

Olivier Elemento

List of Publications by Year in Descending Order

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

365
papers

26,392
citations

78
h-index

158
g-index

402
ext. papers

34,532
ext. citations

12.8
avg, IF

6.93
L-index

#	Paper	IF	Citations
365	Extracellular Matrix in Synthetic Hydrogel-Based Prostate Cancer Organoids Regulate Therapeutic Response to EZH2 and DRD2 Inhibitors (Adv. Mater. 2/2022). <i>Advanced Materials</i> , 2022 , 34, 2270014	24	
364	Serial ctDNA analysis predicts clinical progression in patients with advanced urothelial carcinoma.. <i>British Journal of Cancer</i> , 2022 ,	8.7	1
363	System-wide transcriptome damage and tissue identity loss in COVID-19 patients.. <i>Cell Reports Medicine</i> , 2022 , 3, 100522	18	2
362	Histone 3 Methyltransferases Alter Melanoma Initiation and Progression Through Discrete Mechanisms.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 814216	5.7	
361	Serial ctDNA evaluation to predict clinical progression in patients with advanced urothelial carcinoma.. <i>Journal of Clinical Oncology</i> , 2022 , 40, 532-532	2.2	
360	Simple Linear Cancer Risk Prediction Models With Novel Features Outperform Complex Approaches.. <i>JCO Clinical Cancer Informatics</i> , 2022 , 6, e2100166	5.2	
359	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. <i>Cancer Research</i> , 2022 , 82, P2-06-03-P2-06-03	10.1	
358	Genomic instability is enriched in localized prostate cancers from men of African ancestry.. <i>Journal of Clinical Oncology</i> , 2022 , 40, 270-270	2.2	
357	Abstract P2-06-04: Pathognomonic long molecule footprints of backup repair pathways in homologous recombination deficient cancers. <i>Cancer Research</i> , 2022 , 82, P2-06-04-P2-06-04	10.1	
356	Association of circulating tumor cell RB1 loss RNA signature with outcomes and immune phenotypes in men with mCRPC.. <i>Journal of Clinical Oncology</i> , 2022 , 40, 139-139	2.2	
355	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. <i>Cancer Research</i> , 2022 , 82, P5-05-02-P5-05-02	10.1	
354	Utility of multimodality molecular profiling for pediatric patients with central nervous system tumors.. <i>Neuro-Oncology Advances</i> , 2022 , 4, vdac031	0.9	
353	RET Fusion-Positive Papillary Thyroid Cancers are Associated with a More Aggressive Phenotype.. <i>Annals of Surgical Oncology</i> , 2022 , 1	3.1	0
352	Global evolution of the tumor microenvironment associated with progression from preinvasive invasive to invasive human lung adenocarcinoma.. <i>Cell Reports</i> , 2022 , 39, 110639	10.6	1
351	Inflammatory Responses in the Placenta upon SARS-CoV-2 Infection Late in Pregnancy.. <i>IScience</i> , 2022 , 104223	6.1	6
350	ASO Visual Abstract: RET Fusion-Positive Papillary Thyroid Cancers are Associated with a More Aggressive Phenotype.. <i>Annals of Surgical Oncology</i> , 2022 , 1	3.1	
349	The lactate-NAD axis activates cancer-associated fibroblasts by downregulating p62.. <i>Cell Reports</i> , 2022 , 39, 110792	10.6	2

348	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes.. <i>Cancer Cell</i> , 2022 , 40, 524-544.e5	24.3	2
347	Alterations in transcriptional networks in cancer: the role of noncoding somatic driver mutations. <i>Current Opinion in Genetics and Development</i> , 2022 , 75, 101919	4.9	1
346	LGG-47. Single-cell RNA Sequencing Reveals Immunosuppressive Myeloid Cell Diversity During Malignant Progression in Glioma. <i>Neuro-Oncology</i> , 2022 , 24, i99-i99	1	
345	Metabolic and Immune Markers for Precise Monitoring of COVID-19 Severity and Treatment.. <i>Frontiers in Immunology</i> , 2021 , 12, 809937	8.4	4
344	Stage-specific regulation of DNA methylation by TET enzymes during human cardiac differentiation. <i>Cell Reports</i> , 2021 , 37, 110095	10.6	3
343	GCN2 kinase activation by ATP-competitive kinase inhibitors.. <i>Nature Chemical Biology</i> , 2021 ,	11.7	2
342	Detecting neuroendocrine prostate cancer through tissue-informed cell-free DNA methylation analysis.. <i>Clinical Cancer Research</i> , 2021 ,	12.9	1
341	Metastasis and Immune Evasion from Extracellular cGAMP Hydrolysis. <i>Cancer Discovery</i> , 2021 , 11, 1212-1227	27	29
340	Dynamic Immune Surveillance in Durable Clinical Response to Combined BTK and BCL2 Inhibition in MCL at Longitudinal Single-Cell Resolution. <i>Blood</i> , 2021 , 138, 1323-1323	2.2	
339	Selective STAT3 Degradation Dissect Peripheral T-Cell Lymphomas Vulnerabilities Empowering Personalized Regimens. <i>Blood</i> , 2021 , 138, 865-865	2.2	
338	Single Cell ATAC Lineage Deconvolution Reveals Overlapping Subclones in Epigenetically Distinct AML Samples. <i>Blood</i> , 2021 , 138, 2381-2381	2.2	
337	BTG1 Mutation Promotes Aggressive Lymphoma Development By Lowering the Threshold to MYC Activation and Generating "Super-Competitor" B Cells. <i>Blood</i> , 2021 , 138, 359-359	2.2	0
336	Molecular Evolution of Classical Hodgkin Lymphoma Revealed Through Whole Genome Sequencing of Hodgkin and Reed-Sternberg Cells. <i>Blood</i> , 2021 , 138, 805-805	2.2	
335	HHV-6 in the Lymphoma Microenvironment: Both Chicken and Egg?. <i>Blood</i> , 2021 , 138, 1377-1377	2.2	
334	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. <i>Blood</i> , 2021 , 138, 138-138	2.2	0
333	285 Breaking through the resistance of breast cancer to immune checkpoint blockers in a unique mouse model of HR+ disease 2021 , 9, A309-A309		
332	FOXO1 Dependent Transcription Network Is a Targetable Vulnerability of Mantle Cell Lymphoma. <i>Blood</i> , 2021 , 138, 30-30	2.2	
331	A Predictive Endothelial-Leukemia Pre-Clinical Platform to Uncover Drug Vulnerabilities for Personalized Treatments. <i>Blood</i> , 2021 , 138, 704-704	2.2	

