Assam El-Osta

List of Publications by Year
in descending order

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Version: 2024-02-01

204	13,474	22099	24915
papers	citations	59 h-index	109 g-index

210	210	210	19825
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Î³H2AX: a sensitive molecular marker of DNA damage and repair. Leukemia, 2010, 24, 679-686.	3.3	1,078
2	Transient high glucose causes persistent epigenetic changes and altered gene expression during subsequent normoglycemia. Journal of Experimental Medicine, 2008, 205, 2409-2417.	4.2	931
3	High-Fiber Diet and Acetate Supplementation Change the Gut Microbiota and Prevent the Development of Hypertension and Heart Failure in Hypertensive Mice. Circulation, 2017, 135, 964-977.	1.6	695
4	Hyperglycemia Induces a Dynamic Cooperativity of Histone Methylase and Demethylase Enzymes Associated With Gene-Activating Epigenetic Marks That Coexist on the Lysine Tail. Diabetes, 2009, 58, 1229-1236.	0.3	468
5	Microparticles: major transport vehicles for distinct microRNAs in circulation. Cardiovascular Research, 2012, 93, 633-644.	1.8	418
6	NADPH Oxidase 1 Plays a Key Role in Diabetes Mellitusâ€“Accelerated Atherosclerosis. Circulation, 2013, 127, 1888-1902.	1.6	325
7	Genetic Targeting or Pharmacologic Inhibition of NADPH Oxidase Nox4 Provides Renoprotection in Long-Term Diabetic Nephropathy. Journal of the American Society of Nephrology: JASN, 2014, 25, 1237-1254.	3.0	301
8	Brahma links the SWI/SNF chromatin-remodeling complex with MeCP2-dependent transcriptional silencing. Nature Genetics, 2005, 37, 254-264.	9.4	277
9	Epigenetics and Metabolism. Circulation Research, 2015, 116, 715-736.	2.0	258
10	Multicellular Transcriptional Analysis of Mammalian Heart Regeneration. Circulation, 2017, 136, 1123-1139.	1.6	222
11	Epigenetic phenomena linked to diabetic complications. Nature Reviews Endocrinology, 2010, 6, 665-675.	4.3	202
12	Modulation of Soluble Receptor for Advanced Glycation End Products by Angiotensin-Converting Enzyme-1 Inhibition in Diabetic Nephropathy. Journal of the American Society of Nephrology: JASN, 2005, 16, 2363-2372.	3.0	200
13	Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. Genome Research, 2011, 21, 1601-1615.	2.4	198
14	Epigenetics. Circulation Research, 2010, 107, 1403-1413.	2.0	185
15	Epigenetic changes to the MDR1 locus in response to chemotherapeutic drugs. Oncogene, 2005, 24, 8061-8075.	2.6	184
16	Precipitous Release of Methyl-CpG Binding Protein 2 and Histone Deacetylase 1 from the Methylated Human Multidrug Resistance Gene (MDR1) on Activation. Molecular and Cellular Biology, 2002, 22, 1844-1857.	1.1	177
17	Deficiency of Prebiotic Fiber and Insufficient Signaling Through Gut Metabolite-Sensing Receptors Leads to Cardiovascular Disease. Circulation, 2020, 141, 1393-1403.	1.6	176
18	Deep sequencing reveals increased DNA methylation in chronic rat epilepsy. Acta Neuropathologica, 2013, 126, 741-756.	3.9	172

