

# Winship Herr

## List of Publications by Year in descending order

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97  
papers

12,508  
citations

50566

48  
h-index

39744

98  
g-index

101  
all docs

101  
docs citations

101  
times ranked

7808  
citing authors

#	ARTICLE	IF	CITATIONS
1	THAP11F80L cobalamin disorder-associated mutation reveals normal and pathogenic THAP11 functions in gene expression and cell proliferation. <i>PLoS ONE</i> , 2020, 15, e0224646.	1.1	8
2	Cortical and Commissural Defects Upon HCF-1 Loss in <i>Nkx2.1</i> -Derived Embryonic Neurons and Glia. <i>Developmental Neurobiology</i> , 2019, 79, 578-595.	1.5	7
3	HCF-2 inhibits cell proliferation and activates differentiation-gene expression programs. <i>Nucleic Acids Research</i> , 2019, 47, 5792-5808.	6.5	3
4	Differential regulation of RNA polymerase III genes during liver regeneration. <i>Nucleic Acids Research</i> , 2019, 47, 1786-1796.	6.5	12
5	Rapid Recapitulation of Nonalcoholic Steatohepatitis upon Loss of Host Cell Factor 1 Function in Mouse Hepatocytes. <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	11
6	Cycles of gene expression and genome response during mammalian tissue regeneration. <i>Epigenetics and Chromatin</i> , 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. <i>Journal of Biological Chemistry</i> , 2018, 293, 17754-17768.	1.6	7
8	Segregated hepatocyte proliferation and metabolic states within the regenerating mouse liver. <i>Hepatology Communications</i> , 2017, 1, 871-885.	2.0	13
9	Proteolysis of HCF-1 by Ser/Thr glycosylation-incompetent <i>O</i> -GlcNAc transferase:UDP-GlcNAc complexes. <i>Genes and Development</i> , 2016, 30, 960-972.	2.7	21
10	Compensatory embryonic response to allele-specific inactivation of the murine X-linked gene <i>Hcfc1</i> . <i>Developmental Biology</i> , 2016, 412, 1-17.	0.9	12
11	Epiblast-specific loss of HCF-1 leads to failure in anterior-posterior axis specification. <i>Developmental Biology</i> , 2016, 418, 75-88.	0.9	9
12	Distinct OGT-Binding Sites Promote HCF-1 Cleavage. <i>PLoS ONE</i> , 2015, 10, e0136636.	1.1	15
13	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. <i>Genome Research</i> , 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. <i>PLoS Genetics</i> , 2014, 10, e1004155.	1.5	45
15	HCF-1 Is Cleaved in the Active Site of O-GlcNAc Transferase. <i>Science</i> , 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. <i>Genome Research</i> , 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. <i>PLoS Biology</i> , 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. <i>Genome Research</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17430-17435.	3.3	11
20	O-GlcNAc Transferase Catalyzes Site-Specific Proteolysis of HCF-1. <i>Cell</i> , 2011, 144, 376-388.	13.5	199
21	<i>Drosophila melanogaster</i> dHCF Interacts with both PcG and TrxG Epigenetic Regulators. <i>PLoS ONE</i> , 2011, 6, e27479.	1.1	16
22	Role of the HCF-1 Basic Region in Sustaining Cell Proliferation. <i>PLoS ONE</i> , 2010, 5, e9020.	1.1	25
23	<i>Drosophila Myc</i> Interacts with Host Cell Factor (dHCF) to Activate Transcription and Control Growth. <i>Journal of Biological Chemistry</i> , 2010, 285, 39623-39636.	1.6	14
24	E2F1 mediates DNA damage and apoptosis through HCF-1 and the MLL family of histone methyltransferases. <i>EMBO Journal</i> , 2009, 28, 3185-3195.	3.5	50
25	Species Selectivity of Mixed-Lineage Leukemia/Trithorax and HCF Proteolytic Maturation Pathways. <i>Molecular and Cellular Biology</i> , 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. <i>Molecular Cell</i> , 2007, 27, 107-119.	4.5	218
27	Epigenetic Regulation of Histone H3 Serine 10 Phosphorylation Status by HCF-1 Proteins in <i>C. elegans</i> and Mammalian Cells. <i>PLoS ONE</i> , 2007, 2, e1213.	1.1	21
28	Mutational analysis of BTAF1-TBP interaction: BTAF1 can rescue DNA-binding defective TBP mutants. <i>Nucleic Acids Research</i> , 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. <i>Molecular and Cellular Biology</i> , 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. <i>Molecular and Cellular Biology</i> , 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. <i>Molecular Cell</i> , 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. <i>EMBO Journal</i> , 2003, 22, 2360-2369.	3.5	108
33	The herpes simplex virus VP16-induced complex: the makings of a regulatory switch. <i>Trends in Biochemical Sciences</i> , 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. <i>Molecular Cell</i> , 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. <i>Molecular and Cellular Biology</i> , 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. <i>Genes and Development</i> , 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. <i>Molecular and Cellular Biology</i> , 2002, 22, 6767-6778.	1.1	23
38	Spontaneous Reversion of tsBN67 Cell Proliferation and Cytokinesis Defects in the Absence of HCF-1 Function. <i>Experimental Cell Research</i> , 2002, 277, 119-130.	1.2	23
39	A Regulated Two-Step Mechanism of TBP Binding to DNA. <i>Cell</i> , 2002, 108, 615-627.	13.5	70
40	Developmental and Cell-Cycle Regulation of <i>Caenorhabditis elegans</i> HCF Phosphorylation. <i>Biochemistry</i> , 2001, 40, 5786-5794.	1.2	17