330	Profiling of immune dysfunction in COVID-19 patients allows early prediction of disease progression. <i>Life Science Alliance</i> , 2021 , 4,	5.8	25
329	Extracellular Matrix in Synthetic Hydrogel-Based Prostate Cancer Organoids Regulate Therapeutic Response to EZH2 and DRD2 Inhibitors. <i>Advanced Materials</i> , 2021 , e2100096	24	3
328	CLIP-170S is a microtubule- β TIP variant that confers resistance to taxanes by impairing drug-target engagement. <i>Developmental Cell</i> , 2021 , 56, 3264-3275.e7	10.2	0
327	Prediction of primary venous thromboembolism based on clinical and genetic factors within the U.K. Biobank. <i>Scientific Reports</i> , 2021 , 11, 21340	4.9	0
326	Towards artificial intelligence-driven pathology assessment for hematological malignancies. <i>Blood Cancer Discovery</i> , 2021 , 2, 195-197	7	0
325	Genome-wide investigation identifies a rare copy-number variant burden associated with human spina bifida. <i>Genetics in Medicine</i> , 2021 , 23, 1211-1218	8.1	3
324	FSMP-10. CYSTEINE INDUCES CYTOTOXICITY IN GLIOBLASTOMA THROUGH MITOCHONDRIAL HYDROGEN PEROXIDE PRODUCTION. <i>Neuro-Oncology Advances</i> , 2021 , 3, i18-i18	0.9	78
323	Systemic Tissue and Cellular Disruption from SARS-CoV-2 Infection revealed in COVID-19 Autopsies and Spatial Omics Tissue Maps 2021 ,		3
322	The spatial landscape of lung pathology during COVID-19 progression. <i>Nature</i> , 2021 , 593, 564-569	50.4	72
321	RNA-sequencing data-driven dissection of human plasma cell differentiation reveals new potential transcription regulators. <i>Leukemia</i> , 2021 , 35, 1451-1462	10.7	4
320	Artificial intelligence in oncology: From bench to clinic. <i>Seminars in Cancer Biology</i> , 2021 ,	12.7	3
319	A molecular single-cell lung atlas of lethal COVID-19. <i>Nature</i> , 2021 , 595, 114-119	50.4	81
318	QSER1 protects DNA methylation valleys from de novo methylation. <i>Science</i> , 2021 , 372,	33.3	18
317	Artificial Intelligence in Cancer Research and Precision Medicine. <i>Cancer Discovery</i> , 2021 , 11, 900-915	24.4	26
316	Discovery of Candidate DNA Methylation Cancer Driver Genes. <i>Cancer Discovery</i> , 2021 , 11, 2266-2281	24.4	12
315	Deep learning predicts chromosomal instability from histopathology images. <i>IScience</i> , 2021 , 24, 102394	6.1	5
314	Leptin Mediates Obesity-Induced DNA Damage in BRCA1 Breast Epithelial Cells. <i>Journal of the Endocrine Society</i> , 2021 , 5, A1024-A1024	0.4	
313	Temporal evolution of cellular heterogeneity during the progression to advanced AR-negative prostate cancer. <i>Nature Communications</i> , 2021 , 12, 3372	17.4	3

312	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2021 ,	12.7	7
311	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2021 ,	12.7	3
310	Blood biomarkers reflect the effects of obesity and inflammation on the human breast transcriptome. <i>Carcinogenesis</i> , 2021 , 42, 1281-1292	4.6	0
309	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. <i>Seminars in Cancer Biology</i> , 2021 ,	12.7	3
308	Mutation landscape, clonal evolution pattern, and potential pathogenic pathways in B-lymphoblastic transformation of follicular lymphoma. <i>Leukemia</i> , 2021 , 35, 1203-1208	10.7	1
307	Integration of whole-exome and anchored PCR-based next generation sequencing significantly increases detection of actionable alterations in precision oncology. <i>Translational Oncology</i> , 2021 , 14, 100944	4.9	2
306	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021 , 589, 299-305	50.4	56
305	Leveraging phenotypic variability to identify genetic interactions in human phenotypes. <i>American Journal of Human Genetics</i> , 2021 , 108, 49-67	11	10
304	Limitations of Detecting Genetic Variants from the RNA Sequencing Data in Tissue and Fine-Needle Aspiration Samples. <i>Thyroid</i> , 2021 , 31, 589-595	6.2	4
303	Building biorepositories in the midst of a pandemic. <i>Journal of Clinical and Translational Science</i> , 2021 , 5, e92	0.4	2
302	Chemical systems biology reveals mechanisms of glucocorticoid receptor signaling. <i>Nature Chemical Biology</i> , 2021 , 17, 307-316	11.7	7
301	Single-cell DNA targeted sequencing (scDNA-seq) to test therapeutic vulnerabilities in urothelial cancer (UC) patient-derived organoids (PDO).. <i>Journal of Clinical Oncology</i> , 2021 , 39, 464-464	2.2	
300	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
299	Diet-regulated production of PDGF α by macrophages controls energy storage. <i>Science</i> , 2021 , 373,	33.3	12
298	Functional comparison of exome capture-based methods for transcriptomic profiling of formalin-fixed paraffin-embedded tumors. <i>Npj Genomic Medicine</i> , 2021 , 6, 66	6.2	2
297	Validation of a Circulating Tumor DNA-Based Next-Generation Sequencing Assay in a Cohort of Patients with Solid tumors: A Proposed Solution for Decentralized Plasma Testing. <i>Oncologist</i> , 2021 , 26, e1971-e1981	5.7	1
296	The role of machine learning in clinical research: transforming the future of evidence generation. <i>Trials</i> , 2021 , 22, 537	2.8	9
295	Artificial intelligence in cancer research, diagnosis and therapy. <i>Nature Reviews Cancer</i> , 2021 , 21, 747-753	31.3	11

294	OCT2 pre-positioning facilitates cell fate transition and chromatin architecture changes in humoral immunity. <i>Nature Immunology</i> , 2021 , 22, 1327-1340	19.1	3
293	Reshaping of the androgen-driven chromatin landscape in normal prostate cells by early cancer drivers and effect on therapeutic sensitivity. <i>Cell Reports</i> , 2021 , 36, 109625	10.6	4
292	Cohesin Core Complex Gene Dosage Contributes to Germinal Center Derived Lymphoma Phenotypes and Outcomes. <i>Frontiers in Immunology</i> , 2021 , 12, 688493	8.4	2
291	Dissecting bulk transcriptomes of diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2021 , 39, 1305-1307	24.3	1
290	The NF- κ B Transcriptional Footprint Is Essential for SARS-CoV-2 Replication. <i>Journal of Virology</i> , 2021 , 95, e0125721	6.6	11
289	A polygenic-score-based approach for identification of gene-drug interactions stratifying breast cancer risk. <i>American Journal of Human Genetics</i> , 2021 , 108, 1752-1764	11	1
288	Multi-platform profiling characterizes molecular subgroups and resistance networks in chronic lymphocytic leukemia. <i>Nature Communications</i> , 2021 , 12, 5395	17.4	1
287	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. <i>Nature Immunology</i> , 2021 , 22, 240-253	19.1	12
286	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
285	Pan-cancer analysis reveals molecular patterns associated with age. <i>Cell Reports</i> , 2021 , 37, 110100	10.6	0
284	Precision medicine and artificial intelligence: overview and relevance to reproductive medicine. <i>Fertility and Sterility</i> , 2020 , 114, 908-913	4.8	6
283	Predictive modeling in reproductive medicine: Where will the future of artificial intelligence research take us?. <i>Fertility and Sterility</i> , 2020 , 114, 934-940	4.8	9
282	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. <i>Cancers</i> , 2020 , 12,	6.6	8
281	Demographic and genetic factors influence the abundance of infiltrating immune cells in human tissues. <i>Nature Communications</i> , 2020 , 11, 2213	17.4	11
280	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020 , 26, 1161-1165	50.5	16
279	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020 , 37, 655-673.e11	24.3	47
278	Lineage Reversion Drives WNT Independence in Intestinal Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1590-1609	24.4	16
277	The INPP4B Tumor Suppressor Modulates EGFR Trafficking and Promotes Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1226-1239	24.4	12

