

CITATION REPORT

List of articles citing

SomaticSignatures: inferring mutational signatures from single-nucleotide variants

DOI: 10.1093/bioinformatics/btv408
Bioinformatics, 2015, 31, 3673-5.

Source: <https://exaly.com/paper-pdf/62405248/citation-report.pdf>

Version: 2024-04-23

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
218	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. <i>Nature Communications</i> , 2015 , 6, 8940	17.4	175
217	Patient-specific factors influence somatic variation patterns in von Hippel-Lindau disease renal tumours. <i>Nature Communications</i> , 2016 , 7, 11588	17.4	19
216	Genomic landscape of colorectal cancer in Japan: clinical implications of comprehensive genomic sequencing for precision medicine. 2016 , 8, 136		48
215	Understanding mutagenesis through delineation of mutational signatures in human cancer. 2016 , 37, 531-40		66
214	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. 2016 , 48, 1131-41		233
213	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. 2016 , 128, 1735-44		129
212	Ancestral-derived effects on the mutational landscape of laryngeal cancer. 2016 , 107, 76-82		13
211	Mutational signatures and mutable motifs in cancer genomes. 2018 , 19, 1085-1101		25
210	Exploring background mutational processes to decipher cancer genetic heterogeneity. 2017 , 45, W514-W522		41
209	Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline :c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. 2017 , 3,		6
208	Selective analysis of cancer-cell intrinsic transcriptional traits defines novel clinically relevant subtypes of colorectal cancer. <i>Nature Communications</i> , 2017 , 8, 15107	17.4	129
207	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. 2017 , 214, 2073-2088		23
206	Mutational Signatures in Breast Cancer: The Problem at the DNA Level. 2017 , 23, 2617-2629		73
205	Merkel Cell Polyomavirus Exhibits Dominant Control of the Tumor Genome and Transcriptome in Virus-Associated Merkel Cell Carcinoma. 2017 , 8,		73
204	Nuclear topology modulates the mutational landscapes of cancer genomes. 2017 , 24, 1000-1006		22
203	Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia. 2017 , 9,		184
202	BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. <i>Nature Communications</i> , 2017 , 8, 319	17.4	139

201	Mutational signatures efficiently identify different mutational processes underlying cancers with similar somatic mutation spectra. 2017 , 806, 27-30		2
200	Genome-wide genetic and epigenetic analyses of pancreatic acinar cell carcinomas reveal aberrations in genome stability. <i>Nature Communications</i> , 2017 , 8, 1323	17.4	38
199	Multilevel genomics of colorectal cancers with microsatellite instability-clinical impact of JAK1 mutations and consensus molecular subtype 1. 2017 , 9, 46		53
198	Whole exome sequencing identified sixty-five coding mutations in four neuroblastoma tumors. 2017 , 7, 17787		7
197	Mutational patterns in chemotherapy resistant muscle-invasive bladder cancer. <i>Nature Communications</i> , 2017 , 8, 2193	17.4	62
196	Genomic profiles of a hepatoblastoma from a patient with Beckwith-Wiedemann syndrome with uniparental disomy on chromosome 11p15 and germline mutation of APC and PALB2. 2017 , 8, 91950-91957		10
195	Interpreting whole genome and exome sequencing data of individual gastric cancer samples. 2017 , 18, 517		6
194	Somatic Mitochondrial DNA Mutations in Diffuse Large B-Cell Lymphoma. 2018 , 8, 3623		3
193	mSignatureDB: a database for deciphering mutational signatures in human cancers. 2018 , 46, D964-D970		37
192	Mutational signatures and chromosome alteration profiles of squamous cell carcinomas of the vulva. 2018 , 50, e442		27
191	NSAID use and somatic exomic mutations in Barrett's esophagus. 2018 , 10, 17		10
190	MutationalPatterns: comprehensive genome-wide analysis of mutational processes. 2018 , 10, 33		268
189	Validating the concept of mutational signatures with isogenic cell models. <i>Nature Communications</i> , 2018 , 9, 1744	17.4	87
188	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. 2018 , 33, 690-705.e9		277
187	Comparative genomics reveals that loss of lunatic fringe (LFNG) promotes melanoma metastasis. 2018 , 12, 239-255		12
186	Helmsman: fast and efficient mutation signature analysis for massive sequencing datasets. 2018 , 19, 845		12
185	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. 2018 , 128, 4441-4453		84
184	A recurrent novel fusion identifies a new subtype of high-grade spindle cell sarcoma. 2018 , 4,		20

