

Barbara Majello

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67

papers

2,698

citations

29

h-index

51

g-index

69

ext. papers

2,954

ext. citations

7.7

avg, IF

4.97

L-index

#	Paper	IF	Citations
67	Towards a comprehensive view of 8-oxo-7,8-dihydro-2'-deoxyguanosine: Highlighting the intertwined roles of DNA damage and epigenetics in genomic instability. <i>DNA Repair</i> , 2021 , 97, 103027	4.3	11
66	Genome-wide mapping of genomic DNA damage: methods and implications. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 6745-6762	10.3	2
65	The genomic landscape of 8-oxodG reveals enrichment at specific inherently fragile promoters. <i>Nucleic Acids Research</i> , 2020 , 48, 4309-4324	20.1	14
64	Autophagy Roles in Genome Maintenance. <i>Cancers</i> , 2020 , 12,	6.6	14
63	Expanding the Role of the Histone Lysine-Specific Demethylase LSD1 in Cancer. <i>Cancers</i> , 2019 , 11,	6.6	60
62	Inhibition of lysine-specific demethylase LSD1 induces senescence in Glioblastoma cells through a HIF-1 β -dependent pathway. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019 , 1862, 535-546	6	6
61	Knowledge Generation with Rule Induction in Cancer Omics. <i>International Journal of Molecular Sciences</i> , 2019 , 21,	6.3	3
60	Histone methyl-transferases and demethylases in the autophagy regulatory network: the emerging role of KDM1A/LSD1 demethylase. <i>Autophagy</i> , 2019 , 15, 187-196	10.2	15
59	Genome-wide mapping of 8-oxo-7,8-dihydro-2'-deoxyguanosine reveals accumulation of oxidatively-generated damage at DNA replication origins within transcribed long genes of mammalian cells. <i>Nucleic Acids Research</i> , 2019 , 47, 221-236	20.1	38
58	Targeting Histone Demethylase LSD1/KDM1a in Neurodegenerative Diseases. <i>Journal of Experimental Neuroscience</i> , 2018 , 12, 1179069518765743	3.6	12
57	Mitochondrial AKAP1 supports mTOR pathway and tumor growth. <i>Cell Death and Disease</i> , 2017 , 8, e28428	2.8	32
56	Epigenetic regulation of epithelial to mesenchymal transition by the Lysine-specific demethylase LSD1/KDM1A. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017 , 1860, 905-910	6	31
55	Lysine-specific demethylase LSD1 regulates autophagy in neuroblastoma through SESN2-dependent pathway. <i>Oncogene</i> , 2017 , 36, 6701-6711	9.2	49
54	LSD1 mediates MYCN control of epithelial-mesenchymal transition through silencing of metastatic suppressor NDRG1 gene. <i>Oncotarget</i> , 2017 , 8, 3854-3869	3.3	28
53	Cell cycle-dependent resolution of DNA double-strand breaks. <i>Oncotarget</i> , 2016 , 7, 4949-60	3.3	16
52	MYC impairs resolution of site-specific DNA double-strand breaks repair. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015 , 774, 6-13	3.3	10
51	Chemical characterization, antioxidant and cytotoxic activities of the methanolic extract of <i>Hymenocrater longiflorus</i> grown in Iraq. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2015 , 70, 227-35	1.7	6

