

# Roel G W Verhaak

## List of Publications by Year in descending order

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145  
papers

43,605  
citations

16411

64  
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20307

116  
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151  
all docs

151  
docs citations

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times ranked

47318  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010, 17, 98-110.	7.7	6,138
2	Inferring tumour purity and stromal and immune cell admixture from expression data. <i>Nature Communications</i> , 2013, 4, 2612.	5.8	5,788
3	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
4	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
5	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	7.7	2,078
6	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
7	Tumor Evolution of Glioma-Intrinsic Gene Expression Subtypes Associates with Immunological Changes in the Microenvironment. <i>Cancer Cell</i> , 2017, 32, 42-56.e6.	7.7	1,282
8	Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2004, 350, 1617-1628.	13.9	1,232
9	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.	13.7	1,020
10	Gene expression-based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. <i>Nature Medicine</i> , 2008, 14, 822-827.	15.2	1,015
11	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
12	SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. <i>Nature Genetics</i> , 2009, 41, 1238-1242.	9.4	862
13	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
14	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
15	Transformation by the (R)-enantiomer of 2-hydroxyglutarate linked to EGLN activation. <i>Nature</i> , 2012, 483, 484-488.	13.7	630
16	GlioVis data portal for visualization and analysis of brain tumor expression datasets. <i>Neuro-Oncology</i> , 2017, 19, 139-141.	0.6	622
17	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604
18	Mosaic Analysis with Double Markers Reveals Tumor Cell of Origin in Glioma. <i>Cell</i> , 2011, 146, 209-221.	13.5	571

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19	Glioblastoma in adults: a Society for Neuro-Oncology (SNO) and European Society of Neuro-Oncology (EANO) consensus review on current management and future directions. <i>Neuro-Oncology</i> , 2020, 22, 1073-1113.	0.6	543
20	Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 908-913.	3.6	524
21	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
22	Systematic analysis of telomere length and somatic alterations in 31 cancer types. <i>Nature Genetics</i> , 2017, 49, 349-357.	9.4	476
23	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 517-25.	3.9	462
24	Suppression of lung adenocarcinoma progression by Nkx2-1. <i>Nature</i> , 2011, 473, 101-104.	13.7	383
25	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015, 25, 316-327.	2.4	343
26	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	13.7	343
27	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	13.7	320
28	Prediction of molecular subtypes in acute myeloid leukemia based on gene expression profiling. <i>Haematologica</i> , 2009, 94, 131-134.	1.7	300
29	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. <i>Nature Biotechnology</i> , 2011, 29, 393-396.	9.4	289
30	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. <i>Nature Genetics</i> , 2020, 52, 891-897.	9.4	273
31	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VT11A-TCF7L2 fusion. <i>Nature Genetics</i> , 2011, 43, 964-968.	9.4	270
32	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , 2010, 20, 413-427.	2.4	248
33	Osteopontin mediates glioblastoma-associated macrophage infiltration and is a potential therapeutic target. <i>Journal of Clinical Investigation</i> , 2018, 129, 137-149.	3.9	242
34	Predicting drug susceptibility of non-small cell lung cancers based on genetic lesions. <i>Journal of Clinical Investigation</i> , 2009, 119, 1727-1740.	3.9	230
35	Glioma: experimental models and reality. <i>Acta Neuropathologica</i> , 2017, 133, 263-282.	3.9	223
36	Extrachromosomal oncogene amplification in tumour pathogenesis and evolution. <i>Nature Reviews Cancer</i> , 2019, 19, 283-288.	12.8	219

