization of the genome following DNA damage facilitates chromosome translocations via nuclear actin polymerization. Nature Structural and Molecular Biology, 2023, 30, 99-106.	3.6	22
1394	Spatial biology of cancer evolution. Nature Reviews Genetics, 2023, 24, 295-313.	7.7	42
1397	The genomic and immune landscape of long-term survivors of high-grade serous ovarian cancer. Nature Genetics, 2022, 54, 1853-1864.	9.4	24
1399	The underexplored links between cancer and the internal body climate: Implications for cancer prevention and treatment. Frontiers in Oncology, 0, 12, .	1.3	0
1400	Estimation of Neutral Mutation Rates and Quantification of Somatic Variant Selection Using cancereffectsizeR. Cancer Research, 2023, 83, 500-505.	0.4	5
1401	Pan-cancer landscape of AID-related mutations, composite mutations, and their potential role in the ICI response. Npj Precision Oncology, 2022, 6, .	2.3	2
1402	Clinical and genomic characterization of mutational signatures across human cancers. International Journal of Cancer, 0, , .	2.3	1
1404	Therapy sculpts the complex interplay between cancer and the immune system during tumour evolution. Genome Medicine, 2022, 14, .	3.6	15
1405	Complete genomic characterization in patients with cancer of unknown primary origin in routine diagnostics. ESMO Open, 2022, 7, 100611.	2.0	5
1406	Histopathologic and proteogenomic heterogeneity reveals features of clear cell renal cell carcinoma aggressiveness. Cancer Cell, 2023, 41, 139-163.e17.	7.7	43
1407	An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types. , 2022, 1, e0000151.		0
1408	Ovarian cancer mutational processes drive site-specific immune evasion. Nature, 2022, 612, 778-786.	13.7	51
1409	Mutational Patterns Observed in SARS-CoV-2 Genomes Sampled From Successive Epochs Delimited by Major Public Health Events in Ontario, Canada: Genomic Surveillance Study. JMIR Bioinformatics and Biotechnology, 2022, 3, e42243.	0.4	0
1410	The Cytidine Deaminase APOBEC3G Contributes to Cancer Mutagenesis and Clonal Evolution in Bladder Cancer. Cancer Research, 2023, 83, 506-520.	0.4	15
1411	Cancer Genomics. Archives of Medical Research, 2022, 53, 723-731.	1.5	5

#	ARTICLE	IF	CITATIONS
1412	Molecular Classification of Appendiceal Adenocarcinoma. Journal of Clinical Oncology, 2023, 41, 1553-1564.	0.8	15
1413	Tobacco Smoking-Related Mutational Signatures in Classifying Smoking-Associated and Nonsmoking-Associated NSCLC. Journal of Thoracic Oncology, 2023, 18, 487-498.	0.5	14
1414	Implementation of Whole-Genome and Transcriptome Sequencing Into Clinical Cancer Care. JCO Precision Oncology, 2022, , .	1.5	17
1415	Recurrent repeat expansions in human cancer genomes. Nature, 2023, 613, 96-102.	13.7	21
1416	A prognostic risk model for glioma patients by systematic evaluation of genomic variations. IScience, 2022, 25, 105681.	1.9	1
1417	Dr.Nod: computational framework for discovery of regulatory non-coding drivers in tissue-matched distal regulatory elements. Nucleic Acids Research, 2023, 51, e23-e23.	6.5	1
1418	A heuristic algorithm solving the mutual-exclusivity-sorting problem. Bioinformatics, 2023, 39, .	1.8	1
1419	The Molecular Characterization of Genetic Abnormalities in Esophageal Squamous Cell Carcinoma May Foster the Development of Targeted Therapies. Current Oncology, 2023, 30, 610-640.	0.9	3
1420	High-dose melphalan treatment significantly increases mutational burden at relapse in multiple myeloma. Blood, 2023, 141, 1724-1736.	0.6	15
1421	Mutational Landscape of Bladder Cancer in Mexican Patients: KMT2D Mutations and chr11q15.5 Amplifications Are Associated with Muscle Invasion. International Journal of Molecular Sciences, 2023, 24, 1092.	1.8	1
1422	Concepts of association between cancer and ionising radiation: accounting for specific biological mechanisms. Radiation and Environmental Biophysics, 2023, 62, 1-15.	0.6	3
