Winship Herr

List of Publications by Year
in descending order

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97 papers	12,508 citations	43973 48 h-index	34900 98 g-index
101 all docs	101 docs citations	101 times ranked	6905 citing authors

#	Article	IF	Citations
1	THAP11F80L cobalamin disorder-associated mutation reveals normal and pathogenic THAP11 functions in gene expression and cell proliferation. PLoS ONE, 2020, 15, e0224646.	1.1	8
2	Cortical and Commissural Defects Upon HCFâ€1 Loss in Nkx2.1â€Derived Embryonic Neurons and Glia. Developmental Neurobiology, 2019, 79, 578-595.	1.5	7
3	HCF-2 inhibits cell proliferation and activates differentiation-gene expression programs. Nucleic Acids Research, 2019, 47, 5792-5808.	6.5	3
4	Differential regulation of RNA polymerase III genes during liver regeneration. Nucleic Acids Research, 2019, 47, 1786-1796.	6.5	12
5	Rapid Recapitulation of Nonalcoholic Steatohepatitis upon Loss of Host Cell Factor 1 Function in Mouse Hepatocytes. Molecular and Cellular Biology, 2019, 39, .	1.1	11
6	Cycles of gene expression and genome response during mammalian tissue regeneration. Epigenetics and Chromatin, 2018, 11, 52.	1.8	13
7	The conserved threonine-rich region of the HCF-1PRO repeat activates promiscuous OGT:UDP-GlcNAc glycosylation and proteolysis activities. Journal of Biological Chemistry, 2018, 293, 17754-17768.	1.6	7
8	Segregated hepatocyte proliferation and metabolic states within the regenerating mouse liver. Hepatology Communications, 2017, 1, 871-885.	2.0	13
9	Proteolysis of HCF-1 by Ser/Thr glycosylation-incompetent O-GlcNAc transferase:UDP-GlcNAc complexes. Genes and Development, 2016, 30, 960-972.	2.7	21
10	Compensatory embryonic response to allele-specific inactivation of the murine X-linked gene Hcfc1. Developmental Biology, 2016, 412, 1-17.	0.9	12
11	Epiblast-specific loss of HCF-1 leads to failure in anterior-posterior axis specification. Developmental Biology, 2016, 418, 75-88.	0.9	9
12	Distinct OGT-Binding Sites Promote HCF-1 Cleavage. PLoS ONE, 2015, 10, e0136636.	1.1	15
13	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. Genome Research, 2014, 24, 1157-1168.	2.4	143
14	Genome-Wide Analysis of SREBP1 Activity around the Clock Reveals Its Combined Dependency on Nutrient and Circadian Signals. PLoS Genetics, 2014, 10, e1004155.	1.5	45
15	HCF-1 Is Cleaved in the Active Site of O-GlcNAc Transferase. Science, 2013, 342, 1235-1239.	6.0	162
16	HCFC1 is a common component of active human CpG-island promoters and coincides with ZNF143, THAP11, YY1, and GABP transcription factor occupancy. Genome Research, 2013, 23, 907-916.	2.4	91
17	Genome-Wide RNA Polymerase II Profiles and RNA Accumulation Reveal Kinetics of Transcription and Associated Epigenetic Changes During Diurnal Cycles. PLoS Biology, 2012, 10, e1001442.	2.6	178
18	A multiplicity of factors contributes to selective RNA polymerase III occupancy of a subset of RNA polymerase III genes in mouse liver. Genome Research, 2012, 22, 666-680.	2.4	56

