Bruno Amati

List of Publications by Year
in descending order

76 papers	10,424 citations	53794 45 h-index	76900 74 g-index
82 all docs	82 docs citations	82 times ranked	14652 citing authors

#	Article	IF	Citations
1	Targeting mitochondrial respiration and the BCL2 family in highâ€grade MYCâ€associated Bâ€cell lymphoma. Molecular Oncology, 2022, 16, 1132-1152.	4.6	10
2	Polycomb group ring finger protein 6 suppresses Myc-induced lymphomagenesis. Life Science Alliance, 2022, 5, e202101344.	2.8	4
3	Integrated requirement of nonâ€specific and sequenceâ€specific DNA binding in Mycâ€driven transcription. EMBO Journal, 2021, 40, e105464.	7.8	24
4	Cooperation Between MYC and Î²â€Catenin in Liver Tumorigenesis Requires Yap/Taz. Hepatology, 2020, 72, 1430-1443.	7.3	51
5	Reactivation of Myc transcription in the mouse heart unlocks its proliferative capacity. Nature Communications, 2020, 11, 1827.	12.8	38
6	An early Mycâ€dependent transcriptional program orchestrates cell growth during Bâ€cell activation. EMBO Reports, 2019, 20, e47987.	4.5	44
7	<scp>MYC</scp> in Germinal Centerâ€derived lymphomas: Mechanisms and therapeutic opportunities. Immunological Reviews, 2019, 288, 178-197.	6.0	42
8	p53 Loss in Breast Cancer Leads to Myc Activation, Increased Cell Plasticity, and Expression of a Mitotic Signature with Prognostic Value. Cell Reports, 2019, 26, 624-638.e8.	6.4	47
9	Abstract 108: Reactivation of Myc Transcription in the Heart Unlocks its Proliferative Capacity. Circulation Research, 2019, 125, .	4.5	0
10	Therapeutic synergy between tigecycline and venetoclax in a preclinical model of MYC / BCL2 double-hit B cell lymphoma. Science Translational Medicine, 2018, 10, .	12.4	41
11	YAP and TAZ are dispensable for physiological and malignant haematopoiesis. Leukemia, 2018, 32, 2037-2040.	7.2	42
12	BRD4 and MYCâ€”clarifying regulatory specificity. Science, 2018, 360, 713-714.	12.6	19
13	X-box Binding Protein 1 Regulates Unfolded Protein, Acute-Phase, and DNA Damage Responses During RegenerationÂof Mouse Liver. Gastroenterology, 2017, 152, 1203-1216.e15.	1.3	39
14	FunChIP: an R/Bioconductor package for functional classification of ChIP-seq shapes. Bioinformatics, 2017, 33, 2570-2572.	4.1	5
15	Opposing macrophage polarization programs show extensive epigenomic and transcriptional cross-talk. Nature Immunology, 2017, 18, 530-540.	14.5	164
16	Integrative analysis of RNA polymerase II and transcriptional dynamics upon MYC activation. Genome Research, 2017, 27, 1658-1664.	5.5	50
17	Transcriptional integration of mitogenic and mechanical signals by Myc and YAP. Genes and Development, 2017, 31, 2017-2022.	5.9	65
18	Mutual epitheliumâ€macrophage dependency in liver carcinogenesis mediated by ST18. Hepatology, 2017, 65, 1708-1719.	7.3	19

