Marc Zapatka

List of Publications by Year
in descending order

136 papers	21,332 citations	38742 50 h-index	17592 121 g-index
150 all docs	150 docs citations	150 times ranked	29714 citing authors

#	Article	IF	Citations
1	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	27.8	2,129
2	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
3	DNA methylation-based classification of central nervous system tumours. Nature, 2018, 555, 469-474.	27.8	1,872
4	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. Cancer Cell, 2012, 22, 425-437.	16.8	1,551
5	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
6	Resistance Mechanisms for the Bruton's Tyrosine Kinase Inhibitor Ibrutinib. New England Journal of Medicine, 2014, 370, 2286-2294.	27.0	1,042
7	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
8	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
9	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
10	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
11	Reduced H3K27me3 and DNA Hypomethylation Are Major Drivers of Gene Expression in K27M Mutant Pediatric High-Grade Gliomas. Cancer Cell, 2013, 24, 660-672.	16.8	633
12	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
13	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
14	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
15	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
16	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
17	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	21.4	261
18	IL4I1 Is a Metabolic Immune Checkpoint that Activates the AHR and Promotes Tumor Progression. Cell, 2020, 182, 1252-1270.e34.	28.9	259

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19	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. Nature Genetics, 2016, 48, 253-264.	21.4	254
20	Robust molecular subgrouping and copy-number profiling of medulloblastoma from small amounts of archival tumour material using high-density DNA methylation arrays. Acta Neuropathologica, 2013, 125, 913-916.	7.7	244
21	Somatic CRISPR/Cas9-mediated tumour suppressor disruption enables versatile brain tumour modelling. Nature Communications, 2015, 6, 7391.	12.8	244
22	Tumor-derived exosomes modulate PD-L1 expression in monocytes. Science Immunology, 2017, 2, .	11.9	236
23	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
24	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. Nature Medicine, 2016, 22, 1314-1320.	30.7	183
25	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. Nature, 2018, 553, 101-105.	27.8	170
26	Differential Clinical Significance of Individual NKG2D Ligands in Melanoma: Soluble ULBP2 as an Indicator of Poor Prognosis Superior to S100B. Clinical Cancer Research, 2009, 15, 5208-5215.	7.0	168
27	Merkel Cell Polyomavirus Status Is Not Associated with Clinical Course of Merkel Cell Carcinoma. Journal of Investigative Dermatology, 2011, 131, 1631-1638.	0.7	153
28	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. Cell Death and Differentiation, 2011, 18, 974-984.	11.2	133
29	Drug-perturbation-based stratification of blood cancer. Journal of Clinical Investigation, 2017, 128, 427-445.	8.2	124
30	RNAi screening in glioma stem-like cells identifies PFKFB4 as a key molecule important for cancer cell survival. Oncogene, 2012, 31, 3235-3243.	5.9	123
31	Serum Amyloid A As a Prognostic Marker in Melanoma Identified by Proteomic Profiling. Journal of Clinical Oncology, 2009, 27, 2199-2208.	1.6	107
32	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
33	Relevance of PTEN loss in brain metastasis formation in breast cancer patients. Breast Cancer Research, 2012, 14, R49.	5.0	93
34	Differential proteome analysis of conditioned media to detect Smad4 regulated secreted biomarkers in colon cancer. Proteomics, 2005, 5, 2587-2601.	2.2	86
35	Impact of the CCR5 gene polymorphism on the survival of metastatic melanoma patients receiving immunotherapy. Cancer Immunology, Immunotherapy, 2008, 57, 685-691.	4.2	83
36	MiR-328 promotes glioma cell invasion via SFRP1-dependent Wnt-signaling activation. Neuro-Oncology, 2014, 16, 179-190.	1.2	78