276	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	10.6	84
275	SLFN11 Expression in Advanced Prostate Cancer and Response to Platinum-based Chemotherapy. <i>Molecular Cancer Therapeutics</i> , 2020 , 19, 1157-1164	6.1	23
274	Computational methods in tumor immunology. <i>Methods in Enzymology</i> , 2020 , 636, 209-259	1.7	1
273	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020 , 52, 448-457	36.3	58
272	Tumor Microenvironment Is Critical for the Maintenance of Cellular States Found in Primary Glioblastomas. <i>Cancer Discovery</i> , 2020 , 10, 964-979	24.4	57
271	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. <i>Cell</i> , 2020 , 182, 297-316.e27	56.2	23
270	Small Cell Carcinoma of the Ovary, Hypercalcemic Type (SCCOHT) beyond Mutations: A Comprehensive Genomic Analysis. <i>Cells</i> , 2020 , 9,	7.9	14
269	Multicenter Phase II Study of Cabazitaxel in Advanced Gastroesophageal Cancer: Association of HER2 Expression and M2-Like Tumor-Associated Macrophages with Patient Outcome. <i>Clinical Cancer Research</i> , 2020 , 26, 4756-4766	12.9	6
268	A reference single-cell transcriptomic atlas of human skeletal muscle tissue reveals bifurcated muscle stem cell populations. <i>Skeletal Muscle</i> , 2020 , 10, 19	5.1	39
267	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	11.5	32
266	Inhibition of EZH2 Catalytic Activity Selectively Targets a Metastatic Subpopulation in Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2020 , 30, 755-770.e6	10.6	30
265	Stable reduction of STARD4 alters cholesterol regulation and lipid homeostasis. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2020 , 1865, 158609	5	7
264	Integrative multiplatform molecular profiling of benign prostatic hyperplasia identifies distinct subtypes. <i>Nature Communications</i> , 2020 , 11, 1987	17.4	14
263	EXTH-74. IND-ENABLING CHARACTERIZATION OF DUAL DRD2- AND ClpP-TARGETING AGENT ONC206 AS THE NEXT IMIPRIDONE FOR CLINICAL NEURO-ONCOLOGY. <i>Neuro-Oncology</i> , 2020 , 22, ii103-ii103	1	1
262	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , 2020 , 136, 33-34	2.2	
261	TAMI-38. CYSTEINE-PROMOTING COMPOUNDS INDUCE MITOCHONDRIAL TOXICITY IN GLIOBLASTOMA THROUGH ALTERED PYRUVATE AND SERINE METABOLISM. <i>Neuro-Oncology</i> , 2020 , 22, ii221-ii221	1	
260	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. <i>Journal of Clinical Investigation</i> , 2020 , 130, 1653-1668	15.9	56
259	Clinical, regional, and genetic characteristics of Covid-19 patients from UK Biobank. <i>PLoS ONE</i> , 2020 , 15, e0241264	3.7	20

258	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. <i>Archives of Pathology and Laboratory Medicine</i> , 2020 , 144, 1535-1546	5	4
257	Epithelial plasticity can generate multi-lineage phenotypes in human and murine bladder cancers. <i>Nature Communications</i> , 2020 , 11, 2540	17.4	15
256	The future of precision medicine: towards a more predictive personalized medicine. <i>Emerging Topics in Life Sciences</i> , 2020 , 4, 175-177	3.5	5
255	Urinary Cell Transcriptome Profiling and Identification of ITM2A, SLAMF6, and IKZF3 as Biomarkers of Acute Rejection in Human Kidney Allografts. <i>Transplantation Direct</i> , 2020 , 6, e588	2.3	4
254	Clinical and Genetic Characteristics of Covid-19 Patients from UK Biobank 2020 ,		5
253	Longitudinal immune profiling of mild and severe COVID-19 reveals innate and adaptive immune dysfunction and provides an early prediction tool for clinical progression 2020 ,		7
252	Differential Contributions of Pre- and Post-EMT Tumor Cells in Breast Cancer Metastasis. <i>Cancer Research</i> , 2020 , 80, 163-169	10.1	33
251	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020 , 183, 197-210.e32	56.2	45
250	High-resolution mouse subventricular zone stem-cell niche transcriptome reveals features of lineage, anatomy, and aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 31448-31458	11.5	13
249	Unique Immune Cell Coactivators Specify Locus Control Region Function and Cell Stage. <i>Molecular Cell</i> , 2020 , 80, 845-861.e10	17.6	9
248	Common germline-somatic variant interactions in advanced urothelial cancer. <i>Nature Communications</i> , 2020 , 11, 6195	17.4	6
247	Selective dysregulation of ROCK2 activity promotes aberrant transcriptional networks in ABC diffuse large B-cell lymphoma. <i>Scientific Reports</i> , 2020 , 10, 13094	4.9	1
246	A machine learning and network framework to discover new indications for small molecules. <i>PLoS Computational Biology</i> , 2020 , 16, e1008098	5	8
245	Single-cell profiling reveals an endothelium-mediated immunomodulatory pathway in the eye choroid. <i>Journal of Experimental Medicine</i> , 2020 , 217,	16.6	19
244	Adaptable haemodynamic endothelial cells for organogenesis and tumorigenesis. <i>Nature</i> , 2020 , 585, 426-432	50.4	54
243	Graph convolutional networks for computational drug development and discovery. <i>Briefings in Bioinformatics</i> , 2020 , 21, 919-935	13.4	87
242	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. <i>Blood Cancer Journal</i> , 2019 , 9, 69	7	2
241	Clinical features of neuroendocrine prostate cancer. <i>European Journal of Cancer</i> , 2019 , 121, 7-18	7.5	79

240	Cancer-Specific Thresholds Adjust for Whole Exome Sequencing-based Tumor Mutational Burden Distribution. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	8
239	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	15
238	The Transcriptional Regulator Sin3A Contributes to the Oncogenic Potential of STAT3. <i>Cancer Research</i> , 2019 , 79, 3076-3087	10.1	20
237	Imipridone ONC212 activates orphan G protein-coupled receptor GPR132 and integrated stress response in acute myeloid leukemia. <i>Leukemia</i> , 2019 , 33, 2805-2816	10.7	21
236	Radiation therapy and anti-tumor immunity: exposing immunogenic mutations to the immune system. <i>Genome Medicine</i> , 2019 , 11, 40	14.4	94
235	Function and clinical relevance of RHAMM isoforms in pancreatic tumor progression. <i>Molecular Cancer</i> , 2019 , 18, 92	42.1	19
234	A Recurrent Activating Missense Mutation in Waldenström Macroglobulinemia Affects the DNA Binding of the ETS Transcription Factor SPI1 and Enhances Proliferation. <i>Cancer Discovery</i> , 2019 , 9, 796-811 ⁴	24.4	11
233	Dynamic transcriptome profiles within spermatogonial and spermatocyte populations during postnatal testis maturation revealed by single-cell sequencing. <i>PLoS Genetics</i> , 2019 , 15, e1007810	6	47
232	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	12.1	28
231	Precision Targeting with EZH2 and HDAC Inhibitors in Epigenetically Dysregulated Lymphomas. <i>Clinical Cancer Research</i> , 2019 , 25, 5271-5283	12.9	38
230	CHD1 Loss Alters AR Binding at Lineage-Specific Enhancers and Modulates Distinct Transcriptional Programs to Drive Prostate Tumorigenesis. <i>Cancer Cell</i> , 2019 , 35, 603-617.e8	24.3	29
229	Deep learning enables robust assessment and selection of human blastocysts after in vitro fertilization. <i>Npj Digital Medicine</i> , 2019 , 2, 21	15.7	126
228	Generation of pulmonary neuroendocrine cells and SCLC-like tumors from human embryonic stem cells. <i>Journal of Experimental Medicine</i> , 2019 , 216, 674-687	16.6	47
227	Obesity-Associated Extracellular Matrix Remodeling Promotes a Macrophage Phenotype Similar to Tumor-Associated Macrophages. <i>American Journal of Pathology</i> , 2019 , 189, 2019-2035	5.8	38
226	The Missing Pieces of Artificial Intelligence in Medicine. <i>Trends in Pharmacological Sciences</i> , 2019 , 40, 555-564	13.2	26
225	Upper tract urothelial carcinoma has a luminal-papillary T-cell depleted contexture and activated FGFR3 signaling. <i>Nature Communications</i> , 2019 , 10, 2977	17.4	71
224	3055 Reconstruction of Patient-specific Distal Airway Regeneration Patterns in COPD. <i>Journal of Clinical and Translational Science</i> , 2019 , 3, 154-154	0.4	78
223	Organotypic tumor slice cultures provide a versatile platform for immuno-oncology and drug discovery. <i>Oncolmmunology</i> , 2019 , 8, e1670019	7.2	24

