David T W Jones

List of Publications by Year
in descending order

267 papers	50,632 citations	2675 95 h-index	1715 213 g-index
285 all docs	285 docs citations	285 times ranked	44955 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	27.8	2,129
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	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. Cancer Cell, 2015, 27, 728-743.	16.8	933
7	Molecular subgroups of medulloblastoma: an international meta-analysis of transcriptome, genetic aberrations, and clinical data of WNT, SHH, Group 3, and Group 4 medulloblastomas. Acta Neuropathologica, 2012, 123, 473-484.	7.7	863
8	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
9	Tandem Duplication Producing a Novel Oncogenic BRAF Fusion Gene Defines the Majority of Pilocytic Astrocytomas. Cancer Research, 2008, 68, 8673-8677.	0.9	786
10	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
11	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
12	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
13	Integrated Molecular Meta-Analysis of 1,000 Pediatric High-Grade and Diffuse Intrinsic Pontine Glioma. Cancer Cell, 2017, 32, 520-537.e5.	16.8	716
14	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	28.9	702
15	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. Nature, 2012, 488, 106-110.	27.8	675
16	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
17	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
18	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627

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19	DNA methylation-based classification and grading system for meningioma: a multicentre, retrospective analysis. Lancet Oncology, The, 2017, 18, 682-694.	10.7	586
20	Medulloblastomics: the end of the beginning. Nature Reviews Cancer, 2012, 12, 818-834.	28.4	560
21	Challenges to curing primary brain tumours. Nature Reviews Clinical Oncology, 2019, 16, 509-520.	27.6	540
22	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
23	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
24	IDH1 mutations are present in the majority of common adult gliomas but rare in primary glioblastomas. Neuro-Oncology, 2009, 11, 341-347.	1.2	504
25	Delineation of Two Clinically and Molecularly Distinct Subgroups of Posterior Fossa Ependymoma. Cancer Cell, 2011, 20, 143-157.	16.8	494
26	Paediatric and adult glioblastoma: multiform (epi)genomic culprits emerge. Nature Reviews Cancer, 2014, 14, 92-107.	28.4	469
27	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
28	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
29	Subgroup-Specific Prognostic Implications of TP53 Mutation in Medulloblastoma. Journal of Clinical Oncology, 2013, 31, 2927-2935.	1.6	381
30	Recurrent somatic mutations in ACVR1 in pediatric midline high-grade astrocytoma. Nature Genetics, 2014, 46, 462-466.	21.4	381
31	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
32	ATRX and IDH1-R132H immunohistochemistry with subsequent copy number analysis and IDH sequencing as a basis for an â€œintegratedâ€•diagnostic approach for adult astrocytoma, oligodendroglioma and glioblastoma. Acta Neuropathologica, 2015, 129, 133-146.	7.7	378
33	Frequent ATRX mutations and loss of expression in adult diffuse astrocytic tumors carrying IDH1/IDH2 and TP53 mutations. Acta Neuropathologica, 2012, 124, 615-625.	7.7	376
34	Pilocytic astrocytoma: pathology, molecular mechanisms and markers. Acta Neuropathologica, 2015, 129, 775-788.	7.7	328
35	Meningeal hemangiopericytoma and solitary fibrous tumors carry the NAB2-STAT6 fusion and can be diagnosed by nuclear expression of STAT6 protein. Acta Neuropathologica, 2013, 125, 651-658.	7.7	324
36	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318