1423	Etiological Insights into TNBC and their Related Catastrophic Risks. , 2023, , 1-25.		0
1424	Review: The Key Factors to Melanomagenesis. Life, 2023, 13, 181.	1.1	5
1425	African inclusion in prostate cancer genomic studies provides the first glimpses into addressing health disparities through tailored clinical care. Clinical and Translational Medicine, 2023, 13, .	1.7	3
1426	Genomic Patterns of Malignant Peripheral Nerve Sheath Tumor (MPNST) Evolution Correlate with Clinical Outcome and Are Detectable in Cell-Free DNA. Cancer Discovery, 2023, 13, 654-671.	7.7	15
1429	Mutagenesis induced by protonation of single-stranded DNA is linked to glycolytic sugar metabolism. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2023, 826, 111814.	0.4	1
1430	Comprehensive multi-omic profiling of somatic mutations in malformations of cortical development. Nature Genetics, 2023, 55, 209-220.	9.4	34
1433	Somatic Mutations in Normal Tissues: New Perspectives on Early Carcinogenesis. Annual Review of Cancer Biology, 2023, 7, 189-205.	2.3	4

#	Article	IF	Citations
1434	Homologous Recombination Repair Deficiency: An Overview for Pathologists. Modern Pathology, 2023, 36, 100049.	2.9	17
1436	Fast, accurate, and racially unbiased pan-cancer tumor-only variant calling with tabular machine learning. Npj Precision Oncology, 2023, 7, .	2.3	2
1437	Whole-Genome Sequencing Reveals Mutational Signatures Related to Radiation-Induced Sarcomas and DNA-Damage-Repair Pathways. Modern Pathology, 2023, 36, 100004.	2.9	3
1438	Germline TP53 mutations undergo copy number gain years prior to tumor diagnosis. Nature Communications, 2023, 14, .	5.8	8
1439	Integrated multi-omics profiling yields a clinically relevant molecular classification for esophageal squamous cell carcinoma. Cancer Cell, 2023, 41, 181-195.e9.	7.7	30
1440	Comparative genomic analysis of esophageal squamous cell carcinoma among different geographic regions. Frontiers in Oncology, 0, 12, .	1.3	0
1441	DNA damage and somatic mutations in mammalian cells after irradiation with a nail polish dryer. Nature Communications, 2023, 14, .	5.8	7
1442	Evolutionary history of transformation from chronic lymphocytic leukemia to Richter syndrome. Nature Medicine, 2023, 29, 158-169.	15.2	25
1443	Genomic Profiling of Metastatic Basal cell Carcinoma Reveals Candidate Drivers of Disease and Therapeutic Targets. Modern Pathology, 2023, 36, 100099.	2.9	0
1444	Unravelling the instability of mutational signatures extraction via archetypal analysis. Frontiers in Genetics, 0, 13, .	1.1	0
1445	Updates in pathology and molecular diagnostics to inform the evolving landscape of thoracic surgery and oncology. Journal of Surgical Oncology, 2023, 127, 244-257.	0.8	1
1446	Immune checkpoint blockade in glioblastoma: from tumor heterogeneity to personalized treatment. Journal of Clinical Investigation, 2023, 133, .	3.9	39
1447	Prognosis, immune microenvironment, and personalized treatment prediction in Rho GTPase-activating protein 4-mutant cervical cancer: Computer strategies for precision oncology. Life Sciences, 2023, 315, 121360.	2.0	0
1448	Intracellular calprotectin (S100A8/A9) facilitates DNA damage responses and promotes apoptosis in head and neck squamous cell carcinoma. Oral Oncology, 2023, 137, 106304.	0.8	4
1449	The clinical utility of integrative genomics in childhood cancer extends beyond targetable mutations. Nature Cancer, 2023, 4, 203-221.	5.7	28
1450	Enhancing childhood cancer targetability. Nature Cancer, 0, , .	5.7	0
1451	Biology and genetics of acquired and congenital melanocytic naevi. Pathology, 2023, 55, 169-177.	0.3	3
1452	Optimized detection of homologous recombination deficiency improves the prediction of clinical outcomes in cancer. Npj Precision Oncology, 2022, 6, .	2.3	8

#	ARTICLE	IF	CITATIONS
1453	Genomics of PDGFR-rearranged hypereosinophilic syndrome. Blood Advances, 0, , .	2.5	0