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37	The landscape of chromothripsis across adult cancer types. Nature Communications, 2020, 11, 2320.	12.8	75
38	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. Breast Cancer Research and Treatment, 2008, 108, 137-149.	2.5	74
39	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. PLoS ONE, 2013, 8, e66621.	2.5	74
40	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell Reports, 2019, 29, 2338-2354.e7.	6.4	74
41	Oligonucleotide arrayâ€based comparative genomic hybridization (aCGH) of 90 neuroblastomas reveals aberration patterns closely associated with relapse pattern and outcome. Genes Chromosomes and Cancer, 2006, 45, 1130-1142.	2.8	72
42	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. Breast Cancer Research and Treatment, 2010, 119, 201-211.	2.5	70
43	Survivin-specific T-cell reactivity correlates with tumor response and patient survival: a phase-II peptide vaccination trial in metastatic melanoma. Cancer Immunology, Immunotherapy, 2012, 61, 2091-2103.	4.2	69
44	Capture and Amplification by Tailing and Switching (CATS). RNA Biology, 2014, 11, 817-828.	3.1	68
45	Microphthalmia-Associated Transcription Factor Gene Amplification in Metastatic Melanoma Is a Prognostic Marker for Patient Survival, But Not a Predictive Marker for Chemosensitivity and Chemotherapy Response. Clinical Cancer Research, 2007, 13, 6344-6350.	7.0	67
46	Defective DNA damage repair leads to frequent catastrophic genomic events in murine and human tumors. Nature Communications, 2018, 9, 4760.	12.8	66
47	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. Cancer Cell, 2019, 35, 95-110.e8.	16.8	65
48	The branched-chain amino acid transaminase 1 sustains growth of antiestrogen-resistant and ERÎ±-negative breast cancer. Oncogene, 2017, 36, 4124-4134.	5.9	60
49	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. Neuron, 2009, 63, 585-591.	8.1	58
50	Polymorphisms in the BRCA1 and ABCB1 genes modulate menopausal hormone therapy associated breast cancer risk in postmenopausal women. Breast Cancer Research and Treatment, 2010, 120, 727-736.	2.5	58
51	Interleukin-10 receptor signaling promotes the maintenance of a PD-1int TCF-1+ CD8+ TÂcell population that sustains anti-tumor immunity. Immunity, 2021, 54, 2825-2841.e10.	14.3	57
52	Lsd1 as a therapeutic target in Gfi1-activated medulloblastoma. Nature Communications, 2019, 10, 332.	12.8	55
53	MiRâ€16â€5p is frequently downâ€regulated in astrocytic gliomas and modulates glioma cell proliferation, apoptosis and response to cytotoxic therapy. Neuropathology and Applied Neurobiology, 2019, 45, 441-458.	3.2	50
54	Molecular subgrouping of primary pineal parenchymal tumors reveals distinct subtypes correlated with clinical parameters and genetic alterations. Acta Neuropathologica, 2020, 139, 243-257.	7.7	50

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55	Loss of Smad4 correlates with loss of the invasion suppressor E-cadherin in advanced colorectal carcinomas. Journal of Pathology, 2004, 202, 412-420.	4.5	48
56	Genomic profiling of Acute lymphoblastic leukemia in ataxia telangiectasia patients reveals tight link between ATM mutations and chromothripsis. Leukemia, 2017, 31, 2048-2056.	7.2	47
57	Analysis of Epstein-Barr Virus Genomes and Expression Profiles in Gastric Adenocarcinoma. Journal of Virology, 2018, 92, .	3.4	47
58	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. PLoS Genetics, 2014, 10, e1004345.	3.5	44
59	Monitoring CSF Proteome Alterations in Amyotrophic Lateral Sclerosis: Obstacles and Perspectives in Translating a Novel Marker Panel to the Clinic. PLoS ONE, 2012, 7, e44401.	2.5	44
60	The FRA2C common fragile site maps to the borders of MYCN amplicons in neuroblastoma and is associated with gross chromosomal rearrangements in different cancers. Human Molecular Genetics, 2011, 20, 1488-1501.	2.9	42
61	Telomere dysfunction and chromothripsis. International Journal of Cancer, 2016, 138, 2905-2914.	5.1	42
62	The Phospholipase CÎ³2 Mutants R665W and L845F Identified in Ibrutinib-resistant Chronic Lymphocytic Leukemia Patients Are Hypersensitive to the Rho GTPase Rac2 Protein. Journal of Biological Chemistry, 2016, 291, 22136-22148.	3.4	42
63	Tumor suppressor Smad4 mediates downregulation of the anti-adhesive invasion-promoting matricellular protein SPARC: Landscaping activity of Smad4 as revealed by aâ€œsecretomeâ€•analysis. Proteomics, 2004, 4, 1324-1334.	2.2	41
64	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. Molecular Systems Biology, 2019, 15, e8339.	7.2	39
65	Reprogramming of the ERRÎ± and ERÎ± Target Gene Landscape Triggers Tamoxifen Resistance in Breast Cancer. Cancer Research, 2015, 75, 720-731.	0.9	36
66	Smad4 deficiency in cervical carcinoma cells. Oncogene, 2005, 24, 810-819.	5.9	35
67	Chromosome 17/17q gain and unaltered profiles in high resolution arrayâ€CGH are prognostically informative in neuroblastoma. Genes Chromosomes and Cancer, 2014, 53, 639-649.	2.8	34
68	The onset of p53 loss of heterozygosity is differentially induced in various stem cell types and may involve the loss of either allele. Cell Death and Differentiation, 2014, 21, 1419-1431.	11.2	34
69	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
70	Genome-wide identification of translationally inhibited and degraded miR-155 targets using RNA-interacting protein-IP. RNA Biology, 2013, 10, 1017-1029.	3.1	33
71	Basement membrane component laminin-5 is a target of the tumor suppressor Smad4. Oncogene, 2007, 26, 1417-1427.	5.9	32
72	NoBP, a Nuclear Fibroblast Growth Factor 3 Binding Protein, Is Cell Cycle Regulated and Promotes Cell Growth. Molecular and Cellular Biology, 2001, 21, 4996-5007.	2.3	29

