

# Olivier Elemento

## List of Publications by Year in descending order

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Version: 2024-02-01

370  
papers

39,756  
citations

3531

90  
h-index

3323

184  
g-index

402  
all docs

402  
docs citations

402  
times ranked

57289  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and near Stop Codons. <i>Cell</i> , 2012, 149, 1635-1646.	28.9	3,152
2	Integrative Clinical Genomics of Advanced Prostate Cancer. <i>Cell</i> , 2015, 161, 1215-1228.	28.9	2,660
3	5' UTR m6A Promotes Cap-Independent Translation. <i>Cell</i> , 2015, 163, 999-1010.	28.9	1,414
4	Double-stranded DNA in exosomes: a novel biomarker in cancer detection. <i>Cell Research</i> , 2014, 24, 766-769.	12.0	1,282
5	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , 2016, 375, 443-453.	27.0	1,205
6	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. <i>Nature Medicine</i> , 2016, 22, 298-305.	30.7	1,193
7	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	28.9	1,107
8	Chromosomal instability drives metastasis through a cytosolic DNA response. <i>Nature</i> , 2018, 553, 467-472.	27.8	1,002
9	Reversible methylation of m6Am in the 5' cap controls mRNA stability. <i>Nature</i> , 2017, 541, 371-375.	27.8	797
10	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
11	Personalized <i>In Vitro</i> and <i>In Vivo</i> Cancer Models to Guide Precision Medicine. <i>Cancer Discovery</i> , 2017, 7, 462-477.	9.4	735
12	Vitamin C selectively kills <i>KRAS</i> and <i>BRAF</i> mutant colorectal cancer cells by targeting GAPDH. <i>Science</i> , 2015, 350, 1391-1396.	12.6	722
13	EZH2 Is Required for Germinal Center Formation and Somatic EZH2 Mutations Promote Lymphoid Transformation. <i>Cancer Cell</i> , 2013, 23, 677-692.	16.8	706
14	Molecular Signatures of Tissue-Specific Microvascular Endothelial Cell Heterogeneity in Organ Maintenance and Regeneration. <i>Developmental Cell</i> , 2013, 26, 204-219.	7.0	548
15	The oestrogen receptor alpha-regulated lncRNA NEAT1 is a critical modulator of prostate cancer. <i>Nature Communications</i> , 2014, 5, 5383.	12.8	522
16	The fat mass and obesity associated gene ( <i>Fto</i> ) regulates activity of the dopaminergic midbrain circuitry. <i>Nature Neuroscience</i> , 2013, 16, 1042-1048.	14.8	414
17	A molecular single-cell lung atlas of lethal COVID-19. <i>Nature</i> , 2021, 595, 114-119.	27.8	411
18	N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. <i>Cancer Cell</i> , 2016, 30, 563-577.	16.8	394

