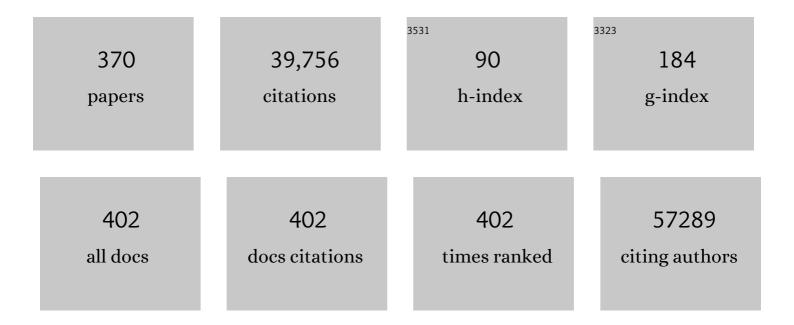
Olivier Elemento

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Artificial intelligence in oncology: From bench to clinic. Seminars in Cancer Biology, 2022, 84, 113-128.	9.6	16
2	Clinical utility of whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 32-39.	9.6	35
3	Analytical demands to use whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 16-22.	9.6	22
4	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. Seminars in Cancer Biology, 2022, 84, 23-31.	9.6	10
5	Extracellular Matrix in Synthetic Hydrogelâ€Based Prostate Cancer Organoids Regulate Therapeutic Response to EZH2 and DRD2 Inhibitors. Advanced Materials, 2022, 34, e2100096.	21.0	24
6	Allele-specific genomic data elucidate the role of somatic gain and copy-number neutral loss of heterozygosity in cancer. Cell Systems, 2022, 13, 183-193.e7.	6.2	13
7	Extracellular Matrix in Synthetic Hydrogelâ€Based Prostate Cancer Organoids Regulate Therapeutic Response to EZH2 and DRD2 Inhibitors (Adv. Mater. 2/2022). Advanced Materials, 2022, 34, .	21.0	0
8	Serial ctDNA analysis predicts clinical progression in patients with advanced urothelial carcinoma. British Journal of Cancer, 2022, 126, 430-439.	6.4	15
9	Collision tumors revealed by prospectively assessing subtype-defining molecular alterations in 904 individual prostate cancer foci. JCl Insight, 2022, 7, .	5.0	6
10	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522.	6.5	24
11	Histone 3 Methyltransferases Alter Melanoma Initiation and Progression Through Discrete Mechanisms. Frontiers in Cell and Developmental Biology, 2022, 10, 814216.	3.7	2
12	GCN2 kinase activation by ATP-competitive kinase inhibitors. Nature Chemical Biology, 2022, 18, 207-215.	8.0	19
13	Detecting Neuroendocrine Prostate Cancer Through Tissue-Informed Cell-Free DNA Methylation Analysis. Clinical Cancer Research, 2022, 28, 928-938.	7.0	29
14	Serial ctDNA evaluation to predict clinical progression in patients with advanced urothelial carcinoma Journal of Clinical Oncology, 2022, 40, 532-532.	1.6	0
15	Simple Linear Cancer Risk Prediction Models With Novel Features Outperform Complex Approaches. JCO Clinical Cancer Informatics, 2022, 6, e2100166.	2.1	2
16	Abstract P2-06-03: Obesity is associated with DNA damage in the breast epithelium of BRCA1 and BRCA2 mutation carriers: A role for estrogens & strategies for prevention. Cancer Research, 2022, 82, P2-06-03-P2-06-03.	0.9	0
17	Genomic instability is enriched in localized prostate cancers from men of African ancestry Journal of Clinical Oncology, 2022, 40, 270-270.	1.6	1
18	Abstract P2-06-04: Pathognomonic long molecule footprints of backup repair pathways in homologous recombination deficient cancers. Cancer Research, 2022, 82, P2-06-04-P2-06-04.	0.9	0

#	Article	IF	CITATIONS
19	Association of circulating tumor cell RB1 loss RNA signature with outcomes and immune phenotypes in men with mCRPC Journal of Clinical Oncology, 2022, 40, 139-139.	1.6	0
20	Abstract P5-05-02: Extracellular vesicles from obese human breast adipose tissue promote breast cancer cell proliferation by increasing mitochondrial mass and stimulating mitochondrial respiration. Cancer Research, 2022, 82, P5-05-02-P5-05-02.	0.9	0
21	Utility of multimodality molecular profiling for pediatric patients with central nervous system tumors. Neuro-Oncology Advances, 2022, 4, vdac031.	0.7	1
22	RET Fusion-Positive Papillary Thyroid Cancers are Associated with a More Aggressive Phenotype. Annals of Surgical Oncology, 2022, , 1.	1.5	8
23	The genomic landscape of metastatic clear cell renal cell carcinoma after systemic therapy. Molecular Oncology, 2022, 16, 2384-2395.	4.6	5
24	Global evolution of the tumor microenvironment associated with progression from preinvasive invasive to invasive human lung adenocarcinoma. Cell Reports, 2022, 39, 110639.	6.4	15
25	Molecular and Pharmacological Bladder Cancer Therapy Screening: Discovery of Clofarabine as a Highly Active Compound. European Urology, 2022, 82, 261-270.	1.9	11
26	Inflammatory responses in the placenta upon SARS-CoV-2 infection late in pregnancy. IScience, 2022, 25, 104223.	4.1	58
