## Janet L Stein

List of Publications by Year in descending order

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IANET I STEIN

#	Article	IF	CITATIONS
1	Titanium with nanotopography attenuates the osteoclast-induced disruption of osteoblast differentiation by regulating histone methylation. Materials Science and Engineering C, 2022, 134, 112548.	7.3	10
2	The breast pre-cancer atlas illustrates the molecular and micro-environmental diversity of ductal carcinoma in situ. Npj Breast Cancer, 2022, 8, 6.	5.2	13
3	The Shared Core Resource as a Partner in Innovative Scientific Research: Illustration from an Academic Microscopy Imaging Center. Journal of Biomolecular Techniques, 2022, 33, 3fc1f5fe.2507f36c.	1.5	4
4	LncMIR181A1HG is a novel chromatin-bound epigenetic suppressor of early stage osteogenic lineage commitment. Scientific Reports, 2022, 12, 7770.	3.3	4
5	Mesenchymal stem cells overexpressing BMP-9 by CRISPR-Cas9 present high in vitro osteogenic potential and enhance in vivo bone formation. Gene Therapy, 2021, 28, 748-759.	4.5	20
6	Hypoxiaâ€inducible factor 2α is a novel inhibitor of chondrocyte maturation. Journal of Cellular Physiology, 2021, 236, 6963-6973.	4.1	4
7	Hinfp is a guardian of the somatic genome by repressing transposable elements. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	7
8	CXCR4 Mediates Enhanced Cell Migration in CALM-AF10 Leukemia. Frontiers in Oncology, 2021, 11, 708915.	2.8	1
9	Ezh2â€dependent H3K27me3 modification dynamically regulates vitamin D3â€dependent epigenetic control of CYP24A1 gene expression in osteoblastic cells. Journal of Cellular Physiology, 2020, 235, 5404-5412.	4.1	6
10	Identification of tRNAâ€derived small RNA (tsRNA) responsive to the tumor suppressor, RUNX1, in breast cancer. Journal of Cellular Physiology, 2020, 235, 5318-5327.	4.1	48
11	Switches in histone modifications epigenetically control vitamin D3â€dependent transcriptional upregulation of the CYP24A1 gene in osteoblastic cells. Journal of Cellular Physiology, 2020, 235, 5328-5339.	4.1	10
12	The Thyroid Hormone Receptor-RUNX2 Axis: A Novel Tumor Suppressive Pathway in Breast Cancer. Hormones and Cancer, 2020, 11, 34-41.	4.9	15
13	RUNX1 and RUNX2 transcription factors function in opposing roles to regulate breast cancer stem cells. Journal of Cellular Physiology, 2020, 235, 7261-7272.	4.1	34
14	Inhibition of the RUNX1-CBFÎ <sup>2</sup> transcription factor complex compromises mammary epithelial cell identity: a phenotype potentially stabilized by mitotic gene bookmarking. Oncotarget, 2020, 11, 2512-2530.	1.8	8
15	Bioactivity-Guided Isolation and Identification of Anti-adipogenic Constituents from the n-Butanol Fraction of Cissus quadrangularis. Critical Reviews in Eukaryotic Gene Expression, 2020, 30, 519-541.	0.9	3
16	Participation of integrin β3 in osteoblast differentiation induced by titanium with nano or microtopography. Journal of Biomedical Materials Research - Part A, 2019, 107, 1303-1313.	4.0	29
17	Osteogenic potential of hexane and dichloromethane fraction of Cissus quadrangularis on murine preosteoblast cell line MC3T3‣1 (subclone 4). Journal of Cellular Physiology, 2019, 234, 23082-23096. 	4.1	13
18	Mllâ€COMPASS complexes mediate H3K4me3 enrichment and transcription of the osteoblast master gene Runx2/p57 in osteoblasts. Journal of Cellular Physiology, 2019, 234, 6244-6253.	4.1	15

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19	Ethyl acetate and nâ€butanol fraction of <i>Cissus quadrangularis</i> promotes the mineralization potential of murine preâ€osteoblast cell line MC3T3â€E1 (subâ€clone 4). Journal of Cellular Physiology, 2019, 234, 10300-10314.	4.1	11
20	Time-varying risks of second events following a DCIS diagnosis in the population-based Vermont DCIS cohort. Breast Cancer Research and Treatment, 2019, 174, 227-235.	2.5	12