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37	Discordant inheritance of chromosomal and extrachromosomal DNA elements contributes to dynamic disease evolution in glioblastoma. <i>Nature Genetics</i> , 2018, 50, 708-717.	9.4	212
38	EGFR heterogeneity and implications for therapeutic intervention in glioblastoma. <i>Neuro-Oncology</i> , 2018, 20, 743-752.	0.6	210
39	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020, 52, 294-305.	9.4	180
40	TumorFusions: an integrative resource for cancer-associated transcript fusions. <i>Nucleic Acids Research</i> , 2018, 46, D1144-D1149.	6.5	179
41	Exosomes from Glioma-Associated Mesenchymal Stem Cells Increase the Tumorigenicity of Glioma Stem-like Cells via Transfer of miR-1587. <i>Cancer Research</i> , 2017, 77, 5808-5819.	0.4	169
42	Essential role of Jun family transcription factors in PU.1 knockdown-induced leukemic stem cells. <i>Nature Genetics</i> , 2006, 38, 1269-1277.	9.4	167
43	The cellular origin for malignant glioma and prospects for clinical advancements. <i>Expert Review of Molecular Diagnostics</i> , 2012, 12, 383-394.	1.5	161
44	Sequential gain of mutations in severe congenital neutropenia progressing to acute myeloid leukemia. <i>Blood</i> , 2012, 119, 5071-5077.	0.6	156
45	PRADA: pipeline for RNA sequencing data analysis. <i>Bioinformatics</i> , 2014, 30, 2224-2226.	1.8	147
46	Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. <i>Nature Genetics</i> , 2018, 50, 1399-1411.	9.4	145
47	The Tandem Duplicator Phenotype Is a Prevalent Genome-Wide Cancer Configuration Driven by Distinct Gene Mutations. <i>Cancer Cell</i> , 2018, 34, 197-210.e5.	7.7	130
48	Genomic and Phenotypic Characterization of a Broad Panel of Patient-Derived Xenografts Reflects the Diversity of Glioblastoma. <i>Clinical Cancer Research</i> , 2020, 26, 1094-1104.	3.2	124
49	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	0.6	119
50	A High Notch Pathway Activation Predicts Response to Î³ Secretase Inhibitors in Proneural Subtype of Glioma Tumor-Initiating Cells. <i>Stem Cells</i> , 2014, 32, 301-312.	1.4	117
51	Immune checkpoint blockade as a potential therapeutic target: surveying CNS malignancies. <i>Neuro-Oncology</i> , 2016, 18, 1357-1366.	0.6	116
52	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. <i>Cancer Cell</i> , 2021, 39, 694-707.e7.	7.7	115
53	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. <i>Nature Genetics</i> , 2021, 53, 1456-1468.	9.4	111
54	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. <i>Nature Communications</i> , 2020, 11, 3883.	5.8	110

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55	A distal single nucleotide polymorphism alters long-range regulation of the PU.1 gene in acute myeloid leukemia. <i>Journal of Clinical Investigation</i> , 2007, 117, 2611-2620.	3.9	109
56	ZFX4 Interacts with the NuRD Core Member CHD4 and Regulates the Glioblastoma Tumor-Initiating Cell State. <i>Cell Reports</i> , 2014, 6, 313-324.	2.9	106
57	Transformation of quiescent adult oligodendrocyte precursor cells into malignant glioma through a multistep reactivation process. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4214-23.	3.3	105
58	Radiotherapy is associated with a deletion signature that contributes to poor outcomes in patients with cancer. <i>Nature Genetics</i> , 2021, 53, 1088-1096.	9.4	94
59	Multigene signature for predicting prognosis of patients with 1p19q co-deletion diffuse glioma. <i>Neuro-Oncology</i> , 2017, 19, 786-795.	0.6	87
60	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.	9.4	79
61	Differential Regulation of Foxo3a Target Genes in Erythropoiesis. <i>Molecular and Cellular Biology</i> , 2007, 27, 3839-3854.	1.1	77
62	Very low mutation burden is a feature of inflamed recurrent glioblastomas responsive to cancer immunotherapy. <i>Nature Communications</i> , 2021, 12, 352.	5.8	77
63	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. <i>Genes and Development</i> , 2013, 27, 1462-1472.	2.7	74
64	Molecular profiling of long-term survivors identifies a subgroup of glioblastoma characterized by chromosome 19/20 co-gain. <i>Acta Neuropathologica</i> , 2015, 130, 419-434.	3.9	74
65	Transcriptional regulatory networks of tumor-associated macrophages that drive malignancy in mesenchymal glioblastoma. <i>Genome Biology</i> , 2020, 21, 216.	3.8	73
66	Glioblastoma-Derived Epidermal Growth Factor Receptor Carboxyl-Terminal Deletion Mutants Are Transforming and Are Sensitive to EGFR-Directed Therapies. <i>Cancer Research</i> , 2011, 71, 7587-7596.	0.4	70
67	Src Inhibition with Saracatinib Reverses Fulvestrant Resistance in ER-Positive Ovarian Cancer Models <i>in Vitro</i> and <i>In Vivo</i> . <i>Clinical Cancer Research</i> , 2012, 18, 5911-5923.	3.2	69
68	Perspective of mesenchymal transformation in glioblastoma. <i>Acta Neuropathologica Communications</i> , 2021, 9, 50.	2.4	63
69	Live-Cell Imaging Shows Uneven Segregation of Extrachromosomal DNA Elements and Transcriptionally Active Extrachromosomal DNA Hubs in Cancer. <i>Cancer Discovery</i> , 2022, 12, 468-483.	7.7	63
70	Histone demethylase JARID1C inactivation triggers genomic instability in sporadic renal cancer. <i>Journal of Clinical Investigation</i> , 2015, 125, 4625-4637.	3.9	62
71	Integrated cisomic and expression analysis of amplified <i>NKX2-1</i> in lung adenocarcinoma identifies <i>LMO3</i> as a functional transcriptional target. <i>Genes and Development</i> , 2013, 27, 197-210.	2.7	61
72	Reconstructing the molecular life history of gliomas. <i>Acta Neuropathologica</i> , 2018, 135, 649-670.	3.9	61

