Volker Hovestadt

List of Publications by Year
in descending order

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86	22,750	25034 57	56724 83
papers	citations	h-index	g-index

89	89	89	25082
all docs	docs citations	times ranked	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	DNA methylation-based classification of central nervous system tumours. Nature, 2018, 555, 469-474.	27.8	1,872
3	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. Cancer Cell, 2012, 22, 425-437.	16.8	1,551
4	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. Cancer Cell, 2015, 27, 728-743.	16.8	933
5	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
6	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
7	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
8	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	28.9	702
9	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
10	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. Cell, 2019, 176, 1265-1281.e24.	28.9	642
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	DNA methylation-based classification and grading system for meningioma: a multicentre, retrospective analysis. Lancet Oncology, The, 2017, 18, 682-694.	10.7	586
14	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
15	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	12.6	461
16	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
17	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	21.4	389
18	BCAT1 promotes cell proliferation through amino acid catabolism in gliomas carrying wild-type IDH1. Nature Medicine, 2013, 19, 901-908.	30.7	388

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19	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
20	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
21	MicroRNA Sequence and Expression Analysis in Breast Tumors by Deep Sequencing. Cancer Research, 2011, 71, 4443-4453.	0.9	331
22	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
23	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. Cell, 2021, 184, 2503-2519.e17.	28.9	312
24	Practical implementation of DNA methylation and copy-number-based CNS tumor diagnostics: the Heidelberg experience. Acta Neuropathologica, 2018, 136, 181-210.	7.7	308
25	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
26	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	27.8	273
27	IDH mutant diffuse and anaplastic astrocytomas have similar age at presentation and little difference in survival: a grading problem for WHO. Acta Neuropathologica, 2015, 129, 867-873.	7.7	272
28	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
29	Somatic CRISPR/Cas9-mediated tumour suppressor disruption enables versatile brain tumour modelling. Nature Communications, 2015, 6, 7391.	12.8	244
30	Adult IDH wild type astrocytomas biologically and clinically resolve into other tumor entities. Acta Neuropathologica, 2015, 130, 407-417.	7.7	237
31	Sarcoma classification by DNA methylation profiling. Nature Communications, 2021, 12, 498.	12.8	237
32	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
33	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
34	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
35	Second-generation molecular subgrouping of medulloblastoma: an international meta-analysis of Group 3 and Group 4 subtypes. Acta Neuropathologica, 2019, 138, 309-326.	7.7	180
36	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

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37	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
38	Tagmentation-based whole-genome bisulfite sequencing. Nature Protocols, 2013, 8, 2022-2032.	12.0	161
39	Methylation-based classification of benign and malignant peripheral nerve sheath tumors. Acta Neuropathologica, 2016, 131, 877-887.	7.7	151
40	Medulloblastomics revisited: biological and clinical insights from thousands of patients. Nature Reviews Cancer, 2020, 20, 42-56.	28.4	147
41	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
42	Poorly differentiated chordoma with SMARCB1/INI1 loss: a distinct molecular entity with dismal prognosis. Acta Neuropathologica, 2016, 132, 149-151.	7.7	127
43	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
44	A biobank of patient-derived pediatric brain tumor models. Nature Medicine, 2018, 24, 1752-1761.	30.7	124
45	Treatment of Children and Adolescents With Metastatic Medulloblastoma and Prognostic Relevance of Clinical and Biologic Parameters. Journal of Clinical Oncology, 2016, 34, 4151-4160.	1.6	121
46	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. Nature Genetics, 2015, 47, 1316-1325.	21.4	119
47	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	21.4	112
48	Histone Variant and Cell Context Determine H3K27M Reprogramming of the Enhancer Landscape and Oncogenic State. Molecular Cell, 2019, 76, 965-980.e12.	9.7	110
49	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	27.8	94
50	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. Cancer Cell, 2020, 38, 44-59.e9.	16.8	94
51	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
52	Differential expression and methylation of brain developmental genes define location-specific subsets of pilocytic astrocytoma. Acta Neuropathologica, 2013, 126, 291-301.	7.7	84
53	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. Genome Biology, 2013, 14, r137.	9.6	78
54	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