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73	Polymorphisms in genes of the steroid receptor superfamily modify postmenopausal breast cancer risk associated with menopausal hormone therapy. International Journal of Cancer, 2010, 126, 2935-2946.	5.1	29
74	<scp>MED</scp>12 mutations and <scp>NOTCH</scp> signalling in chronic lymphocytic leukaemia. British Journal of Haematology, 2017, 179, 421-429.	2.5	29
75	ERCC5 p.Asp1104His and ERCC2 p.Lys751Gln Polymorphisms Are Independent Prognostic Factors for the Clinical Course of Melanoma. Journal of Investigative Dermatology, 2011, 131, 1280-1290.	0.7	28
76	Whole-Exome Sequencing Revealed No Recurrent Mutations within the PI3K Pathway in Relapsed Chronic Lymphocytic Leukemia Patients Progressing Under Idelalisib Treatment. Blood, 2016, 128, 2770-2770.	1.4	26
77	A novel cloning strategy for one-step assembly of multiplex CRISPR vectors. Scientific Reports, 2018, 8, 17499.	3.3	25
78	Proteomic analysis of field cancerization in pharynx and oesophagus: a prospective pilot study. Journal of Pathology, 2010, 221, 462-470.	4.5	24
79	DECIPHER pooled shRNA library screen identifies PP2A and FGFR signaling as potential therapeutic targets for diffuse intrinsic pontine gliomas. Neuro-Oncology, 2019, 21, 867-877.	1.2	24
80	Identification of serum proteins as prognostic and predictive markers of colorectal cancer using surface enhanced laser desorption ionization-time of flight mass spectrometry. Oncology Reports, 2010, 24, 57-64.	2.6	20
81	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. JCO Precision Oncology, 2021, 5, 676-686.	3.0	20
82	Postmenopausal estrogen monotherapyâ€“associated breast cancer risk is modified by CYP17A1_-34_T>C polymorphism. Breast Cancer Research and Treatment, 2010, 120, 737-744.	2.5	19
83	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. Cancer Research, 2019, 79, 3125-3138.	0.9	19
84	Unraveling most abundant mutational signatures in head and neck cancer. International Journal of Cancer, 2021, 148, 115-127.	5.1	19
85	Use of tumor genomic profiling to reveal mechanisms of resistance to the BTK inhibitor ibrutinib in chronic lymphocytic leukemia (CLL).. Journal of Clinical Oncology, 2013, 31, 7014-7014.	1.6	19
86	Discovering functional gene expression patterns in the metabolic network of Escherichia coli with wavelets transforms. BMC Bioinformatics, 2006, 7, 119.	2.6	17
87	CD8⁺ T-cells of CLL-bearing mice acquire a transcriptional program of T-cell activation and exhaustion. Leukemia and Lymphoma, 2020, 61, 351-356.	1.3	17
88	CITED4 gene silencing in colorectal cancer cells modulates adherens/tight junction gene expression and reduces cell proliferation. Journal of Cancer Research and Clinical Oncology, 2016, 142, 225-237.	2.5	15
89	Divergent mechanisms underlie Smad4-mediated positive regulation of the three genes encoding the basement membrane component laminin-332 (laminin-5). BMC Cancer, 2008, 8, 215.	2.6	14
90	qPCR in gastrointestinal stromal tumors: Evaluation of reference genes and expression analysis of KIT and the alternative receptor tyrosine kinases FLT3, CSF1-R, PDGFRB, MET and AXL. BMC Molecular Biology, 2010, 11, 100.	3.0	14