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73	Comparative Molecular Life History of Spontaneous Canine and Human Gliomas. <i>Cancer Cell</i> , 2020, 37, 243-257.e7.	7.7	59
74	BMP signaling mediates glioma stem cell quiescence and confers treatment resistance in glioblastoma. <i>Scientific Reports</i> , 2019, 9, 14569.	1.6	57
75	A cancer drug atlas enables synergistic targeting of independent drug vulnerabilities. <i>Nature Communications</i> , 2020, 11, 2935.	5.8	57
76	Mir-21â€“Sox2 Axis Delineates Glioblastoma Subtypes with Prognostic Impact. <i>Journal of Neuroscience</i> , 2015, 35, 15097-15112.	1.7	53
77	Ets Factors Regulate Neural Stem Cell Depletion and Gliogenesis in Ras Pathway Glioma. <i>Cell Reports</i> , 2015, 12, 258-271.	2.9	53
78	Predicting time to ovarian carcinoma recurrence using protein markers. <i>Journal of Clinical Investigation</i> , 2013, 123, 3740-50.	3.9	46
79	HUGO Gene Nomenclature Committee (HGNC) recommendations for the designation of gene fusions. <i>Leukemia</i> , 2021, 35, 3040-3043.	3.3	42
80	Novel therapeutic strategy for cervical cancer harboring FGFR3-TACC3 fusions. <i>Oncogenesis</i> , 2018, 7, 4.	2.1	41
81	PAF promotes stemness and radioresistance of glioma stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9086-E9095.	3.3	40
82	Silent Mutations Make Some Noise. <i>Cell</i> , 2014, 156, 1129-1131.	13.5	33
83	Engineering and Functional Characterization of Fusion Genes Identifies Novel Oncogenic Drivers of Cancer. <i>Cancer Research</i> , 2017, 77, 3502-3512.	0.4	31
84	The evolutionary pattern of mutations in glioblastoma reveals therapy-mediated selection. <i>Oncotarget</i> , 2018, 9, 7844-7858.	0.8	29
85	Significance of Murine Retroviral Mutagenesis for Identification of Disease Genes in Human Acute Myeloid Leukemia. <i>Cancer Research</i> , 2006, 66, 622-626.	0.4	26
86	Studying a Complex Tumor. <i>Cancer Journal (Sudbury, Mass )</i> , 2012, 18, 107-114.	1.0	26
87	<i>EGFR</i> Amplification Induces Increased DNA Damage Response and Renders Selective Sensitivity to Talazoparib (PARP Inhibitor) in Glioblastoma. <i>Clinical Cancer Research</i> , 2020, 26, 1395-1407.	3.2	26
88	MSK1-Mediated Î²-Catenin Phosphorylation Confers Resistance to PI3K/mTOR Inhibitors in Glioblastoma. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1656-1668.	1.9	25
89	Moving the needle: Optimizing classification for glioma. <i>Science Translational Medicine</i> , 2016, 8, 350fs14.	5.8	24
90	Spatiotemporal dynamics of clonal selection and diversification in normal endometrial epithelium. <i>Nature Communications</i> , 2022, 13, 943.	5.8	24