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19	HCF-1 self-association via an interdigitated Fn3 structure facilitates transcriptional regulatory complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17430-17435.	3.3	11
20	O-GlcNAc Transferase Catalyzes Site-Specific Proteolysis of HCF-1. Cell, 2011, 144, 376-388.	13.5	199
21	Drosophila melanogaster dHCF Interacts with both PcG and TrxG Epigenetic Regulators. PLoS ONE, 2011, 6, e27479.	1.1	16
22	Role of the HCF-1 Basic Region in Sustaining Cell Proliferation. PLoS ONE, 2010, 5, e9020.	1.1	25
23	Drosophila Myc Interacts with Host Cell Factor (dHCF) to Activate Transcription and Control Growth. Journal of Biological Chemistry, 2010, 285, 39623-39636.	1.6	14
24	E2F1 mediates DNA damage and apoptosis through HCF-1 and the MLL family of histone methyltransferases. EMBO Journal, 2009, 28, 3185-3195.	3.5	50
25	Species Selectivity of Mixed-Lineage Leukemia/Trithorax and HCF Proteolytic Maturation Pathways. Molecular and Cellular Biology, 2007, 27, 7063-7072.	1.1	55
26	E2F Activation of S Phase Promoters via Association with HCF-1 and the MLL Family of Histone H3K4 Methyltransferases. Molecular Cell, 2007, 27, 107-119.	4.5	218
27	Epigenetic Regulation of Histone H3 Serine 10 Phosphorylation Status by HCF-1 Proteins in C. elegans and Mammalian Cells. PLoS ONE, 2007, 2, e1213.	1.1	21
28	Mutational analysis of BTAF1-TBP interaction: BTAF1 can rescue DNA-binding defective TBP mutants. Nucleic Acids Research, 2005, 33, 5426-5436.	6.5	18
29	A Nonconserved Surface of the TFIIB Zinc Ribbon Domain Plays a Direct Role in RNA Polymerase II Recruitment. Molecular and Cellular Biology, 2004, 24, 2863-2874.	1.1	22
30	Leukemia Proto-Oncoprotein MLL Forms a SET1-Like Histone Methyltransferase Complex with Menin To Regulate Hox Gene Expression. Molecular and Cellular Biology, 2004, 24, 5639-5649.	1.1	581
31	A Switch in Mitotic Histone H4 Lysine 20 Methylation Status Is Linked to M Phase Defects upon Loss of HCF-1. Molecular Cell, 2004, 14, 713-725.	4.5	91
32	Proteolytic processing is necessary to separate and ensure proper cell growth and cytokinesis functions of HCF-1. EMBO Journal, 2003, 22, 2360-2369.	3.5	108
33	The herpes simplex virus VP16-induced complex: the makings of a regulatory switch. Trends in Biochemical Sciences, 2003, 28, 294-304.	3.7	265
34	A Shared Surface of TBP Directs RNA Polymerase II and III Transcription via Association with Different TFIIB Family Members. Molecular Cell, 2003, 11, 151-161.	4.5	18
35	Role of the Inhibitory DNA-Binding Surface of Human TATA-Binding Protein in Recruitment of Human TFIIB Family Members. Molecular and Cellular Biology, 2003, 23, 8152-8160.	1.1	3
36	Human Sin3 deacetylase and trithorax-related Set1/Ash2 histone H3-K4 methyltransferase are tethered together selectively by the cell-proliferation factor HCF-1. Genes and Development, 2003, 17, 896-911.	2.7	356

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37	Inactivation of the Retinoblastoma Protein Family Can Bypass the HCF-1 Defect in tsBN67 Cell Proliferation and Cytokinesis. Molecular and Cellular Biology, 2002, 22, 6767-6778.	1.1	23
38	Spontaneous Reversion of tsBN67 Cell Proliferation and Cytokinesis Defects in the Absence of HCF-1 Function. Experimental Cell Research, 2002, 277, 119-130.	1.2	23
39	A Regulated Two-Step Mechanism of TBP Binding to DNA. Cell, 2002, 108, 615-627.	13.5	70
40	Developmental and Cell-Cycle Regulation of Caenorhabditis elegans HCF Phosphorylation. Biochemistry, 2001, 40, 5786-5794.	1.2	17
41	DNA Recognition by the Herpes Simplex Virus Transactivator VP16: a Novel DNA-Binding Structure. Molecular and Cellular Biology, 2001, 21, 4700-4712.	1.1	32
42	Loss of HCF-1â€“Chromatin Association Precedes Temperature-Induced Growth Arrest of tsBN67 Cells. Molecular and Cellular Biology, 2001, 21, 3820-3829.	1.1	175
43	Stabilization but Not the Transcriptional Activity of Herpes Simplex Virus VP16-Induced Complexes Is Evolutionarily Conserved among HCF Family Members. Journal of Virology, 2001, 75, 12402-12411.	1.5	19
44	HCF-1 Amino- and Carboxy-Terminal Subunit Association through Two Separate Sets of Interaction Modules: Involvement of Fibronectin Type 3 Repeats. Molecular and Cellular Biology, 2000, 20, 6721-6730.	1.1	45
45	Selected Elements of Herpes Simplex Virus Accessory Factor HCF Are Highly Conserved in Caenorhabditis elegans. Molecular and Cellular Biology, 1999, 19, 909-915.	1.1	21
46	Crystal structure of the conserved core of the herpes simplex virus transcriptional regulatory protein VP16. Genes and Development, 1999, 13, 1692-1703.	2.7	50
47	The mouse telomerase RNA 5'-end lies just upstream of the telomerase template sequence. Nucleic Acids Research, 1998, 26, 532-536.	6.5	46
48	The Herpes Simplex Virus VP16-induced Complex: Mechanisms of Combinatorial Transcriptional Regulation. Cold Spring Harbor Symposia on Quantitative Biology, 1998, 63, 599-608.	2.0	41
49	Viral mimicry: common mode of association with HCF by VP16 and the cellular protein LZIP. Genes and Development, 1997, 11, 3122-3127.	2.7	121
50	Structural flexibility in transcription complex formation revealed by protein-DNA photocrosslinking. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 8450-8455.	3.3	28
51	A single-point mutation in HCF causes temperature-sensitive cell-cycle arrest and disrupts VP16 function.. Genes and Development, 1997, 11, 726-737.	2.7	139
52	Selective Use of TBP and TFIIB Revealed by a TATA-TBP-TFIIB Array with Altered Specificity. Science, 1997, 275, 829-831.	6.0	41
53	TAFs: Guilt by Association?. Cell, 1997, 88, 729-732.	13.5	82
54	N-Oct 5 is generated by in vitro proteolysis of the neural POU-domain protein N-Oct 3. Oncogene, 1997, 14, 1287-1294.	2.6	9