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19	The histone lysine methyltransferase KMT2D sustains a gene expression program that represses B cell lymphoma development. <i>Nature Medicine</i> , 2015, 21, 1199-1208.	30.7	359
20	Phenotype, penetrance, and treatment of 133 cytotoxic T-lymphocyte antigen 4-insufficient subjects. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1932-1946.	2.9	344
21	Deep learning-based classification of mesothelioma improves prediction of patient outcome. <i>Nature Medicine</i> , 2019, 25, 1519-1525.	30.7	332
22	The BRAF Pseudogene Functions as a Competitive Endogenous RNA and Induces Lymphoma In Vivo. <i>Cell</i> , 2015, 161, 319-332.	28.9	293
23	Flow sorting and exome sequencing reveal the oncogenome of primary Hodgkin and Reed-Sternberg cells. <i>Blood</i> , 2015, 125, 1061-1072.	1.4	281
24	A Universal Framework for Regulatory Element Discovery across All Genomes and Data Types. <i>Molecular Cell</i> , 2007, 28, 337-350.	9.7	277
25	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. <i>JAMA Oncology</i> , 2015, 1, 466.	7.1	264
26	EZH2-mediated epigenetic silencing in germinal center B cells contributes to proliferation and lymphomagenesis. <i>Blood</i> , 2010, 116, 5247-5255.	1.4	262
27	Stem Cell Lineage Infidelity Drives Wound Repair and Cancer. <i>Cell</i> , 2017, 169, 636-650.e14.	28.9	255
28	Obesity-dependent changes in interstitial ECM mechanics promote breast tumorigenesis. <i>Science Translational Medicine</i> , 2015, 7, 301ra130.	12.4	252
29	Synergistic Activation of Inflammatory Cytokine Genes by Interferon- $\gamma$ -Induced Chromatin Remodeling and Toll-like Receptor Signaling. <i>Immunity</i> , 2013, 39, 454-469.	14.3	250
30	Clonal evolution of chemotherapy-resistant urothelial carcinoma. <i>Nature Genetics</i> , 2016, 48, 1490-1499.	21.4	250
31	The spatial landscape of lung pathology during COVID-19 progression. <i>Nature</i> , 2021, 593, 564-569.	27.8	249
32	Cell-Cycle Reprogramming for PI3K Inhibition Overrides a Relapse-Specific C481S BTK Mutation Revealed by Longitudinal Functional Genomics in Mantle Cell Lymphoma. <i>Cancer Discovery</i> , 2014, 4, 1022-1035.	9.4	247
33	Patient derived organoids to model rare prostate cancer phenotypes. <i>Nature Communications</i> , 2018, 9, 2404.	12.8	246
34	Deep learning enables robust assessment and selection of human blastocysts after in vitro fertilization. <i>Npj Digital Medicine</i> , 2019, 2, 21.	10.9	246
35	Unmasking Activation of the Zygotic Genome Using Chromosomal Deletions in the <i>Drosophila</i> Embryo. <i>PLoS Biology</i> , 2007, 5, e117.	5.6	241
36	Deep Convolutional Neural Networks Enable Discrimination of Heterogeneous Digital Pathology Images. <i>EBioMedicine</i> , 2018, 27, 317-328.	6.1	240

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37	Graph convolutional networks for computational drug development and discovery. <i>Briefings in Bioinformatics</i> , 2020, 21, 919-935.	6.5	227
38	Single-Cell Analysis of the Muscle Stem Cell Hierarchy Identifies Heterotypic Communication Signals Involved in Skeletal Muscle Regeneration. <i>Cell Reports</i> , 2020, 30, 3583-3595.e5.	6.4	227
39	Identification and Genome-Wide Prediction of DNA Binding Specificities for the ApiAP2 Family of Regulators from the Malaria Parasite. <i>PLoS Pathogens</i> , 2010, 6, e1001165.	4.7	226
40	<i>CREBBP</i> Inactivation Promotes the Development of HDAC3-Dependent Lymphomas. <i>Cancer Discovery</i> , 2017, 7, 38-53.	9.4	218
41	Efficient Direct Reprogramming of Mature Amniotic Cells into Endothelial Cells by ETS Factors and TGF $\beta$ 2 Suppression. <i>Cell</i> , 2012, 151, 559-575.	28.9	212
42	Reprogramming human endothelial cells to haematopoietic cells requires vascular induction. <i>Nature</i> , 2014, 511, 312-318.	27.8	211
43	Artificial Intelligence in Cancer Research and Precision Medicine. <i>Cancer Discovery</i> , 2021, 11, 900-915.	9.4	209
44	The BCL6 transcriptional program features repression of multiple oncogenes in primary B cells and is deregulated in DLBCL. <i>Blood</i> , 2009, 113, 5536-5548.	1.4	205
45	Differentiation of human pluripotent stem cells to cells similar to cord-blood endothelial colony-forming cells. <i>Nature Biotechnology</i> , 2014, 32, 1151-1157.	17.5	203
46	EZH2 and BCL6 Cooperate to Assemble CBX8-BCOR Complex to Repress Bivalent Promoters, Mediate Germinal Center Formation and Lymphomagenesis. <i>Cancer Cell</i> , 2016, 30, 197-213.	16.8	200
47	Clinical features of neuroendocrine prostate cancer. <i>European Journal of Cancer</i> , 2019, 121, 7-18.	2.8	195
48	Revealing Global Regulatory Perturbations across Human Cancers. <i>Molecular Cell</i> , 2009, 36, 900-911.	9.7	193
49	Conversion of adult endothelium to immunocompetent haematopoietic stem cells. <i>Nature</i> , 2017, 545, 439-445.	27.8	191
50	Single-cell RNA sequencing reveals a signature of sexual commitment in malaria parasites. <i>Nature</i> , 2017, 551, 95-99.	27.8	189
51	Radiation therapy and anti-tumor immunity: exposing immunogenic mutations to the immune system. <i>Genome Medicine</i> , 2019, 11, 40.	8.2	179
52	Histone Methyltransferase MMSET/NSD2 Alters EZH2 Binding and Reprograms the Myeloma Epigenome through Global and Focal Changes in H3K36 and H3K27 Methylation. <i>PLoS Genetics</i> , 2014, 10, e1004566.	3.5	178
53	A Hybrid Mechanism of Action for BCL6 in B Cells Defined by Formation of Functionally Distinct Complexes at Enhancers and Promoters. <i>Cell Reports</i> , 2013, 4, 578-588.	6.4	161
54	TET proteins safeguard bivalent promoters from de novo methylation in human embryonic stem cells. <i>Nature Genetics</i> , 2018, 50, 83-95.	21.4	156

