

# Bruno Amati

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Genomic targets of the human c-Myc protein. <i>Genes and Development</i> , 2003, 17, 1115-1129.	5.9	819
2	Oncogenic activity of the c-Myc protein requires dimerization with Max. <i>Cell</i> , 1993, 72, 233-245.	28.9	538
3	Transcriptional activation by the human c-Myc oncoprotein in yeast requires interaction with Max. <i>Nature</i> , 1992, 359, 423-426.	27.8	455
4	Binding of c-Myc to chromatin mediates mitogen-induced acetylation of histone H4 and gene activation. <i>Genes and Development</i> , 2001, 15, 2069-2082.	5.9	441
5	Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. <i>Nature</i> , 2014, 511, 488-492.	27.8	411
6	Methylation of histone H3R2 by PRMT6 and H3K4 by an MLL complex are mutually exclusive. <i>Nature</i> , 2007, 449, 933-937.	27.8	402
7	MYC: connecting selective transcriptional control to global RNA production. <i>Nature Reviews Cancer</i> , 2015, 15, 593-607.	28.4	388
8	Myc represses transcription through recruitment of DNA methyltransferase corepressor. <i>EMBO Journal</i> , 2005, 24, 336-346.	7.8	375
9	Myc-Max-Mad: a transcription factor network controlling cell cycle progression, differentiation and death. <i>Current Opinion in Genetics and Development</i> , 1994, 4, 102-108.	3.3	351
10	Exploiting oncogene-induced replicative stress for the selective killing of Myc-driven tumors. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1331-1335.	8.2	342
11	Myc-binding-site recognition in the human genome is determined by chromatin context. <i>Nature Cell Biology</i> , 2006, 8, 764-770.	10.3	333
12	MYC recruits the TIP60 histone acetyltransferase complex to chromatin. <i>EMBO Reports</i> , 2003, 4, 575-580.	4.5	331
13	Myc and the cell cycle. <i>Frontiers in Bioscience - Landmark</i> , 1998, 3, d250-268.	3.0	324
14	MYC regulates the core pre-mRNA splicing machinery as an essential step in lymphomagenesis. <i>Nature</i> , 2015, 523, 96-100.	27.8	317
15	Tip60 is a haplo-insufficient tumour suppressor required for an oncogene-induced DNA damage response. <i>Nature</i> , 2007, 448, 1063-1067.	27.8	296
16	Symmetric dimethylation of H3R2 is a newly identified histone mark that supports euchromatin maintenance. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 136-144.	8.2	272
17	Tip60 in DNA damage response and growth control: many tricks in one HAT. <i>Trends in Cell Biology</i> , 2006, 16, 433-442.	7.9	264
18	Cyclins E1 and E2 are required for endoreplication in placental trophoblast giant cells. <i>EMBO Journal</i> , 2003, 22, 4794-4803.	7.8	224