41	DNA Recognition by the Herpes Simplex Virus Transactivator VP16: a Novel DNA-Binding Structure. <i>Molecular and Cellular Biology</i> , 2001, 21, 4700-4712.	1.1	32
42	Loss of HCF-1 Chromatin Association Precedes Temperature-Induced Growth Arrest of tsBN67 Cells. <i>Molecular and Cellular Biology</i> , 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. <i>Journal of Virology</i> , 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. <i>Molecular and Cellular Biology</i> , 2000, 20, 6721-6730.	1.1	45
45	Selected Elements of Herpes Simplex Virus Accessory Factor HCF Are Highly Conserved in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 909-915.	1.1	21
46	Crystal structure of the conserved core of the herpes simplex virus transcriptional regulatory protein VP16. <i>Genes and Development</i> , 1999, 13, 1692-1703.	2.7	50
47	The mouse telomerase RNA 5'-end lies just upstream of the telomerase template sequence. <i>Nucleic Acids Research</i> , 1998, 26, 532-536.	6.5	46
48	The Herpes Simplex Virus VP16-induced Complex: Mechanisms of Combinatorial Transcriptional Regulation. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 599-608.	2.0	41
49	Viral mimicry: common mode of association with HCF by VP16 and the cellular protein LZIP. <i>Genes and Development</i> , 1997, 11, 3122-3127.	2.7	121
50	Structural flexibility in transcription complex formation revealed by protein-DNA photocrosslinking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 8450-8455.	3.3	28
51	A single-point mutation in HCF causes temperature-sensitive cell-cycle arrest and disrupts VP16 function.. <i>Genes and Development</i> , 1997, 11, 726-737.	2.7	139
52	Selective Use of TBP and TFIIB Revealed by a TATA-TBP-TFIIB Array with Altered Specificity. <i>Science</i> , 1997, 275, 829-831.	6.0	41
53	TAFs: Guilt by Association?. <i>Cell</i> , 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. <i>Oncogene</i> , 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 $\lambda$ 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. <i>Cell</i> , 1990, 60, 375-386.	13.5	736
74	The Oct-1 homoeodomain directs formation of a multiprotein-DNA complex with the HSV transactivator VP16. <i>Nature</i> , 1989, 341, 624-630.	13.7	477
75	The SV40 enhancer contains two distinct levels of organization. <i>Nature</i> , 1988, 333, 40-45.	13.7	327
76	The POU domain is a bipartite DNA-binding structure. <i>Nature</i> , 1988, 336, 601-604.	13.7	301
77	The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo box subdomain.. <i>Genes and Development</i> , 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 <i>Caenorhabditis elegans</i> unc-86 gene products.. <i>Genes and Development</i> , 1988, 2, 1513-1516.	2.7	744
79	OBP100 binds remarkably degenerate octamer motifs through specific interactions with flanking sequences.. <i>Genes and Development</i> , 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.. <i>Genes and Development</i> , 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.. <i>Genes and Development</i> , 1987, 1, 1147-1160.	2.7	271
82	The SV40 enhancer is composed of multiple functional elements that can compensate for one another. <i>Cell</i> , 1986, 45, 461-470.	13.5	344
83	Diethyl pyrocarbonate: a chemical probe for secondary structure in negatively supercoiled DNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985, 82, 8009-8013.	3.3	181
84	Duplications of a mutated simian virus 40 enhancer restore its activity. <i>Nature</i> , 1985, 313, 711-714.	13.7	170
85	Nucleotide sequence of AKV murine leukemia virus. <i>Journal of Virology</i> , 1984, 49, 471-478.	1.5	279
86	Isolation and mapping of cDNA hybridization probes specific for ecotropic and nonectropic murine leukemia proviruses. <i>Virology</i> , 1983, 125, 139-154.	1.1	28
87	Monoclonal AKR/J thymic leukemias contain multiple JH immunoglobulin gene rearrangements.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1983, 80, 7433-7436.	3.3	33
88	Nucleotide sequence of the 3' half of AKV. <i>Nucleic Acids Research</i> , 1982, 10, 6931-6944.	6.5	50
89	Germ-line MuLV reintegrations in AKR/J mice. <i>Nature</i> , 1982, 296, 865-868.	13.7	56
90	Chemical probing of the tRNA-ribosome complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1981, 78, 2273-2277.	3.3	70

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91	Secondary structure model for 23S ribosomal RNA. <i>Nucleic Acids Research</i> , 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. <i>Journal of Molecular Biology</i> , 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. <i>Journal of Molecular Biology</i> , 1979, 130, 433-449.	2.0	151
94	Nucleotide sequences of accessible regions of 23S RNA in 50S ribosomal subunits. <i>Biochemistry</i> , 1978, 17, 307-315.	1.2	28
95	A fragment of 23S RNA containing a nucleotide sequence complementary to a region of 5S RNA. <i>FEBS Letters</i> , 1975, 53, 248-252.	1.3	52
96	Nucleotide sequence of the 3' terminus of E. coli 16S ribosomal RNA. <i>Molecular Biology Reports</i> , 1974, 1, 437-439.	1.0	28
97	Accessibility of 5 S RNA in 50 S ribosomal subunits. <i>Journal of Molecular Biology</i> , 1974, 90, 181-184.	2.0	39