222	N-Myc-mediated epigenetic reprogramming drives lineage plasticity in advanced prostate cancer. <i>Journal of Clinical Investigation</i> , 2019 , 129, 3924-3940	15.9	55
221	Clinical and molecular analysis of patients treated with prostate-specific membrane antigen (PSMA)-targeted radionuclide therapy.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 272-272	2.2	5
220	UCLH1 loss alters the cell-cycle in metastatic pancreatic neuroendocrine tumors. <i>Endocrine-Related Cancer</i> , 2019 , 26, 411-423	5.7	9
219	Oncogenic Addiction to ERBB2 Signaling Predicts Response to Trastuzumab in Urothelial Cancer. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2019 , 17, 194-200	7.3	3
218	The genomic landscape of metastatic clear cell renal cell carcinoma (ccRCC) after treatment with systemic therapy.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 675-675	2.2	
217	SAT-339 Cross-Talk with Breast Adipose Tissue Contributes to Obesity-induced DNA Damage in BRCA Mutant Breast Epithelial Cells. <i>Journal of the Endocrine Society</i> , 2019 , 3,	0.4	78
216	Heterogeneous Genetic Alterations and Novel Pathogenic Pathways in Relapsed DLBCL Revealed By Whole Exome Sequencing. <i>Blood</i> , 2019 , 134, 2770-2770	2.2	
215	The DNA Helicase Hells Is a New Unconventional Player in ALK- Anaplastic Large Cell Lymphoma Biology. <i>Blood</i> , 2019 , 134, 1477-1477	2.2	
214	Immune Sculpting of Clonal Hematopoiesis in Advanced and Metastatic Solid Tumors. <i>Blood</i> , 2019 , 134, 3721-3721	2.2	
213	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. <i>Nature Communications</i> , 2019 , 10, 821	17.4	49
212	A Bayesian machine learning approach for drug target identification using diverse data types. <i>Nature Communications</i> , 2019 , 10, 5221	17.4	85
211	EXTH-71. IND-ENABLING CHARACTERIZATION OF ONC206 AS THE NEXT BITOPIC DRD2 ANTAGONIST FOR NEURO-ONCOLOGY. <i>Neuro-Oncology</i> , 2019 , 21, vi97-vi97	1	1
210	Deep learning-based classification of mesothelioma improves prediction of patient outcome. <i>Nature Medicine</i> , 2019 , 25, 1519-1525	50.5	132
209	Dopamine Receptor D5 is a Modulator of Tumor Response to Dopamine Receptor D2 Antagonism. <i>Clinical Cancer Research</i> , 2019 , 25, 2305-2313	12.9	27
208	Drug-Induced Expression-Based Computational Repurposing of Small Molecules Affecting Transcription Factor Activity. <i>Methods in Molecular Biology</i> , 2019 , 1903, 179-184	1.4	1
207	Revisiting the initial steps of sexual development in the malaria parasite Plasmodium falciparum. <i>Nature Microbiology</i> , 2019 , 4, 144-154	26.6	57
206	Prostaglandin E down-regulates sirtuin 1 (SIRT1), leading to elevated levels of aromatase, providing insights into the obesity-breast cancer connection. <i>Journal of Biological Chemistry</i> , 2019 , 294, 361-371	5.4	10
205	Predicting peptide presentation by major histocompatibility complex class I: an improved machine learning approach to the immunopeptidome. <i>BMC Bioinformatics</i> , 2019 , 20, 7	3.6	19

204	Epigenetic analysis identifies factors driving racial disparity in prostate cancer. <i>Cancer Reports</i> , 2019 , 2, e1153	1.5	6
203	TETs Regulate Proepicardial Cell Migration through Extracellular Matrix Organization during Zebrafish Cardiogenesis. <i>Cell Reports</i> , 2019 , 26, 720-732.e4	10.6	15
202	Rapid identification of BCR/ABL1-like acute lymphoblastic leukaemia patients using a predictive statistical model based on quantitative real time-polymerase chain reaction: clinical, prognostic and therapeutic implications. <i>British Journal of Haematology</i> , 2018 , 181, 642-652	4.5	31
201	A Randomized Multicenter Phase II Study of Docosahexaenoic Acid in Patients with a History of Breast Cancer, Premalignant Lesions, or Benign Breast Disease. <i>Cancer Prevention Research</i> , 2018 , 11, 203-214	3.2	11
200	Chromosomal instability drives metastasis through a cytosolic DNA response. <i>Nature</i> , 2018 , 553, 467-472	50.4	536
199	AICDA drives epigenetic heterogeneity and accelerates germinal center-derived lymphomagenesis. <i>Nature Communications</i> , 2018 , 9, 222	17.4	34
198	Analyzing DNA Methylation Patterns During Tumor Evolution. <i>Methods in Molecular Biology</i> , 2018 , 1711, 27-53	1.4	1
197	Bioinformatics Approaches to Predict Drug Responses from Genomic Sequencing. <i>Methods in Molecular Biology</i> , 2018 , 1711, 277-296	1.4	7
196	HN1L Promotes Triple-Negative Breast Cancer Stem Cells through LEPR-STAT3 Pathway. <i>Stem Cell Reports</i> , 2018 , 10, 212-227	8	32
195	Bone biopsy protocol for advanced prostate cancer in the era of precision medicine. <i>Cancer</i> , 2018 , 124, 1008-1015	6.4	24
194	Deep Convolutional Neural Networks Enable Discrimination of Heterogeneous Digital Pathology Images. <i>EBioMedicine</i> , 2018 , 27, 317-328	8.8	152
193	Phosphatidylinositol-5-Phosphate 4-Kinases Regulate Cellular Lipid Metabolism By Facilitating Autophagy. <i>Molecular Cell</i> , 2018 , 70, 531-544.e9	17.6	35
192	Tailoring CD19xCD3-DART exposure enhances T-cells to eradication of B-cell neoplasms. <i>Oncolmmunology</i> , 2018 , 7, e1341032	7.2	9
191	Activating Transcription Factor 4 Modulates TGFβ Induced Aggressiveness in Triple-Negative Breast Cancer via SMAD2/3/4 and mTORC2 Signaling. <i>Clinical Cancer Research</i> , 2018 , 24, 5697-5709	12.9	26
190	Association of T-Cell Receptor Repertoire Use With Response to Combined Trastuzumab-Lapatinib Treatment of HER2-Positive Breast Cancer: Secondary Analysis of the NeoALTTO Randomized Clinical Trial. <i>JAMA Oncology</i> , 2018 , 4, e181564	13.4	8
189	Patient derived organoids to model rare prostate cancer phenotypes. <i>Nature Communications</i> , 2018 , 9, 2404	17.4	149
188	Upper tract urothelial carcinoma is non-basal and T-cell depleted.. <i>Journal of Clinical Oncology</i> , 2018 , 36, 4525-4525	2.2	1
187	CATCH-KB: Establishing a Pharmacogenomics Variant Repository for Chemotherapy-Induced Cardiotoxicity. <i>AMIA Summits on Translational Science Proceedings</i> , 2018 , 2017, 168-177	1.1	2