27	ASO Visual Abstract: RET Fusion-Positive Papillary Thyroid Cancers are Associated with a More Aggressive Phenotype. Annals of Surgical Oncology, 2022, , 1.	1.5	0
28	Inhibition of FGF receptor blocks adaptive resistance to RET inhibition in <i>CCDC6-RET</i> –rearranged thyroid cancer. Journal of Experimental Medicine, 2022, 219, .	8.5	6
29	The lactate-NAD+ axis activates cancer-associated fibroblasts by downregulating p62. Cell Reports, 2022, 39, 110792.	6.4	22
30	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. Cancer Cell, 2022, 40, 524-544.e5.	16.8	23
31	Tumor-immune microenvironment revealed by Imaging Mass Cytometry in a metastatic sarcomatoid urothelial carcinoma with a prolonged response to pembrolizumab Cold Spring Harbor Molecular Case Studies, 2022, 8, .	1.0	6
32	Alterations in transcriptional networks in cancer: the role of noncoding somatic driver mutations. Current Opinion in Genetics and Development, 2022, 75, 101919.	3.3	2
33	Tumor-induced double positive T cells display distinct lineage commitment mechanisms and functions. Journal of Experimental Medicine, 2022, 219, .	8.5	8
34	LGG-47. Single-cell RNA Sequencing Reveals Immunosuppressive Myeloid Cell Diversity During Malignant Progression in Glioma. Neuro-Oncology, 2022, 24, i99-i99.	1.2	0
35	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	17.5	38
36	Gain of Chromosome 1q Perturbs a Competitive Endogenous RNA Network to Promote Melanoma Metastasis. Cancer Research, 2022, 82, 3016-3031.	0.9	2

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37	Mutation landscape, clonal evolution pattern, and potential pathogenic pathways in B-lymphoblastic transformation of follicular lymphoma. Leukemia, 2021, 35, 1203-1208.	7.2	8
38	Integration of whole-exome and anchored PCR-based next generation sequencing significantly increases detection of actionable alterations in precision oncology. Translational Oncology, 2021, 14, 100944.	3.7	10
39	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. Nature, 2021, 589, 299-305.	27.8	155
40	Leveraging phenotypic variability to identify genetic interactions in human phenotypes. American Journal of Human Genetics, 2021, 108, 49-67.	6.2	36
41	Limitations of Detecting Genetic Variants from the RNA Sequencing Data in Tissue and Fine-Needle Aspiration Samples. Thyroid, 2021, 31, 589-595.	4.5	19
42	Building biorepositories in the midst of a pandemic. Journal of Clinical and Translational Science, 2021, 5, e92.	0.6	8
43	Chemical systems biology reveals mechanisms of glucocorticoid receptor signaling. Nature Chemical Biology, 2021, 17, 307-316.	8.0	11
44	Single-cell DNA targeted sequencing (scDNA-seq) to test therapeutic vulnerabilities in urothelial cancer (UC) patient-derived organoids (PDO) Journal of Clinical Oncology, 2021, 39, 464-464.	1.6	0
45	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
46	Toward Artificial Intelligence–Driven Pathology Assessment for Hematologic Malignancies. Blood Cancer Discovery, 2021, 2, 195-197.	5.0	3
47	Genome-wide investigation identifies a rare copy-number variant burden associated with human spina bifida. Genetics in Medicine, 2021, 23, 1211-1218.	2.4	10
48	FSMP-10. CYSTEINE INDUCES CYTOTOXICITY IN GLIOBLASTOMA THROUGH MITOCHONDRIAL HYDROGEN PEROXIDE PRODUCTION. Neuro-Oncology Advances, 2021, 3, i18-i18.	0.7	0
49	The road from Rous sarcoma virus to precision medicine. Journal of Experimental Medicine, 2021, 218, .	8.5	3
50	The spatial landscape of lung pathology during COVID-19 progression. Nature, 2021, 593, 564-569.	27.8	249
51	RNA-sequencing data-driven dissection of human plasma cell differentiation reveals new potential transcription regulators. Leukemia, 2021, 35, 1451-1462.	7.2	30
52	A molecular single-cell lung atlas of lethal COVID-19. Nature, 2021, 595, 114-119.	27.8	411
53	QSER1 protects DNA methylation valleys from de novo methylation. Science, 2021, 372, .	12.6	69
54	Abstract PO-036: Immunological characterization of mouse HR+ mammary tumors relapsing after		0

radiation therapy., 2021, , .