21	Realâ€time detection of breast cancer at the cellular level. Journal of Cellular Physiology, 2019, 234, 5413-5419.	4.1	6
22	RUNX1â€dependent mechanisms in biological control and dysregulation in cancer. Journal of Cellular Physiology, 2019, 234, 8597-8609.	4.1	48
23	Towards a more precise and individualized assessment of breast cancer risk. Aging, 2019, 11, 1305-1316.	3.1	9
24	Mitotically-Associated IncRNA (MANCR) Affects Genomic Stability and Cell Division in Aggressive Breast Cancer. Molecular Cancer Research, 2018, 16, 587-598.	3.4	62
25	Selective expression of long nonâ€coding RNAs in a breast cancer cell progression model. Journal of Cellular Physiology, 2018, 233, 1291-1299.	4.1	22
26	Intranuclear and higherâ€order chromatin organization of the major histone gene cluster in breast cancer. Journal of Cellular Physiology, 2018, 233, 1278-1290.	4.1	40
27	Thyroid Hormone Receptor β Suppression of RUNX2 Is Mediated by Brahma-Related Gene 1–Dependent Chromatin Remodeling. Endocrinology, 2018, 159, 2484-2494.	2.8	15
28	Nuclear organization mediates cancer-compromised genetic and epigenetic control. Advances in Biological Regulation, 2018, 69, 1-10.	2.3	10
29	Epithelialâ€ŧoâ€mesenchymal transition and cancer stem cells contribute to breast cancer heterogeneity. Journal of Cellular Physiology, 2018, 233, 9136-9144.	4.1	80
30	Mitotic Gene Bookmarking: An Epigenetic Program to Maintain Normal and Cancer Phenotypes. Molecular Cancer Research, 2018, 16, 1617-1624.	3.4	19
31	Regulation of osteogenesis by long noncoding RNAs: An epigenetic mechanism contributing to bone formation. Connective Tissue Research, 2018, 59, 35-41.	2.3	21
32	Higher order genomic organization and regulatory compartmentalization for cell cycle control at the G1/Sâ€phase transition. Journal of Cellular Physiology, 2018, 233, 6406-6413.	4.1	13
33	Suppression of Breast Cancer Stem Cells and Tumor Growth by the RUNX1 Transcription Factor. Molecular Cancer Research, 2018, 16, 1952-1964.	3.4	48
34	Dissection of Individual Prostate Lobes in Mouse Models of Prostate Cancer to Obtain High Quality RNA. Journal of Cellular Physiology, 2017, 232, 14-18.	4.1	10
35	Ethanol Extract of <i>Cissus quadrangularis</i> Enhances Osteoblast Differentiation and Mineralization of Murine Pre-Osteoblastic MC3T3-E1 Cells. Journal of Cellular Physiology, 2017, 232, 540-547.	4.1	25
36	The connection between BRG1, CTCF and topoisomerases at TAD boundaries. Nucleus, 2017, 8, 150-155.	2.2	24

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37	Chromatin dynamics regulate mesenchymal stem cell lineage specification and differentiation to osteogenesis. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 438-449.	1.9	55
38	Mitotic Gene Bookmarking: An Epigenetic Mechanism for Coordination of Lineage Commitment, Cell Identity and Cell Growth. Advances in Experimental Medicine and Biology, 2017, 962, 95-102.	1.6	14
39	The BRG1 ATPase of human SWI/SNF chromatin remodeling enzymes as a driver of cancer. Epigenomics, 2017, 9, 919-931.	2.1	108
40	Bivalent Epigenetic Control of Oncofetal Gene Expression in Cancer. Molecular and Cellular Biology, 2017, 37, .	2.3	42
41	Unique Regulatory Mechanisms for the Human Embryonic Stem Cell Cycle. Journal of Cellular Physiology, 2017, 232, 1254-1257.	4.1	3
42	Precocious Phenotypic Transcriptionâ€Factor Expression During Early Development. Journal of Cellular Biochemistry, 2017, 118, 953-958.	2.6	3
43	Identifying Nuclear Matrixâ€Attached DNA Across the Genome. Journal of Cellular Physiology, 2017, 232, 1295-1305.	4.1	19
44	Genome-wide DNase hypersensitivity, and occupancy of RUNX2 and CTCF reveal a highly dynamic gene regulome during MC3T3 pre-osteoblast differentiation. PLoS ONE, 2017, 12, e0188056.	2.5	10