186	Obesity-associated extracellular matrix remodeling promotes a tumor-associated macrophage phenotype in tumor-free breast adipose tissue. <i>FASEB Journal</i> , 2018 , 32, 280.5	0.9	
185	Targeting the Epichaperome As an Effective Precision Medicine Approach in a Novel PML-SYK Fusion Acute Myeloid Leukemia. <i>Blood</i> , 2018 , 132, 1435-1435	2.2	1
184	TET proteins safeguard bivalent promoters from de novo methylation in human embryonic stem cells. <i>Nature Genetics</i> , 2018 , 50, 83-95	36.3	108
183	Identifying and Targeting Sporadic Oncogenic Genetic Aberrations in Mouse Models of Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2018 , 8, 354-369	24.4	40
182	STMN1 is Overexpressed in Adrenocortical Carcinoma and Promotes a More Aggressive Phenotype In Vitro. <i>Annals of Surgical Oncology</i> , 2018 , 25, 792-800	3.1	11
181	Immune reprogramming via PD-1 inhibition enhances early-stage lung cancer survival. <i>JCI Insight</i> , 2018 , 3,	9.9	27
180	TBIO-15. UTILIZING A HISTOLOGY-SPECIFIC SEQUENCING ALGORITHM FOR PRECISION NEURO-ONCOLOGY. <i>Neuro-Oncology</i> , 2018 , 20, i183-i183	1	78
179	DDIS-12. ONC201: THE FIRST SELECTIVE, NON-COMPETITIVE DRD2/3 ANTAGONIST FOR CLINICAL NEURO-ONCOLOGY. <i>Neuro-Oncology</i> , 2018 , 20, vi71-vi71	1	78
178	2566 Personalized models of distal airway epithelial-stromal unit in COPD. <i>Journal of Clinical and Translational Science</i> , 2018 , 2, 23-23	0.4	78
177	DRES-10. DRD5 IS A MODULATOR OF GLIOMA SUSCEPTIBILITY TO DRD2 ANTAGONISM BY ONC201. <i>Neuro-Oncology</i> , 2018 , 20, vi77-vi78	1	78
176	GENE-10. IDENTIFICATION OF MXRA5 AND DSP AS RELEVANT TARGETS IN INFILTRATING ASTROCYTOMAS: A WHOLE EXOME ANALYSIS AT A SINGLE INSTITUTION. <i>Neuro-Oncology</i> , 2018 , 20, vi104-vi105	1	78
175	TMOD-36. PRECISE INVESTIGATION OF CANCER STEM CELLS IN A MOUSE GLIOBLASTOMA MODEL. <i>Neuro-Oncology</i> , 2018 , 20, vi276-vi276	1	78
174	EXTH-17. SELECTIVE, NON-COMPETITIVE DRD2/3 ANTAGONISM BY IMIPRIDONE ONC206 IS EFFECTIVE IN TUMORS WITH DOPAMINE RECEPTOR DYSREGULATION. <i>Neuro-Oncology</i> , 2018 , 20, vi88-vi88	1	78
173	Colonoscopic-Guided Pinch Biopsies in Mice as a Useful Model for Evaluating the Roles of Host and Luminal Factors in Colonic Inflammation. <i>American Journal of Pathology</i> , 2018 , 188, 2811-2825	5.8	1
172	The Role of Next-Generation Sequencing in Precision Medicine: A Review of Outcomes in Oncology. <i>Journal of Personalized Medicine</i> , 2018 , 8,	3.6	53
171	TET2 Deficiency Causes Germinal Center Hyperplasia, Impairs Plasma Cell Differentiation, and Promotes B-cell Lymphomagenesis. <i>Cancer Discovery</i> , 2018 , 8, 1632-1653	24.4	77
170	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
169	CHL1 expression differentiates H ₁ thle cell carcinoma from benign H ₁ thle cell nodules. <i>Journal of Surgical Oncology</i> , 2018 , 118, 1042-1049	2.8	3

168	Accelerated lipid catabolism and autophagy are cancer survival mechanisms under inhibited glutaminolysis. <i>Cancer Letters</i> , 2018 , 430, 133-147	9.9	38
167	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	11.5	204
166	Effective Combination Therapies for B-cell Lymphoma Predicted by a Virtual Disease Model. <i>Cancer Research</i> , 2017 , 77, 1818-1830	10.1	10
165	Regulatory elements in molecular networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2017 , 9, e1374	6.6	9
164	Sox17 drives functional engraftment of endothelium converted from non-vascular cells. <i>Nature Communications</i> , 2017 , 8, 13963	17.4	9
163	Towards a better cancer precision medicine: systems biology meets immunotherapy. <i>Current Opinion in Systems Biology</i> , 2017 , 2, 67-73	3.2	5
162	Cabozantinib Eradicates Advanced Murine Prostate Cancer by Activating Antitumor Innate Immunity. <i>Cancer Discovery</i> , 2017 , 7, 750-765	24.4	77
161	BCL6 Antagonizes NOTCH2 to Maintain Survival of Human Follicular Lymphoma Cells. <i>Cancer Discovery</i> , 2017 , 7, 506-521	24.4	27
160	Melanoma genome evolution across species. <i>BMC Genomics</i> , 2017 , 18, 136	4.5	11
159	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	24.4	69
158	Stem Cell Lineage Infidelity Drives Wound Repair and Cancer. <i>Cell</i> , 2017 , 169, 636-650.e14	56.2	161
157	Global miRNA expression analysis identifies novel key regulators of plasma cell differentiation and malignant plasma cell. <i>Nucleic Acids Research</i> , 2017 , 45, 5639-5652	20.1	28
156	Widespread Mitotic Bookmarking by Histone Marks and Transcription Factors in Pluripotent Stem Cells. <i>Cell Reports</i> , 2017 , 19, 1283-1293	10.6	75
155	Conversion of adult endothelium to immunocompetent haematopoietic stem cells. <i>Nature</i> , 2017 , 545, 439-445	50.4	135
154	An integrated model for detecting significant chromatin interactions from high-resolution Hi-C data. <i>Nature Communications</i> , 2017 , 8, 15454	17.4	41
153	Concerted regulation of retinal pigment epithelium basement membrane and barrier function by angiocrine factors. <i>Nature Communications</i> , 2017 , 8, 15374	17.4	39
152	Lymphatic endothelial S1P promotes mitochondrial function and survival in naive T cells. <i>Nature</i> , 2017 , 546, 158-161	50.4	101
151	Personalized and Cancer Models to Guide Precision Medicine. <i>Cancer Discovery</i> , 2017 , 7, 462-477	24.4	477