1454	Deciphering gene contributions and etiologies of somatic mutational signatures of cancer. Briefings in Bioinformatics, 2023, 24, .	3.2	0
1456	Pathological consequences of DNA damage in the kidney. Nature Reviews Nephrology, 2023, 19, 229-243.	4.1	2
1457	Analysis of genomic and immune intratumor heterogeneity in linitis plastica via multiregional exome and Tâ€cell receptor sequencing. Molecular Oncology, 2023, 17, 1531-1544.	2.1	1
1458	Genomic Complexity Predicts Resistance to Endocrine Therapy and CDK4/6 Inhibition in Hormone Receptorâ€“Positive (HR+)/HER2-Negative Metastatic Breast Cancer. Clinical Cancer Research, 2023, 29, 1719-1729.	3.2	12
1459	Pathogenic Variants in Adult-Onset Cancer Predisposition Genes in Pediatric Cancer: Prevalence and Impact on Tumor Molecular Features and Clinical Management. Clinical Cancer Research, 2023, 29, 1243-1251.	3.2	1
1460	A Review of the Pharmacokinetic Characteristics of Immune Checkpoint Inhibitors and Their Clinical Impact Factors. Pharmacogenomics and Personalized Medicine, 0, Volume 16, 29-36.	0.4	0
1462	The genomic landscape and clonal evolutionary trajectory of classical hairy cell leukemia. Leukemia, 2023, 37, 929-933.	3.3	2
1463	Roles of trans-lesion synthesis (TLS) DNA polymerases in tumorigenesis and cancer therapy. NAR Cancer, 2023, 5, .	1.6	14
1464	Unraveling the impact of a germline heterozygous POLD1 frameshift variant in serrated polyposis syndrome. Frontiers in Molecular Biosciences, 0, 10, .	1.6	2
1466	mSigHdp: hierarchical Dirichlet process mixture modeling for mutational signature discovery. NAR Genomics and Bioinformatics, 2023, 5, .	1.5	2
1467	Racial and ethnic disparities in a real-world precision oncology data registry. Npj Precision Oncology, 2023, 7, .	2.3	9
1469	Whole-genome sequencing of 20 cholangiocarcinoma cases reveals unique profiles in patients with cirrhosis and primary sclerosing cholangitis. Journal of Gastrointestinal Oncology, 2023, 14, 379-389.	0.6	1
1470	Comprehensive analysis of mutational signatures reveals distinct patterns and molecular processes across 27 pediatric cancers. Nature Cancer, 2023, 4, 276-289.	5.7	13
1471	Next-generation sequencing shows the genomic features of ovarian clear cell cancer and compares the genetic architectures of high-grade serous ovarian cancer and clear cell carcinoma in ovarian and endometrial tissues. PeerJ, 0, 11, e14653.	0.9	1
1472	The effects of altered <scp>DNA</scp> damage repair genes on mutational processes and immune cell infiltration in esophageal squamous cell carcinoma. Cancer Medicine, 2023, 12, 10077-10090.	1.3	2
1474	Genetic Predisposition to Colorectal Cancer: How Many and Which Genes to Test?. International Journal of Molecular Sciences, 2023, 24, 2137.	1.8	12
1475	Different Tumor Types Share a Common Nuclear Map of Chromosome Territories. Cancer Informatics, 2023, 22, 117693512211485.	0.9	0

#	ARTICLE	IF	CITATIONS
1476	APOBEC mutagenesis is a common process in normal human small intestine. Nature Genetics, 2023, 55, 246-254.	9.4	9
1477	Proteogenomics decodes the evolution of human ipsilateral breast cancer. Communications Biology, 2023, 6, .	2.0	2
1479	Oncogenic signaling pathways and hallmarks of cancer in Korean patients with acral melanoma. Computers in Biology and Medicine, 2023, 154, 106602.	3.9	0
1480	The genome of IMiD-refractory myeloma. Blood, 2023, 141, 560-561.	0.6	0
1481	Multifaceted Nature of DNA Polymerase Î¸. International Journal of Molecular Sciences, 2023, 24, 3619.	1.8	5
1484	Late-Stage Metastatic Melanoma Emerges through a Diversity of Evolutionary Pathways. Cancer Discovery, 2023, 13, 1364-1385.	7.7	10
1485	The Poly (ADP-ribose) polymerase inhibitor olaparib and pan-ErbB inhibitor neratinib are highly synergistic in HER2 overexpressing epithelial ovarian carcinoma in vitro and in vivo. Gynecologic Oncology, 2023, 170, 172-178.	0.6	0
1486	SNV/indel hypermutator phenotype in biallelic RAD51C variant: Fanconi anemia. Human Genetics, 2023, 142, 721-733.	1.8	0