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55	Abstract PO-051: Radiation therapy enhances the presentation of phosphopeptides by MHC-I on cancer cells. , 2021, , .		0
56	Artificial Intelligence in Cancer Research and Precision Medicine. Cancer Discovery, 2021, 11, 900-915.	9.4	209
57	Discovery of Candidate DNA Methylation Cancer Driver Genes. Cancer Discovery, 2021, 11, 2266-2281.	9.4	42
58	Deep learning predicts chromosomal instability from histopathology images. IScience, 2021, 24, 102394.	4.1	29
59	Leptin Mediates Obesity-Induced DNA Damage in BRCA1 Breast Epithelial Cells. Journal of the Endocrine Society, 2021, 5, A1024-A1024.	0.2	0
60	Temporal evolution of cellular heterogeneity during the progression to advanced AR-negative prostate cancer. Nature Communications, 2021, 12, 3372.	12.8	45
61	Characterization of GECPAR, a noncoding RNA that regulates the transcriptional program of diffuse large B cell lymphoma. Haematologica, 2021, , .	3.5	3
62	Blood biomarkers reflect the effects of obesity and inflammation on the human breast transcriptome. Carcinogenesis, 2021, 42, 1281-1292.	2.8	5
63	Diet-regulated production of PDGFcc by macrophages controls energy storage. Science, 2021, 373, .	12.6	84
64	Functional comparison of exome capture-based methods for transcriptomic profiling of formalin-fixed paraffin-embedded tumors. Npj Genomic Medicine, 2021, 6, 66.	3.8	8
65	Validation of a Circulating Tumor <scp>DNA</scp> -Based <scp>Next-Generation</scp> Sequencing Assay in a Cohort of Patients with Solid tumors: A Proposed Solution for Decentralized Plasma Testing. Oncologist, 2021, 26, e1971-e1981.	3.7	11
66	The role of machine learning in clinical research: transforming the future of evidence generation. Trials, 2021, 22, 537.	1.6	82
67	Artificial intelligence in cancer research, diagnosis and therapy. Nature Reviews Cancer, 2021, 21, 747-752.	28.4	87
68	OCT2 pre-positioning facilitates cell fate transition and chromatin architecture changes in humoral immunity. Nature Immunology, 2021, 22, 1327-1340.	14.5	11
69	Reshaping of the androgen-driven chromatin landscape in normal prostate cells by early cancer drivers and effect on therapeutic sensitivity. Cell Reports, 2021, 36, 109625.	6.4	22
70	Cohesin Core Complex Gene Dosage Contributes to Germinal Center Derived Lymphoma Phenotypes and Outcomes. Frontiers in Immunology, 2021, 12, 688493.	4.8	5
71	RNA-Sequencing-Based Transcriptomic Score with Prognostic and Theranostic Values in Multiple Myeloma. Journal of Personalized Medicine, 2021, 11, 988.	2.5	6
72	Dissecting bulk transcriptomes of diffuse large B cell lymphoma. Cancer Cell, 2021, 39, 1305-1307.	16.8	2

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73	The NF-κB Transcriptional Footprint Is Essential for SARS-CoV-2 Replication. Journal of Virology, 2021, 95, e0125721.	3.4	69
74	A polygenic-score-based approach for identification of gene-drug interactions stratifying breast cancer risk. American Journal of Human Genetics, 2021, 108, 1752-1764.	6.2	7
75	Multi-platform profiling characterizes molecular subgroups and resistance networks in chronic lymphocytic leukemia. Nature Communications, 2021, 12, 5395.	12.8	15
76	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. Nature Immunology, 2021, 22, 240-253.	14.5	24
77	Metastasis and Immune Evasion from Extracellular cGAMP Hydrolysis. Cancer Discovery, 2021, 11, 1212-1227.	9.4	139
78	Profiling of immune dysfunction in COVID-19 patients allows early prediction of disease progression. Life Science Alliance, 2021, 4, e202000955.	2.8	56
79	CLIP-170S is a microtubuleÂ+TIP variant that confers resistance to taxanes by impairing drug-target engagement. Developmental Cell, 2021, 56, 3264-3275.e7.	7.0	5