150	Systems Structural Biology Analysis of Ligand Effects on ER Predicts Cellular Response to Environmental Estrogens and Anti-hormone Therapies. <i>Cell Chemical Biology</i> , 2017 , 24, 35-45	8.2	23
149	Reversible methylation of mA in the 5' cap controls mRNA stability. <i>Nature</i> , 2017 , 541, 371-375	50.4	540
148	Mechanisms of Acquired Drug Resistance to the HDAC6 Selective Inhibitor Ricolinostat Reveals Rational Drug-Drug Combination with Ibrutinib. <i>Clinical Cancer Research</i> , 2017 , 23, 3084-3096	12.9	20
147	Single-cell RNA sequencing reveals a signature of sexual commitment in malaria parasites. <i>Nature</i> , 2017 , 551, 95-99	50.4	121
146	EZH2 enables germinal centre formation through epigenetic silencing of CDKN1A and an Rb-E2F1 feedback loop. <i>Nature Communications</i> , 2017 , 8, 877	17.4	87
145	Next-Generation Rapid Autopsies Enable Tumor Evolution Tracking and Generation of Preclinical Models. <i>JCO Precision Oncology</i> , 2017 , 2017,	3.6	23
144	Broad Targeting Specificity during Bacterial Type III CRISPR-Cas Immunity Constrains Viral Escape. <i>Cell Host and Microbe</i> , 2017 , 22, 343-353.e3	23.4	81
143	Flow-sorting and Exome Sequencing of the Reed-Sternberg Cells of Classical Hodgkin Lymphoma. <i>Journal of Visualized Experiments</i> , 2017 ,	1.6	3
142	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	24.6	102
141	R-Spondin chromosome rearrangements drive Wnt-dependent tumour initiation and maintenance in the intestine. <i>Nature Communications</i> , 2017 , 8, 15945	17.4	69
140	Systematic Discovery of Chromatin-Bound Protein Complexes from CHIP-seq Datasets. <i>Methods in Molecular Biology</i> , 2017 , 1507, 43-58	1.4	1
139	CREBBP Inactivation Promotes the Development of HDAC3-Dependent Lymphomas. <i>Cancer Discovery</i> , 2017 , 7, 38-53	24.4	159
138	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	8.6	66
137	Oncogenic BRAF disrupts thyroid morphogenesis and function via twist expression. <i>ELife</i> , 2017 , 6,	8.9	34
136	Identification of a nucleoside analog active against adenosine kinase-expressing plasma cell malignancies. <i>Journal of Clinical Investigation</i> , 2017 , 127, 2066-2080	15.9	5
135	A Computational Approach for Identifying Synergistic Drug Combinations. <i>PLoS Computational Biology</i> , 2017 , 13, e1005308	5	40
134	Cancer stem cell-related gene expression as a potential biomarker of response for first-in-class imipridone ONC201 in solid tumors. <i>PLoS ONE</i> , 2017 , 12, e0180541	3.7	22
133	Pathogen identification in prostate cancer biopsies using transcriptome sequencing.. <i>Journal of Clinical Oncology</i> , 2017 , 35, e16545-e16545	2.2	

132	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	12.5	95
131	Epigenetic profiles signify cell fate plasticity in unipotent spermatogonial stem and progenitor cells. <i>Nature Communications</i> , 2016 , 7, 11275	17.4	19
130	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	32.3	82
129	A Data-Driven Approach to Predicting Successes and Failures of Clinical Trials. <i>Cell Chemical Biology</i> , 2016 , 23, 1294-1301	8.2	66
128	Clonal evolution of chemotherapy-resistant urothelial carcinoma. <i>Nature Genetics</i> , 2016 , 48, 1490-1499	36.3	161
127	Development and validation of a whole-exome sequencing test for simultaneous detection of point mutations, indels and copy-number alterations for precision cancer care. <i>Npj Genomic Medicine</i> , 2016 , 1,	6.2	51
126	A Computational Drug Repositioning Approach for Targeting Oncogenic Transcription Factors. <i>Cell Reports</i> , 2016 , 15, 2348-56	10.6	25
125	Nuclear envelope expansion is crucial for proper chromosomal segregation during a closed mitosis. <i>Journal of Cell Science</i> , 2016 , 129, 1250-9	5.3	22
124	A primer on precision medicine informatics. <i>Briefings in Bioinformatics</i> , 2016 , 17, 145-53	13.4	30
123	Practical Analysis of Genome Contact Interaction Experiments. <i>Methods in Molecular Biology</i> , 2016 , 1418, 177-89	1.4	
122	Disruption of Adipose Rab10-Dependent Insulin Signaling Causes Hepatic Insulin Resistance. <i>Diabetes</i> , 2016 , 65, 1577-89	0.9	33
121	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. <i>Nature Medicine</i> , 2016 , 22, 298-305	50.5	775
120	Rationally designed BCL6 inhibitors target activated B cell diffuse large B cell lymphoma. <i>Journal of Clinical Investigation</i> , 2016 , 126, 3351-62	15.9	92
119	AICDA Introduces Epigenetic Plasticity in Germinal Center-Derived Lymphomas and Accelerates Lymphomagenesis. <i>Blood</i> , 2016 , 128, 1045-1045	2.2	1
118	Inherited mutations in DNA repair genes in men with metastatic castration-resistant prostate cancer.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 5009-5009	2.2	1
117	Generating a neoantigen map of advanced urothelial carcinoma by whole exome sequencing.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 354-354	2.2	3
116	Discovery and clinical introduction of first-in-class imipridone ONC201. <i>Oncotarget</i> , 2016 , 7, 74380-74393	3.3	83
115	Therapeutic efficacy of the bromodomain inhibitor OTX015/MK-8628 in ALK-positive anaplastic large cell lymphoma: an alternative modality to overcome resistant phenotypes. <i>Oncotarget</i> , 2016 , 7, 79637-79653	3.3	18

114	Integrated whole exome and RNA sequencing to reveal distinct genomic and transcriptomic landscape of upper tract urothelial carcinoma.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 379-379	2.2	
113	Patterns of Microrna in Plasma Cells: From Normal Differentiation to Multiple Myeloma. <i>Blood</i> , 2016 , 128, 2069-2069	2.2	
112	PRMT5 Targets Tumor Suppressor Micro RNAs to Regulate Cyclin D1 and c-MYC in Mantle Cell Lymphoma. <i>Blood</i> , 2016 , 128, 2937-2937	2.2	
111	An Epigenomic Approach to Improving Response to Neoadjuvant Cisplatin Chemotherapy in Bladder Cancer. <i>Biomolecules</i> , 2016 , 6,	5.9	33
110	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , 2016 , 375, 443-53	59.2	791
109	Predictive features of ligand-specific signaling through the estrogen receptor. <i>Molecular Systems Biology</i> , 2016 , 12, 864	12.2	29
108	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	14.4	74
107	Endothelial-specific inhibition of NF- κ B enhances functional haematopoiesis. <i>Nature Communications</i> , 2016 , 7, 13829	17.4	27
106	N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. <i>Cancer Cell</i> , 2016 , 30, 563-577	24.3	256
105	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	24.3	150
104	Transcriptome analysis of individual stromal cell populations identifies stroma-tumor crosstalk in mouse lung cancer model. <i>Cell Reports</i> , 2015 , 10, 1187-201	10.6	73
103	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	10.6	97
102	The chromatin Remodeler CHD8 is required for activation of progesterone receptor-dependent enhancers. <i>PLoS Genetics</i> , 2015 , 11, e1005174	6	25
101	Mechanosensitive pannexin-1 channels mediate microvascular metastatic cell survival. <i>Nature Cell Biology</i> , 2015 , 17, 943-52	23.4	85
100	Selective inhibition of protein arginine methyltransferase 5 blocks initiation and maintenance of B-cell transformation. <i>Blood</i> , 2015 , 125, 2530-43	2.2	96
99	The BRAF pseudogene functions as a competitive endogenous RNA and induces lymphoma in vivo. <i>Cell</i> , 2015 , 161, 319-32	56.2	233
98	5' UTR m(6)A Promotes Cap-Independent Translation. <i>Cell</i> , 2015 , 163, 999-1010	56.2	933
97	Vitamin C selectively kills KRAS and BRAF mutant colorectal cancer cells by targeting GAPDH. <i>Science</i> , 2015 , 350, 1391-6	33.3	537