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37	Selumetinib in paediatric patients with BRAF-aberrant or neurofibromatosis type 1-associated recurrent, refractory, or progressive low-grade glioma: a multicentre, phase 2 trial. Lancet Oncology, The, 2019, 20, 1011-1022.	10.7	315
38	Practical implementation of DNA methylation and copy-number-based CNS tumor diagnostics: the Heidelberg experience. Acta Neuropathologica, 2018, 136, 181-210.	7.7	308
39	Recurrence patterns across medulloblastoma subgroups: an integrated clinical and molecular analysis. Lancet Oncology, The, 2013, 14, 1200-1207.	10.7	307
40	Novel, improved grading system(s) for IDH-mutant astrocytic gliomas. Acta Neuropathologica, 2018, 136, 153-166.	7.7	298
41	Integrated analysis of pediatric glioblastoma reveals a subset of biologically favorable tumors with associated molecular prognostic markers. Acta Neuropathologica, 2015, 129, 669-678.	7.7	277
42	Prognostic value of medulloblastoma extent of resection after accounting for molecular subgroup: a retrospective integrated clinical and molecular analysis. Lancet Oncology, The, 2016, 17, 484-495.	10.7	274
43	Farewell to oligoastrocytoma: in situ molecular genetics favor classification as either oligodendroglioma or astrocytoma. Acta Neuropathologica, 2014, 128, 551-559.	7.7	268
44	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
45	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
46	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
47	Cytogenetic Prognostication Within Medulloblastoma Subgroups. Journal of Clinical Oncology, 2014, 32, 886-896.	1.6	263
48	Next-generation personalised medicine for high-risk paediatric cancer patients â€“ The INFORM pilot study. European Journal of Cancer, 2016, 65, 91-101.	2.8	262
49	Distribution of TERT promoter mutations in pediatric and adult tumors of the nervous system. Acta Neuropathologica, 2013, 126, 907-915.	7.7	254
50	Mutations in SETD2 and genes affecting histone H3K36 methylation target hemispheric high-grade gliomas. Acta Neuropathologica, 2013, 125, 659-669.	7.7	250
51	Clinical, Radiologic, Pathologic, and Molecular Characteristics of Long-Term Survivors of Diffuse Intrinsic Pontine Glioma (DIPG): A Collaborative Report From the International and European Society for Pediatric Oncology DIPG Registries. Journal of Clinical Oncology, 2018, 36, 1963-1972.	1.6	250
52	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
53	Somatic CRISPR/Cas9-mediated tumour suppressor disruption enables versatile brain tumour modelling. Nature Communications, 2015, 6, 7391.	12.8	244
54	Adult IDH wild type astrocytomas biologically and clinically resolve into other tumor entities. Acta Neuropathologica, 2015, 130, 407-417.	7.7	237

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55	Sarcoma classification by DNA methylation profiling. Nature Communications, 2021, 12, 498.	12.8	237
56	Pediatric Gliomas: Current Concepts on Diagnosis, Biology, and Clinical Management. Journal of Clinical Oncology, 2017, 35, 2370-2377.	1.6	223
57	Pediatric high-grade glioma: biologically and clinically in need of new thinking. Neuro-Oncology, 2017, 19, now101.	1.2	217
58	Methylation of the TERT promoter and risk stratification of childhood brain tumours: an integrative genomic and molecular study. Lancet Oncology, The, 2013, 14, 534-542.	10.7	212
59	Oncogenic FAM131Bâ€“BRAF fusion resulting from 7q34 deletion comprises an alternative mechanism of MAPK pathway activation in pilocytic astrocytoma. Acta Neuropathologica, 2011, 121, 763-774.	7.7	211
60	Secretory meningiomas are defined by combined KLF4 K409Q and TRAF7 mutations. Acta Neuropathologica, 2013, 125, 351-358.	7.7	208
61	Next-generation sequencing in routine brain tumor diagnostics enables an integrated diagnosis and identifies actionable targets. Acta Neuropathologica, 2016, 131, 903-910.	7.7	203
62	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	7.7	199
63	Embryonal tumor with abundant neuropil and true rosettes (ETANTR), ependymoblastoma, and medulloepithelioma share molecular similarity and comprise a single clinicopathological entity. Acta Neuropathologica, 2014, 128, 279-289.	7.7	191
64	Anaplastic astrocytoma with piloid features, a novel molecular class of IDH wildtype glioma with recurrent MAPK pathway, CDKN2A/B and ATRX alterations. Acta Neuropathologica, 2018, 136, 273-291.	7.7	190
65	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. Nature Medicine, 2016, 22, 1314-1320.	30.7	183
66	MAPK pathway activation in pilocytic astrocytoma. Cellular and Molecular Life Sciences, 2012, 69, 1799-1811.	5.4	177
67	Integrated DNA methylation and copy-number profiling identify three clinically and biologically relevant groups of anaplastic glioma. Acta Neuropathologica, 2014, 128, 561-571.	7.7	176
68	Phase II study of sorafenib in children with recurrent or progressive low-grade astrocytomas. Neuro-Oncology, 2014, 16, 1408-1416.	1.2	175
69	Polymorphous low-grade neuroepithelial tumor of the young (PLNTY): an epileptogenic neoplasm with oligodendroglioma-like components, aberrant CD34 expression, and genetic alterations involving the MAP kinase pathway. Acta Neuropathologica, 2017, 133, 417-429.	7.7	172
70	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. Nature, 2018, 553, 101-105.	27.8	170
71	Radiomic subtyping improves disease stratification beyond key molecular, clinical, and standard imaging characteristics in patients with glioblastoma. Neuro-Oncology, 2018, 20, 848-857.	1.2	170
72	cIMPACT-NOW update 4: diffuse gliomas characterized by MYB, MYBL1, or FGFR1 alterations or BRAFV600E mutation. Acta Neuropathologica, 2019, 137, 683-687.	7.7	170