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91	Prognostic Relevance of Tumor Purity and Interaction with MGMT Methylation in Glioblastoma. <i>Molecular Cancer Research</i> , 2017, 15, 532-540.	1.5	23
92	Homozygous MTAP deletion in primary human glioblastoma is not associated with elevation of methylthioadenosine. <i>Nature Communications</i> , 2021, 12, 4228.	5.8	21
93	Spatial concordance of DNA methylation classification in diffuse glioma. <i>Neuro-Oncology</i> , 2021, 23, 2054-2065.	0.6	19
94	The polo-like kinase 1 inhibitor volasertib synergistically increases radiation efficacy in glioma stem cells. <i>Oncotarget</i> , 2018, 9, 10497-10509.	0.8	18
95	Prospective Clinical Sequencing of Adult Glioma. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 991-1000.	1.9	15
96	Transcriptional mimicry by tumor-associated stroma. <i>Nature Genetics</i> , 2015, 47, 307-309.	9.4	14
97	Unifying Gene Expression Measures from Multiple Platforms Using Factor Analysis. <i>PLoS ONE</i> , 2011, 6, e17691.	1.1	12
98	Biphasic components of sarcomatoid clear cell renal cell carcinomas are molecularly similar to each other, but distinct from, non-sarcomatoid renal carcinomas. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 212-224.	1.3	12
99	iGLASS: imaging integration into the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2020, 22, 1545-1546.	0.6	12
100	Novel kinase fusion transcripts found in endometrial cancer. <i>Scientific Reports</i> , 2016, 5, 18657.	1.6	11
101	TMIC-14. TUMOR EVOLUTION OF GLIOMA INTRINSIC GENE EXPRESSION SUBTYPE ASSOCIATES WITH IMMUNOLOGICAL CHANGES IN THE MICROENVIRONMENT. <i>Neuro-Oncology</i> , 2016, 18, vi202-vi202.	0.6	11
102	Molecular and clonal evolution in recurrent metastatic gliosarcoma. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a004671.	0.5	10
103	A validated integrated clinical and molecular glioblastoma long-term survival-predictive nomogram. <i>Neuro-Oncology Advances</i> , 2021, 3, vdaa146.	0.4	10
104	Evolving Insights into the Molecular Neuropathology of Diffuse Gliomas in Adults. <i>Neurologic Clinics</i> , 2018, 36, 421-437.	0.8	9
105	Longitudinal genomic characterization of brain tumors for identification of therapeutic vulnerabilities: Table 1. <i>Neuro-Oncology</i> , 2016, 18, 1037-1039.	0.6	8
106	Doomed from the TERT? A Two-Stage Model of Tumorigenesis in IDH-Wild-Type Glioblastoma. <i>Cancer Cell</i> , 2019, 35, 542-544.	7.7	8
107	Seek and Destroy: Relating Cancer Drivers to Therapies. <i>Cancer Cell</i> , 2015, 27, 319-321.	7.7	5
108	Serum cell-free DNA epigenetic biomarkers aid glioma diagnostics and monitoring. <i>Neuro-Oncology</i> , 2021, 23, 1423-1424.	0.6	5