96	Epigenomic evolution in diffuse large B-cell lymphomas. <i>Nature Communications</i> , 2015 , 6, 6921	17.4	81
95	Vascular Platform to Define Hematopoietic Stem Cell Factors and Enhance Regenerative Hematopoiesis. <i>Stem Cell Reports</i> , 2015 , 5, 881-894	8	37
94	Obesity-dependent changes in interstitial ECM mechanics promote breast tumorigenesis. <i>Science Translational Medicine</i> , 2015 , 7, 301ra130	17.5	175
93	DNA Methylation Dynamics of Germinal Center B Cells Are Mediated by AID. <i>Cell Reports</i> , 2015 , 12, 2086-2096	11.8	68
92	The histone lysine methyltransferase KMT2D sustains a gene expression program that represses B cell lymphoma development. <i>Nature Medicine</i> , 2015 , 21, 1199-208	50.5	247
91	Transcriptome sequencing reveals thousands of novel long non-coding RNAs in B cell lymphoma. <i>Genome Medicine</i> , 2015 , 7, 110	14.4	50
90	Use of RNA sequencing to evaluate rheumatic disease patients. <i>Arthritis Research and Therapy</i> , 2015 , 17, 167	5.7	21
89	Flow sorting and exome sequencing reveal the oncogenome of primary Hodgkin and Reed-Sternberg cells. <i>Blood</i> , 2015 , 125, 1061-72	2.2	206
88	CCMCL1: a new model of aggressive mantle cell lymphoma. <i>Blood</i> , 2015 , 125, 2730-2	2.2	5
87	Vascular niche promotes hematopoietic multipotent progenitor formation from pluripotent stem cells. <i>Journal of Clinical Investigation</i> , 2015 , 125, 1243-54	15.9	80
86	VDJ-Seq: Deep Sequencing Analysis of Rearranged Immunoglobulin Heavy Chain Gene to Reveal Clonal Evolution Patterns of B Cell Lymphoma. <i>Journal of Visualized Experiments</i> , 2015 , e53215	1.6	5
85	Prediction of Genetic Interactions Using Machine Learning and Network Properties. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 172	5.8	21
84	Identification of Reprogrammed Myeloid Cell Transcriptomes in NSCLC. <i>PLoS ONE</i> , 2015 , 10, e0129123	3.7	17
83	Integrative clinical genomics of advanced prostate cancer. <i>Cell</i> , 2015 , 161, 1215-1228	56.2	1765
82	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. <i>JAMA Oncology</i> , 2015 , 1, 466-74	13.4	207
81	Lymphoblastic transformation of follicular lymphoma: a clinicopathologic and molecular analysis of 7 patients. <i>Human Pathology</i> , 2015 , 46, 260-71	3.7	50
80	Whole exome sequencing to reveal chemotherapy-driven evolution of platinum-resistant metastatic urothelial cancer.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 4513-4513	2.2	1
79	Defining a molecular subclass of treatment resistant prostate cancer.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 5004-5004	2.2	3

78	Precision medicine program for whole-exome sequencing (WES) provides new insight on platinum sensitivity in advanced prostate cancer (PCa).. <i>Journal of Clinical Oncology</i> , 2015 , 33, 158-158	2.2	1
77	Clonal heterogeneity in platinum-resistant metastatic urothelial cancer.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 290-290	2.2	
76	Exquisite Sensitivity of Plasma Cell Malignancies to a Novel Nucleoside Analog Is Mediated By Overexpressed Adenosine Kinase. <i>Blood</i> , 2015 , 126, 1812-1812	2.2	
75	Transcriptome Sequencing Reveals Thousands of Novel Long Non-Coding RNAs in B-Cell Lymphoma. <i>Blood</i> , 2015 , 126, 2427-2427	2.2	
74	A Chromatin Reader That Acts As a Key to Lock in and Coordinate Recruitment of Transcription Factors and a Novel Polycomb Complex to Bivalent Chromatin Thus Driving Formation of Germinal Centers and B-Cell Lymphomas. <i>Blood</i> , 2015 , 126, 434-434	2.2	
73	Double-stranded DNA in exosomes: a novel biomarker in cancer detection. <i>Cell Research</i> , 2014 , 24, 766-924.7	987	
72	Tracing the roots of cancer evolution. <i>Cancer Discovery</i> , 2014 , 4, 995-7	24.4	2
71	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, 1022-33	24.4	203
70	Differentiation of human pluripotent stem cells to cells similar to cord-blood endothelial colony-forming cells. <i>Nature Biotechnology</i> , 2014 , 32, 1151-1157	44.5	164
69	Deep sequencing reveals clonal evolution patterns and mutation events associated with relapse in B-cell lymphomas. <i>Genome Biology</i> , 2014 , 15, 432	18.3	56
68	Molecular diagnosis of autosomal dominant polycystic kidney disease using next-generation sequencing. <i>Journal of Molecular Diagnostics</i> , 2014 , 16, 216-28	5.1	45
67	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, 7325-30	11.5	78
66	Reprogramming human endothelial cells to haematopoietic cells requires vascular induction. <i>Nature</i> , 2014 , 511, 312-8	50.4	171
65	DrugTargetSeqR: a genomics- and CRISPR-Cas9-based method to analyze drug targets. <i>Nature Chemical Biology</i> , 2014 , 10, 626-8	11.7	84
64	Impact of ERBB2 mutations on in vitro sensitivity of bladder cancer to lapatinib. <i>Cancer Biology and Therapy</i> , 2014 , 15, 1239-47	4.6	24
63	Tbx5 is required for avian and Mammalian epicardial formation and coronary vasculogenesis. <i>Circulation Research</i> , 2014 , 115, 834-44	15.7	23
62	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	6	137
61	ELAVL1 modulates transcriptome-wide miRNA binding in murine macrophages. <i>Cell Reports</i> , 2014 , 9, 2330-43	10.6	43