80	Prediction of primary venous thromboembolism based on clinical and genetic factors within the U.K. Biobank. Scientific Reports, 2021, 11, 21340.	3.3	7
81	Dynamic Immune Surveillance in Durable Clinical Response to Combined BTK and BCL2 Inhibition in MCL at Longitudinal Single-Cell Resolution. Blood, 2021, 138, 1323-1323.	1.4	0
82	Selective STAT3 Degraders Dissect Peripheral T-Cell Lymphomas Vulnerabilities Empowering Personalized Regimens. Blood, 2021, 138, 865-865.	1.4	0
83	Single Cell ATAC Lineage Deconvolution Reveals Overlapping Subclones in Epigenetically Distinct AML Samples. Blood, 2021, 138, 2381-2381.	1.4	0
84	BTG1 Mutation Promotes Aggressive Lymphoma Development By Lowering the Threshold to MYC Activation and Generating "Super-Competitor" B Cells. Blood, 2021, 138, 359-359.	1.4	2
85	Molecular Evolution of Classical Hodgkin Lymphoma Revealed Though Whole Genome Sequencing of Hodgkin and Reed-Sternberg Cells. Blood, 2021, 138, 805-805.	1.4	1
86	HHV-6 in the Lymphoma Microenvironment: Both Chicken and Egg?. Blood, 2021, 138, 1377-1377.	1.4	0
87	High Rates of Remission with the Initial Treatment of Oral Azacitidine Plus CHOP for Peripheral T-Cell Lymphoma (PTCL): Clinical Outcomes and Biomarker Analysis of a Multi-Center Phase II Study. Blood, 2021, 138, 138-138.	1.4	5
88	285â€Breaking through the resistance of breast cancer to immune checkpoint blockers in a unique mouse model of HR+ disease. , 2021, 9, A309-A309.		0
89	FOXO1 Dependent Transcription Network Is a Targetable Vulnerability of Mantle Cell Lymphoma. Blood, 2021, 138, 30-30.	1.4	0
90	A Predictive Endothelial-Leukemia Pre-Clinical Platform to Uncover Drug Vulnerabilities for Personalized Treatments. Blood, 2021, 138, 704-704.	1.4	0

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91	Metabolic and Immune Markers for Precise Monitoring of COVID-19 Severity and Treatment. Frontiers in Immunology, 2021, 12, 809937.	4.8	13
92	Stage-specific regulation of DNA methylation by TET enzymes during human cardiac differentiation. Cell Reports, 2021, 37, 110095.	6.4	10
93	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
94	Pan-cancer analysis reveals molecular patterns associated with age. Cell Reports, 2021, 37, 110100.	6.4	26
95	Graph convolutional networks for computational drug development and discovery. Briefings in Bioinformatics, 2020, 21, 919-935.	6.5	227
96	Differential Contributions of Pre- and Post-EMT Tumor Cells in Breast Cancer Metastasis. Cancer Research, 2020, 80, 163-169.	0.9	62
97	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	28.9	141
98	High-resolution mouse subventricular zone stem-cell niche transcriptome reveals features of lineage, anatomy, and aging. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31448-31458.	7.1	39
99	Unique Immune Cell Coactivators Specify Locus Control Region Function and Cell Stage. Molecular Cell, 2020, 80, 845-861.e10.	9.7	21
100	Common germline-somatic variant interactions in advanced urothelial cancer. Nature Communications, 2020, 11, 6195.	12.8	21
101	Selective dysregulation of ROCK2 activity promotes aberrant transcriptional networks in ABC diffuse large B-cell lymphoma. Scientific Reports, 2020, 10, 13094.	3.3	8
102	A machine learning and network framework to discover new indications for small molecules. PLoS Computational Biology, 2020, 16, e1008098.	3.2	8
103	Single-cell profiling reveals an endothelium-mediated immunomodulatory pathway in the eye choroid. Journal of Experimental Medicine, 2020, 217, .	8.5	55
104	Adaptable haemodynamic endothelial cells for organogenesis and tumorigenesis. Nature, 2020, 585, 426-432.	27.8	145
105	Precision medicine and artificial intelligence: overview and relevance to reproductive medicine. Fertility and Sterility, 2020, 114, 908-913.	1.0	16