45	An AML1-ETO/miR-29b-1 regulatory circuit modulates phenotypic properties of acute myeloid leukemia cells. Oncotarget, 2017, 8, 39994-40005.	1.8	15
46	Runx1 stabilizes the mammary epithelial cell phenotype and prevents epithelial to mesenchymal transition. Oncotarget, 2017, 8, 17610-17627.	1.8	53
47	Development of a predictive miRNA signature for breast cancer risk among high-risk women. Oncotarget, 2017, 8, 112170-112183.	1.8	30
48	Transcriptional Auto-Regulation of RUNX1 P1 Promoter. PLoS ONE, 2016, 11, e0149119.	2.5	22
49	Oncofetal Epigenetic Bivalency in Breast Cancer Cells: H3K4 and H3K27 Tri-Methylation as a Biomarker for Phenotypic Plasticity. Journal of Cellular Physiology, 2016, 231, 2474-2481.	4.1	25
50	Chromosomes at Work: Organization of Chromosome Territories in the Interphase Nucleus. Journal of Cellular Biochemistry, 2016, 117, 9-19.	2.6	39
51	Transient RUNX1 Expression during Early Mesendodermal Differentiation ofÂhESCs Promotes Epithelial to Mesenchymal Transition through TGFB2 Signaling. Stem Cell Reports, 2016, 7, 884-896.	4.8	21
52	Maternal expression and early induction of histone gene transcription factor Hinfp sustains development in pre-implantation embryos. Developmental Biology, 2016, 419, 311-320.	2.0	13
53	Câ€ing the Genome: A Compendium of Chromosome Conformation Capture Methods to Study Higherâ€Order Chromatin Organization. Journal of Cellular Physiology, 2016, 231, 31-35.	4.1	50
54	WWOX and p53 Dysregulation Synergize to Drive the Development of Osteosarcoma. Cancer Research, 2016, 76, 6107-6117.	0.9	38

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55	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1389-1397.	1.9	60
56	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. Genome Research, 2016, 26, 1188-1201.	5.5	90
57	Expression of Ribosomal RNA and Protein Genes in Human Embryonic Stem Cells Is Associated With the Activating H3K4me3 Histone Mark. Journal of Cellular Physiology, 2016, 231, 2007-2013.	4.1	13
58	Thyroid Hormone Receptor-β (TRβ) Mediates Runt-Related Transcription Factor 2 (Runx2) Expression in Thyroid Cancer Cells: A Novel Signaling Pathway in Thyroid Cancer. Endocrinology, 2016, 157, 3278-3292.	2.8	26
59	Genome-Wide Studies Reveal that H3K4me3 Modification in Bivalent Genes Is Dynamically Regulated during the Pluripotent Cell Cycle and Stabilized upon Differentiation. Molecular and Cellular Biology, 2016, 36, 615-627.	2.3	53
60	MicroRNA-378-mediated suppression of Runx1 alleviates the aggressive phenotype of triple-negative MDA-MB-231 human breast cancer cells. Tumor Biology, 2016, 37, 8825-8839.	1.8	41
61	Oncogenic epigenetic control. Aging, 2016, 8, 565-566.	3.1	2
62	A microRNA/Runx1/Runx2 network regulates prostate tumor progression from onset to adenocarcinoma in TRAMP mice. Oncotarget, 2016, 7, 70462-70474.	1.8	21
63	Antagonizing miR-218-5p attenuates Wnt signaling and reduces metastatic bone disease of triple negative breast cancer cells. Oncotarget, 2016, 7, 79032-79046.	1.8	68
64	Histone H3 lysine 4 acetylation and methylation dynamics define breast cancer subtypes. Oncotarget, 2016, 7, 5094-5109.	1.8	89
65	The BRG1 chromatin remodeling enzyme links cancer cell metabolism and proliferation. Oncotarget, 2016, 7, 38270-38281.	1.8	51
66	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. Genome Biology, 2015, 16, 214.	8.8	206
67	Runx1 is associated with breast cancer progression in MMTVâ€PyMT transgenic mice and its depletion in vitro inhibits migration and invasion. Journal of Cellular Physiology, 2015, 230, 2522-2532.	4.1	63
68	The SWI/SNF ATPases Are Required for Triple Negative Breast Cancer Cell Proliferation. Journal of Cellular Physiology, 2015, 230, 2683-2694.	4.1	58