60	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, 18309-14	11.5	40
59	The oestrogen receptor alpha-regulated lncRNA NEAT1 is a critical modulator of prostate cancer. <i>Nature Communications</i> , 2014 , 5, 5383	17.4	432
58	Demethylase Activity of Aid during Germinal Center B Cell Maturation Could Contribute to Lymphomagenesis. <i>Blood</i> , 2014 , 124, 59-59	2.2	1
57	A Virtual B Cell Lymphoma Model to Predict Effective Combination Therapy. <i>Blood</i> , 2014 , 124, 928-928	2.2	2
56	Protein Arginine Methyltransferase 5 Directly Targets and Epigenetically Silences microRNAs miR33b and miR96 to Support Constitutive Cyclin D1 Activity in Non-Hodgkin's Lymphoma. <i>Blood</i> , 2014 , 124, 60-60	2.2	
55	A stable transcription factor complex nucleated by oligomeric AML1-ETO controls leukaemogenesis. <i>Nature</i> , 2013 , 500, 93-7	50.4	103
54	The fat mass and obesity associated gene (Fto) regulates activity of the dopaminergic midbrain circuitry. <i>Nature Neuroscience</i> , 2013 , 16, 1042-8	25.5	327
53	Molecular signatures of tissue-specific microvascular endothelial cell heterogeneity in organ maintenance and regeneration. <i>Developmental Cell</i> , 2013 , 26, 204-19	10.2	421
52	Epigenomic alterations in localized and advanced prostate cancer. <i>Neoplasia</i> , 2013 , 15, 373-83	6.4	59
51	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, 578-88	10.6	127
50	Synergistic activation of inflammatory cytokine genes by interferon- γ -induced chromatin remodeling and toll-like receptor signaling. <i>Immunity</i> , 2013 , 39, 454-69	32.3	176
49	NFIB is a governor of epithelial-melanocyte stem cell behaviour in a shared niche. <i>Nature</i> , 2013 , 495, 98-102	50.4	116
48	Punctuated evolution of prostate cancer genomes. <i>Cell</i> , 2013 , 153, 666-77	56.2	862
47	AID stabilizes stem-cell phenotype by removing epigenetic memory of pluripotency genes. <i>Nature</i> , 2013 , 500, 89-92	50.4	70
46	EZH2 is required for germinal center formation and somatic EZH2 mutations promote lymphoid transformation. <i>Cancer Cell</i> , 2013 , 23, 677-92	24.3	547
45	Inferring chromatin-bound protein complexes from genome-wide binding assays. <i>Genome Research</i> , 2013 , 23, 1295-306	9.7	28
44	Aberration in DNA methylation in B-cell lymphomas has a complex origin and increases with disease severity. <i>PLoS Genetics</i> , 2013 , 9, e1003137	6	91
43	Metabolic alterations in lung cancer-associated fibroblasts correlated with increased glycolytic metabolism of the tumor. <i>Molecular Cancer Research</i> , 2013 , 11, 579-92	6.6	69

42	Epigenetic repression of miR-31 disrupts androgen receptor homeostasis and contributes to prostate cancer progression. <i>Cancer Research</i> , 2013 , 73, 1232-44	10.1	137
41	Human ESC-derived hemogenic endothelial cells undergo distinct waves of endothelial to hematopoietic transition. <i>Blood</i> , 2013 , 121, 770-80	2.2	70
40	A novel approach for characterizing microsatellite instability in cancer cells. <i>PLoS ONE</i> , 2013 , 8, e63056	3.7	35
39	Deep Sequencing Reveals Clonal Evolution Patterns and Mutation Events Associated With Relapse In B Cell Lymphomas. <i>Blood</i> , 2013 , 122, 79-79	2.2	1
38	A panel of four miRNAs accurately differentiates malignant from benign indeterminate thyroid lesions on fine needle aspiration. <i>Clinical Cancer Research</i> , 2012 , 18, 2032-8	12.9	127
37	Using transcriptome sequencing to identify mechanisms of drug action and resistance. <i>Nature Chemical Biology</i> , 2012 , 8, 235-7	11.7	122
36	Comprehensive analysis of mRNA methylation reveals enrichment in 3' UTRs and near stop codons. <i>Cell</i> , 2012 , 149, 1635-46	56.2	2100
35	Efficient direct reprogramming of mature amniotic cells into endothelial cells by ETS factors and TGFβ suppression. <i>Cell</i> , 2012 , 151, 559-75	56.2	170
34	Oncogenic transcription factors as master regulators of chromatin topology: a new role for ERG in prostate cancer. <i>Cell Cycle</i> , 2012 , 11, 3380-3	4.7	12
33	Oncogene-mediated alterations in chromatin conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 9083-8	11.5	110
32	Genome-wide detection of genes targeted by non-Ig somatic hypermutation in lymphoma. <i>PLoS ONE</i> , 2012 , 7, e40332	3.7	39
31	An integrated ChIP-seq analysis platform with customizable workflows. <i>BMC Bioinformatics</i> , 2011 , 12, 277	3.6	72
30	DNA methyltransferase 1 and DNA methylation patterning contribute to germinal center B-cell differentiation. <i>Blood</i> , 2011 , 118, 3559-69	2.2	107
29	A Role for BCL6 in the Higher-Order Organization of Genes in DLBCL. <i>Blood</i> , 2011 , 118, 558-558	2.2	
28	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	7.6	172
27	EZH2-mediated epigenetic silencing in germinal center B cells contributes to proliferation and lymphomagenesis. <i>Blood</i> , 2010 , 116, 5247-55	2.2	227
26	DNA methylation signatures define molecular subtypes of diffuse large B-cell lymphoma. <i>Blood</i> , 2010 , 116, e81-9	2.2	124
25	Mutations in FLVCR1 cause posterior column ataxia and retinitis pigmentosa. <i>American Journal of Human Genetics</i> , 2010 , 87, 643-54	11	66

24	Large-scale discovery and characterization of protein regulatory motifs in eukaryotes. <i>PLoS ONE</i> , 2010 , 5, e14444	3.7	25
23	Integrative Genome-Wide DNA Methylation and Gene Expression Analysis Reveals Biological and Clinical Insights In Adult Acute Lymphoblastic Leukemia. <i>Blood</i> , 2010 , 116, 852-852	2.2	0
22	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, 6605-9	5.4	88
21	Revealing global regulatory perturbations across human cancers. <i>Molecular Cell</i> , 2009 , 36, 900-11	17.6	149
20	The BCL6 transcriptional program features repression of multiple oncogenes in primary B cells and is deregulated in DLBCL. <i>Blood</i> , 2009 , 113, 5536-48	2.2	179
19	EZH2 Mediates DNA Methylation-Independent Epigenetic Silencing of a Germinal Center Specific Transcriptional Program That Contributes to Cellular Proliferation and Lymphomagenesis.. <i>Blood</i> , 2009 , 114, 3465-3465	2.2	1
18	ABC and GCB DLBCLs Display Unique Biologically Distinct and Clinically Relevant Epigenetic Signatures.. <i>Blood</i> , 2009 , 114, 619-619	2.2	
17	Unmasking activation of the zygotic genome using chromosomal deletions in the Drosophila embryo. <i>PLoS Biology</i> , 2007 , 5, e117	9.7	201
16	A universal framework for regulatory element discovery across all genomes and data types. <i>Molecular Cell</i> , 2007 , 28, 337-50	17.6	241
15	Fastcompare: a nonalignment approach for genome-scale discovery of DNA and mRNA regulatory elements using network-level conservation. <i>Methods in Molecular Biology</i> , 2007 , 395, 349-66	1.4	5
14	Revealing posttranscriptional regulatory elements through network-level conservation. <i>PLoS Computational Biology</i> , 2005 , 1, e69	5	63
13	Reconstructing the duplication history of tandemly repeated genes. <i>Molecular Biology and Evolution</i> , 2002 , 19, 278-88	8.3	61
12	Prediction of Venous Thromboembolism Based on Clinical and Genetic Factors		1
11	Single-cell analysis of the muscle stem cell hierarchy identifies heterotypic communication signals involved in skeletal muscle regeneration		3
10	A New Big-Data Paradigm for Target Identification and Drug Discovery		9
9	A reference single-cell transcriptomic atlas of human skeletal muscle tissue reveals bifurcated muscle stem cell populations		2
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2	Metabolic and immune markers for precise monitoring of COVID-19 severity and treatment	1
1	A Systematic Framework for Assessing the Clinical Impact of Polygenic Risk Scores. <i>SSRN Electronic Journal</i> ,	1 5