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19	Integrated Systems for NGS Data Management and Analysis: Open Issues and Available Solutions. Frontiers in Genetics, 2016, 7, 75.	2.3	45
20	Smyd2 is a Myc-regulated gene critical for MLL-AF9 induced leukemogenesis. Oncotarget, 2016, 7, 66398-66415.	1.8	19
21	p53 transcriptional programs in B cells upon exposure to genotoxic stress in vivo : Computational analysis of next-generation sequencing data. Genomics Data, 2016, 7, 29-31.	1.3	4
22	Identification of MYC-Dependent Transcriptional Programs in Oncogene-Addicted Liver Tumors. Cancer Research, 2016, 76, 3463-3472.	0.9	54
23	Proteasome machinery is instrumental in a common gain-of-function program of the p53 missense mutants in cancer. Nature Cell Biology, 2016, 18, 897-909.	10.3	205
24	Degradation dynamics of microRNAs revealed by a novel pulse-chase approach. Genome Research, 2016, 26, 554-565.	5.5	155
25	The mitochondrial translation machinery as a therapeutic target in Myc-driven lymphomas. Oncotarget, 2016, 7, 72415-72430.	1.8	56
26	Pin1 is required for sustained B cell proliferation upon oncogenic activation of Myc. Oncotarget, 2016, 7, 21786-21798.	1.8	28
27	methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. BMC Bioinformatics, 2015, 16, 313.	2.6	68
28	INSPEcT: a computational tool to infer mRNA synthesis, processing and degradation dynamics from RNA- and 4sU-seq time course experiments. Bioinformatics, 2015, 31, 2829-2835.	4.1	60
29	MYC regulates the core pre-mRNA splicing machinery as an essential step in lymphomagenesis. Nature, 2015, 523, 96-100.	27.8	317
30	MYC: connecting selective transcriptional control to global RNA production. Nature Reviews Cancer, 2015, 15, 593-607.	28.4	388
31	Selective transcriptional regulation by Myc: Experimental design and computational analysis of high-throughput sequencing data. Data in Brief, 2015, 3, 40-46.	1.0	3
32	Genome-wide analysis of p53 transcriptional programs in B cells upon exposure to genotoxic stress in vivo. Oncotarget, 2015, 6, 24611-24626.	1.8	31
33	Genome Recognition by MYC. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a014191-a014191.	6.2	84
34	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	2.8	24
35	Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. Nature, 2014, 511, 488-492.	27.8	411
36	SUMOylation of Myc-Family Proteins. PLoS ONE, 2014, 9, e91072.	2.5	27

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37	A non-redundant function of cyclin E1 in hematopoietic stem cells. Cell Cycle, 2013, 12, 3663-3672.	2.6	12
38	Two sides of the Myc-induced DNA damage response: from tumor suppression to tumor maintenance. Cell Division, 2012, 7, 6.	2.4	73
39	Symmetric dimethylation of H3R2 is a newly identified histone mark that supports euchromatin maintenance. Nature Structural and Molecular Biology, 2012, 19, 136-144.	8.2	272
40	Exploiting oncogene-induced replicative stress for the selective killing of Myc-driven tumors. Nature Structural and Molecular Biology, 2011, 18, 1331-1335.	8.2	342
41	The Methyltransferase Set7/9 (Setd7) Is Dispensable for the p53-Mediated DNA Damage Response InÂVivo. Molecular Cell, 2011, 43, 681-688.	9.7	77
42	Impairment of Cytoplasmic eIF6 Activity Restricts Lymphomagenesis and Tumor Progression without Affecting Normal Growth. Cancer Cell, 2011, 19, 765-775.	16.8	90
43	Chromatin association and regulation of rDNA transcription by the Ras-family protein RasL11a. EMBO Journal, 2010, 29, 1215-1224.	7.8	19
44	Cdk2 suppresses cellular senescence induced by the c-myc oncogene. Nature Cell Biology, 2010, 12, 54-59.	10.3	218
45	Myc, Cdk2 and cellular senescence: Old players, new game. Cell Cycle, 2010, 9, 3679-3685.	2.6	24
46	TGFÎ²-dependent gene expression shows that senescence correlates with abortive differentiation along several lineages in Myc-induced lymphomas. Cell Cycle, 2010, 9, 4622-4626.	2.6	6
47	Myc, Cdk2 and cellular senescence: Old players, new game. Cell Cycle, 2010, 9, 3655-61.	2.6	17
48	Epigenome Microarray Platform for Proteome-Wide Dissection of Chromatin-Signaling Networks. PLoS ONE, 2009, 4, e6789.	2.5	91
49	Nucleophosmin and its AML-associated mutant regulate c-Myc turnover through Fbw7Î³. Journal of Cell Biology, 2008, 182, 19-26.	5.2	114
50	Immortalization of Human Neural Stem Cells with the c-Myc Mutant T58A. PLoS ONE, 2008, 3, e3310.	2.5	37
51	Analysis of Myc-Induced Histone Modifications on Target Chromatin. PLoS ONE, 2008, 3, e3650.	2.5	120
52	MYC degradation: deubiquitinating enzymes enter the dance. Nature Cell Biology, 2007, 9, 729-731.	10.3	23
53	Tip60 is a haplo-insufficient tumour suppressor required for an oncogene-induced DNA damage response. Nature, 2007, 448, 1063-1067.	27.8	296
54	Methylation of histone H3R2 by PRMT6 and H3K4 by an MLL complex are mutually exclusive. Nature, 2007, 449, 933-937.	27.8	402