1488	The evolution of non-small cell lung cancer metastases in TRACERx. Nature, 2023, 616, 534-542.	13.7	41
1489	Human papillomavirus genomics: Understanding carcinogenicity. Tumour Virus Research, 2023, 15, 200258.	1.5	13
1490	â€œParadoxical neoantigenic mutationsâ€ not simply a driver vs passenger dualism. British Journal of Cancer, 2023, 129, 1-2.	2.9	0
1491	Smoking status in acute myeloid leukemia is associated with worse overall survival and independent of prior nonhematopoietic malignancies, cytogenetic abnormalities, and WHO category. Human Pathology, 2023, 135, 45-53.	1.1	1
1493	Clinically relevant fusion oncogenes: detection and practical implications. Therapeutic Advances in Medical Oncology, 2022, 14, 175883592211441.	1.4	8
1494	A Clonal Evolution Simulator forÂPlanning Somatic Evolution Studies. Lecture Notes in Computer Science, 2022, , 229-242.	1.0	1
1495	Therapy-selected clonal hematopoiesis and its role in myeloid neoplasms. Leukemia Research, 2023, 126, 107020.	0.4	0
1496	Analysis on methylation and expression of <i>PSMB8</i> and its correlation with immunity and immunotherapy in lung adenocarcinoma. Epigenomics, 2022, 14, 1427-1448.	1.0	0
1497	Blocking Genomic Instability Prevents Acquired Resistance to MAPK Inhibitor Therapy in Melanoma. Cancer Discovery, 2023, 13, 880-909.	7.7	19
1498	A molecular phenotypic map of malignant pleural mesothelioma. GigaScience, 2022, 12, .	3.3	4

#	ARTICLE	IF	CITATIONS
1499	Deep genomic analysis of malignant peripheral nerve sheath tumor cell lines challenges current malignant peripheral nerve sheath tumor diagnosis. IScience, 2023, 26, 106096.	1.9	5
1500	Molecular Evolution of Classic Hodgkin Lymphoma Revealed Through Whole-Genome Sequencing of Hodgkin and Reed Sternberg Cells. Blood Cancer Discovery, 2023, 4, 208-227.	2.6	9
1503	Clonal hematopoiesis driven by chromosome 1q/MDM4 trisomy defines a canonical route toward leukemia in Fanconi anemia. Cell Stem Cell, 2023, 30, 153-170.e9.	5.2	22
1504	Distinct breast cancer phenotypes in BRCA 1/2 carriers based on ER status. Breast Cancer Research and Treatment, 2023, 198, 197-205.	1.1	0
1505	Comprehensive genomic profiling of upper tract urothelial carcinoma and urothelial carcinoma of the bladder identifies distinct molecular characterizations with potential implications for targeted therapy & immunotherapy. Frontiers in Immunology, 0, 13, .	2.2	5
1506	APOBEC3B Is Co-Expressed with PKCÎ±/NF-Î°B in Oral and Oropharyngeal Squamous Cell Carcinomas. Diagnostics, 2023, 13, 569.	1.3	0
1507	Evolutionary route of nasopharyngeal carcinoma metastasis and its clinical significance. Nature Communications, 2023, 14, .	5.8	5
1508	Simultaneous sequencing of genetic and epigenetic bases in DNA. Nature Biotechnology, 2023, 41, 1457-1464.	9.4	26
1509	WGS Data Collections: How Do Genomic Databases Transform Medicine?. International Journal of Molecular Sciences, 2023, 24, 3031.	1.8	2
1510	The APOBEC3B cytidine deaminase is an adenovirus restriction factor. PLoS Pathogens, 2023, 19, e1011156.	2.1	0
1511	Germline Cancer Gene Expression Quantitative Trait Loci Are Associated with Local and Global Tumor Mutations. Cancer Research, 2023, 83, 1191-1202.	0.4	3
1513	Spatial genomic diversity associated with <scp>APOBEC</scp> mutagenesis in squamous cell carcinoma arising from ovarian teratoma. Cancer Science, 2023, 114, 2145-2157.	1.7	4
1515	Removal of Aflatoxin B₁ and Zearalenone in Mixed Aqueous Solution by Palygorskite-Montmorillonite Materials In Situ Prepared from Palygorskite Mineral. Langmuir, 2023, 39, 2797-2807.	1.6	0
1516	Integrative proteomic characterization of adenocarcinoma of esophagogastric junction. Nature Communications, 2023, 14, .	5.8	10
1517	Genomic and microenvironmental heterogeneity shaping epithelial-to-mesenchymal trajectories in cancer. Nature Communications, 2023, 14, .	5.8	16