#	Article	IF	Citations
19	The Circadian Syndrome: is the Metabolic Syndrome and much more!. Journal of Internal Medicine, 2019, 286, 181-191.	2.7	172
20	Distinguishing Hyperglycemic Changes by Set7 in Vascular Endothelial Cells. Circulation Research, 2012, 110, 1067-1076.	2.0	147
21	Reactive Oxygen Species Can Provide Atheroprotection via NOX4-Dependent Inhibition of Inflammation and Vascular Remodeling. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 295-307.	1.1	147
22	Clonogenic Assay: Adherent Cells. Journal of Visualized Experiments, 2011, , .	0.2	145
23	Î³H2AX as a molecular marker of aging and disease. Epigenetics, 2010, 5, 129-136.	1.3	134
24	DNA Methylation and Histone Deacetylation in the Control of Gene Expression: Basic Biochemistry to Human Development and Disease. Gene Expression, 2001, 9, 63-75.	0.5	129
25	Epigenetic regulation and fetal programming. Best Practice and Research in Clinical Endocrinology and Metabolism, 2008, 22, 1-16.	2.2	129
26	Gene name errors are widespread in the scientific literature. Genome Biology, 2016, 17, 177.	3.8	123
27	Survival motor neuron gene 2 silencing by DNA methylation correlates with spinal muscular atrophy disease severity and can be bypassed by histone deacetylase inhibition. Human Molecular Genetics, 2009, 18, 304-317.	1.4	116
28	Epigenetic programming, early life nutrition and the risk of metabolic disease. Atherosclerosis, 2017, 266, 31-40.	0.4	114
29	Altered methylation of the human MDR1 promoter is associated with acquired multidrug resistance. Clinical Cancer Research, 1997, 3, 2025-32.	3.2	114
30	RNA interference and potential therapeutic applications of short interfering RNAs. Cancer Gene Therapy, 2005, 12, 787-795.	2.2	113
31	HDAC inhibition attenuates cardiac hypertrophy by acetylation and deacetylation of target genes. Epigenetics, 2015, 10, 418-430.	1.3	111
32	Phosphoinositide 3-kinase as a novel functional target for the regulation of the insulin signaling pathway by SIRT1. Molecular and Cellular Endocrinology, 2011, 335, 166-176.	1.6	109
33	Hepatitis C virus leaves an epigenetic signature post cure of infection by direct-acting antivirals. PLoS Genetics, 2019, 15, e1008181.	1.5	109
34	Metabolic memory and diabetic nephropathy: potential role for epigenetic mechanisms. Nature Reviews Nephrology, 2010, 6, 332-341.	4.1	107
35	Analysis of the IGF2/H19 imprinting control region uncovers new genetic defects, including mutations of OCT-binding sequences, in patients with 11p15 fetal growth disorders. Human Molecular Genetics, 2010, 19, 803-814.	1.4	106
36	Epidemic T2DM, early development and epigenetics: implications of the Chinese Famine. Nature Reviews Endocrinology, 2018, 14, 738-746.	4.3	100

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37	Epigenetic Changes in Diabetes and Cardiovascular Risk. Circulation Research, 2016, 118, 1706-1722.	2.0	98
38	Will broad-spectrum histone deacetylase inhibitors be superseded by more specific compounds?. Leukemia, 2007, 21, 61-65.	3.3	96
39	FOXO1 Regulates the Expression of 4E-BP1 and Inhibits mTOR Signaling in Mammalian Skeletal Muscle. Journal of Biological Chemistry, 2007, 282, 21176-21186.	1.6	89
40	Glycemic memory associated epigenetic changes. Biochemical Pharmacology, 2010, 80, 1853-1859.	2.0	87
41	Contraction-induced Interleukin-6 Gene Transcription in Skeletal Muscle Is Regulated by c-Jun Terminal Kinase/Activator Protein-1. Journal of Biological Chemistry, 2012, 287, 10771-10779.	1.6	87
42	Etiology matters â€“ Genomic DNA Methylation Patterns in Three Rat Models of Acquired Epilepsy. Scientific Reports, 2016, 6, 25668.	1.6	87
43	Human Sympathetic Nerve Biology. Annals of the New York Academy of Sciences, 2008, 1148, 338-348.	1.8	84
44	Downstream targets of methyl CpG binding protein 2 and their abnormal expression in the frontal cortex of the human Rett syndrome brain. BMC Neuroscience, 2010, 11, 53.	0.8	84
45	Modulation of cellular radiation responses by histone deacetylase inhibitors. Oncogene, 2006, 25, 3885-3893.	2.6	83
46	The rise of DNA methylation and the importance of chromatin on multidrug resistance in cancer. Experimental Cell Research, 2003, 290, 177-194.	1.2	81
47	The methylation hypothesis of pharmacoresistance in epilepsy. Epilepsia, 2013, 54, 41-47.	2.6	81
48	Processed foods drive intestinal barrier permeability and microvascular diseases. Science Advances, 2021, 7, .	4.7	80
49	Vascular histone deacetylation by pharmacological HDAC inhibition. Genome Research, 2014, 24, 1271-1284.	2.4	79
50	Epigenetics and precision medicine in cardiovascular patients: from basic concepts to the clinical arena. European Heart Journal, 2018, 39, 4150-4158.	1.0	79
51	Transient Intermittent Hyperglycemia Accelerates Atherosclerosis by Promoting Myelopoiesis. Circulation Research, 2020, 127, 877-892.	2.0	77
52	DNMT cooperativity?the developing links between methylation, chromatin structure and cancer. BioEssays, 2003, 25, 1071-1084.	1.2	76
53	The Set7 Lysine Methyltransferase Regulates Plasticity in Oxidative Phosphorylation Necessary for Trained Immunity Induced by Î²-Glucan. Cell Reports, 2020, 31, 107548.	2.9	76
54	The neuronal noradrenaline transporter, anxiety and cardiovascular disease. Journal of Psychopharmacology, 2006, 20, 60-66.	2.0	73