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55	Myc-binding-site recognition in the human genome is determined by chromatin context. Nature Cell Biology, 2006, 8, 764-770.	10.3	333
56	Tip60 in DNA damage response and growth control: many tricks in one HAT. Trends in Cell Biology, 2006, 16, 433-442.	7.9	264
57	Myc represses transcription through recruitment of DNA methyltransferase corepressor. EMBO Journal, 2005, 24, 336-346.	7.8	375
58	E2F-Dependent Histone Acetylation and Recruitment of the Tip60 Acetyltransferase Complex to Chromatin in Late G 1. Molecular and Cellular Biology, 2004, 24, 4546-4556.	2.3	194
59	Myc degradation: Dancing with ubiquitin ligases. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8843-8844.	7.1	66
60	Cyclins E1 and E2 are required for endoreplication in placental trophoblast giant cells. EMBO Journal, 2003, 22, 4794-4803.	7.8	224
61	MYC recruits the TIP60 histone acetyltransferase complex to chromatin. EMBO Reports, 2003, 4, 575-580.	4.5	331
62	Deacetylase Activity Is Required for Recruitment of the Basal Transcription Machinery and Transactivation by STAT5. Molecular and Cellular Biology, 2003, 23, 4162-4173.	2.3	128
63	Werner syndrome protein limits MYC-induced cellular senescence. Genes and Development, 2003, 17, 1569-1574.	5.9	157
64	Genomic targets of the human c-Myc protein. Genes and Development, 2003, 17, 1115-1129.	5.9	819
65	Recruitment of TRRAP required for oncogenic transformation by E1A. Oncogene, 2001, 20, 8270-8275.	5.9	75
66	Integrating Myc and TGF-Î² signalling in cell-cycle control. Nature Cell Biology, 2001, 3, E112-E113.	10.3	38
67	Function of the c-Myc oncoprotein in chromatin remodeling and transcription. Biochimica Et Biophysica Acta: Reviews on Cancer, 2001, 1471, M135-M145.	7.4	102
68	Binding of c-Myc to chromatin mediates mitogen-induced acetylation of histone H4 and gene activation. Genes and Development, 2001, 15, 2069-2082.	5.9	441
69	Kip1 meets SKP2: new links in cell-cycle control. Nature Cell Biology, 1999, 1, E91-E93.	10.3	57
70	Cyclin E2: a novel CDK2 partner in the late G1 and S phases of the mammalian cell cycle. Oncogene, 1998, 17, 2637-2643.	5.9	130
71	Myc and the cell cycle. Frontiers in Bioscience - Landmark, 1998, 3, d250-268.	3.0	324
72	Integrated control of cell proliferation and cell death by the c-myc oncogene. , 1995, , 33-39.		1

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73	Mycâ€”Maxâ€”Mad: a transcription factor network controlling cell cycle progression, differentiation and death. Current Opinion in Genetics and Development, 1994, 4, 102-108.	3.3	351
74	Oncogenic activity of the c-Myc protein requires dimerization with Max. Cell, 1993, 72, 233-245.	28.9	538
75	Distinct DNA binding preferences for the c-Myc/Max and Max/Max dimers. Nucleic Acids Research, 1993, 21, 5372-5376.	14.5	102
76	Transcriptional activation by the human c-Myc oncoprotein in yeast requires interaction with Max. Nature, 1992, 359, 423-426.	27.8	455