1518	Limited role of generation time changes in driving the evolution of the mutation spectrum in humans. ELife, 0, 12, .	2.8	10
1519	Potential Role of the Fragile Histidine Triad in Cancer Evo-Dev. Cancers, 2023, 15, 1144.	1.7	2
1520	Copy number footprints of platinum-based anticancer therapies. PLoS Genetics, 2023, 19, e1010634.	1.5	1

#	Article	IF	Citations
1521	Genotoxins: The Mechanistic Links between Escherichia coli and Colorectal Cancer. Cancers, 2023, 15, 1152.	1.7	6
1522	APOBEC3A Catalytic Inactivity Mutation Induces Tertiary Structure Destabilization. ACS Medicinal Chemistry Letters, 2023, 14, 338-343.	1.3	1
1523	Immuno-photodynamic Therapy (IPDT): Organic Photosensitizers and Their Application in Cancer Ablation. Jacs Au, 2023, 3, 682-699.	3.6	21
1525	An Integrative Analysis of Nasopharyngeal Carcinoma Genomes Unraveled Unique Processes Driving a Viral-Positive Cancer. Cancers, 2023, 15, 1243.	1.7	0
1528	Widespread perturbation of ETS factor binding sites in cancer. Nature Communications, 2023, 14, .	5.8	1
1530	Using comprehensive genomic and functional analyses for resolving genotypeâ€“phenotype mismatches in children with suspected CMMRD in Lebanon: an IRRDC study. Human Genetics, 2023, 142, 563-576.	1.8	0
1531	The etiology of clonal mosaicism in human aging and disease. Aging and Cancer, 2023, 4, 3-20.	0.5	2
1532	Pan-cancer clinical impact of latent drivers from double mutations. Communications Biology, 2023, 6, .	2.0	3
1534	Functional Homologous Recombination Assay on FFPE Specimens of Advanced High-Grade Serous Ovarian Cancer Predicts Clinical Outcomes. Clinical Cancer Research, 2023, 29, 3110-3123.	3.2	6
1536	Prognostic and Predictive Biomarkers in Familial Breast Cancer. Cancers, 2023, 15, 1346.	1.7	0
1537	The repertoire of copy number alteration signatures in human cancer. Briefings in Bioinformatics, 2023, 24, .	3.2	3
1538	Clinical Next-Generation Sequencing Panels Reveal Molecular Differences Between Merkel Cell Polyomavirusâ€“Negative Merkel Cell Carcinomas and Neuroendocrine Carcinomas. American Journal of Clinical Pathology, 2023, 159, 395-406.	0.4	2
1541	Association between hepatic angiosarcoma and endâ€stage renal disease: nationwide populationâ€based evidence and enriched mutational signature of aristolochic acid exposure. Journal of Pathology, 2023, 260, 165-176.	2.1	1
1543	Predicting Cancer Risk from Germline Whole-exome Sequencing Data Using a Novel Context-based Variant Aggregation Approach. Cancer Research Communications, 2023, 3, 483-488.	0.7	1
1546	Olaparib in the Setting of Radiotherapy-Associated Sarcoma: What Can Precision Medicine Offer For Rare Cancers?. JCO Precision Oncology, 2023, , .	1.5	0
1547	Carcinogenicity Assessment. , 2023, , 125-172.		0
1548	Primary refractory plasmablastic lymphoma: A precision oncology approach. Frontiers in Oncology, 0, 13, .	1.3	4
1549	Multiomic analysis of homologous recombination-deficient end-stage high-grade serous ovarian cancer. Nature Genetics, 2023, 55, 437-450.	9.4	12

#	Article	IF	Citations
1550	Accumulation of STR-Loci Aberrations in Subclones of Jurkat Cell Line as a Model of Tumor Clonal Evolution. Genes, 2023, 14, 571.	1.0	1
1551	DNA Damage and DNA Repair. , 2023, , 51-73.		0
1553	Characterization of POLE c.1373Aâ€‰>â€‰T p.(Tyr458Phe), causing high cancer risk. Molecular Genetics and Genomics, 0, , .	1.0	0
1555	Integrative Pan-Cancer Genomic and Transcriptomic Analyses of Refractory Metastatic Cancer. Cancer Discovery, 2023, 13, 1116-1143.	7.7	11
1557	An oncospace for human cancers. BioEssays, 2023, 45, .	1.2	2
1558	A Biterm Topic Model for Sparse Mutation Data. Cancers, 2023, 15, 1601.	1.7	0
1559	Genotype-phenotype mapping of a patient-derived lung cancer organoid biobank identifies NKX2-1-defined Wnt dependency in lung adenocarcinoma. Cell Reports, 2023, 42, 112212.	2.9	12