106	Predictive modeling in reproductive medicine: Where will the future of artificial intelligence research take us?. Fertility and Sterility, 2020, 114, 934-940.	1.0	27
107	Identification of Distinct Heterogenic Subtypes and Molecular Signatures Associated with African Ancestry in Triple Negative Breast Cancer Using Quantified Genetic Ancestry Models in Admixed Race Populations. Cancers, 2020, 12, 1220.	3.7	19
108	Demographic and genetic factors influence the abundance of infiltrating immune cells in human tissues. Nature Communications, 2020, 11, 2213.	12.8	23

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109	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
110	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. Cancer Cell, 2020, 37, 655-673.e11.	16.8	93
111	Lineage Reversion Drives WNT Independence in Intestinal Cancer. Cancer Discovery, 2020, 10, 1590-1609.	9.4	52
112	The INPP4B Tumor Suppressor Modulates EGFR Trafficking and Promotes Triple-Negative Breast Cancer. Cancer Discovery, 2020, 10, 1226-1239.	9.4	32
113	Single-Cell Analysis of the Muscle Stem Cell Hierarchy Identifies Heterotypic Communication Signals Involved in Skeletal Muscle Regeneration. Cell Reports, 2020, 30, 3583-3595.e5.	6.4	227
114	SLFN11 Expression in Advanced Prostate Cancer and Response to Platinum-based Chemotherapy. Molecular Cancer Therapeutics, 2020, 19, 1157-1164.	4.1	44
115	Computational methods in tumor immunology. Methods in Enzymology, 2020, 636, 209-259.	1.0	3
116	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
117	Tumor Microenvironment Is Critical for the Maintenance of Cellular States Found in Primary Glioblastomas. Cancer Discovery, 2020, 10, 964-979.	9.4	102
118	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. Cell, 2020, 182, 297-316.e27.	28.9	63
119	Small Cell Carcinoma of the Ovary, Hypercalcemic Type (SCCOHT) beyond SMARCA4 Mutations: A Comprehensive Genomic Analysis. Cells, 2020, 9, 1496.	4.1	29
120	Multicenter Phase II Study of Cabazitaxel in Advanced Gastroesophageal Cancer: Association of HER2 Expression and M2-Like Tumor-Associated Macrophages with Patient Outcome. Clinical Cancer Research, 2020, 26, 4756-4766.	7.0	7
121	A reference single-cell transcriptomic atlas of human skeletal muscle tissue reveals bifurcated muscle stem cell populations. Skeletal Muscle, 2020, 10, 19.	4.2	121
122	The aging skin microenvironment dictates stem cell behavior. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5339-5350.	7.1	101
123	Inhibition of EZH2 Catalytic Activity Selectively Targets a Metastatic Subpopulation in Triple-Negative Breast Cancer. Cell Reports, 2020, 30, 755-770.e6.	6.4	65
124	Stable reduction of STARD4 alters cholesterol regulation and lipid homeostasis. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2020, 1865, 158609.	2.4	14
125	Integrative multiplatform molecular profiling of benign prostatic hyperplasia identifies distinct subtypes. Nature Communications, 2020, 11, 1987.	12.8	29
126	Epithelial plasticity can generate multi-lineage phenotypes in human and murine bladder cancers. Nature Communications, 2020, 11, 2540.	12.8	40

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127	The future of precision medicine: towards a more predictive personalized medicine. Emerging Topics in Life Sciences, 2020, 4, 175-177.	2.6	31
128	Urinary Cell Transcriptome Profiling and Identification of ITM2A, SLAMF6, and IKZF3 as Biomarkers of Acute Rejection in Human Kidney Allografts. Transplantation Direct, 2020, 6, e588.	1.6	8
129	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. Journal of Clinical Investigation, 2020, 130, 1653-1668.	8.2	122