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55	Transcriptional regulation by the Set7 lysine methyltransferase. Epigenetics, 2013, 8, 361-372.	1.3	71
56	Epigenetic changes in diabetes. Clinical Genetics, 2013, 84, 1-10.	1.0	70
57	Disparity of histone deacetylase inhibition on repair of radiation-induced DNA damage on euchromatin and constitutive heterochromatin compartments. Oncogene, 2007, 26, 3963-3971.	2.6	67
58	Epigenetics in diabetic nephropathy, immunity and metabolism. Diabetologia, 2018, 61, 6-20.	2.9	65
59	Genetic Examination of SETD7 and SUV39H1/H2 Methyltransferases and the Risk of Diabetes Complications in Patients With Type 1 Diabetes. Diabetes, 2011, 60, 3073-3080.	0.3	62
60	DNA damage repair and transcription. Cellular and Molecular Life Sciences, 2004, 61, 2137-47.	2.4	61
61	Genomic <scp>DNA</scp> methylation distinguishes subtypes of human focal cortical dysplasia. Epilepsia, 2019, 60, 1091-1103.	2.6	61
62	Maternal Overnutrition Programs Changes in the Expression of Skeletal Muscle Genes That Are Associated with Insulin Resistance and Defects of Oxidative Phosphorylation in Adult Male Rat Offspring. Journal of Nutrition, 2014, 144, 237-244.	1.3	59
63	The primary microRNA-208b interacts with Polycomb-group protein, Ezh2, to regulate gene expression in the heart. Nucleic Acids Research, 2014, 42, 790-803.	6.5	57
64	Dynamic changes in the cardiac methylome during postnatal development. FASEB Journal, 2015, 29, 1329-1343.	0.2	56
65	Evaluation of microRNA alignment techniques. Rna, 2016, 22, 1120-1138.	1.6	56
66	Chromatin modifications remodel cardiac gene expression. Cardiovascular Research, 2014, 103, 7-16.	1.8	55
67	Genetic and epigenetic events in diabetic wound healing. International Wound Journal, 2011, 8, 12-21.	1.3	53
68	New insights into the pathogenesis of beckwith-wiedemann and silver-russell syndromes: Contribution of small copy number variations to 11p15 imprinting defects. Human Mutation, 2011, 32, 1171-1182.	1.1	53
69	Chromatin context and ncRNA highlight targets of MeCP2 in brain. RNA Biology, 2013, 10, 1741-1757.	1.5	52
70	Glycemic Memories and the Epigenetic Component of Diabetic Nephropathy. Current Diabetes Reports, 2013, 13, 574-581.	1.7	48
71	Lipoxins Regulate the Early Growth Responseâ€“1 Network and Reverse Diabetic Kidney Disease. Journal of the American Society of Nephrology: JASN, 2018, 29, 1437-1448.	3.0	48
72	Complement C5a Induces Renal Injury in Diabetic Kidney Disease by Disrupting Mitochondrial Metabolic Agility. Diabetes, 2020, 69, 83-98.	0.3	48