69	p53 checkpoint ablation exacerbates the phenotype of Hinfp dependent histone H4 deficiency. Cell Cycle, 2015, 14, 2501-2508.	2.6	14
70	Multiple levels of epigenetic control for bone biology and pathology. Bone, 2015, 81, 733-738.	2.9	18
71	Genome-wide co-occupancy of AML1-ETO and N-CoR defines the t(8;21) AML signature in leukemic cells. BMC Genomics, 2015, 16, 309.	2.8	30
72	Subnuclear domain proteins in cancer cells support transcription factor RUNX2 functions in DNA damage response. Journal of Cell Science, 2015, 128, 728-40.	2.0	21

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73	Targeting of Runx2 by miR-135 and miR-203 Impairs Progression of Breast Cancer and Metastatic Bone Disease. Cancer Research, 2015, 75, 1433-1444.	0.9	164
74	Runx1 Activities in Superficial Zone Chondrocytes, Osteoarthritic Chondrocyte Clones and Response to Mechanical Loading. Journal of Cellular Physiology, 2015, 230, 440-448.	4.1	25
75	Chromatin modifiers and histone modifications in bone formation, regeneration, and therapeutic intervention for bone-related disease. Bone, 2015, 81, 739-745.	2.9	66
76	Cell cycle gene expression networks discovered using systems biology: Significance in carcinogenesis. Journal of Cellular Physiology, 2015, 230, 2533-2542.	4.1	16
77	Epigenetic Control of the Bone-master Runx2 Gene during Osteoblast-lineage Commitment by the Histone Demethylase JARID1B/KDM5B. Journal of Biological Chemistry, 2015, 290, 28329-28342.	3.4	68
78	Could IncRNAs be the Missing Links in Control of Mesenchymal Stem Cell Differentiation?. Journal of Cellular Physiology, 2015, 230, 526-534.	4.1	72
79	The bone-specific Runx2-P1 promoter displays conserved three-dimensional chromatin structure with the syntenic Supt3h promoter. Nucleic Acids Research, 2014, 42, 10360-10372.	14.5	28
80	CBFβ and the Leukemogenic Fusion Protein CBFβâ€ <b>5</b> MMHC Associate With Mitotic Chromosomes to Epigenetically Regulate Ribosomal Genes. Journal of Cellular Biochemistry, 2014, 115, 2155-2164.	2.6	11
81	Genomic occupancy of Runx2 with global expression profiling identifies a novel dimension to control of osteoblastogenesis. Genome Biology, 2014, 15, R52.	9.6	122
82	Fidelity of Histone Gene Regulation Is Obligatory for Genome Replication and Stability. Molecular and Cellular Biology, 2014, 34, 2650-2659.	2.3	25
83	MicroRNAs in the control of metastatic bone disease. Trends in Endocrinology and Metabolism, 2014, 25, 320-327.	7.1	60
84	The Dynamic Architectural and Epigenetic Nuclear Landscape: Developing the Genomic Almanac of Biology and Disease. Journal of Cellular Physiology, 2014, 229, 711-727.	4.1	11
85	Bookmarking Target Genes in Mitosis: A Shared Epigenetic Trait of Phenotypic Transcription Factors and Oncogenes?. Cancer Research, 2014, 74, 420-425.	0.9	33
86	hsa-mir-30c promotes the invasive phenotype of metastatic breast cancer cells by targeting NOV/CCN3. Cancer Cell International, 2014, 14, 73.	4.1	46
87	Epigenetic landscape during osteoblastogenesis defines a differentiation-dependent Runx2 promoter region. Gene, 2014, 550, 1-9.	2.2	28
88	Targeting deregulated epigenetic control in cancer. Journal of Cellular Physiology, 2013, 228, 2103-2108.	4.1	22
89	MicroRNA-34c Inversely Couples the Biological Functions of the Runt-related Transcription Factor RUNX2 and the Tumor Suppressor p53 in Osteosarcoma. Journal of Biological Chemistry, 2013, 288, 21307-21319.	3.4	95
90	miR-218 Directs a Wnt Signaling Circuit to Promote Differentiation of Osteoblasts and Osteomimicry of Metastatic Cancer Cells. Journal of Biological Chemistry, 2012, 287, 42084-42092.	3.4	251