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55	A Bayesian machine learning approach for drug target identification using diverse data types. <i>Nature Communications</i> , 2019, 10, 5221.	12.8	156
56	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	27.8	155
57	A Data-Driven Approach to Predicting Successes and Failures of Clinical Trials. <i>Cell Chemical Biology</i> , 2016, 23, 1294-1301.	5.2	154
58	A Predictive Model for Selective Targeting of the Warburg Effect through GAPDH Inhibition with a Natural Product. <i>Cell Metabolism</i> , 2017, 26, 648-659.e8.	16.2	154
59	Lymphatic endothelial S1P promotes mitochondrial function and survival in naive T cells. <i>Nature</i> , 2017, 546, 158-161.	27.8	153
60	Epigenetic Repression of miR-31 Disrupts Androgen Receptor Homeostasis and Contributes to Prostate Cancer Progression. <i>Cancer Research</i> , 2013, 73, 1232-1244.	0.9	150
61	Using transcriptome sequencing to identify mechanisms of drug action and resistance. <i>Nature Chemical Biology</i> , 2012, 8, 235-237.	8.0	148
62	Adaptable haemodynamic endothelial cells for organogenesis and tumorigenesis. <i>Nature</i> , 2020, 585, 426-432.	27.8	145
63	NFIB is a governor of epithelial melanocyte stem cell behaviour in a shared niche. <i>Nature</i> , 2013, 495, 98-102.	27.8	144
64	Oncogene-mediated alterations in chromatin conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9083-9088.	7.1	142
65	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	28.9	141
66	A Panel of Four miRNAs Accurately Differentiates Malignant from Benign Indeterminate Thyroid Lesions on Fine Needle Aspiration. <i>Clinical Cancer Research</i> , 2012, 18, 2032-2038.	7.0	140
67	Upper tract urothelial carcinoma has a luminal-papillary T-cell depleted contexture and activated FGFR3 signaling. <i>Nature Communications</i> , 2019, 10, 2977.	12.8	140
68	Metastasis and Immune Evasion from Extracellular cGAMP Hydrolysis. <i>Cancer Discovery</i> , 2021, 11, 1212-1227.	9.4	139
69	DNA methylation signatures define molecular subtypes of diffuse large B-cell lymphoma. <i>Blood</i> , 2010, 116, e81-e89.	1.4	138
70	Deep Sequencing of T-cell Receptor DNA as a Biomarker of Clonally Expanded TILs in Breast Cancer after Immunotherapy. <i>Cancer Immunology Research</i> , 2016, 4, 835-844.	3.4	138
71	Transcriptome Analysis of Individual Stromal Cell Populations Identifies Stroma-Tumor Crosstalk in Mouse Lung Cancer Model. <i>Cell Reports</i> , 2015, 10, 1187-1201.	6.4	137
72	A stable transcription factor complex nucleated by oligomeric AML1-ETO controls leukaemogenesis. <i>Nature</i> , 2013, 500, 93-97.	27.8	134