1560	Influence network model uncovers relations between biological processes and mutational signatures. Genome Medicine, 2023, 15, .	3.6	2
1563	Evolution of synchronous female bilateral breast cancers and response to treatment. Nature Medicine, 2023, 29, 646-655.	15.2	2
1564	Defining clonal hematopoiesis of indeterminate potential: evolutionary dynamics and detection under aging and inflammation. Journal of Physical Education and Sports Management, 2023, 9, a006251.	0.5	2
1565	Pan-cancer association of DNA repair deficiencies with whole-genome mutational patterns. ELife, 0, 12, .	2.8	0
1570	The hereditary N363K POLE exonuclease mutant extends PPAP tumor spectrum to glioblastomas by causing DNA damage and aneuploidy in addition to increased mismatch mutagenicity. NAR Cancer, 2023, 5, .	1.6	1
1571	Strand asymmetries across genomic processes. Computational and Structural Biotechnology Journal, 2023, 21, 2036-2047.	1.9	0
1574	Antitumor Activity of PEGylated and TEGylated Phenothiazine Derivatives: Structureâ€"Activity Relationship. International Journal of Molecular Sciences, 2023, 24, 5449.	1.8	3
1575	A generalizable machine learning framework for classifying DNA repair defects using ctDNA exomes. Npj Precision Oncology, 2023, 7, .	2.3	3
1576	The Driverless Triple-Wild-Type (BRAF, RAS, KIT) Cutaneous Melanoma: Whole Genome Sequencing Discoveries. Cancers, 2023, 15, 1712.	1.7	3
1577	Heterocyclic aromatic amines (HAA), exposure, metabolism, macromolecular adducts, and cancer risk. , 2024, , 187-206.		1
1578	Molecular Profile of MSH6-Associated Colorectal Carcinomas Shows Distinct Features From Other Lynch Syndromeâ€"Associated Colorectal Carcinomas. Gastroenterology, 2023, 165, 271-274.e2.	0.6	6

#	Article	IF	Citations
1579	Discovering cryptic splice mutations in cancers via a deep neural network framework. NAR Cancer, 2023, 5, .	1.6	0
1580	Multiomic analysis of malignant pleural mesothelioma identifies molecular axes and specialized tumor profiles driving intertumor heterogeneity. Nature Genetics, 2023, 55, 607-618.	9.4	18
1581	Clonal Evolution in Healthy and Premalignant Tissues: Implications for Early Cancer Interception Strategies. Cancer Prevention Research, 2023, 16, 369-378.	0.7	3
1582	Phenotypic Heterogeneity Analysis of APC-Mutant Colon Cancer by Proteomics and Phosphoproteomics Identifies RAI14 as a Key Prognostic Determinant in East Asians and Westerners. Molecular and Cellular Proteomics, 2023, 22, 100532.	2.5	7
1584	Clinical and Mechanistic Implications of R-Loops in Human Leukemias. International Journal of Molecular Sciences, 2023, 24, 5966.	1.8	2
1585	Involvement of APOBEC3A/B Deletion in Mouse Mammary Tumor Virus (MMTV)-like Positive Human Breast Cancer. Diagnostics, 2023, 13, 1196.	1.3	0
1586	Prospects of POLD1 in Human Cancers: A Review. Cancers, 2023, 15, 1905.	1.7	2
1587	Whole-genome and Epigenomic Landscapes of Malignant Gastrointestinal Stromal Tumors Harboring<i>KIT</i>Exon 11 557â€“558 Deletion Mutations. Cancer Research Communications, 2023, 3, 684-696.	0.7	1
1588	Homologous recombination deficiency signatures in gastrointestinal and thoracic cancers correlate with platinum therapy duration. Npj Precision Oncology, 2023, 7, .	2.3	6
1589	Computational Methods Summarizing Mutational Patterns in Cancer: Promise and Limitations for Clinical Applications. Cancers, 2023, 15, 1958.	1.7	1
1590	DNA repair mechanisms that promote insertion-deletion events during immunoglobulin gene diversification. Science Immunology, 2023, 8, .	5.6	4
1591	Clonal origin and development of high hyperdiploidy in childhood acute lymphoblastic leukaemia. Nature Communications, 2023, 14, .	5.8	3
1592	Personalized Immuno-Oncology with Immunodeficiency Mouse Models. , 2023, , .		0
1594	Seeing Beyond the Smoke: Reclassifying Lung Cancer by Smoking-Related Mutational Signatures. Journal of Thoracic Oncology, 2023, 18, 396-398.	0.5	0
