Roel G W Verhaak

List of Publications by Year
in descending order

145 papers	43,605 citations	16411 64 h-index	20307 116 g-index
151 all docs	151 docs citations	151 times ranked	47318 citing authors

#	Article	IF	Citations
1	Live-Cell Imaging Shows Uneven Segregation of Extrachromosomal DNA Elements and Transcriptionally Active Extrachromosomal DNA Hubs in Cancer. Cancer Discovery, 2022, 12, 468-483.	7.7	63
2	Spatiotemporal dynamics of clonal selection and diversification in normal endometrial epithelium. Nature Communications, 2022, 13, 943.	5.8	24
3	Very low mutation burden is a feature of inflamed recurrent glioblastomas responsive to cancer immunotherapy. Nature Communications, 2021, 12, 352.	5.8	77
4	Perspective of mesenchymal transformation in glioblastoma. Acta Neuropathologica Communications, 2021, 9, 50.	2.4	63
5	Radiotherapy is associated with a deletion signature that contributes to poor outcomes in patients with cancer. Nature Genetics, 2021, 53, 1088-1096.	9.4	94
6	Spatial concordance of DNA methylation classification in diffuse glioma. Neuro-Oncology, 2021, 23, 2054-2065.	0.6	19
7	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. Cancer Cell, 2021, 39, 694-707.e7.	7.7	115
8	Serum cell-free DNA epigenetic biomarkers aid glioma diagnostics and monitoring. Neuro-Oncology, 2021, 23, 1423-1424.	0.6	5
9	OMRT-3. Longitudinal analysis of diffuse glioma reveals cell state dynamics at recurrence associated with changes in genetics and the microenvironment. Neuro-Oncology Advances, 2021, 3, ii7-ii8.	0.4	1
10	OTEH-10. Evolutionary trajectory of epigenomic of gliomas. Neuro-Oncology Advances, 2021, 3, ii12-ii12.	0.4	0
11	Abstract 2084: Single-cell multimodal glioma analyses reveal epigenetic regulators of cellular plasticity and environmental stress response. , 2021, , .		0
12	Homozygous MTAP deletion in primary human glioblastoma is not associated with elevation of methylthioadenosine. Nature Communications, 2021, 12, 4228.	5.8	21
13	Abstract 2068: Radiotherapy is associated with a deletion signature that contributes to poor cancer patient outcomes. , 2021, , .		0
14	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. Nature Genetics, 2021, 53, 1456-1468.	9.4	111
15	HUGO Gene Nomenclature Committee (HGNC) recommendations for the designation of gene fusions. Leukemia, 2021, 35, 3040-3043.	3.3	42
16	A validated integrated clinical and molecular glioblastoma long-term survival-predictive nomogram. Neuro-Oncology Advances, 2021, 3, vdaa146.	0.4	10
17	INNV-08. LOW AND INTERMEDIATE GRADE GLIOMA UMBRELLA STUDY OF MOLECULAR GUIDED THERAPIES (LUMOS) STUDY. Neuro-Oncology, 2021, 23, vi106-vi107.	0.6	0
18	EPCO-09. LONGITUDINAL ANALYSIS OF DIFFUSE GLIOMA REVEALS CELL STATE DYNAMICS AT RECURRENCE ASSOCIATED WITH CHANGES IN GENETICS AND THE MICROENVIRONMENT. Neuro-Oncology, 2021, 23, vi3-vi3.	0.6	0