183	Mitochondrial RNA Expression and Single Nucleotide Variants in Association with Clinical Parameters in Primary Breast Cancers. 2018 , 10,	5
182	The genetic landscape of 5T models for multiple myeloma. 2018 , 8, 15030	10
181	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. <i>Nature Communications</i> , 2018 , 9, 4181	17.4 45
180	Predominance of triple wild-type and IGF2R mutations in mucosal melanomas. 2018 , 18, 1054	10
179	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease-Associated Colorectal Cancers. 2018 , 24, 5133-5142	17
178	Chromatin loop anchors are associated with genome instability in cancer and recombination hotspots in the germline. 2018 , 19, 101	34
177	Mutational Signatures in Cancer (MuSiCa): a web application to implement mutational signatures analysis in cancer samples. 2018 , 19, 224	50
176	Timing somatic events in the evolution of cancer. 2018 , 19, 95	41
175	Genomic Hallmarks and Structural Variation in Metastatic Prostate Cancer. 2018 , 174, 758-769.e9	234
174	Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer. 2018 , 3, 18	23
173	Characterization of BK Polyomaviruses from Kidney Transplant Recipients Suggests a Role for APOBEC3 in Driving In-Host Virus Evolution. 2018 , 23, 628-635.e7	39
172	The effects of mutational processes and selection on driver mutations across cancer types. <i>Nature Communications</i> , 2018 , 9, 1857	17.4 59
171	Genomic features of renal cell carcinoma with venous tumor thrombus. 2018 , 8, 7477	9
170	Copy number signatures and mutational processes in ovarian carcinoma. 2018 , 50, 1262-1270	155
169	Forward and reverse mutations in stages of cancer development. 2018 , 12, 40	8
168	Impact of DNA lesion repair, replication and formation on the mutational spectra of environmental carcinogens: Aflatoxin B as a case study. 2018 , 71, 12-22	14
167	Whole exome sequencing in the rat. 2018 , 19, 487	3
166	Inactivation of CDK12 Delineates a Distinct Immunogenic Class of Advanced Prostate Cancer. 2018 , 173, 1770-1782.e14	256

165	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. <i>Nature Communications</i> , 2018 , 9, 2378	17.4	50
164	Canine osteosarcoma genome sequencing identifies recurrent mutations in and the histone methyltransferase gene. 2019 , 2, 266		28
163	Modeling clinical and molecular covariates of mutational process activity in cancer. <i>Bioinformatics</i> , 2019 , 35, i492-i500	7.2	9
162	A practical guide for mutational signature analysis in hematological malignancies. <i>Nature Communications</i> , 2019 , 10, 2969	17.4	73
161	Distinctive mutational spectrum and karyotype disruption in long-term cisplatin-treated urothelial carcinoma cell lines. 2019 , 9, 14476		3
160	Identification of Recurrent Activating Mutations in Primary Canine Pulmonary Adenocarcinoma. 2019 , 25, 5866-5877		13
159	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. 2019 , 20, 685		56
158	The molecular origin and taxonomy of mucinous ovarian carcinoma. <i>Nature Communications</i> , 2019 , 10, 3935	17.4	59
157	Computational tools to detect signatures of mutational processes in DNA from tumours: A review and empirical comparison of performance. 2019 , 14, e0221235		25
156	The Effects of Neoadjuvant Chemoradiation in Locally Advanced Rectal Cancer-The Impact in Intratumoral Heterogeneity. <i>Frontiers in Oncology</i> , 2019 , 9, 974	5.3	8
155	Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. <i>Nature Communications</i> , 2019 , 10, 353	17.4	53
154	Paternal exposure to benzo(a)pyrene induces genome-wide mutations in mouse offspring. 2019 , 2, 228		15
153	Integrative analysis of genomic and transcriptomic characteristics associated with progression of aggressive thyroid cancer. <i>Nature Communications</i> , 2019 , 10, 2764	17.4	80
152	Germline variants and somatic mutation signatures of breast cancer across populations of African and European ancestry in the US and Nigeria. 2019 , 145, 3321-3333		5
151	Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes. 2019 , 8, 446-455.e8		29
150	Mutational signatures of redox stress in yeast single-strand DNA and of aging in human mitochondrial DNA share a common feature. 2019 , 17, e3000263		13
149	Portrait of a cancer: mutational signature analyses for cancer diagnostics. 2019 , 19, 457		51
148	Implication of DNA repair genes in Lynch-like syndrome. 2019 , 18, 331-342		12