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91	Genomic Promoter Occupancy of Runt-related Transcription Factor RUNX2 in Osteosarcoma Cells Identifies Genes Involved in Cell Adhesion and Motility. Journal of Biological Chemistry, 2012, 287, 4503-4517.	3.4	75
92	A Runx2-HDAC1 co-repressor complex regulates rRNA gene expression by modulating UBF acetylation. Journal of Cell Science, 2012, 125, 2732-9.	2.0	36
93	Epigenetic Control of Cell Cycle-Dependent Histone Gene Expression Is a Principal Component of the Abbreviated Pluripotent Cell Cycle. Molecular and Cellular Biology, 2012, 32, 3860-3871.	2.3	25
94	Bookmarking the Genome: Maintenance of Epigenetic Information. Journal of Biological Chemistry, 2011, 286, 18355-18361.	3.4	76
95	An architectural genetic and epigenetic perspective. Integrative Biology (United Kingdom), 2011, 3, 297-303.	1.3	6
96	Functional coupling of transcription factor HiNF-P and histone H4 gene expression during pre- and post-natal mouse development. Gene, 2011, 483, 1-10.	2.2	9
97	Live cell imaging of the cancerâ€related transcription factor RUNX2 during mitotic progression. Journal of Cellular Physiology, 2011, 226, 1383-1389.	4.1	17
98	Epigenetic Regulation of Early Osteogenesis and Mineralized Tissue Formation by a HOXA10-PBX1-Associated Complex. Cells Tissues Organs, 2011, 194, 146-150.	2.3	52
99	Mitotic bookmarking of genes: a novel dimension to epigenetic control. Nature Reviews Genetics, 2010, 11, 583-589.	16.3	142
100	Architectural Epigenetics: Mitotic Retention of Mammalian Transcriptional Regulatory Information. Molecular and Cellular Biology, 2010, 30, 4758-4766.	2.3	46
101	Pbx1 Represses Osteoblastogenesis by Blocking Hoxa10-Mediated Recruitment of Chromatin Remodeling Factors. Molecular and Cellular Biology, 2010, 30, 3531-3541.	2.3	64
102	The Histone Deacetylase Inhibitor, Vorinostat, Reduces Tumor Growth at the Metastatic Bone Site and Associated Osteolysis, but Promotes Normal Bone Loss. Molecular Cancer Therapeutics, 2010, 9, 3210-3220.	4.1	47
103	Transcriptional corepressor TLE1 functions with Runx2 in epigenetic repression of ribosomal RNA genes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4165-4169.	7.1	41
104	Recruitment and subnuclear distribution of the regulatory machinery during 1α,25-dihydroxy vitamin D3-mediated transcriptional upregulation in osteoblasts. Journal of Steroid Biochemistry and Molecular Biology, 2010, 121, 156-158.	2.5	8
105	Control of the Human Pluripotent Cell Cycle. , 2010, , 235-251.		2
106	Co-stimulation of the Bone-related Runx2 P1 Promoter in Mesenchymal Cells by SP1 and ETS Transcription Factors at Polymorphic Purine-rich DNA Sequences (Y-repeats). Journal of Biological Chemistry, 2009, 284, 3125-3135.	3.4	70
107	Specific Residues of RUNX2 Are Obligatory for Formation of BMP2-Induced RUNX2-SMAD Complex to Promote Osteoblast Differentiation. Cells Tissues Organs, 2009, 189, 133-137.	2.3	76
108	Ectopic Runx2 Expression in Mammary Epithelial Cells Disrupts Formation of Normal Acini Structure: Implications for Breast Cancer Progression. Cancer Research, 2009, 69, 6807-6814.	0.9	80

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109	Altered Runx1 Subnuclear Targeting Enhances Myeloid Cell Proliferation and Blocks Differentiation by Activating a miR-24/MKP-7/MAPK Network. Cancer Research, 2009, 69, 8249-8255.	0.9	100
110	The histone gene activator HINFP is a nonredundant cyclin E/CDK2 effector during early embryonic cell cycles. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12359-12364.	7.1	31
111	Subnuclear targeting of the Runx3 tumor suppressor and its epigenetic association with mitotic chromosomes. Journal of Cellular Physiology, 2009, 218, 473-479.	4.1	40
112	CDK inhibitors selectively diminish cell cycle controlled activation of the histone H4 gene promoter by p220 <sup>NPAT</sup> and HiNFâ€P. Journal of Cellular Physiology, 2009, 219, 438-448.	4.1	14
