MarÃ-a Dolores Tabernero

List of Publications by Year
in descending order

29 papers	1,281 citations	361413 20 h-index	477307 29 g-index
29 all docs	29 docs citations	29 times ranked	2085 citing authors

#	Article	IF	Citations
1	Tumor cell and immune cell profiles in primary human glioblastoma: Impact on patient outcome. Brain Pathology, 2021, 31, 365-380.	4.1	27
2	Whole-Exome Sequencing Reveals Recurrent but Heterogeneous Mutational Profiles in Sporadic WHO Grade 1 Meningiomas. Frontiers in Oncology, 2021, 11, 740782.	2.8	5
3	Multivariate analysis reveals differentially expressed genes among distinct subtypes of diffuse astrocytic gliomas: diagnostic implications. Scientific Reports, 2020, 10, 11270.	3.3	11
4	Heterogeneous EGFR, CDK4, MDM4, and PDGFRA Gene Expression Profiles in Primary GBM: No Association with Patient Survival. Cancers, 2020, 12, 231.	3.7	13
5	Prognostic stratification of adult primary glioblastoma multiforme patients based on their tumor gene amplification profiles. Oncotarget, 2018, 9, 28083-28102.	1.8	5
6	Tumor infiltrating immune cells in gliomas and meningiomas. Brain, Behavior, and Immunity, 2016, 53, 1-15.	4.1	228
7	Genetic/molecular alterations of meningiomas and the signaling pathways targeted. Oncotarget, 2015, 6, 10671-10688.	1.8	58
8	The protein expression profile of meningioma cells is associated with distinct cytogenetic tumour subgroups. Neuropathology and Applied Neurobiology, 2015, 41, 319-332.	3.2	10
9	Molecular and Genomic Alterations in Glioblastoma Multiforme. American Journal of Pathology, 2015, 185, 1820-1833.	3.8	141
10	Proposal for a new risk stratification classification for meningioma based on patient age, WHO tumor grade, size, localization, and karyotype. Neuro-Oncology, 2014, 16, 735-747.	1.2	98
11	Association between mutation of the NF2gene and monosomy 22 in menopausal women with sporadic meningiomas. BMC Medical Genetics, 2013, 14, 114.	2.1	16
12	Association between Inflammatory Infiltrates and Isolated Monosomy 22/del(22q) in Meningiomas. PLoS ONE, 2013, 8, e74798.	2.5	31
13	Amplified and Homozygously Deleted Genes in Glioblastoma: Impact on Gene Expression Levels. PLoS ONE, 2012, 7, e46088.	2.5	38
14	Delineation of commonly deleted chromosomal regions in meningiomas by highâ€density single nucleotide polymorphism genotyping arrays. Genes Chromosomes and Cancer, 2012, 51, 606-617.	2.8	15
15	Detailed Characterization of Alterations of Chromosomes 7, 9, and 10 in Glioblastomas as Assessed by Single-Nucleotide Polymorphism Arrays. Journal of Molecular Diagnostics, 2011, 13, 634-647.	2.8	55
16	Intratumoral patterns of clonal evolution in gliomas. Neurogenetics, 2010, 11, 227-239.	1.4	23
17	Gene expression profiles of human glioblastomas are associated with both tumor cytogenetics and histopathology. Neuro-Oncology, 2010, 12, 991-1003.	1.2	45
18	Gene Expression Profiles of Meningiomas are Associated with Tumor Cytogenetics and Patient Outcome. Brain Pathology, 2009, 19, 409-420.	4.1	42

#	Article	IF	Citations
19	Array-based comparative genomic hybridization of mapped BAC DNA clones to screen for chromosome 14 copy number abnormalities in meningiomas. European Journal of Human Genetics, 2008, 16, 1450-1458.	2.8	6
20	Early recurrences in histologically benign/grade I meningiomas are associated with large tumors and coexistence of monosomy 14 and del(1p36) in the ancestral tumor cell clone. Neuro-Oncology, 2007, 9, 438-446.	1.2	74
21	Patient Gender Is Associated with Distinct Patterns of Chromosomal Abnormalities and Sex Chromosomeâ€“Linked Gene-Expression Profiles in Meningiomas. Oncologist, 2007, 12, 1225-1236.	3.7	37
22	Microarray-Based Analysis of Spinal versus Intracranial Meningiomas: Different Clinical, Biological, and Genetic Characteristics Associated with Distinct Patterns of Gene Expression. Journal of Neuropathology and Experimental Neurology, 2006, 65, 445-454.	1.7	48
23	The Cytogenetic Relationship between Primary and Recurrent Meningiomas Points to the Need for New Treatment Strategies in Cases at High Risk of Relapse. Clinical Cancer Research, 2006, 12, 772-780.	7.0	37
24	Characterization of Chromosome 14 Abnormalities by Interphase In Situ Hybridization and Comparative Genomic Hybridization in 124 Meningiomas. American Journal of Clinical Pathology, 2005, 123, 744-751.	0.7	34
25	Characterization of chromosome 14 abnormalities by interphase in situ hybridization and comparative genomic hybridization in 124 meningiomas: correlation with clinical, histopathologic, and prognostic features. American Journal of Clinical Pathology, 2005, 123, 744-51.	0.7	9
26	Intratumoral Patterns of Clonal Evolution in Meningiomas as Defined by Multicolor Interphase Fluorescence in Situ Hybridization (FISH). Journal of Molecular Diagnostics, 2004, 6, 316-325.	2.8	42
27	New Classification Scheme for the Prognostic Stratification of Meningioma on the Basis of Chromosome 14 Abnormalities, Patient Age, and Tumor Histopathology. Journal of Clinical Oncology, 2003, 21, 3285-3295.	1.6	71
28	Incidence of numerical chromosome aberrations in meningioma tumors as revealed by fluorescence in situ hybridization using 10 chromosome-specific probes. Cytometry, 2002, 50, 153-159.	1.8	28
29	Gains of chromosome 22 by fluorescence in situ hybridization in the context of an hyperdiploid karyotype are associated with aggressive clinical features in meningioma patients. Cancer, 2001, 92, 377-385.	4.1	34