#	Article	IF	Citations
19	TMOD-13. IDENTIFYING DRIVERS IN THE CONVERGING SYNTENIC REGIONS OF SPONTANEOUS CANINE AND PEDIATRIC HIGH-GRADE GLIOMA USING IMAGING BASED CRISPR-CAS9 ARRAY SCREEN. Neuro-Oncology, 2021, 23, vi218-vi218.	0.6	0
20	BIOM-41. LIVE-CELL IMAGING SHOWS UNEVEN SEGREGATION OF EXTRACHROMOSOMAL DNA ELEMENTS AND TRANSCRIPTIONALLY ACTIVE EXTRACHROMOSOMAL DNA CLUSTERS IN CANCER. Neuro-Oncology, 2021, 23, vi20-vi20.	0.6	0
21	EPCO-17. METHYLATION ANALYSIS OF MATCHED PRIMARY AND RECURRENT IDHmt ASTROCYTOMA; AN UPDATE FROM THE GLIOMA LONGITUDINAL ANALYSIS NL (GLASS-NL) CONSORTIUM. Neuro-Oncology, 2021, 23, vi5-vi5.	0.6	0
22	BIOM-20. TUMOR-INTRINSIC AND PERIPHERAL FEATURES ASSOCIATE WITH SURVIVAL AFTER POLIO VIROTHERAPY IN RECURRENT GBM. Neuro-Oncology, 2021, 23, vi14-vi15.	0.6	0
23	EPCO-13. MULTIOMIC SINGLE NUCLEUS RNA- AND ATACseq PROFILING REVEALS REGULATORS OF GLIOMA CELL STATE DIVERSITY. Neuro-Oncology, 2021, 23, vi4-vi4.	0.6	0
24	LUMOS - Low and Intermediate Grade Glioma Umbrella Study of Molecular Guided TherapieS at relapse: Protocol for a pilot study. BMJ Open, 2021, 11, e054075.	0.8	2
25	*EGFR* Amplification Induces Increased DNA Damage Response and Renders Selective Sensitivity to Talazoparib (PARP Inhibitor) in Glioblastoma. Clinical Cancer Research, 2020, 26, 1395-1407.	3.2	26
26	Molecular and clonal evolution in recurrent metastatic gliosarcoma. Journal of Physical Education and Sports Management, 2020, 6, a004671.	0.5	10
27	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	9.4	79
28	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. Nature Communications, 2020, 11, 3883.	5.8	110
29	Transcriptional regulatory networks of tumor-associated macrophages that drive malignancy in mesenchymal glioblastoma. Genome Biology, 2020, 21, 216.	3.8	73
30	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. Nature Genetics, 2020, 52, 891-897.	9.4	273
31	A cancer drug atlas enables synergistic targeting of independent drug vulnerabilities. Nature Communications, 2020, 11, 2935.	5.8	57
32	iGLASS: imaging integration into the Glioma Longitudinal Analysis Consortium. Neuro-Oncology, 2020, 22, 1545-1546.	0.6	12
33	Comparative Molecular Life History of Spontaneous Canine and Human Gliomas. Cancer Cell, 2020, 37, 243-257.e7.	7.7	59
34	Genomic and Phenotypic Characterization of a Broad Panel of Patient-Derived Xenografts Reflects the Diversity of Glioblastoma. Clinical Cancer Research, 2020, 26, 1094-1104.	3.2	124
35	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. Nature Genetics, 2020, 52, 294-305.	9.4	180
36	Glioblastoma in adults: a Society for Neuro-Oncology (SNO) and European Society of Neuro-Oncology (EANO) consensus review on current management and future directions. Neuro-Oncology, 2020, 22, 1073-1113.	0.6	543