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73	Epigenetic Modification of the Norepinephrine Transporter Gene in Postural Tachycardia Syndrome. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 1910-1916.	1.1	47
74	Galectin-3 deficiency ameliorates fibrosis and remodeling in dilated cardiomyopathy mice with enhanced Mst1 signaling. American Journal of Physiology - Heart and Circulatory Physiology, 2019, 316, H45-H60.	1.5	47
75	The histone deacetylase inhibitor, trichostatin A, enhances radiation sensitivity and accumulation of gammaH2A.X. Cancer Biology and Therapy, 2005, 4, 787-793.	1.5	46
76	Development of Novel Activin-Targeted Therapeutics. Molecular Therapy, 2015, 23, 434-444.	3.7	46
77	MDR1, Chemotherapy and chromatin remodeling. Cancer Biology and Therapy, 2004, 3, 819-824.	1.5	44
78	The Epigenetic Modifier, Valproic Acid, Enhances Radiation Sensitivity. Epigenetics, 2006, 1, 131-137.	1.3	42
79	Effect of valproic acid on radiation-induced DNA damage in euchromatic and heterochromatic compartments. Cell Cycle, 2008, 7, 468-476.	1.3	42
80	Glycemic memory. Current Opinion in Lipidology, 2012, 23, 24-29.	1.2	42
81	Digital expression explorer 2: a repository of uniformly processed RNA sequencing data. GigaScience, 2019, 8, .	3.3	42
82	Sex-Specific Control of Human Heart Maturation by the Progesterone Receptor. Circulation, 2021, 143, 1614-1628.	1.6	42
83	Trichostatin A accentuates doxorubicin-induced hypertrophy in cardiac myocytes. Aging, 2010, 2, 659-668.	1.4	42
84	siRNAs: Mechanism of RNA interference, In vivo and potential clinical applications. Cancer Biology and Therapy, 2004, 3, 1069-1074.	1.5	41
85	Role of Histone Acetylation in the Stimulatory Effect of Valproic Acid on Vascular Endothelial Tissue-Type Plasminogen Activator Expression. PLoS ONE, 2012, 7, e31573.	1.1	41
86	Immunomodulatory Effects of Histone Deacetylase Inhibitors. Current Molecular Medicine, 2013, 13, 640-647.	0.6	41
87	Cardiac ventricular chambers are epigenetically distinguishable. Cell Cycle, 2010, 9, 612-617.	1.3	40
88	Investigation into the biological properties of the olive polyphenol, hydroxytyrosol: mechanistic insights by genome-wide mRNA-Seq analysis. Genes and Nutrition, 2012, 7, 343-355.	1.2	40
89	The rise and fall of genomic methylation in cancer. Leukemia, 2004, 18, 233-237.	3.3	38
90	The Paradox of Histone Deacetylase Inhibitor-Mediated Modulation of Cellular Responses to Radiation. Cell Cycle, 2006, 5, 288-295.	1.3	37

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91	Demethylation using the epigenetic modifier, 5-azacytidine, increases the efficiency of transient transfection of macrophages. Journal of Lipid Research, 2005, 46, 356-365.	2.0	36
92	Methylation of the SLC6a2 Gene Promoter in Major Depression and Panic Disorder. PLoS ONE, 2013, 8, e83223.	1.1	36
93	Interplay of chromatin modifications and non-coding RNAs in the heart. Epigenetics, 2014, 9, 101-112.	1.3	36
94	Clinical Potential of Histone Deacetylase Inhibitors as Stand Alone Therapeutics and in Combination with other Chemotherapeutics or Radiotherapy for Cancer. Epigenetics, 2006, 1, 121-126.	1.3	35
95	Chromatin modifications and DNA double-strand breaks: the current state of play. Leukemia, 2007, 21, 195-200.	3.3	35
96	Chromatin Modifications Associated with Diabetes. Journal of Cardiovascular Translational Research, 2012, 5, 399-412.	1.1	33
97	Expression analysis of the epigenetic methyltransferases and Methyl-CpG binding protein families in the normal B-cell and B-cell chronic lymphocytic leukemia (CLL). Cancer Biology and Therapy, 2004, 3, 989-994.	1.5	32
98	Chromatin modifying agents â€“ the cutting edge of anticancer therapy. Drug Discovery Today, 2011, 16, 543-547.	3.2	32
99	Analysis of the barley leaf transcriptome under salinity stress using mRNA-Seq. Acta Physiologiae Plantarum, 2013, 35, 1915-1924.	1.0	32
100	Ubiquitinâ€specific protease 2â€69 in macrophages potentially modulates metainflammation. FASEB Journal, 2013, 27, 4940-4953.	0.2	31
101	Epigenetic mechanisms in the pathogenesis of diabetic foot ulcers. Journal of Diabetes and Its Complications, 2012, 26, 554-561.	1.2	29
102	The emerging role of epigenetic modifications and chromatin remodeling in spinal muscular atrophy. Journal of Neurochemistry, 2009, 109, 1557-1569.	2.1	28
103	Transcription factors Tp73, Cebpd, Pax6, and Spi1 rather than DNA methylation regulate chronic transcriptomics changes after experimental traumatic brain injury. Acta Neuropathologica Communications, 2018, 6, 17.	2.4	28
104	The circadian syndrome predicts cardiovascular disease better than metabolic syndrome in Chinese adults. Journal of Internal Medicine, 2021, 289, 851-860.	2.7	28
105	Î³-radiation-induced Î³H2AX formation occurs preferentially in actively transcribing euchromatic loci. Cellular and Molecular Life Sciences, 2010, 67, 291-294.	2.4	27
106	Alleviating Transcriptional Inhibition of the NorepinephrineSlc6a2Transporter Gene in Depolarized Neurons. Journal of Neuroscience, 2010, 30, 1494-1501.	1.7	26
107	Cardiac genes show contextual SWI/SNF interactions with distinguishable gene activities. Epigenetics, 2011, 6, 760-768.	1.3	26
108	Effects of the Histone Deacetylase Inhibitor, Trichostatin A, in a Chronic Allergic Airways Disease Model in Mice. Archivum Immunologiae Et Therapiae Experimentalis, 2012, 60, 295-306.	1.0	26