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73	Mechanosensitive pannexin-1 channels mediate microvascular metastatic cell survival. <i>Nature Cell Biology</i> , 2015, 17, 943-952.	10.3	134
74	Rationally designed BCL6 inhibitors target activated B cell diffuse large B cell lymphoma. <i>Journal of Clinical Investigation</i> , 2016, 126, 3351-3362.	8.2	133
75	EZH2 enables germinal centre formation through epigenetic silencing of CDKN1A and an Rb-E2F1 feedback loop. <i>Nature Communications</i> , 2017, 8, 877.	12.8	132
76	Selective inhibition of protein arginine methyltransferase 5 blocks initiation and maintenance of B-cell transformation. <i>Blood</i> , 2015, 125, 2530-2543.	1.4	125
77	DNA methyltransferase 1 and DNA methylation patterning contribute to germinal center B-cell differentiation. <i>Blood</i> , 2011, 118, 3559-3569.	1.4	123
78	Widespread Mitotic Bookmarking by Histone Marks and Transcription Factors in Pluripotent Stem Cells. <i>Cell Reports</i> , 2017, 19, 1283-1293.	6.4	122
79	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 1653-1668.	8.2	122
80	A reference single-cell transcriptomic atlas of human skeletal muscle tissue reveals bifurcated muscle stem cell populations. <i>Skeletal Muscle</i> , 2020, 10, 19.	4.2	121
81	TET2 Deficiency Causes Germinal Center Hyperplasia, Impairs Plasma Cell Differentiation, and Promotes B-cell Lymphomagenesis. <i>Cancer Discovery</i> , 2018, 8, 1632-1653.	9.4	120
82	Broad Targeting Specificity during Bacterial Type III CRISPR-Cas Immunity Constrains Viral Escape. <i>Cell Host and Microbe</i> , 2017, 22, 343-353.e3.	11.0	118
83	N-Myc-mediated epigenetic reprogramming drives lineage plasticity in advanced prostate cancer. <i>Journal of Clinical Investigation</i> , 2019, 129, 3924-3940.	8.2	115
84	Multi-tiered Reorganization of the Genome during B Cell Affinity Maturation Anchored by a Germinal Center-Specific Locus Control Region. <i>Immunity</i> , 2016, 45, 497-512.	14.3	112
85	Cabozantinib Eradicates Advanced Murine Prostate Cancer by Activating Antitumor Innate Immunity. <i>Cancer Discovery</i> , 2017, 7, 750-765.	9.4	112
86	Epigenomic evolution in diffuse large B-cell lymphomas. <i>Nature Communications</i> , 2015, 6, 6921.	12.8	111
87	Discovery and clinical introduction of first-in-class imipridone ONC201. <i>Oncotarget</i> , 2016, 7, 74380-74392.	1.8	111
88	DrugTargetSeqR: a genomics- and CRISPR-Cas9-based method to analyze drug targets. <i>Nature Chemical Biology</i> , 2014, 10, 626-628.	8.0	110
89	Deficiency of UBE2T, the E2 Ubiquitin Ligase Necessary for FANCD2 and FANCI Ubiquitination, Causes FA-T Subtype of Fanconi Anemia. <i>Cell Reports</i> , 2015, 12, 35-41.	6.4	107
90	Single-cell TCRseq: paired recovery of entire T-cell alpha and beta chain transcripts in T-cell receptors from single-cell RNAseq. <i>Genome Medicine</i> , 2016, 8, 80.	8.2	107