#	Article	IF	Citations
37	Extrachromosomal DNA (ecDNA) carrying amplified oncogenes as a biomarker for insensitivity to pembrolizumab treatment in gastric cancer patients.. Journal of Clinical Oncology, 2020, 38, 3123-3123.	0.8	5
38	EPCO-27. GLIOMA SINGLE CELL MULTI-OMIC ANALYSES REVEALS REGULATORS OF PLASTICITY AND ADAPTIVE STRESS RESPONSE. Neuro-Oncology, 2020, 22, ii75-ii75.	0.6	0
39	EPCO-11. IN VIVO FUNCTIONAL GENOMIC SCREEN IDENTIFIES WISP1 AS AN OVEREXPRESSED DRIVER OF GLIOBLASTOMA. Neuro-Oncology, 2020, 22, ii71-ii71.	0.6	0
40	TMOD-13. RESEARCH RESOURCES FOR OLIGODENDROGLIOMA NOW AVAILABLE TO RESEARCH COMMUNITY. Neuro-Oncology, 2020, 22, ii230-ii230.	0.6	0
41	EPCO-29. EPIGENOMICS OF THE GLIOMA LONGITUDINAL ANALYSIS (GLASS) CONSORTIUM. Neuro-Oncology, 2020, 22, ii75-ii75.	0.6	0
42	EPCO-15. TUMOR TREATMENT WITH IONIZING RADIATION IS ASSOCIATED WITH A CLINICALLY RELEVANT DELETION SIGNATURE. Neuro-Oncology, 2020, 22, ii72-ii72.	0.6	0
43	EPCO-08. TUMOR-IMMUNE INTERACTIONS ARE DYNAMIC AND INFLUENCE THE EVOLUTIONARY TRAJECTORY OF ADULT DIFFUSE GLIOMA. Neuro-Oncology, 2020, 22, ii70-ii71.	0.6	0
44	EPCO-09. STEREOTACTIC IMAGE-GUIDED EPIGENOME PROFILING REVEALS DIVERSE EVOLUTIONARY GROWTH ROUTES IN DIFFUSE GLIOMAS. Neuro-Oncology, 2020, 22, ii71-ii71.	0.6	0
45	BMP signaling mediates glioma stem cell quiescence and confers treatment resistance in glioblastoma. Scientific Reports, 2019, 9, 14569.	1.6	57
46	Doomed from the TERT? A Two-Stage Model of Tumorigenesis in IDH-Wild-Type Glioblastoma. Cancer Cell, 2019, 35, 542-544.	7.7	8
47	Extrachromosomal oncogene amplification in tumour pathogenesis and evolution. Nature Reviews Cancer, 2019, 19, 283-288.	12.8	219
48	Prospective Clinical Sequencing of Adult Glioma. Molecular Cancer Therapeutics, 2019, 18, 991-1000.	1.9	15
49	PATH-48. THE DNA METHYLATION LANDSCAPE OF CORE AND PERIPHERAL DIFFUSE GLIOMA REGIONS SHOWS LITTLE SPATIAL SUBTYPE HETEROGENEITY AFTER CONSIDERING TUMOR PURITY. Neuro-Oncology, 2019, 21, vi154-vi154.	0.6	0
50	COMP-15. MOLECULAR AND CLONAL EVOLUTION IN RECURRENT METASTATIC GLIOSARCOMA. Neuro-Oncology, 2019, 21, vi64-vi64.	0.6	0
51	EPID-23. PURSUIT OF AN INTERNATIONAL LANGUAGE OF GLIOMA RESEARCH: COMMON DATA ELEMENTS FOR THE LONGITUDINAL STUDY OF ADULT MALIGNANT GLIOMA. Neuro-Oncology, 2019, 21, vi79-vi79.	0.6	1
52	GENE-40. CHARACTERIZING EPIGENETIC INTRATUMORAL HETEROGENEITY IN GLIOMA USING SINGLE-CELL BISULFITE SEQUENCING. Neuro-Oncology, 2019, 21, vi106-vi106.	0.6	0
53	GENE-57. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA. Neuro-Oncology, 2019, 21, vi110-vi110.	0.6	0
54	GENE-28. LONGITUDINAL MOLECULAR TRAJECTORIES OF DIFFUSE GLIOMA IN ADULTS. Neuro-Oncology, 2019, 21, vi103-vi103.	0.6	1