130	Clinical, regional, and genetic characteristics of Covid-19 patients from UK Biobank. PLoS ONE, 2020, 15, e0241264.	2.5	40
131	Performance Characteristics of a Targeted Sequencing Platform for Simultaneous Detection of Single Nucleotide Variants, Insertions/Deletions, Copy Number Alterations, and Gene Fusions in Cancer Genome. Archives of Pathology and Laboratory Medicine, 2020, 144, 1535-1546.	2.5	10
132	EXTH-74. IND-ENABLING CHARACTERIZATION OF DUAL DRD2- AND ClpP-TARGETING AGENT ONC206 AS THE NEXT IMIPRIDONE FOR CLINICAL NEURO-ONCOLOGY. Neuro-Oncology, 2020, 22, ii103-ii103.	1.2	2
133	Robust Discovery of Candidate DNA Methylation Cancer Drivers. Blood, 2020, 136, 33-34.	1.4	0
134	TAMI-38. CYSTEINE-PROMOTING COMPOUNDS INDUCE MITOCHONDRIAL TOXICITY IN GLIOBLASTOMA THROUGH ALTERED PYRUVATE AND SERINE METABOLISM. Neuro-Oncology, 2020, 22, ii221-ii221.	1.2	0
135	Obesity-Associated Extracellular Matrix Remodeling Promotes a Macrophage Phenotype Similar to Tumor-Associated Macrophages. American Journal of Pathology, 2019, 189, 2019-2035.	3.8	62
136	The Missing Pieces of Artificial Intelligence in Medicine. Trends in Pharmacological Sciences, 2019, 40, 555-564.	8.7	46
137	Upper tract urothelial carcinoma has a luminal-papillary T-cell depleted contexture and activated FGFR3 signaling. Nature Communications, 2019, 10, 2977.	12.8	140
138	Artificial intelligence: its applications in reproductive medicine and the assisted reproductive technologies. Fertility and Sterility, 2019, 112, 28-30.	1.0	34
139	3055 Reconstruction of Patient-specific Distal Airway Regeneration Patterns in COPD. Journal of Clinical and Translational Science, 2019, 3, 154-154.	0.6	0
140	Organotypic tumor slice cultures provide a versatile platform for immuno-oncology and drug discovery. Oncolmmunology, 2019, 8, e1670019.	4.6	51
141	Exploring tumor clonal evolution in bone marrow of patients with diffuse large B-cell lymphoma by deep IGH sequencing and its potential relevance in relapse. Blood Cancer Journal, 2019, 9, 69.	6.2	4
142	Clinical features of neuroendocrine prostate cancer. European Journal of Cancer, 2019, 121, 7-18.	2.8	195
143	Cancer-Specific Thresholds Adjust for Whole Exome Sequencing–Based Tumor Mutational Burden Distribution. JCO Precision Oncology, 2019, 3, 1-12.	3.0	21
144	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. JCO Precision Oncology, 2019, 3, 1-12.	3.0	24

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145	The Transcriptional Regulator Sin3A Contributes to the Oncogenic Potential of STAT3. Cancer Research, 2019, 79, 3076-3087.	0.9	30
146	Imipridone ONC212 activates orphan G protein-coupled receptor GPR132 and integrated stress response in acute myeloid leukemia. Leukemia, 2019, 33, 2805-2816.	7.2	47
147	Radiation therapy and anti-tumor immunity: exposing immunogenic mutations to the immune system. Genome Medicine, 2019, 11, 40.	8.2	179
148	Function and clinical relevance of RHAMM isoforms in pancreatic tumor progression. Molecular Cancer, 2019, 18, 92.	19.2	33
149	A Recurrent Activating Missense Mutation in Waldenström Macroglobulinemia Affects the DNA Binding of the ETS Transcription Factor SPI1 and Enhances Proliferation. Cancer Discovery, 2019, 9, 796-811.	9.4	30
150	Dynamic transcriptome profiles within spermatogonial and spermatocyte populations during postnatal testis maturation revealed by single-cell sequencing. PLoS Genetics, 2019, 15, e1007810.	3.5	80
151	Comprehensive characterization of the mutational landscape in multiple myeloma cell lines reveals potential drivers and pathways associated with tumor progression and drug resistance. Theranostics, 2019, 9, 540-553.	10.0	49
152	Precision Targeting with EZH2 and HDAC Inhibitors in Epigenetically Dysregulated Lymphomas. Clinical Cancer Research, 2019, 25, 5271-5283.	7.0	59
