

Volker Hovestadt

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

22,750
citations

25034

57
h-index

56724

83
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89
all docs

89
docs citations

89
times ranked

25082
citing authors

#	ARTICLE	IF	CITATIONS
1	ATRT-10. Single-cell transcriptional profiling of ATRTs reveals heterogeneous signatures of tumor and non-malignant cell populations. <i>Neuro-Oncology</i> , 2022, 24, i4-i5.	1.2	0
2	GLI3s Associated With Neuronal Differentiation in SHH-Activated and WNT-Activated Medulloblastoma. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021, 80, 129-136.	1.7	5
3	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. <i>Cancer Discovery</i> , 2021, 11, 2282-2299.	9.4	21
4	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	28.9	312
5	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , 2021, 39, 1086-1094.	17.5	28
6	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
7	Systematic detection of m6A-modified transcripts at single-molecule and single-cell resolution. <i>Cell Reports Methods</i> , 2021, 1, 100061.	2.9	8
8	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498.	12.8	237
9	Machine learning workflows to estimate class probabilities for precision cancer diagnostics on DNA methylation microarray data. <i>Nature Protocols</i> , 2020, 15, 479-512.	12.0	89
10	Medulloblastomics revisited: biological and clinical insights from thousands of patients. <i>Nature Reviews Cancer</i> , 2020, 20, 42-56.	28.4	147
11	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. <i>Cancer Cell</i> , 2020, 38, 44-59.e9.	16.8	94
12	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. <i>Genome Biology</i> , 2020, 21, 174.	8.8	59
13	EPEN-21. IMPAIRED NEURONAL-GLIAL FATE SPECIFICATION IN PEDIATRIC EPENDYMOMA REVEALED BY SINGLE-CELL RNA-SEQ. <i>Neuro-Oncology</i> , 2020, 22, iii311-iii312.	1.2	0
14	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	27.8	273
15	Histone Variant and Cell Context Determine H3K27M Reprogramming of the Enhancer Landscape and Oncogenic State. <i>Molecular Cell</i> , 2019, 76, 965-980.e12.	9.7	110
16	Second-generation molecular subgrouping of medulloblastoma: an international meta-analysis of Group 3 and Group 4 subtypes. <i>Acta Neuropathologica</i> , 2019, 138, 309-326.	7.7	180
17	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. <i>Cell</i> , 2019, 176, 1265-1281.e24.	28.9	642
18	The molecular landscape of ETMR at diagnosis and relapse. <i>Nature</i> , 2019, 576, 274-280.	27.8	94

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19	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	12.6	461
20	A Novel Method for Rapid Molecular Subgrouping of Medulloblastoma. <i>Clinical Cancer Research</i> , 2018, 24, 1355-1363.	7.0	24
21	DNA methylation-based classification of central nervous system tumours. <i>Nature</i> , 2018, 555, 469-474.	27.8	1,872
22	Anaplastic astrocytoma with piloid features, a novel molecular class of IDH wildtype glioma with recurrent MAPK pathway, CDKN2A/B and ATRX alterations. <i>Acta Neuropathologica</i> , 2018, 136, 273-291.	7.7	190
23	Methylation profiling of paediatric pilocytic astrocytoma reveals variants specifically associated with tumour location and predictive of recurrence. <i>Molecular Oncology</i> , 2018, 12, 1219-1232.	4.6	14
24	The case for DNA methylation based molecular profiling to improve diagnostic accuracy for central nervous system embryonal tumors (not otherwise specified) in adults. <i>Journal of Clinical Neuroscience</i> , 2018, 47, 163-167.	1.5	8
25	A biobank of patient-derived pediatric brain tumor models. <i>Nature Medicine</i> , 2018, 24, 1752-1761.	30.7	124
26	MBRS-28. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2018, 20, i134-i134.	1.2	0
27	Practical implementation of DNA methylation and copy-number-based CNS tumor diagnostics: the Heidelberg experience. <i>Acta Neuropathologica</i> , 2018, 136, 181-210.	7.7	308
28	DIPG-52. ACTIVE CHROMATIN IN H3K27M DIPG REVEALS DISTINCT EPIGENETIC SUBTYPES AND SUBTYPE-SPECIFIC MECHANISMS OF PATHOGENESIS. <i>Neuro-Oncology</i> , 2018, 20, i59-i59.	1.2	0
29	Recurrent homozygous deletion of DROSHA and microduplication of PDE4DIP in pineoblastoma. <i>Nature Communications</i> , 2018, 9, 2868.	12.8	54
30	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.	21.4	112
31	H3-/IDH-wild type pediatric glioblastoma is comprised of molecularly and prognostically distinct subtypes with associated oncogenic drivers. <i>Acta Neuropathologica</i> , 2017, 134, 507-516.	7.7	144
32	Telomerase activation in posterior fossa group A ependymomas is associated with dismal prognosis and chromosome 1q gain. <i>Neuro-Oncology</i> , 2017, 19, 1183-1194.	1.2	31
33	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	12.6	743
34	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
35	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
36	Cribiform neuroepithelial tumor: molecular characterization of a SMARCB1-deficient non-rhabdoid tumor with favorable long-term outcome. <i>Brain Pathology</i> , 2017, 27, 411-418.	4.1	58