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55	The ability to associate with activation domains in vitro is not required for the TATA box-binding protein to support activated transcription in vivo.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 10550-10554.	3.3	40
56	The POU domain: versatility in transcriptional regulation by a flexible two-in-one DNA-binding domain.. Genes and Development, 1995, 9, 1679-1693.	2.7	353
57	Basal promoter elements as a selective determinant of transcriptional activator function. Nature, 1995, 374, 657-660.	13.7	117
58	The HCF repeat is an unusual proteolytic cleavage signal.. Genes and Development, 1995, 9, 2445-2458.	2.7	86
59	The gene encoding the VP16-accessory protein HCF (HCFC1) resides in human Xq28 and is highly expressed in fetal tissues and the adult kidney. Genomics, 1995, 25, 462-468.	1.3	44
60	Multiple regions of TBP participate in the response to transcriptional activators in vivo.. Genes and Development, 1994, 8, 2756-2769.	2.7	68
61	Crystal structure of the Oct-1 POU domain bound to an octamer site: DNA recognition with tethered DNA-binding modules. Cell, 1994, 77, 21-32.	13.5	496
62	The SV40 enhancer: Transcriptional regulation through a hierarchy of combinatorial interactions. Seminars in Virology, 1993, 4, 3-13.	4.1	14
63	The solution structure of the Oct-1 POU-specific domain reveals a striking similarity to the bacteriophage Î» repressor DNA-binding domain. Cell, 1993, 73, 193-205.	13.5	144
64	The VP16 accessory protein HCF is a family of polypeptides processed from a large precursor protein. Cell, 1993, 74, 115-125.	13.5	259
65	Differential positive control by Oct-1 and Oct-2: activation of a transcriptionally silent motif through Oct-1 and VP16 corecruitment.. Genes and Development, 1993, 7, 72-83.	2.7	91
66	A single amino acid exchange transfers VP16-induced positive control from the Oct-1 to the Oct-2 homeo domain.. Genes and Development, 1992, 6, 2058-2065.	2.7	141
67	Ethidium bromide provides a simple tool for identifying genuine DNA-independent protein associations.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 6958-6962.	3.3	458
68	Promoter-selective activation domains in Oct-1 and Oct-2 direct differential activation of an snRNA and mRNA promoter. Cell, 1992, 68, 755-767.	13.5	234
69	An agent of suppression. Nature, 1991, 350, 554-555.	13.7	4
70	The herpes simplex virus trans-activator VP16 recognizes the Oct-1 homeo domain: evidence for a homeo domain recognition subdomain.. Genes and Development, 1991, 5, 2555-2566.	2.7	138
71	Regulation of eukaryotic RNA polymerase II transcription by sequence-specific DNA-binding proteins. Molecular Aspects of Cellular Regulation, 1991, 6, 25-56.	1.4	5
72	The gene for the ubiquitous octamer-binding protein Oct-1 is on human chromosome 1, region cen-q32, and near Ly-22 and Ltw-4 on mouse chromosome 1. Genomics, 1990, 6, 666-672.	1.3	41