#	Article	IF	Citations
55	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	13.7	343
56	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	13.7	320
57	Discordant inheritance of chromosomal and extrachromosomal DNA elements contributes to dynamic disease evolution in glioblastoma. Nature Genetics, 2018, 50, 708-717.	9.4	212
58	Reconstructing the molecular life history of gliomas. Acta Neuropathologica, 2018, 135, 649-670.	3.9	61
59	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. Neuro-Oncology, 2018, 20, 873-884.	0.6	119
60	Novel therapeutic strategy for cervical cancer harboring FGFR3-TACC3 fusions. Oncogenesis, 2018, 7, 4.	2.1	41
61	TumorFusions: an integrative resource for cancer-associated transcript fusions. Nucleic Acids Research, 2018, 46, D1144-D1149.	6.5	179
62	EGFR heterogeneity and implications for therapeutic intervention in glioblastoma. Neuro-Oncology, 2018, 20, 743-752.	0.6	210
63	DDIS-03. EGFR AMPLIFICATION INDUCED INCREASED DNA DAMAGE RESPONSE AND PREDICTED SELECTIVE SENSITIVITY TO TALAZOPARIB (PARP INHIBITOR) IN GLIOBLASTOMA STEM-LIKE CELLS. Neuro-Oncology, 2018, 20, vi69-vi69.	0.6	0
64	COMP-07. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA. Neuro-Oncology, 2018, 20, vi64-vi65.	0.6	1
65	IMMU-36. IMMUNE RESPONSES IN CANINE GLIOMAS ARE ENRICHED AT THE INFILTRATING EDGE OF ASTROCYTOMAS. Neuro-Oncology, 2018, 20, vi129-vi129.	0.6	0
66	TMOD-18. THE PATIENT DERIVED XENOGRAFT NATIONAL RESOURCE: A COMPREHENSIVE COLLECTION OF HIGH-GRADE GLIOMA MODELS FOR PRE-CLINICAL AND TRANSLATIONAL STUDIES. Neuro-Oncology, 2018, 20, vi272-vi272.	0.6	0
67	The evolutionary pattern of mutations in glioblastoma reveals therapy-mediated selection. Oncotarget, 2018, 9, 7844-7858.	0.8	29
68	DRES-05. MOLECULAR EVOLUTION OF DIFFUSE GLIOMAS AND THE GLIOMA LONGITUDINAL ANALYSIS CONSORTIUM. Neuro-Oncology, 2018, 20, vi76-vi76.	0.6	0
69	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. Neuro-Oncology, 2018, 20, vi235-vi235.	0.6	1
70	Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. Nature Genetics, 2018, 50, 1399-1411.	9.4	145
71	Evolving Insights into the Molecular Neuropathology of Diffuse Gliomas in Adults. Neurologic Clinics, 2018, 36, 421-437.	0.8	9
72	The Tandem Duplicator Phenotype Is a Prevalent Genome-Wide Cancer Configuration Driven by Distinct Gene Mutations. Cancer Cell, 2018, 34, 197-210.e5.	7.7	130

#	Article	IF	Citations
73	Osteopontin mediates glioblastoma-associated macrophage infiltration and is a potential therapeutic target. Journal of Clinical Investigation, 2018, 129, 137-149.	3.9	242
74	The polo-like kinase 1 inhibitor volasertib synergistically increases radiation efficacy in glioma stem cells. Oncotarget, 2018, 9, 10497-10509.	0.8	18
75	Systematic analysis of telomere length and somatic alterations in 31 cancer types. Nature Genetics, 2017, 49, 349-357.	9.4	476
76	Glioma: experimental models and reality. Acta Neuropathologica, 2017, 133, 263-282.	3.9	223
77	Prognostic Relevance of Tumor Purity and Interaction with MGMT Methylation in Glioblastoma. Molecular Cancer Research, 2017, 15, 532-540.	1.5	23
78	Engineering and Functional Characterization of Fusion Genes Identifies Novel Oncogenic Drivers of Cancer. Cancer Research, 2017, 77, 3502-3512.	0.4	31
79	Multigene signature for predicting prognosis of patients with 1p19q co-deletion diffuse glioma. Neuro-Oncology, 2017, 19, 786-795.	0.6	87
80	PAF promotes stemness and radioresistance of glioma stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9086-E9095.	3.3	40
81	Navigating the Cancer Transcriptome by Decoding Divergent Oncogenic States. Cell Systems, 2017, 5, 90-92.	2.9	0
82	Exosomes from Glioma-Associated Mesenchymal Stem Cells Increase the Tumorigenicity of Glioma Stem-like Cells via Transfer of miR-1587. Cancer Research, 2017, 77, 5808-5819.	0.4	169
83	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	7.7	642
84	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
85	Tumor Evolution of Glioma-Intrinsic Gene Expression Subtypes Associates with Immunological Changes in the Microenvironment. Cancer Cell, 2017, 32, 42-56.e6.	7.7	1,282
86	GlioVis data portal for visualization and analysis of brain tumor expression datasets. Neuro-Oncology, 2017, 19, 139-141.	0.6	622
87	TMOD-31. AN INFLAMMATION RESPONSE GENE SIGNATURE IS ASSOCIATED WITH PROGNOSIS OF GLIOMA PATIENTS WITH 1p/19q CO-DELETION TUMORS. Neuro-Oncology, 2016, 18, vi213-vi213.	0.6	0
88	Immune checkpoint blockade as a potential therapeutic target: surveying CNS malignancies. Neuro-Oncology, 2016, 18, 1357-1366.	0.6	116
89	Longitudinal genomic characterization of brain tumors for identification of therapeutic vulnerabilities: TableÂ1.. Neuro-Oncology, 2016, 18, 1037-1039.	0.6	8
90	MSK1-Mediated Î²-Catenin Phosphorylation Confers Resistance to PI3K/mTOR Inhibitors in Glioblastoma. Molecular Cancer Therapeutics, 2016, 15, 1656-1668.	1.9	25