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109	Extrachromosomal DNA (ecDNA) carrying amplified oncogenes as a biomarker for insensitivity to pembrolizumab treatment in gastric cancer patients.. <i>Journal of Clinical Oncology</i> , 2020, 38, 3123-3123.	0.8	5
110	LUMOS - Low and Intermediate Grade Glioma Umbrella Study of Molecular Guided Therapies at relapse: Protocol for a pilot study. <i>BMJ Open</i> , 2021, 11, e054075.	0.8	2
111	Intragenic breakpoint. <i>Cell Cycle</i> , 2013, 12, 3705-3706.	1.3	1
112	COMP-07. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA. <i>Neuro-Oncology</i> , 2018, 20, vi64-vi65.	0.6	1
113	RBTT-07. NUTMEG: A RANDOMISED PHASE II STUDY OF NIVOLUMAB AND TEMOZOLOMIDE (TMZ) VS TMZ ALONE IN ELDERLY PATIENTS WITH NEWLY DIAGNOSED GLIOBLASTOMA (GBM): TRIAL IN PROGRESS. <i>Neuro-Oncology</i> , 2018, 20, vi235-vi235.	0.6	1
114	EPID-23. PURSUIT OF AN INTERNATIONAL LANGUAGE OF GLIOMA RESEARCH: COMMON DATA ELEMENTS FOR THE LONGITUDINAL STUDY OF ADULT MALIGNANT GLIOMA. <i>Neuro-Oncology</i> , 2019, 21, vi79-vi79.	0.6	1
115	GENE-28. LONGITUDINAL MOLECULAR TRAJECTORIES OF DIFFUSE GLIOMA IN ADULTS. <i>Neuro-Oncology</i> , 2019, 21, vi103-vi103.	0.6	1
116	OMRT-3. Longitudinal analysis of diffuse glioma reveals cell state dynamics at recurrence associated with changes in genetics and the microenvironment. <i>Neuro-Oncology Advances</i> , 2021, 3, ii7-ii8.	0.4	1
117	EPIG-14EPIGENOMIC (DNA METHYLATION AND EXPRESSION) SIGNATURES DEFINE SUBSETS OF BOTH IDHmut AND IDHwt GLIOMA WITH DISTINCT CLINICAL OUTCOMES. <i>Neuro-Oncology</i> , 2015, 17, v89.2-v89.	0.6	0
118	GENO-36GLIOMA SPHERE-FORMING CELLS REVEAL INTRINSIC GLOBAL HYPERMETHYLATION ASSOCIATED WITH GBM RADIATION RESISTANCE. <i>Neuro-Oncology</i> , 2015, 17, v99.5-v100.	0.6	0
119	TMOD-31. AN INFLAMMATION RESPONSE GENE SIGNATURE IS ASSOCIATED WITH PROGNOSIS OF GLIOMA PATIENTS WITH 1p/19q CO-DELETION TUMORS. <i>Neuro-Oncology</i> , 2016, 18, vi213-vi213.	0.6	0
120	Navigating the Cancer Transcriptome by Decoding Divergent Oncogenic States. <i>Cell Systems</i> , 2017, 5, 90-92.	2.9	0
121	DDIS-03. EGFR AMPLIFICATION INDUCED INCREASED DNA DAMAGE RESPONSE AND PREDICTED SELECTIVE SENSITIVITY TO TALAZOPARIB (PARP INHIBITOR) IN GLIOBLASTOMA STEM-LIKE CELLS. <i>Neuro-Oncology</i> , 2018, 20, vi69-vi69.	0.6	0
122	IMMU-36. IMMUNE RESPONSES IN CANINE GLIOMAS ARE ENRICHED AT THE INFILTRATING EDGE OF ASTROCYTOMAS. <i>Neuro-Oncology</i> , 2018, 20, vi129-vi129.	0.6	0
123	TMOD-18. THE PATIENT DERIVED XENOGRAFT NATIONAL RESOURCE: A COMPREHENSIVE COLLECTION OF HIGH-GRADE GLIOMA MODELS FOR PRE-CLINICAL AND TRANSLATIONAL STUDIES. <i>Neuro-Oncology</i> , 2018, 20, vi272-vi272.	0.6	0
124	DRES-05. MOLECULAR EVOLUTION OF DIFFUSE GLIOMAS AND THE GLIOMA LONGITUDINAL ANALYSIS CONSORTIUM. <i>Neuro-Oncology</i> , 2018, 20, vi76-vi76.	0.6	0
125	PATH-48. THE DNA METHYLATION LANDSCAPE OF CORE AND PERIPHERAL DIFFUSE GLIOMA REGIONS SHOWS LITTLE SPATIAL SUBTYPE HETEROGENEITY AFTER CONSIDERING TUMOR PURITY. <i>Neuro-Oncology</i> , 2019, 21, vi154-vi154.	0.6	0
126	COMP-15. MOLECULAR AND CLONAL EVOLUTION IN RECURRENT METASTATIC GLIOSARCOMA. <i>Neuro-Oncology</i> , 2019, 21, vi64-vi64.	0.6	0