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91	Proteomic Bronchiolitis Obliterans Syndrome Risk Monitoring in Lung Transplant Recipients. Transplantation, 2011, 92, 477-485.	1.0	13
92	Low p14ARF expression in neuroblastoma cells is associated with repressed histone mark status, and enforced expression induces growth arrest and apoptosis. Human Molecular Genetics, 2013, 22, 1735-1745.	2.9	13
93	Mismatch Repair Deficiency Drives Durable Complete Remission by Targeting Programmed Death Receptor 1 in a Metastatic Luminal Breast Cancer Patient. Breast Care, 2019, 14, 53-59.	1.4	13
94	Bronchoalveolar lavage fluid of lung cancer patients: Mapping the uncharted waters using proteomics technology. Lung Cancer, 2011, 72, 136-138.	2.0	12
95	Association of mutation signature effectuating processes with mutation hotspots in driver genes and non-coding regions. Nature Communications, 2022, 13, 178.	12.8	12
96	Using gene expression data and network topology to detect substantial pathways, clusters and switches during oxygen deprivation of Escherichia coli. BMC Bioinformatics, 2007, 8, 149.	2.6	11
97	Chromothripsis in Human Breast Cancer. Cancer Research, 2020, 80, 4918-4931.	0.9	11
98	Clonal evolution in chronic lymphocytic leukemia is scant in relapsed but accelerated in refractory cases after chemo(immune) therapy. Haematologica, 2022, 107, 604-614.	3.5	11
99	Tumorâ€“microenvironment interactions studied by zonal transcriptional profiling of squamous cell lung carcinoma. Genes Chromosomes and Cancer, 2013, 52, 250-264.	2.8	10
100	In silico SNP analysis of the breast cancer antigen NY-BR-1. BMC Cancer, 2016, 16, 901.	2.6	10
101	Pilocytic astrocytoma demethylation and transcriptional landscapes link bZIP transcription factors to immune response. Neuro-Oncology, 2020, 22, 1327-1338.	1.2	10
102	Postoperative serum proteomic profiles may predict recurrence-free survival in high-risk primary breast cancer. Journal of Cancer Research and Clinical Oncology, 2011, 137, 1773-1783.	2.5	9
103	confFuse: High-Confidence Fusion Gene Detection across Tumor Entities. Frontiers in Genetics, 2017, 8, 137.	2.3	9
104	Secondary resistance to idelalisib is characterized by upregulation of IGF1R rather than by MAPK/ERK pathway mutations. Blood, 2022, 139, 3340-3344.	1.4	9
105	High-level inducible Smad4-reexpression in the cervical cancer cell line C4-II is associated with a gene expression profile that predicts a preferential role of Smad4 in extracellular matrix composition. BMC Cancer, 2007, 7, 209.	2.6	8
106	Implementation of Smith-Waterman Algorithm in OpenCL for GPUs. , 2010, , .		8
107	Carbon ion radiotherapy eradicates medulloblastomas with chromothripsis in an orthotopic Li-Fraumeni patient-derived mouse model. Neuro-Oncology, 2021, 23, 2028-2041.	1.2	7
108	The age of adult pilocytic astrocytoma cells. Oncogene, 2021, 40, 2830-2841.	5.9	6