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73	Differential transcriptional activation by Oct-1 and Oct-2: Interdependent activation domains induce Oct-2 phosphorylation. Cell, 1990, 60, 375-386.	13.5	736
74	The Oct-1 homoeodomain directs formation of a multiprotein-DNA complex with the HSV transactivator VP16. Nature, 1989, 341, 624-630.	13.7	477
75	The SV40 enhancer contains two distinct levels of organization. Nature, 1988, 333, 40-45.	13.7	327
76	The POU domain is a bipartite DNA-binding structure. Nature, 1988, 336, 601-604.	13.7	301
77	The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo box subdomain.. Genes and Development, 1988, 2, 1582-1599.	2.7	682
78	The POU domain: a large conserved region in the mammalian pit-1, oct-1, oct-2, and Caenorhabditis elegans unc-86 gene products.. Genes and Development, 1988, 2, 1513-1516.	2.7	744
79	OBP100 binds remarkably degenerate octamer motifs through specific interactions with flanking sequences.. Genes and Development, 1988, 2, 1400-1413.	2.7	201
80	Activation of the U2 snRNA promoter by the octamer motif defines a new class of RNA polymerase II enhancer elements.. Genes and Development, 1988, 2, 1764-1778.	2.7	186
81	A 100-kD HeLa cell octamer binding protein (OBP100) interacts differently with two separate octamer-related sequences within the SV40 enhancer.. Genes and Development, 1987, 1, 1147-1160.	2.7	271
82	The SV40 enhancer is composed of multiple functional elements that can compensate for one another. Cell, 1986, 45, 461-470.	13.5	344
83	Diethyl pyrocarbonate: a chemical probe for secondary structure in negatively supercoiled DNA.. Proceedings of the National Academy of Sciences of the United States of America, 1985, 82, 8009-8013.	3.3	181
84	Duplications of a mutated simian virus 40 enhancer restore its activity. Nature, 1985, 313, 711-714.	13.7	170
85	Nucleotide sequence of AKV murine leukemia virus. Journal of Virology, 1984, 49, 471-478.	1.5	279
86	Isolation and mapping of cDNA hybridization probes specific for ecotropic and nonecotropic murine leukemia proviruses. Virology, 1983, 125, 139-154.	1.1	28
87	Monoclonal AKR/J thymic leukemias contain multiple JH immunoglobulin gene rearrangements.. Proceedings of the National Academy of Sciences of the United States of America, 1983, 80, 7433-7436.	3.3	33
88	Nucleotide sequence of the 3â€² half of AKV. Nucleic Acids Research, 1982, 10, 6931-6944.	6.5	50
89	Germ-line MuLV reintegrations in AKR/J mice. Nature, 1982, 296, 865-868.	13.7	56
90	Chemical probing of the tRNA–ribosome complex.. Proceedings of the National Academy of Sciences of the United States of America, 1981, 78, 2273-2277.	3.3	70

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91	Secondary structure model for 23S ribosomal RNA. Nucleic Acids Research, 1981, 9, 6167-6189.	6.5	397
92	Protection of specific sites in 23 S and 5 S RNA from chemical modification by association of 30 S and 50 S ribosomes. Journal of Molecular Biology, 1979, 130, 421-432.	2.0	83
93	Mechanism of ribosomal subunit association: Discrimination of specific sites in 16 S RNA essential for association activity. Journal of Molecular Biology, 1979, 130, 433-449.	2.0	151
94	Nucleotide sequences of accessible regions of 23S RNA in 50S ribosomal subunits. Biochemistry, 1978, 17, 307-315.	1.2	28
95	A fragment of 23S RNA containing a nucleotide sequence complementary to a region of 5S RNA. FEBS Letters, 1975, 53, 248-252.	1.3	52
96	Nucleotide sequence of the 3? terminus of E. coli 16S ribosomal RNA. Molecular Biology Reports, 1974, 1, 437-439.	1.0	28
97	Accessibility of 5 S RNA in 50 S ribosomal subunits. Journal of Molecular Biology, 1974, 90, 181-184.	2.0	39