1595	Characterization of somatic mutations of colorectal tumor in a patient with concurrent APC and MLH1 germline mutations. Genes and Diseases, 2023, , .	1.5	1
1596	Molecular origins of mutational spectra produced by the environmental carcinogen<i>N</i>-nitrosodimethylamine and SN1 chemotherapeutic agents. NAR Cancer, 2023, 5, .	1.6	2
1597	Understanding Head and Neck Cancer Evolution to Guide Therapeutic Approaches. , 2023, , 63-81.		0
1598	Undifferentiated and Dedifferentiated Metastatic Melanomas Masquerading as Soft Tissue Sarcomas: Mutational Signature Analysis and Immunotherapy Response. Modern Pathology, 2023, 36, 100165.	2.9	2

#	Article	IF	Citations
1599	Neuroblastoma arises in early fetal development and its evolutionary duration predicts outcome. Nature Genetics, 2023, 55, 619-630.	9.4	10
1600	Dissection of Cancer Mutational Signatures with Individual Components of Cigarette Smoking. Chemical Research in Toxicology, 2023, 36, 714-723.	1.7	2
1601	APOBEC3-mediated mutagenesis in cancer: causes, clinical significance and therapeutic potential. Journal of Hematology and Oncology, 2023, 16, .	6.9	10
1602	Comprehensive proteogenomic characterization of early duodenal cancer reveals the carcinogenesis tracks of different subtypes. Nature Communications, 2023, 14, .	5.8	3
1604	Clonal hematopoiesis detection in patients with cancer using cell-free DNA sequencing. Science Translational Medicine, 2023, 15, .	5.8	6
1606	Clinical Targeted Next-Generation Panel Sequencing Reveals <i>MYC</i> Amplification Is a Poor Prognostic Factor in Osteosarcoma. JCO Precision Oncology, 2023, , .	1.5	2
1608	Mutation bias and the predictability of evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2023, 378, .	1.8	7
1609	T cell immune deficiency rather than chromosome instability predisposes patients with short telomere syndromes to squamous cancers. Cancer Cell, 2023, 41, 807-817.e6.	7.7	12
1611	Circulating Cell-Free Nucleic Acids as Biomarkers for Diagnosis and Prognosis of Pancreatic Cancer. Biomedicines, 2023, 11, 1069.	1.4	1
1612	Detection of rare mutations, copy number alterations, and methylation in the same template DNA molecules. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	8
1613	NAGS, CPS1, and SLC25A13 (Citrin) at the Crossroads of Arginine and Pyrimidines Metabolism in Tumor Cells. International Journal of Molecular Sciences, 2023, 24, 6754.	1.8	1
1614	Spectra and characteristics of somatic mutations induced by ionizing radiation in hematopoietic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	1
1615	Atypical teratoid/rhabdoid tumoroids reveal subgroup-specific drug vulnerabilities. Oncogene, 2023, 42, 1661-1671.	2.6	5
1616	Emerging predictive biomarkers in the management of bone and soft tissue sarcomas. Expert Review of Anticancer Therapy, 0, , 1-8.	1.1	1
1617	New Molecular and Biological Markers in Cutaneous T Cell Lymphoma: Therapeutic Implications. Current Hematologic Malignancy Reports, 0, , .	1.2	1
1618	Predicting response to enzalutamide and abiraterone in metastatic prostate cancer using whole-omics machine learning. Nature Communications, 2023, 14, .	5.8	4
1620	Genomicâ€“transcriptomic evolution in lung cancer and metastasis. Nature, 2023, 616, 543-552.	13.7	44
1621	Genome-wide contributions of the MutSÎ±- and MutSÎ²-dependent DNA mismatch repair pathways to the maintenance of genetic stability in S. cerevisiae. Journal of Biological Chemistry, 2023, , 104705.	1.6	0

#	Article	IF	Citations
1622	The evolution of lung cancer and impact of subclonal selection in TRACERx. Nature, 2023, 616, 525-533.	13.7	62
1623	Accelerating the understanding of cancer biology through the lens of genomics. Cell, 2023, 186, 1755-1771.	13.5	9
1624	The origins and functional effects of postzygotic mutations throughout the human life span. Science, 2023, 380, .	6.0	6