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37	Papillary Tumor of the Pineal Region: A Distinct Molecular Entity. <i>Brain Pathology</i> , 2016, 26, 199-205.	4.1	39
38	Telomere dysfunction and chromothripsis. <i>International Journal of Cancer</i> , 2016, 138, 2905-2914.	5.1	42
39	Somatic mutations of <i>DICER1</i> and <i>KMT2D</i> are frequent in intraocular medulloepitheliomas. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 418-427.	2.8	34
40	Pseudoprogression in children, adolescents and young adults with non-brainstem high grade glioma and diffuse intrinsic pontine glioma. <i>Journal of Neuro-Oncology</i> , 2016, 129, 109-121.	2.9	30
41	Poorly differentiated chordoma with SMARCB1/INI1 loss: a distinct molecular entity with dismal prognosis. <i>Acta Neuropathologica</i> , 2016, 132, 149-151.	7.7	127
42	Treatment of Children and Adolescents With Metastatic Medulloblastoma and Prognostic Relevance of Clinical and Biologic Parameters. <i>Journal of Clinical Oncology</i> , 2016, 34, 4151-4160.	1.6	121
43	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , 2016, 530, 57-62.	27.8	318
44	Methylation-based classification of benign and malignant peripheral nerve sheath tumors. <i>Acta Neuropathologica</i> , 2016, 131, 877-887.	7.7	151
45	Methylation profiling of choroid plexus tumors reveals 3 clinically distinct subgroups. <i>Neuro-Oncology</i> , 2016, 18, 790-796.	1.2	67
46	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , 2016, 29, 379-393.	16.8	438
47	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. <i>Cell</i> , 2016, 164, 1060-1072.	28.9	702
48	Gliomatosis cerebri: no evidence for a separate brain tumor entity. <i>Acta Neuropathologica</i> , 2016, 131, 309-319.	7.7	74
49	Histologically distinct neuroepithelial tumors with histone 3 G34 mutation are molecularly similar and comprise a single nosologic entity. <i>Acta Neuropathologica</i> , 2016, 131, 137-146.	7.7	162
50	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016, 7, 28169-28182.	1.8	62
51	Comparative integrated molecular analysis of intraocular medulloepitheliomas and central nervous system embryonal tumors with multilayered rosettes confirms that they are distinct nosologic entities. <i>Neuropathology</i> , 2015, 35, 538-544.	1.2	38
52	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. <i>Cancer Cell</i> , 2015, 27, 728-743.	16.8	933
53	IDH mutant diffuse and anaplastic astrocytomas have similar age at presentation and little difference in survival: a grading problem for WHO. <i>Acta Neuropathologica</i> , 2015, 129, 867-873.	7.7	272
54	Melanotic Tumors of the Nervous System are Characterized by Distinct Mutational, Chromosomal and Epigenomic Profiles. <i>Brain Pathology</i> , 2015, 25, 202-208.	4.1	66