147	Single-cell whole-genome sequencing reveals the functional landscape of somatic mutations in B lymphocytes across the human lifespan. 2019 , 116, 9014-9019		101
146	Integrative molecular profiling identifies a novel cluster of estrogen receptor-positive breast cancer in very young women. 2019 , 110, 1760-1770		5
145	Genomic stratification and liquid biopsy in a rare adrenocortical carcinoma (ACC) case, with dual lung metastases. 2019 , 5,		7
144	Integrated structural variation and point mutation signatures in cancer genomes using correlated topic models. 2019 , 15, e1006799		19
143	Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy. <i>Nature Communications</i> , 2019 , 10, 657	17.4	30
142	Whole-genome sequencing identifies ADGRG6 enhancer mutations and FRS2 duplications as angiogenesis-related drivers in bladder cancer. <i>Nature Communications</i> , 2019 , 10, 720	17.4	37
141	Evaluation of Whole Genome Sequencing Data. 2019 , 1956, 321-336		2
140	Establishment, molecular and biological characterization of HCB-514: a novel human cervical cancer cell line. 2019 , 9, 1913		7
139	Integrative molecular and clinical modeling of clinical outcomes to PD1 blockade in patients with metastatic melanoma. 2019 , 25, 1916-1927		227
138	Somatic mutation signatures in primary liver tumors of workers exposed to ionizing radiation. 2019 , 9, 18199		4
137	Comparison of somatic variant detection algorithms using Ion Torrent targeted deep sequencing data. 2019 , 12, 181		3
136	Deep multi-region whole-genome sequencing reveals heterogeneity and gene-by-environment interactions in treatment-naive, metastatic lung cancer. 2019 , 38, 1661-1675		10
135	In Utero Exposure to Benzo[a]pyrene Induces Ovarian Mutations at Doses That Deplete Ovarian Follicles in Mice. 2019 , 60, 410-420		11
134	Computational approaches for discovery of mutational signatures in cancer. 2019 , 20, 77-88		25
133	Analysis pipelines for cancer genome sequencing in mice. 2020 , 15, 266-315		12
132	Whole-exome sequencing reveals the impact of UVA light mutagenesis in xeroderma pigmentosum variant human cells. 2020 , 48, 1941-1953		10
131	Characteristics of mutational signatures of unknown etiology. 2020 , 2, zcaa026		8
130	Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis. <i>Bioinformatics</i> , 2021 , 37, 1590-1592	7.2	4