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91	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	21.4	104
92	let-7 Overexpression Leads to an Increased Fraction of Cells in G2/M, Direct Down-regulation of Cdc34, and Stabilization of Wee1 Kinase in Primary Fibroblasts. <i>Journal of Biological Chemistry</i> , 2009, 284, 6605-6609.	3.4	102
93	Aberration in DNA Methylation in B-Cell Lymphomas Has a Complex Origin and Increases with Disease Severity. <i>PLoS Genetics</i> , 2013, 9, e1003137.	3.5	102
94	Tumor Microenvironment Is Critical for the Maintenance of Cellular States Found in Primary Glioblastomas. <i>Cancer Discovery</i> , 2020, 10, 964-979.	9.4	102
95	Epigenetic Identity in AML Depends on Disruption of Nonpromoter Regulatory Elements and Is Affected by Antagonistic Effects of Mutations in Epigenetic Modifiers. <i>Cancer Discovery</i> , 2017, 7, 868-883.	9.4	101
96	The aging skin microenvironment dictates stem cell behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5339-5350.	7.1	101
97	R-Spondin chromosome rearrangements drive Wnt-dependent tumour initiation and maintenance in the intestine. <i>Nature Communications</i> , 2017, 8, 15945.	12.8	97
98	Vascular niche promotes hematopoietic multipotent progenitor formation from pluripotent stem cells. <i>Journal of Clinical Investigation</i> , 2015, 125, 1243-1254.	8.2	96
99	Histone variant H3.3 is an essential maternal factor for oocyte reprogramming. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7325-7330.	7.1	95
100	Revisiting the initial steps of sexual development in the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Microbiology</i> , 2019, 4, 144-154.	13.3	95
101	The Role of Next-Generation Sequencing in Precision Medicine: A Review of Outcomes in Oncology. <i>Journal of Personalized Medicine</i> , 2018, 8, 30.	2.5	94
102	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020, 37, 655-673.e11.	16.8	93
103	The cancer precision medicine knowledge base for structured clinical-grade mutations and interpretations. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 513-519.	4.4	88
104	DNA Methylation Dynamics of Germinal Center B Cells Are Mediated by AID. <i>Cell Reports</i> , 2015, 12, 2086-2098.	6.4	87
105	Artificial intelligence in cancer research, diagnosis and therapy. <i>Nature Reviews Cancer</i> , 2021, 21, 747-752.	28.4	87
106	Mutations in FLVCR1 Cause Posterior Column Ataxia and Retinitis Pigmentosa. <i>American Journal of Human Genetics</i> , 2010, 87, 643-654.	6.2	86
107	Diet-regulated production of PDGF $\alpha$ by macrophages controls energy storage. <i>Science</i> , 2021, 373, .	12.6	84
108	The role of machine learning in clinical research: transforming the future of evidence generation. <i>Trials</i> , 2021, 22, 537.	1.6	82