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73	Aberrant patterns of H3K4 and H3K27 histone lysine methylation occur across subgroups in medulloblastoma. Acta Neuropathologica, 2013, 125, 373-384.	7.7	169
74	Histologically distinct neuroepithelial tumors with histone 3 G34 mutation are molecularly similar and comprise a single nosologic entity. Acta Neuropathologica, 2016, 131, 137-146.	7.7	162
75	Therapeutic Impact of Cytoreductive Surgery and Irradiation of Posterior Fossa Ependymoma in the Molecular Era: A Retrospective Multicohort Analysis. Journal of Clinical Oncology, 2016, 34, 2468-2477.	1.6	160
76	Infant High-Grade Gliomas Comprise Multiple Subgroups Characterized by Novel Targetable Gene Fusions and Favorable Outcomes. Cancer Discovery, 2020, 10, 942-963.	9.4	157
77	Global epigenetic profiling identifies methylation subgroups associated with recurrence-free survival in meningioma. Acta Neuropathologica, 2017, 133, 431-444.	7.7	155
78	Methylation-based classification of benign and malignant peripheral nerve sheath tumors. Acta Neuropathologica, 2016, 131, 877-887.	7.7	151
79	Risk-adapted therapy for young children with medulloblastoma (SJYC07): therapeutic and molecular outcomes from a multicentre, phase 2 trial. Lancet Oncology, The, 2018, 19, 768-784.	10.7	151
80	TERT promoter mutations are highly recurrent in SHH subgroup medulloblastoma. Acta Neuropathologica, 2013, 126, 917-929.	7.7	146
81	H3-/IDH-wild type pediatric glioblastoma is comprised of molecularly and prognostically distinct subtypes with associated oncogenic drivers. Acta Neuropathologica, 2017, 134, 507-516.	7.7	144
82	Molecular, Pathological, Radiological, and Immune Profiling of Non-brainstem Pediatric High-Grade Glioma from the HERBY Phase II Randomized Trial. Cancer Cell, 2018, 33, 829-842.e5.	16.8	140
83	Adamantinomatous and papillary craniopharyngiomas are characterized by distinct epigenomic as well as mutational and transcriptomic profiles. Acta Neuropathologica Communications, 2016, 4, 20.	5.2	136
84	Genetic Aberrations Leading to MAPK Pathway Activation Mediate Oncogene-Induced Senescence in Sporadic Pilocytic Astrocytomas. Clinical Cancer Research, 2011, 17, 4650-4660.	7.0	135
85	Poorly differentiated chordoma with SMARCB1/INI1 loss: a distinct molecular entity with dismal prognosis. Acta Neuropathologica, 2016, 132, 149-151.	7.7	127
86	Prognostic significance of clinical, histopathological, and molecular characteristics of medulloblastomas in the prospective HIT2000 multicenter clinical trial cohort. Acta Neuropathologica, 2014, 128, 137-149.	7.7	125
87	A biobank of patient-derived pediatric brain tumor models. Nature Medicine, 2018, 24, 1752-1761.	30.7	124
88	Chd7 is indispensable for mammalian brain development through activation of a neuronal differentiation programme. Nature Communications, 2017, 8, 14758.	12.8	118
89	Molecularly defined diffuse leptomeningeal glioneuronal tumor (DLGNT) comprises two subgroups with distinct clinical and genetic features. Acta Neuropathologica, 2018, 136, 239-253.	7.7	118
90	Pediatric low-grade gliomas: next biologically driven steps. Neuro-Oncology, 2018, 20, 160-173.	1.2	116