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109	Deep sequencing reveals novel Set7 networks. Cellular and Molecular Life Sciences, 2014, 71, 4471-4486.	2.4	26
110	Evaluation of the efficacy of radiation-modifying compounds using Î³H2AX as a molecular marker of DNA double-strand breaks. Genome Integrity, 2011, 2, 3.	1.0	25
111	Epigenetics, cardiovascular disease, and cellular reprogramming. Journal of Molecular and Cellular Cardiology, 2019, 128, 129-133.	0.9	25
112	Epigenetic and Genetic Mechanisms of Abnormal 11p15 Genomic Imprinting in Silver-Russell and Beckwith-Wiedemann Syndromes. Current Medicinal Chemistry, 2011, 18, 1740-1750.	1.2	24
113	DNA damage repair and transcription. Cellular and Molecular Life Sciences, 2004, 61, 2173-80.	2.4	23
114	RAGE Deletion Confers Renoprotection by Reducing Responsiveness to Transforming Growth Factor-Î² and Increasing Resistance to Apoptosis. Diabetes, 2018, 67, 960-973.	0.3	23
115	Metabolic Karmaâ€”The Atherogenic Legacy of Diabetes: The 2017 Edwin Bierman Award Lecture. Diabetes, 2018, 67, 785-790.	0.3	22
116	Protective effects of valproic acid against airway hyperresponsiveness and airway remodeling in a mouse model of allergic airways disease. Epigenetics, 2011, 6, 1463-1470.	1.3	21
117	Redox Mediating Epigenetic Changes Confer Metabolic Memories. Circulation Research, 2012, 111, 262-264.	2.0	21
118	DNA methylation patterns from peripheral blood separate coronary artery disease patients with and without heart failure. ESC Heart Failure, 2020, 7, 2468-2478.	1.4	21
119	Histone deacetylase inhibitors augment doxorubicin-induced DNA damage in cardiomyocytes. Cellular and Molecular Life Sciences, 2011, 68, 4101-4114.	2.4	20
120	Systems approach to the pharmacological actions of HDAC inhibitors reveals EP300 activities and convergent mechanisms of regulation in diabetes. Epigenetics, 2017, 12, 991-1003.	1.3	20
121	Analysis of Chromatin-Immunopurified MeCP2-Associated Fragments. Biochemical and Biophysical Research Communications, 2001, 289, 733-737.	1.0	19
122	Rapid Development of Non-Alcoholic Steatohepatitis in Psammomys obesus (Israeli Sand Rat). PLoS ONE, 2014, 9, e92656.	1.1	19
123	Quantification of γH2AX Foci in Response to Ionising Radiation. Journal of Visualized Experiments, 2010, , .	0.2	18
124	Epigenetic Regulation of Multidrug Resistance 1 Gene Expression: Profiling CpG Methylation Status Using Bisulphite Sequencing. Methods in Molecular Biology, 2010, 596, 183-198.	0.4	18
125	Yap regulates skeletal muscle fatty acid oxidation and adiposity in metabolic disease. Nature Communications, 2021, 12, 2887.	5.8	18
126	Valproic acid influences the expression of genes implicated with hyperglycaemia-induced complement and coagulation pathways. Scientific Reports, 2021, 11, 2163.	1.6	18