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109	An integrated ChIP-seq analysis platform with customizable workflows. BMC Bioinformatics, 2011, 12, 277.	2.6	80
110	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
111	Metabolic Alterations in Lung Cancerâ€Associated Fibroblasts Correlated with Increased Glycolytic Metabolism of the Tumor. Molecular Cancer Research, 2013, 11, 579-592.	3.4	79
112	AID stabilizes stem-cell phenotype by removing epigenetic memory of pluripotency genes. Nature, 2013, 500, 89-92.	27.8	78
113	Human ESC-derived hemogenic endothelial cells undergo distinct waves of endothelial to hematopoietic transition. Blood, 2013, 121, 770-780.	1.4	78
114	A Computational Approach for Identifying Synergistic Drug Combinations. PLoS Computational Biology, 2017, 13, e1005308.	3.2	77
115	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. Nature Communications, 2019, 10, 821.	12.8	73
116	Reconstructing the Duplication History of Tandemly Repeated Genes. Molecular Biology and Evolution, 2002, 19, 278-288.	8.9	71
117	Deep sequencing reveals clonal evolution patterns and mutation events associated with relapse in B-cell lymphomas. Genome Biology, 2014, 15, 432.	8.8	71
118	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
119	Epigenomic Alterations in Localized and Advanced Prostate Cancer. Neoplasia, 2013, 15, 373-IN5.	5.3	69
120	QSER1 protects DNA methylation valleys from de novo methylation. Science, 2021, 372, .	12.6	69
121	The NF-ÎB Transcriptional Footprint Is Essential for SARS-CoV-2 Replication. Journal of Virology, 2021, 95, e0125721.	3.4	69
122	Revealing Posttranscriptional Regulatory Elements Through Network-Level Conservation. PLoS Computational Biology, 2005, 1, e69.	3.2	68
123	Development and validation of a whole-exome sequencing test for simultaneous detection of point mutations, indels and copy-number alterations for precision cancer care. Npj Genomic Medicine, 2016, 1, .	3.8	68
124	Phosphatidylinositol-5-Phosphate 4-Kinases Regulate Cellular Lipid Metabolism By Facilitating Autophagy. Molecular Cell, 2018, 70, 531-544.e9.	9.7	68
125	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
126	An integrated model for detecting significant chromatin interactions from high-resolution Hi-C data. Nature Communications, 2017, 8, 15454.	12.8	66



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127	Inhibition of EZH2 Catalytic Activity Selectively Targets a Metastatic Subpopulation in Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2020, 30, 755-770.e6.	6.4	65
128	Concerted regulation of retinal pigment epithelium basement membrane and barrier function by angiocrine factors. <i>Nature Communications</i> , 2017, 8, 15374.	12.8	64
129	Lymphoblastic transformation of follicular lymphoma: a clinicopathologic and molecular analysis of 7 patients. <i>Human Pathology</i> , 2015, 46, 260-271.	2.0	63
130	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. <i>Cell</i> , 2020, 182, 297-316.e27.	28.9	63
131	Transcriptome sequencing reveals thousands of novel long non-coding RNAs in B cell lymphoma. <i>Genome Medicine</i> , 2015, 7, 110.	8.2	62
132	Identifying and Targeting Sporadic Oncogenic Genetic Aberrations in Mouse Models of Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2018, 8, 354-369.	9.4	62
133	Obesity-Associated Extracellular Matrix Remodeling Promotes a Macrophage Phenotype Similar to Tumor-Associated Macrophages. <i>American Journal of Pathology</i> , 2019, 189, 2019-2035.	3.8	62
134	Differential Contributions of Pre- and Post-EMT Tumor Cells in Breast Cancer Metastasis. <i>Cancer Research</i> , 2020, 80, 163-169.	0.9	62
135	Molecular Diagnosis of Autosomal Dominant Polycystic Kidney Disease Using Next-Generation Sequencing. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 216-228.	2.8	59
136	Precision Targeting with EZH2 and HDAC Inhibitors in Epigenetically Dysregulated Lymphomas. <i>Clinical Cancer Research</i> , 2019, 25, 5271-5283.	7.0	59
137	Inflammatory responses in the placenta upon SARS-CoV-2 infection late in pregnancy. <i>iScience</i> , 2022, 25, 104223.	4.1	58
138	Profiling of immune dysfunction in COVID-19 patients allows early prediction of disease progression. <i>Life Science Alliance</i> , 2021, 4, e202000955.	2.8	56
139	Single-cell profiling reveals an endothelium-mediated immunomodulatory pathway in the eye choroid. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	55
140	ELAVL1 Modulates Transcriptome-wide miRNA Binding in Murine Macrophages. <i>Cell Reports</i> , 2014, 9, 2330-2343.	6.4	54
141	ELAVL1 regulates alternative splicing of eIF4E transporter to promote postnatal angiogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18309-18314.	7.1	54
142	Accelerated lipid catabolism and autophagy are cancer survival mechanisms under inhibited glutaminolysis. <i>Cancer Letters</i> , 2018, 430, 133-147.	7.2	54
143	Lineage Reversion Drives WNT Independence in Intestinal Cancer. <i>Cancer Discovery</i> , 2020, 10, 1590-1609.	9.4	52
144	AICDA drives epigenetic heterogeneity and accelerates germinal center-derived lymphomagenesis. <i>Nature Communications</i> , 2018, 9, 222.	12.8	51