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109	Serum proteomics and disease-specific biomarkers of patients with advanced gastric cancer. Oncology Letters, 2010, 1, 327-333.	1.8	5
110	A synergistic interaction between HDACâ€•and PARP inhibitors in childhood tumors with chromothripsis. International Journal of Cancer, 2022, 151, 590-606.	5.1	5
111	Comparative parallel multi-omics analysis during the induction of pluripotent and trophectoderm states. Nature Communications, 2022, 13, .	12.8	4
112	Data-Mining in klinischen DatensÃtzen â€“ Bericht der Arbeitsgruppe Bioinformatik der DGKL. Laboratoriums Medizin, 2010, 34, 227-233.	0.6	3
113	STAT3 Single Nucleotide Polymorphism rs4796793 SNP Does Not Correlate with Response to Adjuvant IFNÃŽÂ± Therapy in Stage III Melanoma Patients. Frontiers in Medicine, 2014, 1, 47.	2.6	3
114	A versatile system to introduce clusters of genomic doubleâ€strand breaks in large cell populations. Genes Chromosomes and Cancer, 2021, 60, 303-313.	2.8	3
115	Longitudinal analyses of CLL in mice identify leukemia-related clonal changes including a Myc gain predicting poor outcome in patients. Leukemia, 2021, , .	7.2	3
116	Ontological Analysis and Pathway Modelling in Drug Discovery. Pharmaceutical Medicine, 2008, 22, 99-105.	1.9	2
117	Abstract 4872: ICGC PedBrain Tumor - Next-generation sequencing identifies novel subgroup-specific mutations and copy number aberrations in medulloblastoma. Cancer Research, 2012, 72, 4872-4872.	0.9	1
118	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 2436-2436.	1.4	1
119	CLL Exosome-Derived Y RNA hY4 Induces TLR7/8-Mediated Inflammation and PD-L1 Expression in Monocytes. Blood, 2016, 128, 3217-3217.	1.4	1
120	GENE-06. DISTINCT MOLECULAR SUBGROUPS OF TUMORS OF THE PINEAL REGION CORRELATE WITH CLINICAL PARAMETERS AND GENETIC ALTERATIONS. Neuro-Oncology, 2019, 21, ii81-ii82.	1.2	0
121	Tumor suppressor Smad4 mediates down-regulation of the anti-adhesive invasion-promoting matricellular protein SPARC. , 0, 2004, .		0
122	CCR5 gene polymorphism in patients with cutaneous melanoma: Impact on survival following immunotherapy. Journal of Clinical Oncology, 2007, 25, 21071-21071.	1.6	0
123	Abstract 4724: Identification of a CpG-island methylator phenotype (CIMP) in a subgroup of pilocytic astrocytoma with favorable prognosis. , 2011, , .		0
124	Abstract 3084: Epigenetic deregulation in H3.3-K27M mutant pediatric high-grade gliomas. , 2014, , .		0
125	Abstract B25: Progressive epigenetic programming during B cell maturation yields a continuum of clonal disease phenotypes with distinct etiologies in chronic lymphocytic leukemia.. , 2015, , .		0
126	Abstract PR02: Somatic CRISPR/Cas9-mediated tumor suppressor disruption enables versatile brain tumor modeling. , 2015, , .		0

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127	Abstract A30: Chronic lymphocytic leukemia-derived extracellular vesicles mediate NFkB signaling and pro-inflammatory cytokine release in monocytes. , 2016, , .		0
128	Abstract 509: Genomic profiling of acute lymphoblastic leukemia in ataxia telangiectasia patients reveals tight link betweenATMmutations and chromothripsis. , 2017, , .		0
129	Abstract 1352: Inactivation of factors of DNA double-strand break repair by homologous recombination or non-homologous end-joining leads to frequent catastrophic genomic events in murine and human tumors. , 2018, , .		0
130	Abstract 5109: Somatic CRISPR/Cas9-mediated gene editing enables versatile brain tumor modeling. , 2018, , .		0
131	Abstract 1686: Comprehensive genomic and transcriptomic profiling of gastrointestinal stromal tumors. , 2019, , .		0
132	Abstract PD2-01: Exploring CDK4/6 inhibitor therapy response and drug resistance development at the single cell level in metastatic breast cancer CTCs. , 2020, , .		0
133	Viren und Krebs: Umfassende Suche nach viralen Sequenzen. , 0, , .		0
134	Immune Suppression in CLL Is Mediated By the L-Amino Acid Oxidase IL4I1, a Reason for the Treatment Failure of IDO1 Inhibitors. Blood, 2020, 136, 34-34.	1.4	0
135	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. Blood, 2020, 136, 10-11.	1.4	0
136	Abstract 3496: Defective DNA damage repair leads to frequent catastrophic genomic events in murine and human tumors. , 2019, , .		0