153	CHD1 Loss Alters AR Binding at Lineage-Specific Enhancers and Modulates Distinct Transcriptional Programs to Drive Prostate Tumorigenesis. Cancer Cell, 2019, 35, 603-617.e8.	16.8	70
154	Deep learning enables robust assessment and selection of human blastocysts after in vitro fertilization. Npj Digital Medicine, 2019, 2, 21.	10.9	246
155	Generation of pulmonary neuroendocrine cells and SCLC-like tumors from human embryonic stem cells. Journal of Experimental Medicine, 2019, 216, 674-687.	8.5	68
156	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. Nature Communications, 2019, 10, 821.	12.8	73
157	A Bayesian machine learning approach for drug target identification using diverse data types. Nature Communications, 2019, 10, 5221.	12.8	156
158	EXTH-71. IND-ENABLING CHARACTERIZATION OF ONC206 AS THE NEXT BITOPIC DRD2 ANTAGONIST FOR NEURO-ONCOLOGY. Neuro-Oncology, 2019, 21, vi97-vi97.	1.2	1
159	Deep learning-based classification of mesothelioma improves prediction of patient outcome. Nature Medicine, 2019, 25, 1519-1525.	30.7	332
160	Dopamine Receptor D5 is a Modulator of Tumor Response to Dopamine Receptor D2 Antagonism. Clinical Cancer Research, 2019, 25, 2305-2313.	7.0	43
161	Drug-Induced Expression-Based Computational Repurposing of Small Molecules Affecting Transcription Factor Activity. Methods in Molecular Biology, 2019, 1903, 179-184.	0.9	2
162	Revisiting the initial steps of sexual development in the malaria parasite Plasmodium falciparum. Nature Microbiology, 2019, 4, 144-154.	13.3	95

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163	Prostaglandin E2 down-regulates sirtuin 1 (SIRT1), leading to elevated levels of aromatase, providing insights into the obesity–breast cancer connection. Journal of Biological Chemistry, 2019, 294, 361-371.	3.4	18
164	Predicting peptide presentation by major histocompatibility complex class I: an improved machine learning approach to the immunopeptidome. BMC Bioinformatics, 2019, 20, 7.	2.6	45
165	Epigenetic analysis identifies factors driving racial disparity in prostate cancer. Cancer Reports, 2019, 2, e1153.	1.4	11
166	TETs Regulate Proepicardial Cell Migration through Extracellular Matrix Organization during Zebrafish Cardiogenesis. Cell Reports, 2019, 26, 720-732.e4.	6.4	22
167	N-Myc–mediated epigenetic reprogramming drives lineage plasticity in advanced prostate cancer. Journal of Clinical Investigation, 2019, 129, 3924-3940.	8.2	115
168	Clinical and molecular analysis of patients treated with prostate-specific membrane antigen (PSMA)-targeted radionuclide therapy Journal of Clinical Oncology, 2019, 37, 272-272.	1.6	8
169	UCHL1 loss alters the cell cycle in metastatic pancreatic neuroendocrine tumors. Endocrine-Related Cancer, 2019, 26, 411-423.	3.1	17
170	Oncogenic Addiction to ERBB2 Signaling Predicts Response to Trastuzumab in Urothelial Cancer. Journal of the National Comprehensive Cancer Network: JNCCN, 2019, 17, 194-200.	4.9	6
171	The genomic landscape of metastatic clear cell renal cell carcinoma (ccRCC) after treatment with systemic therapy Journal of Clinical Oncology, 2019, 37, 675-675.	1.6	Ο
172	SAT-339 Cross-Talk with Breast Adipose Tissue Contributes to Obesity-induced DNA Damage in BRCA Mutant Breast Epithelial Cells. Journal of the Endocrine Society, 2019, 3, .	0.2	0
173	Heterogeneous Genetic Alterations and Novel Pathogenic Pathways in Relapsed DLBCL Revealed By Whole Exome Sequencing. Blood, 2019, 134, 2770-2770.	1.4	0
174	The DNA Helicase Hells Is a New Unconventional Player in ALK- Anaplastic Large Cell Lymphoma Biology. Blood, 2019, 134, 1477-1477.	1.4	0
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