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19	Cdk2 suppresses cellular senescence induced by the c-myc oncogene. <i>Nature Cell Biology</i> , 2010, 12, 54-59.	10.3	218
20	Proteasome machinery is instrumental in a common gain-of-function program of the p53 missense mutants in cancer. <i>Nature Cell Biology</i> , 2016, 18, 897-909.	10.3	205
21	E2F-Dependent Histone Acetylation and Recruitment of the Tip60 Acetyltransferase Complex to Chromatin in Late G 1. <i>Molecular and Cellular Biology</i> , 2004, 24, 4546-4556.	2.3	194
22	Opposing macrophage polarization programs show extensive epigenomic and transcriptional cross-talk. <i>Nature Immunology</i> , 2017, 18, 530-540.	14.5	164
23	Werner syndrome protein limits MYC-induced cellular senescence. <i>Genes and Development</i> , 2003, 17, 1569-1574.	5.9	157
24	Degradation dynamics of microRNAs revealed by a novel pulse-chase approach. <i>Genome Research</i> , 2016, 26, 554-565.	5.5	155
25	Cyclin E2: a novel CDK2 partner in the late G1 and S phases of the mammalian cell cycle. <i>Oncogene</i> , 1998, 17, 2637-2643.	5.9	130
26	Deacetylase Activity Is Required for Recruitment of the Basal Transcription Machinery and Transactivation by STAT5. <i>Molecular and Cellular Biology</i> , 2003, 23, 4162-4173.	2.3	128
27	Analysis of Myc-Induced Histone Modifications on Target Chromatin. <i>PLoS ONE</i> , 2008, 3, e3650.	2.5	120
28	Nucleophosmin and its AML-associated mutant regulate c-Myc turnover through Fbw7 <sup>13</sup> . <i>Journal of Cell Biology</i> , 2008, 182, 19-26.	5.2	114
29	Distinct DNA binding preferences for the c-Myc/Max and Max/Max dimers. <i>Nucleic Acids Research</i> , 1993, 21, 5372-5376.	14.5	102
30	Function of the c-Myc oncoprotein in chromatin remodeling and transcription. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2001, 1471, M135-M145.	7.4	102
31	Epigenome Microarray Platform for Proteome-Wide Dissection of Chromatin-Signaling Networks. <i>PLoS ONE</i> , 2009, 4, e6789.	2.5	91
32	Impairment of Cytoplasmic eIF6 Activity Restricts Lymphomagenesis and Tumor Progression without Affecting Normal Growth. <i>Cancer Cell</i> , 2011, 19, 765-775.	16.8	90
33	Genome Recognition by MYC. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a014191-a014191.	6.2	84
34	The Methyltransferase Set7/9 (Setd7) Is Dispensable for the p53-Mediated DNA Damage Response In Vivo. <i>Molecular Cell</i> , 2011, 43, 681-688.	9.7	77
35	Recruitment of TRRAP required for oncogenic transformation by E1A. <i>Oncogene</i> , 2001, 20, 8270-8275.	5.9	75
36	Two sides of the Myc-induced DNA damage response: from tumor suppression to tumor maintenance. <i>Cell Division</i> , 2012, 7, 6.	2.4	73

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37	methyPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. BMC Bioinformatics, 2015, 16, 313.	2.6	68
38	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
39	Transcriptional integration of mitogenic and mechanical signals by Myc and YAP. Genes and Development, 2017, 31, 2017-2022.	5.9	65
40	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
41	Kip1 meets SKP2: new links in cell-cycle control. Nature Cell Biology, 1999, 1, E91-E93.	10.3	57
42	The mitochondrial translation machinery as a therapeutic target in Myc-driven lymphomas. Oncotarget, 2016, 7, 72415-72430.	1.8	56
43	Identification of MYC-Dependent Transcriptional Programs in Oncogene-Addicted Liver Tumors. Cancer Research, 2016, 76, 3463-3472.	0.9	54
44	Cooperation Between MYC and $\beta$ -Catenin in Liver Tumorigenesis Requires Yap/Taz. Hepatology, 2020, 72, 1430-1443.	7.3	51
45	Integrative analysis of RNA polymerase II and transcriptional dynamics upon MYC activation. Genome Research, 2017, 27, 1658-1664.	5.5	50
46	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
47	Integrated Systems for NGS Data Management and Analysis: Open Issues and Available Solutions. Frontiers in Genetics, 2016, 7, 75.	2.3	45
48	An early Myc-dependent transcriptional program orchestrates cell growth during B-cell activation. EMBO Reports, 2019, 20, e47987.	4.5	44
49	YAP and TAZ are dispensable for physiological and malignant haematopoiesis. Leukemia, 2018, 32, 2037-2040.	7.2	42
50	MYC in Germinal Center-derived lymphomas: Mechanisms and therapeutic opportunities. Immunological Reviews, 2019, 288, 178-197.	6.0	42
51	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
52	X-box Binding Protein 1 Regulates Unfolded Protein, Acute-Phase, and DNA Damage Responses During Regeneration of Mouse Liver. Gastroenterology, 2017, 152, 1203-1216.e15.	1.3	39
53	Integrating Myc and TGF- $\beta$ signalling in cell-cycle control. Nature Cell Biology, 2001, 3, E112-E113.	10.3	38
54	Reactivation of Myc transcription in the mouse heart unlocks its proliferative capacity. Nature Communications, 2020, 11, 1827.	12.8	38