113	Transcription-factor-mediated epigenetic control of cell fate and lineage commitmentThis paper is one of a selection of papers published in this Special Issue, entitled CSBMCB's 51st Annual Meeting– Epigenetics and Chromatin Dynamics, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology 2009 87 1-6	2.0	20
114	1α,25â€dihydroxy vitamin D <sub>3</sub> â€enhanced expression of the osteocalcin gene involves increased promoter occupancy of basal transcription regulators and gradual recruitment of the 1α,25â€dihydroxy vitamin D <sub>3</sub> receptorâ€SRCâ€1 coactivator complex. Journal of Cellular Physiology, 2008, 214, 740-749.	4.1	38
115	Phenotypic transcription factors epigenetically mediate cell growth control. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6632-6637.	7.1	86
116	The Histone Gene Cell Cycle Regulator HiNF-P Is a Unique Zinc Finger Transcription Factor with a Novel Conserved Auxiliary DNA-Binding Motif. Biochemistry, 2008, 47, 11415-11423.	2.5	11
117	Staged assembly of histone gene expression machinery at subnuclear foci in the abbreviated cell cycle of human embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16964-16969.	7.1	76
118	The leukemogenic t(8;21) fusion protein AML1-ETO controls rRNA genes and associates with nucleolar-organizing regions at mitotic chromosomes. Journal of Cell Science, 2008, 121, 3981-3990.	2.0	48
119	Runx2 Transcriptional Activation of Indian Hedgehog and a Downstream Bone Metastatic Pathway in Breast Cancer Cells. Cancer Research, 2008, 68, 7795-7802.	0.9	160
120	Synergistic regulation of the Runx2 P1 promoter in mesenchymal cells by a conserved HLH box and purineâ€rich elements (GAY motifs). FASEB Journal, 2008, 22, 782.17.	0.5	0
121	Mitotic retention of gene expression patterns by the cell fate-determining transcription factor Runx2. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3189-3194.	7.1	152
122	The HiNF-P/p220NPAT Cell Cycle Signaling Pathway Controls Nonhistone Target Genes. Cancer Research, 2007, 67, 10334-10342.	0.9	23
123	Chromatin Remodeling by SWI/SNF Results in Nucleosome Mobilization to Preferential Positions in the Rat Osteocalcin Gene Promoter. Journal of Biological Chemistry, 2007, 282, 9445-9457.	3.4	27
124	An architectural perspective of vitamin D responsiveness. Archives of Biochemistry and Biophysics, 2007, 460, 293-299.	3.0	14
125	The 1α,25-dihydroxy Vitamin D3 receptor preferentially recruits the coactivator SRC-1 during up-regulation of the osteocalcin gene. Journal of Steroid Biochemistry and Molecular Biology, 2007, 103, 420-424.	2.5	25
126	Establishment of histone gene regulation and cell cycle checkpoint control in human embryonic stem cells. Journal of Cellular Physiology, 2007, 210, 517-526.	4.1	80

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127	Cell cycle dependent phosphorylation and subnuclear organization of the histone gene regulator p220NPAT in human embryonic stem cells. Journal of Cellular Physiology, 2007, 213, 9-17.	4.1	62
128	Nuclear microenvironments in biological control and cancer. Nature Reviews Cancer, 2007, 7, 454-463.	28.4	144
129	Mitotic occupancy and lineage-specific transcriptional control of rRNA genes by Runx2. Nature, 2007, 445, 442-446.	27.8	218
130	Organization of transcriptional regulatory machinery in nuclear microenvironments: Implications for biological control and cancer. Advances in Enzyme Regulation, 2007, 47, 242-250.	2.6	21
131	The Histone Gene Transcription Factor HiNF-P Stabilizes Its Cell Cycle Regulatory Co-Activator p220NPATâ€. Biochemistry, 2006, 45, 15915-15920.	2.5	17
132	Networks and hubs for the transcriptional control of osteoblastogenesis. Reviews in Endocrine and Metabolic Disorders, 2006, 7, 1-16.	5.7	397