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145	Organotypic tumor slice cultures provide a versatile platform for immuno-oncology and drug discovery. <i>Oncolmmunology</i> , 2019, 8, e1670019.	4.6	51
146	Immune reprogramming via PD-1 inhibition enhances early-stage lung cancer survival. <i>JCI Insight</i> , 2018, 3, .	5.0	49
147	Comprehensive characterization of the mutational landscape in multiple myeloma cell lines reveals potential drivers and pathways associated with tumor progression and drug resistance. <i>Theranostics</i> , 2019, 9, 540-553.	10.0	49
148	A Novel Approach for Characterizing Microsatellite Instability in Cancer Cells. <i>PLoS ONE</i> , 2013, 8, e63056.	2.5	47
149	Oncogenic BRAF disrupts thyroid morphogenesis and function via twist expression. <i>ELife</i> , 2017, 6, .	6.0	47
150	Imipridone ONC212 activates orphan G protein-coupled receptor GPR132 and integrated stress response in acute myeloid leukemia. <i>Leukemia</i> , 2019, 33, 2805-2816.	7.2	47
151	Disruption of Adipose Rab10-Dependent Insulin Signaling Causes Hepatic Insulin Resistance. <i>Diabetes</i> , 2016, 65, 1577-1589.	0.6	46
152	Rapid identification of <i>BCR&lt;sc&gt;/sc&gt;ABL&lt;sc&gt;/sc&gt;1</i> like acute lymphoblastic leukaemia patients using a predictive statistical model based on quantitative real time PCR polymerase chain reaction: clinical, prognostic and therapeutic implications. <i>British Journal of Haematology</i> , 2018, 181, 642-652.	2.5	46
153	The Missing Pieces of Artificial Intelligence in Medicine. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 555-564.	8.7	46
154	Predicting peptide presentation by major histocompatibility complex class I: an improved machine learning approach to the immunopeptidome. <i>BMC Bioinformatics</i> , 2019, 20, 7.	2.6	45
155	Temporal evolution of cellular heterogeneity during the progression to advanced AR-negative prostate cancer. <i>Nature Communications</i> , 2021, 12, 3372.	12.8	45
156	The Chromatin Remodeler CHD8 Is Required for Activation of Progesterone Receptor-Dependent Enhancers. <i>PLoS Genetics</i> , 2015, 11, e1005174.	3.5	44
157	An Epigenomic Approach to Improving Response to Neoadjuvant Cisplatin Chemotherapy in Bladder Cancer. <i>Biomolecules</i> , 2016, 6, 37.	4.0	44
158	SLFN11 Expression in Advanced Prostate Cancer and Response to Platinum-based Chemotherapy. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1157-1164.	4.1	44
159	Genome-Wide Detection of Genes Targeted by Non-Ig Somatic Hypermutation in Lymphoma. <i>PLoS ONE</i> , 2012, 7, e40332.	2.5	44
160	Vascular Platform to Define Hematopoietic Stem Cell Factors and Enhance Regenerative Hematopoiesis. <i>Stem Cell Reports</i> , 2015, 5, 881-894.	4.8	43
161	BCL6 Antagonizes NOTCH2 to Maintain Survival of Human Follicular Lymphoma Cells. <i>Cancer Discovery</i> , 2017, 7, 506-521.	9.4	43
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