

Konstantin Okonechnikov

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

2,998
citations

567281

15
h-index

526287

27
g-index

29
all docs

29
docs citations

29
times ranked

6702
citing authors

#	ARTICLE	IF	CITATIONS
1	The genetic landscape of choroid plexus tumors in children and adults. <i>Neuro-Oncology</i> , 2021, 23, 650-660.	1.2	26
2	Integrated molecular analysis of adult sonic hedgehog (SHH)-activated medulloblastomas reveals two clinically relevant tumor subsets with VEGFA as potent prognostic indicator. <i>Neuro-Oncology</i> , 2021, 23, 1576-1585.	1.2	7
3	Notch Signaling between Cerebellar Granule Cell Progenitors. <i>ENeuro</i> , 2021, 8, ENEURO.0468-20.2021.	1.9	9
4	Cross-Species Genomics Reveals Oncogenic Dependencies in ZFTA/C11orf95 Fusion-Positive Supratentorial Ependymomas. <i>Cancer Discovery</i> , 2021, 11, 2230-2247.	9.4	39
5	Targeting fibroblast growth factor receptors to combat aggressive ependymoma. <i>Acta Neuropathologica</i> , 2021, 142, 339-360.	7.7	14
6	Therapeutic implications of improved molecular diagnostics for rare CNS embryonal tumor entities: results of an international, retrospective study. <i>Neuro-Oncology</i> , 2021, 23, 1597-1611.	1.2	22
7	Notch1 switches progenitor competence in inducing medulloblastoma. <i>Science Advances</i> , 2021, 7, .	10.3	6
8	Recurrent fusions in PLAGL1 define a distinct subset of pediatric-type supratentorial neuroepithelial tumors. <i>Acta Neuropathologica</i> , 2021, 142, 827-839.	7.7	33
9	Subgroup and subtype-specific outcomes in adult medulloblastoma. <i>Acta Neuropathologica</i> , 2021, 142, 859-871.	7.7	34
10	Developmental and evolutionary dynamics of cis-regulatory elements in mouse cerebellar cells. <i>Science</i> , 2021, 373, .	12.6	51
11	Transcriptional profiling of medulloblastoma with extensive nodularity (MBEN) reveals two clinically relevant tumor subsets with VSNL1 as potent prognostic marker. <i>Acta Neuropathologica</i> , 2020, 139, 583-596.	7.7	13
12	Functional loss of a noncanonical BCOR-PRC1.1 complex accelerates SHH-driven medulloblastoma formation. <i>Genes and Development</i> , 2020, 34, 1161-1176.	5.9	16
13	MYCN amplification drives an aggressive form of spinal ependymoma. <i>Acta Neuropathologica</i> , 2019, 138, 1075-1089.	7.7	104
14	Probing Medulloblastoma Initiation at the Single-Cell Level. <i>Trends in Cancer</i> , 2019, 5, 759-761.	7.4	1
15	YAP1 subgroup supratentorial ependymoma requires TEAD and nuclear factor I-mediated transcriptional programmes for tumorigenesis. <i>Nature Communications</i> , 2019, 10, 3914.	12.8	65
16	Molecular progression of SHH-activated medulloblastomas. <i>Acta Neuropathologica</i> , 2019, 138, 327-330.	7.7	2
17	<i>MYC</i> Drives Group 3 Medulloblastoma through Transformation of Sox2+ Astrocyte Progenitor Cells. <i>Cancer Research</i> , 2019, 79, 1967-1980.	0.9	29
18	Desmoplastic/nodular medulloblastomas (DNMB) and medulloblastomas with extensive nodularity (MBEN) disclose similar epigenetic signatures but different transcriptional profiles. <i>Acta Neuropathologica</i> , 2019, 137, 1003-1015.	7.7	9

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19	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , 2018, 553, 101-105.	27.8	170
20	Interrogating the enhancer landscape of intracranial ependymomas: perspectives for precision medicine. <i>Expert Review of Precision Medicine and Drug Development</i> , 2018, 3, 147-149.	0.7	1
21	A mechanistic classification of clinical phenotypes in neuroblastoma. <i>Science</i> , 2018, 362, 1165-1170.	12.6	213
22	Aberrant ERBB4-SRC Signaling as a Hallmark of Group 4 Medulloblastoma Revealed by Integrative Phosphoproteomic Profiling. <i>Cancer Cell</i> , 2018, 34, 379-395.e7.	16.8	104
23	DNA methylation-based classification and grading system for meningioma: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , The, 2017, 18, 682-694.	10.7	586
24	Qualimap 2: advanced multi-sample quality control for high-throughput sequencing data. <i>Bioinformatics</i> , 2016, 32, 292-294.	4.1	1,362
25	InFusion: Advancing Discovery of Fusion Genes and Chimeric Transcripts from Deep RNA-Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0167417.	2.5	62
26	Genetic characterization of an adapted pandemic 2009 H1N1 influenza virus that reveals improved replication rates in human lung epithelial cells. <i>Virology</i> , 2016, 492, 118-129.	2.4	8