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127	GENE-40. CHARACTERIZING EPIGENETIC INTRATUMORAL HETEROGENEITY IN GLIOMA USING SINGLE-CELL BISULFITE SEQUENCING. <i>Neuro-Oncology</i> , 2019, 21, vi106-vi106.	0.6	0
128	GENE-57. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA. <i>Neuro-Oncology</i> , 2019, 21, vi110-vi110.	0.6	0
129	OTEH-10. Evolutionary trajectory of epigenomic of gliomas. <i>Neuro-Oncology Advances</i> , 2021, 3, ii12-ii12.	0.4	0
130	Abstract 2084: Single-cell multimodal glioma analyses reveal epigenetic regulators of cellular plasticity and environmental stress response. , 2021, , .		0
131	Abstract 2068: Radiotherapy is associated with a deletion signature that contributes to poor cancer patient outcomes. , 2021, , .		0
132	INN-08. LOW AND INTERMEDIATE GRADE GLIOMA UMBRELLA STUDY OF MOLECULAR GUIDED THERAPIES (LUMOS) STUDY. <i>Neuro-Oncology</i> , 2021, 23, vi106-vi107.	0.6	0
133	EPCO-09. LONGITUDINAL ANALYSIS OF DIFFUSE GLIOMA REVEALS CELL STATE DYNAMICS AT RECURRENCE ASSOCIATED WITH CHANGES IN GENETICS AND THE MICROENVIRONMENT. <i>Neuro-Oncology</i> , 2021, 23, vi3-vi3.	0.6	0
134	TMOD-13. IDENTIFYING DRIVERS IN THE CONVERGING SYNTENIC REGIONS OF SPONTANEOUS CANINE AND PEDIATRIC HIGH-GRADE GLIOMA USING IMAGING BASED CRISPR-CAS9 ARRAY SCREEN. <i>Neuro-Oncology</i> , 2021, 23, vi218-vi218.	0.6	0
135	BIOM-41. LIVE-CELL IMAGING SHOWS UNEVEN SEGREGATION OF EXTRACHROMOSOMAL DNA ELEMENTS AND TRANSCRIPTIONALLY ACTIVE EXTRACHROMOSOMAL DNA CLUSTERS IN CANCER. <i>Neuro-Oncology</i> , 2021, 23, vi20-vi20.	0.6	0
136	EPCO-17. METHYLATION ANALYSIS OF MATCHED PRIMARY AND RECURRENT IDHmt ASTROCYTOMA; AN UPDATE FROM THE GLIOMA LONGITUDINAL ANALYSIS NL (GLASS-NL) CONSORTIUM. <i>Neuro-Oncology</i> , 2021, 23, vi5-vi5.	0.6	0
137	EPCO-27. GLIOMA SINGLE CELL MULTI-OMIC ANALYSES REVEALS REGULATORS OF PLASTICITY AND ADAPTIVE STRESS RESPONSE. <i>Neuro-Oncology</i> , 2020, 22, ii75-ii75.	0.6	0
138	EPCO-11. IN VIVO FUNCTIONAL GENOMIC SCREEN IDENTIFIES WISP1 AS AN OVEREXPRESSED DRIVER OF GLIOBLASTOMA. <i>Neuro-Oncology</i> , 2020, 22, ii71-ii71.	0.6	0
139	TMOD-13. RESEARCH RESOURCES FOR OLIGODENDROGLIOMA NOW AVAILABLE TO RESEARCH COMMUNITY. <i>Neuro-Oncology</i> , 2020, 22, ii230-ii230.	0.6	0
140	EPCO-29. EPIGENOMICS OF THE GLIOMA LONGITUDINAL ANALYSIS (GLASS) CONSORTIUM. <i>Neuro-Oncology</i> , 2020, 22, ii75-ii75.	0.6	0
141	EPCO-15. TUMOR TREATMENT WITH IONIZING RADIATION IS ASSOCIATED WITH A CLINICALLY RELEVANT DELETION SIGNATURE. <i>Neuro-Oncology</i> , 2020, 22, ii72-ii72.	0.6	0
142	EPCO-08. TUMOR-IMMUNE INTERACTIONS ARE DYNAMIC AND INFLUENCE THE EVOLUTIONARY TRAJECTORY OF ADULT DIFFUSE GLIOMA. <i>Neuro-Oncology</i> , 2020, 22, ii70-ii71.	0.6	0
143	BIOM-20. TUMOR-INTRINSIC AND PERIPHERAL FEATURES ASSOCIATE WITH SURVIVAL AFTER POLIO VIROTHERAPY IN RECURRENT GBM. <i>Neuro-Oncology</i> , 2021, 23, vi14-vi15.	0.6	0
144	EPCO-13. MULTIOMIC SINGLE NUCLEUS RNA- AND ATACseq PROFILING REVEALS REGULATORS OF GLIOMA CELL STATE DIVERSITY. <i>Neuro-Oncology</i> , 2021, 23, vi4-vi4.	0.6	0

#	ARTICLE	IF	CITATIONS
145	EPCO-09. STEREOTACTIC IMAGE-GUIDED EPIGENOME PROFILING REVEALS DIVERSE EVOLUTIONARY GROWTH ROUTES IN DIFFUSE GLIOMAS. <i>Neuro-Oncology</i> , 2020, 22, ii71-ii71.	0.6	0