50	Lysine-specific demethylase (LSD1/KDM1A) and MYCN cooperatively repress tumor suppressor genes in neuroblastoma. <i>Oncotarget</i> , 2015 , 6, 14572-83	3.3	37
49	RNA polymerase II CTD modifications: how many tales from a single tail. <i>Journal of Cellular Physiology</i> , 2014 , 229, 538-44	7	11
48	Role of noncoding RNAs in the regulation of P-TEFb availability and enzymatic activity. <i>BioMed Research International</i> , 2014 , 2014, 643805	3	
47	Myc and PI3K/AKT signaling cooperatively repress FOXO3a-dependent PUMA and GADD45a gene expression. <i>Nucleic Acids Research</i> , 2014 , 42, 2098-2098	20.1	78
46	The histone LSD1 demethylase in stemness and cancer transcription programs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013 , 1829, 981-6	6	138
45	Sequence-specific double strand breaks trigger P-TEFb-dependent Rpb1-CTD hyperphosphorylation. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2013 , 749, 21-7	3.3	10
44	SUMO-activating SAE1 transcription is positively regulated by Myc. <i>American Journal of Cancer Research</i> , 2012 , 2, 330-4	4.4	16
43	Myc and PI3K/AKT signaling cooperatively repress FOXO3a-dependent PUMA and GADD45a gene expression. <i>Nucleic Acids Research</i> , 2011 , 39, 9498-507	20.1	61
42	Epigenetic reprogramming of Myc target genes. <i>American Journal of Cancer Research</i> , 2011 , 1, 413-418	4.4	11
41	LSD1-mediated demethylation of histone H3 lysine 4 triggers Myc-induced transcription. <i>Oncogene</i> , 2010 , 29, 3691-702	9.2	125
40	Caffeine prevents transcription inhibition and P-TEFb/7SK dissociation following UV-induced DNA damage. <i>PLoS ONE</i> , 2010 , 5, e11245	3.7	10
39	DNA oxidation drives Myc mediated transcription. <i>Cell Cycle</i> , 2010 , 9, 3002-4	4.7	29
38	Camptothecin releases P-TEFb from the inactive 7SK snRNP complex. <i>Cell Cycle</i> , 2009 , 8, 1249-55	4.7	17
37	p14ARF is capable of promoting HIV-1 tat degradation. <i>Cell Cycle</i> , 2008 , 7, 1433-9	4.7	11
36	P-TEFb is a crucial co-factor for Myc transactivation. <i>Cell Cycle</i> , 2007 , 6, 2031-7	4.7	62
35	Activation of P-TEFb induces p21 leading to cell cycle arrest. <i>Cell Cycle</i> , 2007 , 6, 1126-9	4.7	8
34	p14ARF interacts with N-Myc and inhibits its transcriptional activity. <i>FEBS Letters</i> , 2007 , 581, 821-5	3.8	10
33	Increased HEXIM1 expression during erythroleukemia and neuroblastoma cell differentiation. <i>Journal of Cellular Physiology</i> , 2006 , 206, 603-10	7	32

32	p14ARF directly interacts with Myc through the Myc BoxII domain. <i>Cancer Biology and Therapy</i> , 2006 , 5, 287-91	4.6	14
31	Identification of proteins interacting with the RNAPII FCP1 phosphatase: FCP1 forms a complex with arginine methyltransferase PRMT5 and it is a substrate for PRMT5-mediated methylation. <i>FEBS Letters</i> , 2005 , 579, 683-9	3.8	59
30	Inhibition of Tat activity by the HEXIM1 protein. <i>Retrovirology</i> , 2005 , 2, 42	3.6	31
29	Catalytic activity of Cdk9 is required for nuclear co-localization of the Cdk9/cyclin T1 (P-TEFb) complex. <i>Journal of Cellular Physiology</i> , 2003 , 197, 1-7	7	16
28	Functional inactivation of Cdk9 through oligomerization chain reaction. <i>Oncogene</i> , 2003 , 22, 4882-8	9.2	13
27	The FCP1 phosphatase interacts with RNA polymerase II and with MEP50 a component of the methylosome complex involved in the assembly of snRNP. <i>Nucleic Acids Research</i> , 2003 , 31, 999-1005	20.1	17
26	CDK9 has the intrinsic property to shuttle between nucleus and cytoplasm, and enhanced expression of cyclin T1 promotes its nuclear localization. <i>Journal of Cellular Physiology</i> , 2002 , 192, 209-15	7	32
25	Role of cyclinT/Cdk9 complex in basal and regulated transcription (Review) 2002 , 21, 171		4
24	Role of cyclinT/Cdk9 complex in basal and regulated transcription (review). <i>International Journal of Oncology</i> , 2002 , 21, 171-7	1	13
23	Distinct regions of cyclinT1 are required for binding to CDK9 and for recruitment to the HIV-1 Tat/TAR complex. <i>Journal of Cellular Biochemistry</i> , 2001 , Suppl 36, 247-53	4.7	18
22	Transcription activation by targeted recruitment of the RNA polymerase II CTD phosphatase FCP1. <i>Nucleic Acids Research</i> , 2001 , 29, 3539-45	20.1	14
21	Control of RNA polymerase II activity by dedicated CTD kinases and phosphatases. <i>Frontiers in Bioscience - Landmark</i> , 2001 , 6, D1358-68	2.8	30
20	Inhibition of Tat transactivation by the RNA polymerase II CTD-phosphatase FCP1. <i>Aids</i> , 2001 , 15, 301-7	3.5	9
19	Control of RNA polymerase II activity by dedicated CTD kinases and phosphatases. <i>Frontiers in Bioscience - Landmark</i> , 2001 , 6, d1358-1368	2.8	22
18	Transcriptional activity of positive transcription elongation factor b kinase in vivo requires the C-terminal domain of RNA polymerase II. <i>Gene</i> , 2000 , 254, 139-45	3.8	44
17	A novel member of the BTB/POZ family, PATZ, associates with the RNF4 RING finger protein and acts as a transcriptional repressor. <i>Journal of Biological Chemistry</i> , 2000 , 275, 7894-901	5.4	69
16	The CDK9-associated cyclins T1 and T2 exert opposite effects on HIV-1 Tat activity. <i>Aids</i> , 1999 , 13, 1453-9	3.5	33
15	Transcriptional regulation by targeted recruitment of cyclin-dependent CDK9 kinase in vivo. <i>Oncogene</i> , 1999 , 18, 4598-605	9.2	63