#	Article	IF	Citations
91	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
92	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	9.4	933
93	Novel kinase fusion transcripts found in endometrial cancer. Scientific Reports, 2016, 5, 18657.	1.6	11
94	Moving the needle: Optimizing classification for glioma. Science Translational Medicine, 2016, 8, 350fs14.	5.8	24
95	TMIC-14. TUMOR EVOLUTION OF GLIOMA INTRINSIC GENE EXPRESSION SUBTYPE ASSOCIATES WITH IMMUNOLOGICAL CHANGES IN THE MICROENVIRONMENT. Neuro-Oncology, 2016, 18, vi202-vi202.	0.6	11
96	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
97	EPIG-14EPIGENOMIC (DNA METHYLATION AND EXPRESSION) SIGNATURES DEFINE SUBSETS OF BOTH IDHmut AND IDHwt GLIOMA WITH DISTINCT CLINICAL OUTCOMES. Neuro-Oncology, 2015, 17, v89.2-v89.	0.6	0
98	Molecular profiling of long-term survivors identifies a subgroup of glioblastoma characterized by chromosome 19/20 co-gain. Acta Neuropathologica, 2015, 130, 419-434.	3.9	74
99	Biphasic components of sarcomatoid clear cell renal cell carcinomas are molecularly similar to each other, but distinct from, non‐sarcomatoid renal carcinomas. Journal of Pathology: Clinical Research, 2015, 1, 212-224.	1.3	12
100	GENO-36GLIOMA SPHERE-FORMING CELLS REVEAL INTRINSIC GLOBAL HYPERMETHYLATION ASSOCIATED WITH GBM RADIATION RESISTANCE. Neuro-Oncology, 2015, 17, v99.5-v100.	0.6	0
101	Mir-21‐Sox2 Axis Delineates Glioblastoma Subtypes with Prognostic Impact. Journal of Neuroscience, 2015, 35, 15097-15112.	1.7	53
102	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. Genome Research, 2015, 25, 316-327.	2.4	343
103	Seek and Destroy: Relating Cancer Drivers to Therapies. Cancer Cell, 2015, 27, 319-321.	7.7	5
104	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	15.2	604
105	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
106	Transcriptional mimicry by tumor-associated stroma. Nature Genetics, 2015, 47, 307-309.	9.4	14
107	Ets Factors Regulate Neural Stem Cell Depletion and Gliogenesis in Ras Pathway Glioma. Cell Reports, 2015, 12, 258-271.	2.9	53
108	Histone demethylase JARID1C inactivation triggers genomic instability in sporadic renal cancer. Journal of Clinical Investigation, 2015, 125, 4625-4637.	3.9	62