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55	Gliomatosis cerebri: no evidence for a separate brain tumor entity. Acta Neuropathologica, 2016, 131, 309-319.	7.7	74
56	Methylation profiling of choroid plexus tumors reveals 3 clinically distinct subgroups. Neuro-Oncology, 2016, 18, 790-796.	1.2	67
57	Melanotic Tumors of the Nervous System are Characterized by Distinct Mutational, Chromosomal and Epigenomic Profiles. Brain Pathology, 2015, 25, 202-208.	4.1	66
58	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. Oncotarget, 2016, 7, 28169-28182.	1.8	62
59	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. Genome Biology, 2020, 21, 174.	8.8	59
60	Stem cell characteristics in glioblastoma are maintained by the ecto-nucleotidase E-NPP1. Cell Death and Differentiation, 2014, 21, 929-940.	11.2	58
61	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
62	Bioinformatic analysis of barcoded cDNA libraries for small RNA profiling by next-generation sequencing. Methods, 2012, 58, 171-187.	3.8	55
63	Recurrent homozygous deletion of DROSHA and microduplication of PDE4DIP in pineoblastoma. Nature Communications, 2018, 9, 2868.	12.8	54
64	Telomere dysfunction and chromothripsis. International Journal of Cancer, 2016, 138, 2905-2914.	5.1	42
65	Papillary Tumor of the Pineal Region: A Distinct Molecular Entity. Brain Pathology, 2016, 26, 199-205.	4.1	39
66	Comparative integrated molecular analysis of intraocular medulloepitheliomas and central nervous system embryonal tumors with multilayered rosettes confirms that they are distinct nosologic entities. Neuropathology, 2015, 35, 538-544.	1.2	38
67	Whole exome sequencing reveals that the majority of schwannomatosis cases remain unexplained after excluding SMARCB1 and LZTR1 germline variants. Acta Neuropathologica, 2014, 128, 449-452.	7.7	36
68	Arhgap36-dependent activation of Gli transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11061-11066.	7.1	35
69	Somatic mutations of DICER1 and KMT2D are frequent in intraocular medulloepitheliomas. Genes Chromosomes and Cancer, 2016, 55, 418-427.	2.8	34
70	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
71	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
72	Telomerase activation in posterior fossa group A ependymomas is associated with dismal prognosis and chromosome 1q gain. Neuro-Oncology, 2017, 19, 1183-1194.	1.2	31

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73	Pseudoprogression in children, adolescents and young adults with non-brainstem high grade glioma and diffuse intrinsic pontine glioma. Journal of Neuro-Oncology, 2016, 129, 109-121.	2.9	30
74	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. Nature Biotechnology, 2021, 39, 1086-1094.	17.5	28
75	A Novel Method for Rapid Molecular Subgrouping of Medulloblastoma. Clinical Cancer Research, 2018, 24, 1355-1363.	7.0	24
76	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. Cancer Discovery, 2021, 11, 2282-2299.	9.4	21
77	Methylation profiling of paediatric pilocytic astrocytoma reveals variants specifically associated with tumour location and predictive of recurrence. Molecular Oncology, 2018, 12, 1219-1232.	4.6	14
78	The case for DNA methylation based molecular profiling to improve diagnostic accuracy for central nervous system embryonal tumors (not otherwise specified) in adults. Journal of Clinical Neuroscience, 2018, 47, 163-167.	1.5	8
79	Systematic detection of m6A-modified transcripts at single-molecule and single-cell resolution. Cell Reports Methods, 2021, 1, 100061.	2.9	8
80	Protein phosphatase 1, regulatory subunit 15B is a survival factor for ERÎ±â€positive breast cancer. International Journal of Cancer, 2013, 132, 2714-2719.	5.1	7
81	GLI3ÂIs Associated With Neuronal Differentiation in SHH-Activated and WNT-Activated Medulloblastoma. Journal of Neuropathology and Experimental Neurology, 2021, 80, 129-136.	1.7	5
82	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.. Journal of Clinical Oncology, 2014, 32, 2017-2017.	1.6	3
83	MBRS-28. SINGLE-CELL TRANSCRIPTOME ANALYSIS OF MEDULLOBLASTOMA. Neuro-Oncology, 2018, 20, i134-i134.	1.2	0
84	DIPG-52. ACTIVE CHROMATIN IN H3K27M DIPG REVEALS DISTINCT EPIGENETIC SUBTYPES AND SUBTYPE-SPECIFIC MECHANISMS OF PATHOGENESIS. Neuro-Oncology, 2018, 20, i59-i59.	1.2	0
85	EPEN-21. IMPAIRED NEURONAL-GLIAL FATE SPECIFICATION IN PEDIATRIC EPENDYMOMA REVEALED BY SINGLE-CELL RNA-SEQ. Neuro-Oncology, 2020, 22, iii311-iii312.	1.2	0
86	ATRT-10. Single-cell transcriptional profiling of ATRTs reveals heterogeneous signatures of tumor and non-malignant cell populations. Neuro-Oncology, 2022, 24, i4-i5.	1.2	0