133	An architectural perspective of cell-cycle control at the G1/S phase cell-cycle transition. Journal of Cellular Physiology, 2006, 209, 706-710.	4.1	58
134	The dynamic organization of geneâ€regulatory machinery in nuclear microenvironments. EMBO Reports, 2005, 6, 128-133.	4.5	107
135	Impaired intranuclear trafficking of Runx2 (AML3/CBFA1) transcription factors in breast cancer cells inhibits osteolysis <i>in vivo</i> . Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1454-1459.	7.1	174
136	HiNF-P Directly Links the Cyclin E/CDK2/p220NPAT Pathway to Histone H4 Gene Regulation at the G1/S Phase Cell Cycle Transition. Molecular and Cellular Biology, 2005, 25, 6140-6153.	2.3	88
137	The Runx2 Osteogenic Transcription Factor Regulates Matrix Metalloproteinase 9 in Bone Metastatic Cancer Cells and Controls Cell Invasion. Molecular and Cellular Biology, 2005, 25, 8581-8591.	2.3	280
138	Coordinate Control and Selective Expression of the Full Complement of Replication-dependent Histone H4 Genes in Normal and Cancer Cells. Journal of Biological Chemistry, 2005, 280, 37400-37407.	3.4	46
139	Regulatory Controls for Osteoblast Growth and Differentiation: Role of Runx/Cbfa/AML Factors. Critical Reviews in Eukaryotic Gene Expression, 2004, 14, 1-42.	0.9	392
140	Bone-Specific Transcription Factor Runx2 Interacts with the 1α,25-Dihydroxyvitamin D 3 Receptor To Up-Regulate Rat Osteocalcin Gene Expression in Osteoblastic Cells. Molecular and Cellular Biology, 2004, 24, 8847-8861.	2.3	126
141	Architectural Organization of the Regulatory Machinery for Transcription, Replication, and Repair: Dynamic Temporal-Spatial Parameters of Cell Cycle Control. , 2004, , 15-92.		0
142	Regulatory controls for osteoblast growth and differentiation: role of Runx/Cbfa/AML factors. Critical Reviews in Eukaryotic Gene Expression, 2004, 14, 1-41.	0.9	194
143	Nuclear microenvironments support physiological control of gene expression. Chromosome Research, 2003, 11, 527-536.	2.2	6
144	Runx2/Cbfa1 Functions: Diverse Regulation of Gene Transcription by Chromatin Remodeling and Co-Regulatory Protein Interactions. Connective Tissue Research, 2003, 44, 141-148.	2.3	56

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145	Regulation of the Bone-Specific Osteocalcin Gene by p300 Requires Runx2/Cbfa1 and the Vitamin D3 Receptor but Not p300 Intrinsic Histone Acetyltransferase Activity. Molecular and Cellular Biology, 2003, 23, 3339-3351.	2.3	190
146	Identification of HiNF-P, a Key Activator of Cell Cycle-Controlled Histone H4 Genes at the Onset of S Phase. Molecular and Cellular Biology, 2003, 23, 8110-8123.	2.3	65
147	Mitotic partitioning and selective reorganization of tissue-specific transcription factors in progeny cells. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14852-14857.	7.1	88
148	Transcriptional Induction of the Osteocalcin Gene During Osteoblast Differentiation Involves Acetylation of Histones H3 and H4. Molecular Endocrinology, 2003, 17, 743-756.	3.7	92
149	Transcription factors RUNX1/AML1 and RUNX2/Cbfa1 dynamically associate with stationary subnuclear domains. Journal of Cell Science, 2002, 115, 4167-4176.	2.0	82
150	Histone Acetylation in Vivo at the Osteocalcin Locus Is Functionally Linked to Vitamin D-dependent, Bone Tissue-specific Transcription. Journal of Biological Chemistry, 2002, 277, 20284-20292.	3.4	66
151	Nonlinear partial differential equations and applications: Multiple subnuclear targeting signals of the leukemia-related AML1/ETO and ETO repressor proteins. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15434-15439.	7.1	56
152	Interaction of the 1α,25-dihydroxyvitamin D3 receptor at the distal promoter region of the bone-specific osteocalcin gene requires nucleosomal remodelling. Biochemical Journal, 2002, 363, 667-676.	3.7	37