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55	Integrated analysis of pediatric glioblastoma reveals a subset of biologically favorable tumors with associated molecular prognostic markers. <i>Acta Neuropathologica</i> , 2015, 129, 669-678.	7.7	277
56	Adult IDH wild type astrocytomas biologically and clinically resolve into other tumor entities. <i>Acta Neuropathologica</i> , 2015, 130, 407-417.	7.7	237
57	Somatic CRISPR/Cas9-mediated tumour suppressor disruption enables versatile brain tumour modelling. <i>Nature Communications</i> , 2015, 6, 7391.	12.8	244
58	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015, 47, 1316-1325.	21.4	119
59	ATRX and IDH1-R132H immunohistochemistry with subsequent copy number analysis and IDH sequencing as a basis for an "integrated" diagnostic approach for adult astrocytoma, oligodendroglioma and glioblastoma. <i>Acta Neuropathologica</i> , 2015, 129, 133-146.	7.7	378
60	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. <i>Neuro-Oncology</i> , 2014, 16, 1630-1638.	1.2	77
61	Arhgap36-dependent activation of Gli transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11061-11066.	7.1	35
62	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	16.8	627
63	Prognostic significance of clinical, histopathological, and molecular characteristics of medulloblastomas in the prospective HIT2000 multicenter clinical trial cohort. <i>Acta Neuropathologica</i> , 2014, 128, 137-149.	7.7	125
64	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014, 510, 537-541.	27.8	378
65	Embryonal tumor with abundant neuropil and true rosettes (ETANTR), ependymoblastoma, and medulloepithelioma share molecular similarity and comprise a single clinicopathological entity. <i>Acta Neuropathologica</i> , 2014, 128, 279-289.	7.7	191
66	Stem cell characteristics in glioblastoma are maintained by the ecto-nucleotidase E-NPP1. <i>Cell Death and Differentiation</i> , 2014, 21, 929-940.	11.2	58
67	Whole exome sequencing reveals that the majority of schwannomatosis cases remain unexplained after excluding SMARCB1 and LZTR1 germline variants. <i>Acta Neuropathologica</i> , 2014, 128, 449-452.	7.7	36
68	Integrated DNA methylation and copy-number profiling identify three clinically and biologically relevant groups of anaplastic glioma. <i>Acta Neuropathologica</i> , 2014, 128, 561-571.	7.7	176
69	Enhancer hijacking activates GF1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	27.8	520
70	Determining the glioma CpG island methylator phenotype, 1p/19q codeletion, and MGMT promoter methylation from epigenome-wide methylation data in the biomarker cohort of the NOA-04 trial. <i>Journal of Clinical Oncology</i> , 2014, 32, 2017-2017.	1.6	3
71	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013, 45, 927-932.	21.4	674
72	Robust molecular subgrouping and copy-number profiling of medulloblastoma from small amounts of archival tumour material using high-density DNA methylation arrays. <i>Acta Neuropathologica</i> , 2013, 125, 913-916.	7.7	244

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73	Tagmentation-based whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2013, 8, 2022-2032.	12.0	161
74	Reduced H3K27me3 and DNA Hypomethylation Are Major Drivers of Gene Expression in K27M Mutant Pediatric High-Grade Gliomas. <i>Cancer Cell</i> , 2013, 24, 660-672.	16.8	633
75	Methylation of the TERT promoter and risk stratification of childhood brain tumours: an integrative genomic and molecular study. <i>Lancet Oncology</i> , The, 2013, 14, 534-542.	10.7	212
76	Differential expression and methylation of brain developmental genes define location-specific subsets of pilocytic astrocytoma. <i>Acta Neuropathologica</i> , 2013, 126, 291-301.	7.7	84
77	BCAT1 promotes cell proliferation through amino acid catabolism in gliomas carrying wild-type IDH1. <i>Nature Medicine</i> , 2013, 19, 901-908.	30.7	388
78	Protein phosphatase 1, regulatory subunit 15B is a survival factor for ER α -positive breast cancer. <i>International Journal of Cancer</i> , 2013, 132, 2714-2719.	5.1	7
79	Genome-wide identification of translationally inhibited and degraded miR-155 targets using RNA-interacting protein-IP. <i>RNA Biology</i> , 2013, 10, 1017-1029.	3.1	33
80	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. <i>Genome Biology</i> , 2013, 14, r137.	9.6	78
81	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. <i>Cancer Cell</i> , 2012, 22, 425-437.	16.8	1,551
82	Bioinformatic analysis of barcoded cDNA libraries for small RNA profiling by next-generation sequencing. <i>Methods</i> , 2012, 58, 171-187.	3.8	55
83	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012, 44, 1316-1320.	21.4	389
84	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. <i>Nature</i> , 2012, 482, 226-231.	27.8	2,129
85	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012, 488, 100-105.	27.8	765
86	MicroRNA Sequence and Expression Analysis in Breast Tumors by Deep Sequencing. <i>Cancer Research</i> , 2011, 71, 4443-4453.	0.9	331