#	Article	IF	Citations
109	A High Notch Pathway Activation Predicts Response to Î³ Secretase Inhibitors in Proneural Subtype of Glioma Tumor-Initiating Cells. Stem Cells, 2014, 32, 301-312.	1.4	117
110	PRADA: pipeline for RNA sequencing data analysis. Bioinformatics, 2014, 30, 2224-2226.	1.8	147
111	Silent Mutations Make Some Noise. Cell, 2014, 156, 1129-1131.	13.5	33
112	Transformation of quiescent adult oligodendrocyte precursor cells into malignant glioma through a multistep reactivation process. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4214-23.	3.3	105
113	ZFHX4 Interacts with the NuRD Core Member CHD4 and Regulates the Glioblastoma Tumor-Initiating Cell State. Cell Reports, 2014, 6, 313-324.	2.9	106
114	Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612.	5.8	5,788
115	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
116	Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer. Nature Structural and Molecular Biology, 2013, 20, 908-913.	3.6	524
117	Integrated cistromic and expression analysis of amplified *NKX2-1* in lung adenocarcinoma identifies *LMO3* as a functional transcriptional target. Genes and Development, 2013, 27, 197-210.	2.7	61
118	Intragenic breakpoint. Cell Cycle, 2013, 12, 3705-3706.	1.3	1
119	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. Genes and Development, 2013, 27, 1462-1472.	2.7	74
120	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. Journal of Clinical Investigation, 2013, 123, 517-25.	3.9	462
121	Predicting time to ovarian carcinoma recurrence using protein markers. Journal of Clinical Investigation, 2013, 123, 3740-50.	3.9	46
122	Src Inhibition with Saracatinib Reverses Fulvestrant Resistance in ER-Positive Ovarian Cancer Models *In Vitro* and *In Vivo*. Clinical Cancer Research, 2012, 18, 5911-5923.	3.2	69
123	Studying a Complex Tumor. Cancer Journal (Sudbury, Mass), 2012, 18, 107-114.	1.0	26
124	Transformation by the (R)-enantiomer of 2-hydroxyglutarate linked to EGLN activation. Nature, 2012, 483, 484-488.	13.7	630
125	The cellular origin for malignant glioma and prospects for clinical advancements. Expert Review of Molecular Diagnostics, 2012, 12, 383-394.	1.5	161
126	Sequential gain of mutations in severe congenital neutropenia progressing to acute myeloid leukemia. Blood, 2012, 119, 5071-5077.	0.6	156

#	Article	IF	Citations
127	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. Nature Biotechnology, 2011, 29, 393-396.	9.4	289
128	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	9.4	270
129	Mosaic Analysis with Double Markers Reveals Tumor Cell of Origin in Glioma. Cell, 2011, 146, 209-221.	13.5	571
130	Glioblastoma-Derived Epidermal Growth Factor Receptor Carboxyl-Terminal Deletion Mutants Are Transforming and Are Sensitive to EGFR-Directed Therapies. Cancer Research, 2011, 71, 7587-7596.	0.4	70
131	Unifying Gene Expression Measures from Multiple Platforms Using Factor Analysis. PLoS ONE, 2011, 6, e17691.	1.1	12
132	Suppression of lung adenocarcinoma progression by Nkx2-1. Nature, 2011, 473, 101-104.	13.7	383
133	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	7.7	6,138
134	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	7.7	2,078
135	Integrative analysis of the melanoma transcriptome. Genome Research, 2010, 20, 413-427.	2.4	248
136	Prediction of molecular subtypes in acute myeloid leukemia based on gene expression profiling. Haematologica, 2009, 94, 131-134.	1.7	300
137	SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. Nature Genetics, 2009, 41, 1238-1242.	9.4	862
138	Predicting drug susceptibility of non–small cell lung cancers based on genetic lesions. Journal of Clinical Investigation, 2009, 119, 1727-1740.	3.9	230
139	Gene expression–based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. Nature Medicine, 2008, 14, 822-827.	15.2	1,015
140	Differential Regulation of Foxo3a Target Genes in Erythropoiesis. Molecular and Cellular Biology, 2007, 27, 3839-3854.	1.1	77
141	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	13.7	1,020
142	A distal single nucleotide polymorphism alters long-range regulation of the PU.1 gene in acute myeloid leukemia. Journal of Clinical Investigation, 2007, 117, 2611-2620.	3.9	109
143	Essential role of Jun family transcription factors in PU.1 knockdown–induced leukemic stem cells. Nature Genetics, 2006, 38, 1269-1277.	9.4	167
144	Significance of Murine Retroviral Mutagenesis for Identification of Disease Genes in Human Acute Myeloid Leukemia. Cancer Research, 2006, 66, 622-626.	0.4	26

#	Article	IF	Citations
145	Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia. New England Journal of Medicine, 2004, 350, 1617-1628.	13.9	1,232