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91	CDKN2A/B homozygous deletion is associated with early recurrence in meningiomas. Acta Neuropathologica, 2020, 140, 409-413.	7.7	116
92	LIN28A immunoreactivity is a potent diagnostic marker of embryonal tumor with multilayered rosettes (ETMR). Acta Neuropathologica, 2012, 124, 875-881.	7.7	115
93	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	21.4	112
94	The Pediatric Precision Oncology INFORM Registry: Clinical Outcome and Benefit for Patients with Very High-Evidence Targets. Cancer Discovery, 2021, 11, 2764-2779.	9.4	110
95	Primary intracranial spindle cell sarcoma with rhabdomyosarcoma-like features share a highly distinct methylation profile and DICER1 mutations. Acta Neuropathologica, 2018, 136, 327-337.	7.7	104
96	MYCN amplification drives an aggressive form of spinal ependymoma. Acta Neuropathologica, 2019, 138, 1075-1089.	7.7	104
97	Histone H3 wild-type DIPG/DMG overexpressing EZHIP extend the spectrum diffuse midline gliomas with PRC2 inhibition beyond H3-K27M mutation. Acta Neuropathologica, 2020, 139, 1109-1113.	7.7	104
98	Nuclear relocation of <scp>STAT</scp>6 reliably predicts NAB2â€“STAT6 fusion for the diagnosis of solitary fibrous tumour. Histopathology, 2014, 65, 613-622.	2.9	101
99	Methylation array profiling of adult brain tumours: diagnostic outcomes in a large, single centre. Acta Neuropathologica Communications, 2019, 7, 24.	5.2	101
100	N2M2 (NOA-20) phase I/II trial of molecularly matched targeted therapies plus radiotherapy in patients with newly diagnosed non-MGMT hypermethylated glioblastoma. Neuro-Oncology, 2019, 21, 95-105.	1.2	100
101	Molecular characteristics and therapeutic vulnerabilities across paediatric solid tumours. Nature Reviews Cancer, 2019, 19, 420-438.	28.4	98
102	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. Nucleic Acids Research, 2015, 43, e10-e10.	14.5	95
103	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	27.8	94
104	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. Nature, 2020, 580, 396-401.	27.8	94
105	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. Cell, 2020, 183, 1617-1633.e22.	28.9	93
106	Integrated Molecular-Morphologic Meningioma Classification: A Multicenter Retrospective Analysis, Retrospectively and Prospectively Validated. Journal of Clinical Oncology, 2021, 39, 3839-3852.	1.6	93
107	Epithelioid glioblastomas stratify into established diagnostic subsets upon integrated molecular analysis. Brain Pathology, 2018, 28, 656-662.	4.1	89
108	Machine learning workflows to estimate class probabilities for precision cancer diagnostics on DNA methylation microarray data. Nature Protocols, 2020, 15, 479-512.	12.0	89