1625	Integrative Analysis of a Large Real-World Cohort of Small Cell Lung Cancer Identifies Distinct Genetic Subtypes and Insights into Histologic Transformation. Cancer Discovery, 2023, 13, 1572-1591.	7.7	13
1626	Calcifications in triple-negative breast cancer: Molecular features and treatment strategies. Npj Breast Cancer, 2023, 9, .	2.3	0
1627	Comparing Genomic Landscapes of Oral and Cutaneous Squamous Cell Carcinoma of the Head and Neck: Quest for Novel Diagnostic Markers. Modern Pathology, 2023, 36, 100190.	2.9	1
1628	Genomic Characterization Revealed PM_{2.5}-Associated Mutational Signatures in Lung Cancer Including Activation of APOBEC3B. Environmental Science & Technology, 2023, 57, 6854-6864.	4.6	1
1629	Aberrant APOBEC3B Expression in Breast Cancer Is Linked to Proliferation and Cell Cycle Phase. Cells, 2023, 12, 1185.	1.8	4
1630	Validation of genetic variants from NGS data using deep convolutional neural networks. BMC Bioinformatics, 2023, 24, .	1.2	0
1631	Genomic mapping of metastatic organotropism in lung adenocarcinoma. Cancer Cell, 2023, 41, 970-985.e3.	7.7	15
1632	Salivary gland cancer organoids are valid for preclinical genotype-oriented medical precision trials. IScience, 2023, 26, 106695.	1.9	1
1633	The evolution of two transmissible cancers in Tasmanian devils. Science, 2023, 380, 283-293.	6.0	20
1634	Changes in metabolic landscapes shape divergent but distinct mutational signatures and cytotoxic consequences of redox stress. Nucleic Acids Research, 0, , .	6.5	0
1635	Relationship between homologous recombination deficiency and clinical features of breast cancer based on genomic scar score. Breast, 2023, , .	0.9	3
1636	ACT-Discover: identifying karyotype heterogeneity in pancreatic cancer evolution using ctDNA. Genome Medicine, 2023, 15, .	3.6	3
1637	Using genomic scars to select immunotherapy beneficiaries in advanced non-small cell lung cancer. Scientific Reports, 2023, 13, .	1.6	3
1638	Speed reading the epigenome and genome. Nature Biotechnology, 0, , .	9.4	0
1642	Progress of Lung Cancer Genomic Epidemiology in China. , 2022, , 243-259.		0

#	Article	IF	Citations
1682	GÃ©nome tumoral. , 2023, , 3-9.		0
1713	Circle Damage Sequencing for Whole-Genome Analysis of DNA Damage. Methods in Molecular Biology, 2023, , 247-262.	0.4	0
1754	Basic Concepts of Carcinogenesis and Immunopathology. , 2023, , 5-27.		0
1776	Somatic mutations in facial skin from countries of contrasting skin cancer risk. Nature Genetics, 2023, 55, 1440-1447.	9.4	5
1782	Alternative Mechanisms of Mutagenesis at mCpG Sites during Replication and Repair. Molecular Biology, 2023, 57, 584-592.	0.4	0
1786	Commonalities and differences in the mutational signature and somatic driver mutation landscape across solid and hollow viscus organs. Oncogene, 0, , .	2.6	1
1801	Editorial: DNA repair and nucleic acid therapeutics in cancer. NAR Cancer, 2023, 5, .	1.6	0
1847	Gene Editing and Gene Therapy in Oncology. , 2023, , 155-180.		4
1860	Carcinogens. , 2023, , 21-67.		0
1902	Genomic Mosaicism of the Brain: Origin, Impact, and Utility. Neuroscience Bulletin, 0, , .	1.5	0
1906	Deubiquitinases in cancer. Nature Reviews Cancer, 2023, 23, 842-862.	12.8	5
1919	Scrambling the genome in cancer: causes and consequences of complex chromosome rearrangements. Nature Reviews Genetics, 2024, 25, 196-210.	7.7	3
1940	The chemotherapeutic drug CX-5461 is a potent mutagen in cultured human cells. Nature Genetics, 2024, 56, 23-26.	9.4	4
1945	Targeting Polymerase Theta (POLÎ¸) for Cancer Therapy. Cancer Treatment and Research, 2023, , 285-298.	0.2	0
2008	Lung cancer in patients who have never smoked â€" an emerging disease. Nature Reviews Clinical Oncology, 2024, 21, 121-146.	12.5	1
2039	Review of gene expression using microarray and RNA-seq. , 2024, , 159-187.		0
2080	DNA-SchÃ¤digung und DNA-Reparatur. , 2024, , 61-87.		0
2093	The Search for Cancer Drivers. Lecture Notes in Computer Science, 2024, , 145-171.	1.0	0

#	ARTICLE	IF	CITATIONS