129	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. 2020 , 52, 790-799		62
128	Integrated analysis of optical mapping and whole-genome sequencing reveals intratumoral genetic heterogeneity in metastatic lung squamous cell carcinoma. 2020 , 9, 670-681		6
127	Multi-Omics Analysis Reveals Novel Subtypes and Driver Genes in Glioblastoma. <i>Frontiers in Genetics</i> , 2020 , 11, 565341	4-5	4
126	Integrated molecular drivers coordinate biological and clinical states in melanoma. 2020 , 52, 1373-1383		11
125	CaMuS: simultaneous fitting and de novo imputation of cancer mutational signature. 2020 , 10, 19316		3
124	Genetic profiling for diffuse type and genomically stable subtypes in gastric cancer. 2020 , 18, 3301-3308		7
123	MutSignatures: an R package for extraction and analysis of cancer mutational signatures. 2020 , 10, 18217		8
122	Mutational Landscape of Esophageal Squamous Cell Carcinoma in an Indian Cohort. <i>Frontiers in Oncology</i> , 2020 , 10, 1457	5-3	11
121	Molecular correlates of cisplatin-based chemotherapy response in muscle invasive bladder cancer by integrated multi-omics analysis. <i>Nature Communications</i> , 2020 , 11, 4858	17.4	41
120	Whole-genome sequencing of 508 patients identifies key molecular features associated with poor prognosis in esophageal squamous cell carcinoma. 2020 , 30, 902-913		42
119	Decoding whole-genome mutational signatures in 37 human pan-cancers by denoising sparse autoencoder neural network. 2020 , 39, 5031-5041		6
118	Epigenetic loss of heterozygosity of Apc and an inflammation-associated mutational signature detected in Lrig1-driven murine colonic adenomas. 2020 , 20, 126		1
117	Mutational landscape differences between young-onset and older-onset breast cancer patients. 2020 , 20, 212		5
116	Mutation signatures specific to DNA alkylating agents in yeast and cancers. 2020 , 48, 3692-3707		13
115	The mutREAD method detects mutational signatures from low quantities of cancer DNA. <i>Nature Communications</i> , 2020 , 11, 3166	17.4	3
114	Measuring single cell divisions in human tissues from multi-region sequencing data. <i>Nature Communications</i> , 2020 , 11, 1035	17.4	17
113	BATCAVE: calling somatic mutations with a tumor- and site-specific prior. 2020 , 2, lqaa004		0
112	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. <i>Nature Communications</i> , 2020 , 11, 435	17.4	20

111	Extreme intratumour heterogeneity and driver evolution in mismatch repair deficient gastro-oesophageal cancer. <i>Nature Communications</i> , 2020 , 11, 139	17.4	22
110	CANCERSIGN: a user-friendly and robust tool for identification and classification of mutational signatures and patterns in cancer genomes. 2020 , 10, 1286		7
109	The repertoire of mutational signatures in human cancer. 2020 , 578, 94-101		849
108	Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. <i>Nature Communications</i> , 2020 , 11, 1528	17.4	25
107	Integrative multiplatform molecular profiling of benign prostatic hyperplasia identifies distinct subtypes. <i>Nature Communications</i> , 2020 , 11, 1987	17.4	14
106	Mechanisms and therapeutic implications of hypermutation in gliomas. 2020 , 580, 517-523		172
105	Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. 2021 , 22,		8
104	Associations among the mutational landscape, immune microenvironment, and prognosis in Chinese patients with hepatocellular carcinoma. 2021 , 70, 377-389		18
103	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. 2021 , 27, 1695-1705		9
102	Integrated Genomic and Transcriptomic Analysis reveals key genes for predicting dual-phenotype Hepatocellular Carcinoma Prognosis. 2021 , 12, 2993-3010		2
101	Identification of Potential Driver Genes Based on Multi-Genomic Data in Cervical Cancer. <i>Frontiers in Genetics</i> , 2021 , 12, 598304	4.5	4
100	Discriminating Spontaneous From Cigarette Smoke and THS 2.2 Aerosol Exposure-Related Proliferative Lung Lesions in A/J Mice by Using Gene Expression and Mutation Spectrum Data.. 2021 , 3, 634035		
99	Integration of comprehensive genomic profiling, tumor mutational burden, and PD-L1 expression to identify novel biomarkers of immunotherapy in non-small cell lung cancer. <i>Cancer Medicine</i> , 2021 , 10, 2216-2231	4.8	9
98	Characterization of Tumor Microenvironment in Lung Adenocarcinoma Identifies Immune Signatures to Predict Clinical Outcomes and Therapeutic Responses. <i>Frontiers in Oncology</i> , 2021 , 11, 581030	5.3	4
97	Histopathological characteristics and artificial intelligence for predicting tumor mutational burden-high colorectal cancer. 2021 , 56, 547-559		4
96	Whole-Exome Sequencing Analysis of Oral Squamous Cell Carcinoma Delineated by Tobacco Usage Habits. <i>Frontiers in Oncology</i> , 2021 , 11, 660696	5.3	3
95	Whole-Genome Sequencing of Common Salivary Gland Carcinomas: Subtype-Restricted and Shared Genetic Alterations. 2021 , 27, 3960-3969		2
94	A novel genomic classification system of gastric cancer via integrating multidimensional genomic characteristics. 2021 , 24, 1227-1241		2