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109	AKT1E17K mutations cluster with meningothelial and transitional meningiomas and can be detected by SFRP1 immunohistochemistry. Acta Neuropathologica, 2013, 126, 757-762.	7.7	88
110	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	12.8	87
111	Differential expression and methylation of brain developmental genes define location-specific subsets of pilocytic astrocytoma. Acta Neuropathologica, 2013, 126, 291-301.	7.7	84
112	Transcriptomic and epigenetic profiling of â€˜diffuse midline gliomas, H3 K27M-mutantâ€™ discriminate two subgroups based on the type of histone H3 mutated and not supratentorial or infratentorial location. Acta Neuropathologica Communications, 2018, 6, 117.	5.2	83
113	Isomorphic diffuse glioma is a morphologically and molecularly distinct tumour entity with recurrent gene fusions of MYBL1 or MYB and a benign disease course. Acta Neuropathologica, 2020, 139, 193-209.	7.7	83
114	MGMT CpG island is invariably methylated in adult astrocytic and oligodendroglial tumors with IDH1 or IDH2 mutations. International Journal of Cancer, 2012, 131, 1104-1113.	5.1	78
115	Assessing CpG island methylator phenotype, 1p/19q codeletion, and MGMT promoter methylation from epigenome-wide data in the biomarker cohort of the NOA-04 trial. Neuro-Oncology, 2014, 16, 1630-1638.	1.2	77
116	Array-based DNA-methylation profiling in sarcomas with small blue round cell histology provides valuable diagnostic information. Modern Pathology, 2018, 31, 1246-1256.	5.5	76
117	A subset of pediatric-type thalamic gliomas share a distinct DNA methylation profile, H3K27me3 loss and frequent alteration of EGFR. Neuro-Oncology, 2021, 23, 34-43.	1.2	75
118	Gliomatosis cerebri: no evidence for a separate brain tumor entity. Acta Neuropathologica, 2016, 131, 309-319.	7.7	74
119	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. Acta Neuropathologica, 2019, 138, 295-308.	7.7	74
120	Pediatric low-grade gliomas: implications of the biologic era. Neuro-Oncology, 2017, 19, now209.	1.2	73
121	Evidence of H3 K27M mutations in posterior fossa ependymomas. Acta Neuropathologica, 2016, 132, 635-637.	7.7	73
122	Super enhancers define regulatory subtypes and cell identity in neuroblastoma. Nature Cancer, 2021, 2, 114-128.	13.2	73
123	Genomic Analysis of Pilocytic Astrocytomas at 0.97 Mb Resolution Shows an Increasing Tendency Toward Chromosomal Copy Number Change With Age. Journal of Neuropathology and Experimental Neurology, 2006, 65, 1049-1058.	1.7	72
124	Next-generation (epi)genetic drivers of childhood brain tumours and the outlook for targeted therapies. Lancet Oncology, The, 2015, 16, e293-e302.	10.7	72
125	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. Nature Communications, 2018, 9, 2378.	12.8	72
126	Response to trametinib treatment in progressive pediatric low-grade glioma patients. Journal of Neuro-Oncology, 2020, 149, 499-510.	2.9	68

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127	An activated mutant BRAF kinase domain is sufficient to induce pilocytic astrocytoma in mice. Journal of Clinical Investigation, 2011, 121, 1344-1348.	8.2	68
128	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67
129	Methylation profiling of choroid plexus tumors reveals 3 clinically distinct subgroups. Neuro-Oncology, 2016, 18, 790-796.	1.2	67
130	Biological and clinical heterogeneity of MYCN-amplified medulloblastoma. Acta Neuropathologica, 2012, 123, 515-527.	7.7	66
131	Melanotic Tumors of the Nervous System are Characterized by Distinct Mutational, Chromosomal and Epigenomic Profiles. Brain Pathology, 2015, 25, 202-208.	4.1	66
132	Defective DNA damage repair leads to frequent catastrophic genomic events in murine and human tumors. Nature Communications, 2018, 9, 4760.	12.8	66
133	Bevacizumab plus hypofractionated radiotherapy versus radiotherapy alone in elderly patients with glioblastoma: the randomized, open-label, phase II ARTE trial. Annals of Oncology, 2018, 29, 1423-1430.	1.2	65
134	YAP1 subgroup supratentorial ependymoma requires TEAD and nuclear factor I-mediated transcriptional programmes for tumorigenesis. Nature Communications, 2019, 10, 3914.	12.8	65
135	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
136	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. Oncotarget, 2016, 7, 28169-28182.	1.8	62
137	EWSR1â€PATZ1 gene fusion may define a new glioneuronal tumor entity. Brain Pathology, 2019, 29, 53-62.	4.1	61
138	DNA methylation-based reclassification of olfactory neuroblastoma. Acta Neuropathologica, 2018, 136, 255-271.	7.7	59
139	FBW7 suppression leads to SOX9 stabilization and increased malignancy in medulloblastoma. EMBO Journal, 2016, 35, 2192-2212.	7.8	58
140	Cribriform neuroepithelial tumor: molecular characterization of a SMARCB1â€deficient nonâ€rhabdoid tumor with favorable longâ€term outcome. Brain Pathology, 2017, 27, 411-418.	4.1	58
141	Extensive Molecular and Clinical Heterogeneity in Patients With Histologically Diagnosed CNS-PNET Treated as a Single Entity: A Report From the Childrenâ€™s Oncology Group Randomized ACNS0332 Trial. Journal of Clinical Oncology, 2018, 36, 3388-3395.	1.6	58
142	Rosette-forming glioneuronal tumors share a distinct DNA methylation profile and mutations in FGFR1, with recurrent co-mutation of PIK3CA and NF1. Acta Neuropathologica, 2019, 138, 497-504.	7.7	57
143	Multicenter pilot study of radiochemotherapy as first-line treatment for adults with medulloblastoma (NOA-07). Neuro-Oncology, 2018, 20, 400-410.	1.2	56
144	FGFR1:TACC1 fusion is a frequent event in molecularly defined extraventricular neurocytoma. Acta Neuropathologica, 2018, 136, 293-302.	7.7	56