153	Reduced CpG methylation is associated with transcriptional activation of the bone-specific rat osteocalcin gene in osteoblasts*. Journal of Cellular Biochemistry, 2002, 85, 112-122.	2.6	93
154	Reduced CpG methylation is associated with transcriptional activation of the bone-specific rat osteocalcin gene in osteoblasts*The contents are solely the responsibility of the authors and do not necessarily represent the official views of the National Institutes of Health Journal of Cellular Biochemistry, 2002, 85, 112.	2.6	1
155	Reduced CpG methylation is associated with transcriptional activation of the bone-specific rat osteocalcin gene in osteoblasts. Journal of Cellular Biochemistry, 2002, 85, 112-22.	2.6	50
156	Modified intranuclear organization of regulatory factors in human acute leukemias: Reversal after treatment. , 2000, 77, 30-43.		10
157	Bone tissue specific transcriptional control. Cancer, 2000, 88, 2899-2902.	4.1	10
158	Leukemia-associated AML1/ETO (8;21) chromosomal translocation protein increases the cellular representation of PML bodies. Journal of Cellular Biochemistry, 2000, 79, 103-112.	2.6	22
159	Subnuclear organization and trafficking of regulatory proteins: Implications for biological control and cancer. Journal of Cellular Biochemistry, 2000, 79, 84-92.	2.6	21
160	Transcriptional autoregulation of the bone related CBFA1/RUNX2 gene. Journal of Cellular Physiology, 2000, 184, 341-350.	4.1	236
161	Molecular characterization of Celtix-1, a bromodomain protein interacting with the transcription factor interferon regulatory factor 2. Journal of Cellular Physiology, 2000, 185, 269-279.	4.1	38
162	Transcriptional autoregulation of the bone related CBFA1/RUNX2 gene. Journal of Cellular Physiology, 2000, 184, 341-350.	4.1	5

#	Article	IF	CITATIONS
163	The homeodomain transcription factor CDP/cut interacts with the cell cycle regulatory element of histone H4 genes packaged into nucleosomes. Molecular Biology Reports, 1999, 26, 185-194.	2.3	17
164	Transcriptional control within the three-dimensional context of nuclear architecture: Requirements for boundaries and direction. Journal of Cellular Biochemistry, 1999, 75, 24-31.	2.6	9
165	Multiple interactions of the transcription factor YY1 with human histone H4 gene regulatory elements. Journal of Cellular Biochemistry, 1999, 72, 507-516.	2.6	24
166	Nuclear structure/gene expression interrelationships. , 1999, 181, 240-250.		11
167	Osteocalcin gene promoter: Unlocking the secrets for regulation of osteoblast growth and differentiation. , 1998, 72, 62-72.		112
168	Targeting of the YY1 transcription factor to the nucleolus and the nuclear matrix in situ: The C-terminus is a principal determinant for nuclear trafficking. , 1998, 68, 500-510.		83
169	Osteocalcin gene promoter: Unlocking the secrets for regulation of osteoblast growth and differentiation. Journal of Cellular Biochemistry, 1998, 72, 62-72.	2.6	4
170	Bipartite structure of the proximal promoter of a human H4 histone gene. Journal of Cellular Biochemistry, 1995, 58, 372-379.	2.6	6
171	Nuclear matrix association of multiple sequence-specific DNA binding activities related to SP-1, ATF, CCAAT, C/EBP, OCT-1, and AP-1. Biochemistry, 1993, 32, 8397-8402.	2.5	173
172	Protein-DNA interactions at the H4-Site III upstream transcriptional element of a cell cycle regulated histone H4 gene: Differences in normal versus tumor cells. Journal of Cellular Biochemistry, 1992, 49, 93-110.	2.6	12
173	Transcriptional element H4-site II of cell cycle regulated human H4 histone genes is a multipartite protein/DNA interaction site for factors HiNF-D, HiNF-M, and HiNF-P: Involvement of phosphorylation. Journal of Cellular Biochemistry, 1991, 46, 174-189.	2.6	51