93	Multi-omics profiling of primary small cell carcinoma of the esophagus reveals RB1 disruption and additional molecular subtypes. <i>Nature Communications</i> , 2021 , 12, 3785	17.4	3
92	Origins and timing of emerging lesions in advanced renal cell carcinoma.		
91	Whole-exome sequencing of alpha-fetoprotein producing gastric carcinoma reveals genomic profile and therapeutic targets. <i>Nature Communications</i> , 2021 , 12, 3946	17.4	5
90	De novo mutational signature discovery in tumor genomes using SparseSignatures. 2021 , 17, e1009119		6
89	Humans with inherited T cell CD28 deficiency are susceptible to skin papillomaviruses but are otherwise healthy. 2021 , 184, 3812-3828.e30		18
88	SUITOR: selecting the number of mutational signatures through cross-validation.		
87	Global mapping of cancers: The Cancer Genome Atlas and beyond. 2021 , 15, 2823-2840		10
86	Whole-Genome Analysis of De Novo Somatic Point Mutations Reveals Novel Mutational Biomarkers in Pancreatic Cancer. 2021 , 13,		2
85	A practical framework RNMF for the potential mechanism of cancer progression with the analysis of genes cumulative contribution abundance.		
84	Rad18 mediates specific mutational signatures and shapes the genomic landscape of carcinogen-induced tumors. 2021 , 3, zcaa037		6
83	SomaMutDB: a database of somatic mutations in normal human tissues. 2021 ,		5
82	Bioinformatic Methods to Identify Mutational Signatures in Cancer. 2021 , 2185, 447-473		2
81	MutationalPatterns: comprehensive genome-wide analysis of mutational processes.		6
80	The effects of mutational processes and selection on driver mutations across cancer types.		2
79	Computational approaches for discovery of mutational signatures in cancer.		3
78	Copy-number signatures and mutational processes in ovarian carcinoma.		3
77	MutSignatures: An R Package for Extraction and Analysis of Cancer Mutational Signatures.		1
76	Evaluating assembly and variant calling software for strain-resolved analysis of large DNA-viruses.		2