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145	TelomereHunter â€“ in silico estimation of telomere content and composition from cancer genomes. BMC Bioinformatics, 2019, 20, 272.	2.6	56
146	H3.3-K27M drives neural stem cell-specific gliomagenesis in a human iPSC-derived model. Cancer Cell, 2021, 39, 407-422.e13.	16.8	56
147	The Senescence-associated Secretory Phenotype Mediates Oncogene-induced Senescence in Pediatric Pilocytic Astrocytoma. Clinical Cancer Research, 2019, 25, 1851-1866.	7.0	55
148	DNA methylation-based profiling for paediatric CNS tumour diagnosis and treatment: a population-based study. The Lancet Child and Adolescent Health, 2020, 4, 121-130.	5.6	55
149	Genomic and transcriptomic analyses match medulloblastoma mouse models to their human counterparts. Acta Neuropathologica, 2014, 128, 123-136.	7.7	54
150	Recurrent homozygous deletion of DROSHA and microduplication of PDE4DIP in pineoblastoma. Nature Communications, 2018, 9, 2868.	12.8	54
151	Primary mismatch repair deficient IDH-mutant astrocytoma (PMMRDIA) is a distinct type with a poor prognosis. Acta Neuropathologica, 2021, 141, 85-100.	7.7	52
152	Histone 3.3 hotspot mutations in conventional osteosarcomas: a comprehensive clinical and molecular characterization of six H3F3A mutated cases. Clinical Sarcoma Research, 2017, 7, 9.	2.3	51
153	Brainstem biopsy in pediatric diffuse intrinsic pontine glioma in the era of precision medicine: the INFORM study experience. European Journal of Cancer, 2019, 114, 27-35.	2.8	51
154	Primary intracranial sarcomas with DICER1 mutation often contain prominent eosinophilic cytoplasmic globules and can occur in the setting of neurofibromatosis type 1. Acta Neuropathologica, 2019, 137, 521-525.	7.7	51
155	DNA methylation profiling distinguishes Ewing-like sarcoma with EWSR1â€“NFATc2 fusion from Ewing sarcoma. Journal of Cancer Research and Clinical Oncology, 2019, 145, 1273-1281.	2.5	50
156	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
157	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
158	Adult grade II diffuse astrocytomas are genetically distinct from and more aggressive than their paediatric counterparts. Acta Neuropathologica, 2011, 121, 753-761.	7.7	46
159	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. Nature Communications, 2021, 12, 1269.	12.8	46
160	Transitioning from genotypes to epigenotypes: Why the time has come for medulloblastoma epigenomics. Neuroscience, 2014, 264, 171-185.	2.3	45
161	From class waivers to precision medicine in paediatric oncology. Lancet Oncology, The, 2017, 18, e394-e404.	10.7	45
162	YAP1-fusions in pediatric NF2-wildtype meningioma. Acta Neuropathologica, 2020, 139, 215-218.	7.7	45

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163	Infratentorial IDH-mutant astrocytoma is a distinct subtype. Acta Neuropathologica, 2020, 140, 569-581.	7.7	45
164	Implications of new understandings of gliomas in children and adults with NF1: report of a consensus conference. Neuro-Oncology, 2020, 22, 773-784.	1.2	44
165	Clinical and molecular heterogeneity of pineal parenchymal tumors: a consensus study. Acta Neuropathologica, 2021, 141, 771-785.	7.7	44
166	Papillary glioneuronal tumor (PGNT) exhibits a characteristic methylation profile and fusions involving PRKCA. Acta Neuropathologica, 2019, 137, 837-846.	7.7	43
167	Establishment and application of a novel patient-derived KIAA1549:BRAF-driven pediatric pilocytic astrocytoma model for preclinical drug testing. Oncotarget, 2017, 8, 11460-11479.	1.8	43
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169	Development of the SIOPE DIPG network, registry and imaging repository: a collaborative effort to optimize research into a rare and lethal disease. Journal of Neuro-Oncology, 2017, 132, 255-266.	2.9	42
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