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55	Immortalization of Human Neural Stem Cells with the c-Myc Mutant T58A. <i>PLoS ONE</i> , 2008, 3, e3310.	2.5	37
56	Genome-wide analysis of p53 transcriptional programs in B cells upon exposure to genotoxic stress <i>in vivo</i> . <i>Oncotarget</i> , 2015, 6, 24611-24626.	1.8	31
57	Pin1 is required for sustained B cell proliferation upon oncogenic activation of Myc. <i>Oncotarget</i> , 2016, 7, 21786-21798.	1.8	28
58	SUMOylation of Myc-Family Proteins. <i>PLoS ONE</i> , 2014, 9, e91072.	2.5	27
59	Myc, Cdk2 and cellular senescence: Old players, new game. <i>Cell Cycle</i> , 2010, 9, 3679-3685.	2.6	24
60	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	2.8	24
61	Integrated requirement of non-specific and sequence-specific DNA binding in Myc-driven transcription. <i>EMBO Journal</i> , 2021, 40, e105464.	7.8	24
62	MYC degradation: deubiquitinating enzymes enter the dance. <i>Nature Cell Biology</i> , 2007, 9, 729-731.	10.3	23
63	Chromatin association and regulation of rDNA transcription by the Ras-family protein RasL11a. <i>EMBO Journal</i> , 2010, 29, 1215-1224.	7.8	19
64	Smyd2 is a Myc-regulated gene critical for MLL-AF9 induced leukemogenesis. <i>Oncotarget</i> , 2016, 7, 66398-66415.	1.8	19
65	Mutual epithelium-macrophage dependency in liver carcinogenesis mediated by ST18. <i>Hepatology</i> , 2017, 65, 1708-1719.	7.3	19
66	BRD4 and MYC clarifying regulatory specificity. <i>Science</i> , 2018, 360, 713-714.	12.6	19
67	Myc, Cdk2 and cellular senescence: Old players, new game. <i>Cell Cycle</i> , 2010, 9, 3655-61.	2.6	17
68	A non-redundant function of cyclin E1 in hematopoietic stem cells. <i>Cell Cycle</i> , 2013, 12, 3663-3672.	2.6	12
69	Targeting mitochondrial respiration and the BCL2 family in high-grade MYC-associated B-cell lymphoma. <i>Molecular Oncology</i> , 2022, 16, 1132-1152.	4.6	10
70	TGF $\beta$ -dependent gene expression shows that senescence correlates with abortive differentiation along several lineages in Myc-induced lymphomas. <i>Cell Cycle</i> , 2010, 9, 4622-4626.	2.6	6
71	FunChIP: an R/Bioconductor package for functional classification of ChIP-seq shapes. <i>Bioinformatics</i> , 2017, 33, 2570-2572.	4.1	5
72	p53 transcriptional programs in B cells upon exposure to genotoxic stress <i>in vivo</i> : Computational analysis of next-generation sequencing data. <i>Genomics Data</i> , 2016, 7, 29-31.	1.3	4

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73	Polycomb group ring finger protein 6 suppresses Myc-induced lymphomagenesis. Life Science Alliance, 2022, 5, e202101344.	2.8	4
74	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
75	Integrated control of cell proliferation and cell death by the c-myc oncogene. , 1995, , 33-39.		1
76	Abstract 108: Reactivation of Myc Transcription in the Heart Unlocks its Proliferative Capacity. Circulation Research, 2019, 125, .	4.5	0