75	Identifying temporal and spatial patterns of variation from multi-modal data using MEFISTO.	6
74	Uncovering novel mutational signatures by de novo extraction with SigProfilerExtractor.	17
73	Integrated single-nucleotide and structural variation signatures of DNA-repair deficient human cancers.	3
72	The Repertoire of Mutational Signatures in Human Cancer.	67
71	sigLASSO: optimizing cancer mutation signatures jointly with sampling likelihood.	1
70	De Novo Mutational Signature Discovery in Tumor Genomes using SparseSignatures.	6
69	Single-cell whole-genome sequencing reveals the functional landscape of somatic mutations in B lymphocytes across the human lifespan.	3
68	Measuring single cell divisions in human cancers from multi-region sequencing data.	1
67	Evolutionary history of metastatic breast cancer reveals minimal seeding from axillary lymph nodes. 2018 , 128, 1355-1370	78
66	Decomposition of mutational context signatures using quadratic programming methods. 5, 1253	4
65	Impact of mutations in Toll-like receptor pathway genes on esophageal carcinogenesis. 2017 , 13, e1006808	12
64	Mutation Processes in 293-Based Clones Overexpressing the DNA Cytosine Deaminase APOBEC3B. 2016 , 11, e0155391	24
63	Deep targeted sequencing in pediatric acute lymphoblastic leukemia unveils distinct mutational patterns between genetic subtypes and novel relapse-associated genes. 2016 , 7, 64071-64088	26
62	The ubiquitous Tancer mutational signatureT5 occurs specifically in cancers with deleted alleles. 2017 , 8, 102199-102211	8
61	Whole exome sequencing identifies mTOR and KEAP1 as potential targets for radiosensitization of HNSCC cells refractory to EGFR and α integrin inhibition. 2018 , 9, 18099-18114	11
60	The Impact of Whole Genome Data on Therapeutic Decision-Making in Metastatic Prostate Cancer: A Retrospective Analysis. 2020 , 12,	5
59	Genomic characterization of rare molecular subclasses of hepatocellular carcinoma. 2021 , 4, 1150	0
58	Genomic Sub-Classification of Ovarian Clear Cell Carcinoma Revealed by Distinct Mutational Signatures. 2021 , 13,	2

- 57 Chromatin loop anchors are associated with genome instability in cancer and recombination hotspots in the germline.
- 56 Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer.
- 55 Androgen receptor binding sites are highly mutated in prostate cancer.
- 54 Helmsman: fast and efficient generation of input matrices for mutation signature analysis.
- 53 The Medical Genome Reference Bank: Whole genomes and phenotype of 2,570 healthy elderly. 1
- 52 Computational tools to detect signatures of mutational processes in DNA from tumours: a review and empirical comparison of performance. 2
- 51 Identification of frequent activating HER2 mutations in primary canine pulmonary adenocarcinoma. 1
- 50 SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events.
- 49 Epigenetic loss of heterozygosity of Apc and an inflammation-associated mutational signature detected in Lrig1+/-driven murine colonic adenomas.
- 48 Extreme intratumour heterogeneity and driver evolution in mismatch repair deficient gastro-oesophageal cancer.
- 47 Integrative genomic, transcriptomic, and epigenomic analyses of benign prostatic hyperplasia reveal new options for therapy.
- 46 BATCAVE: Calling somatic mutations with a tumor- and site-specific prior.
- 45 Sequencing Chemically Induced Mutations in the Mutamouse Lacz Reporter Gene Identifies Human Cancer Mutational Signatures. 0
- 44 Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis.
- 43 A mixture model for signature discovery from sparse mutation data. **2021**, 13, 173 6
- 42 Multidimensional Mutational Profiling of the Indian HNSCC Sub-Population Provides IRAK1, a Novel Driver Gene and Potential Druggable Target. *Frontiers in Oncology*, **2021**, 11, 723162 53 0
- 41 Single-cell Individual Complete mtDNA Sequencing Uncovers Hidden Mitochondrial Heterogeneity in Human and Mouse Oocytes. 1
- 40 MutationalPatterns: The one stop shop for the analysis of mutational processes. 0