14	Transcriptional control by cell-cycle regulators: a review. <i>Journal of Cellular Physiology</i> , 1999 , 179, 134-41		37
13	Retinoblastoma protein tethered to promoter DNA represses TBP-mediated transcription. <i>Journal of Cellular Biochemistry</i> , 1998 , 70, 281-7	4.7	15
12	Recruitment of human TBP selectively activates RNA polymerase II TATA-dependent promoters. <i>Journal of Biological Chemistry</i> , 1998 , 273, 16509-16	5.4	38
11	Recruitment of the TATA-binding protein to the HIV-1 promoter is a limiting step for Tat transactivation. <i>Aids</i> , 1998 , 12, 1957-64	3.5	19
10	Sp3 is a bifunctional transcription regulator with modular independent activation and repression domains. <i>Journal of Biological Chemistry</i> , 1997 , 272, 4021-6	5.4	245
9	Transcriptional regulation by the Sp family proteins. <i>International Journal of Biochemistry and Cell Biology</i> , 1997 , 29, 1313-23	5.6	268
8	Sp3 represses transcription when tethered to promoter DNA or targeted to promoter proximal RNA. <i>Journal of Biological Chemistry</i> , 1996 , 271, 8533-6	5.4	72
7	Different members of the Sp1 multigene family exert opposite transcriptional regulation of the long terminal repeat of HIV-1. <i>Nucleic Acids Research</i> , 1994 , 22, 4914-21	20.1	210
6	Mutational analysis of the human endogenous ERV9 proviruses promoter region. <i>Virology</i> , 1994 , 200, 686-95	3.6	13
5	Identification of regulatory elements within the minimal promoter region of the human endogenous ERV9 proviruses: accurate transcription initiation is controlled by an Inr-like element. <i>Nucleic Acids Research</i> , 1992 , 20, 4129-36	20.1	26
4	Structural and functional organization of the human endogenous retroviral ERV9 sequences. <i>Virology</i> , 1992 , 191, 464-8	3.6	31
3	Characterization of mononuclear-phagocyte terminal maturation by mRNA phenotyping using a set of cloned cDNA probes. <i>FEBS Journal</i> , 1989 , 185, 291-6		10
2	Human c-myc protooncogene: nucleotide sequence of cDNA and organization of the genomic locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986 , 83, 9636-40	11.5	155
1	Activation of major histocompatibility complex class I mRNA containing an Alu-like repeat in polyoma virus-transformed rat cells. <i>Nature</i> , 1985 , 314, 457-9	50.4	37