- 39 Mutagenicity of folic acid deficiency and supplementation is tissue-specific and results in distinct mutation profiles.
- 38 mutSigMapper: an R package to map spectra to mutational signatures based on shot-noise modeling.
- 37 DNASE1L3 as a Novel Diagnostic and Prognostic Biomarker for Lung Adenocarcinoma Based on Data Mining. *Frontiers in Genetics*, **2021**, 12, 699242 4-5 1
- 36 Mutational signatures among young-onset testicular cancers. **2021**, 14, 280
- 35 Accuracy of mutational signature software on correlated signatures.. **2022**, 12, 390 2
- 34 Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO.. **2022**, 5
- 33 MutationalPatterns: the one stop shop for the analysis of mutational processes.. **2022**, 23, 134 4
- 32 APOBEC SBS13 Mutational Signature-A Novel Predictor of Radioactive Iodine Refractory Papillary Thyroid Carcinoma.. **2022**, 14, 0
- 31 SUITOR: Selecting the number of mutational signatures through cross-validation.. **2022**, 18, e1009309 0
- 30 Genomic Variations and Immune-Related Features of TMB, PD-L1 Expression and CD8 T Cell Infiltration in Chinese Pulmonary Sarcomatoid Carcinoma.. **2022**, 15, 4209-4220 0
- 29 Data_Sheet_1.pdf. **2020**,
- 28 Table_1.pdf. **2020**,
- 27 Table_2.pdf. **2020**,
- 26 Table_3.pdf. **2020**,
- 25 Table_4.pdf. **2020**,
- 24 Table_5.pdf. **2020**,
- 23 Table_6.pdf. **2020**,
- 22 Table_7.pdf. **2020**,

21 Table_8.pdf. **2020**,

20 Table_9.pdf. **2020**,

19 Tumor infiltrating lymphocytes-based subtypes and genomic characteristics of EBV- associated lymphoepithelioma-like carcinoma.. **2022**,

18 Establishment and Application of a Prognostic Risk Score Model Based on Characteristics of Different Immunophenotypes for Lung Adenocarcinoma.. *Frontiers in Genetics*, **2022**, 13, 850101 4.5

17 Detection and Localization of Solid Tumors Utilizing the Cancer-Type-Specific Mutational Signatures.. *Frontiers in Bioengineering and Biotechnology*, **2022**, 10, 883791 5.8

16 A practical framework RNMF for exploring the association between mutational signatures and genes using gene cumulative contribution abundance.. *Cancer Medicine*, **2022**, 4.8

15 Cutaneous and acral melanoma cross-OMICs reveals prognostic cancer drivers associated with pathobiology and ultraviolet exposure.

14 Whole-Exome Sequencing Uncovers Specific Genetic Variation Difference Based on Different Modes of Drug Resistance in Small Cell Lung Cancer. *Frontiers in Oncology*, 12, 5.3

13 Cutaneous and acral melanoma cross-OMICs reveals prognostic cancer drivers associated with pathobiology and ultraviolet exposure. *Nature Communications*, **2022**, 13, 17.4 ○

12 Targeted parallel DNA sequencing detects circulating tumor-associated variants of the mitochondrial and nuclear genomes in patients with neuroblastoma. *Cancer Reports*, 1.5

11 Evaluation of the mutagenic effects of Molnupiravir and N4 -hydroxycytidine in bacterial and mammalian cells by HiFi sequencing. 1

10 Collaborative study from the Bladder Cancer Advocacy Network for the genomic analysis of metastatic urothelial cancer. **2022**, 13, ○

9 Cancer classification based on multiple dimensions: SNV patterns. **2022**, 151, 106270 ○

8 Intratumor heterogeneity is associated with less CD8+ T cell infiltration and worse survival in patients with small cell lung cancer. ○

7 Feasibility and tolerability of sintilimab plus anlotinib as the second-line therapy for patients with advanced biliary tract cancers: An open-label, single-arm, phase II clinical trial. ○

6 Whole exome sequencing in Chinese mucinous pulmonary adenocarcinoma uncovers specific genetic variations different from lung adenocarcinoma. 12, ○

5 Diffsig: Associating Risk Factors With Mutational Signatures. ○

4 Computational Methods Summarizing Mutational Patterns in Cancer: Promise and Limitations for Clinical Applications. **2023**, 15, 1958 ○

- 3 APOBEC3B stratifies ovarian clear cell carcinoma with distinct immunophenotype and prognosis. ○
- 2 Characterization of the Mitochondrial Genetic Landscape in Abdominal Aortic Aneurysm. **2023**, 12, ○
- 1 Changes in metabolic landscapes shape divergent but distinct mutational signatures and cytotoxic consequences of redox stress. ○