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127	Profiling methyl-CpG specific determinants on transcriptionally silent chromatin. Molecular Biology Reports, 2001, 28, 209-215.	1.0	17
128	Pharmacological inhibition of arginine and lysine methyltransferases induces nuclear abnormalities and suppresses angiogenesis in human endothelial cells. Biochemical Pharmacology, 2016, 121, 18-32.	2.0	17
129	NET silencing by let-7i in postural tachycardia syndrome. JCI Insight, 2017, 2, e90183.	2.3	17
130	Reply to â€œTesting for association between MeCP2 and the brahma-associated SWI/SNF chromatin-remodeling complexâ€• Nature Genetics, 2006, 38, 964-967.	9.4	16
131	Transient high glucose causes persistent epigenetic changes and altered gene expression during subsequent normoglycemia. Journal of Experimental Medicine, 2008, 205, 2683-2683.	4.2	16
132	Histone modifications regulate the norepinephrine transporter gene. Cell Cycle, 2010, 9, 4600-4601.	1.3	16
133	MeCP2 interacts with chromosomal microRNAs in brain. Epigenetics, 2017, 12, 1028-1037.	1.3	16
134	Silencing Lysine-Specific Histone Demethylase 1 (LSD1) Causes Increased HP1-Positive Chromatin, Stimulation of DNA Repair Processes, and Dysregulation of Proliferation by Chk1 Phosphorylation in Human Endothelial Cells. Cells, 2019, 8, 1212.	1.8	16
135	FMR1 silencing and the signals to chromatin: a unified model of transcriptional regulation. Biochemical and Biophysical Research Communications, 2002, 295, 575-581.	1.0	15
136	Utility of Î³H2AX as a Molecular Marker of DNA Double-Strand Breaks in Nuclear Medicine: Applications to Radionuclide Therapy Employing Auger Electron-Emitting Isotopes. Current Radiopharmaceuticals, 2011, 4, 59-67.	0.3	15
137	Double-strand breaks and the concept of short- and long-term epigenetic memory. Chromosoma, 2011, 120, 129-149.	1.0	15
138	Influence of Natural and Synthetic Histone Deacetylase Inhibitors on Chromatin. Antioxidants and Redox Signaling, 2012, 17, 340-354.	2.5	15
139	Genetic variants within the second intron of theKCNQ1gene affect CTCF binding and confer a risk of Beckwithâ€“Wiedemann syndrome upon maternal transmission. Journal of Medical Genetics, 2014, 51, 502-511.	1.5	15
140	Set7 mediated interactions regulate transcriptional networks in embryonic stem cells. Nucleic Acids Research, 2016, 44, gkw621.	6.5	15
141	HDAC Inhibition in Vascular Endothelial Cells Regulates the Expression of ncRNAs. Non-coding RNA, 2016, 2, 4.	1.3	14
142	Metabolism and chromatin dynamics in health and disease. Molecular Aspects of Medicine, 2017, 54, 1-15.	2.7	14
143	SAHA attenuates Takotsubo-like myocardial injury by targeting an epigenetic Ac/Dc axis. Signal Transduction and Targeted Therapy, 2021, 6, 159.	7.1	14
144	Epigenetic evidence of an Ac/Dc axis by VPA and SAHA. Clinical Epigenetics, 2021, 13, 58.	1.8	13

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145	Atherogenic Factors and Their Epigenetic Relationships. International Journal of Vascular Medicine, 2010, 2010, 1-7.	0.4	12
146	Applicability of Histone Deacetylase Inhibition for the Treatment of Spinal Muscular Atrophy. Neurotherapeutics, 2013, 10, 677-687.	2.1	12
147	Diet during Pregnancy is Implicated in the Regulation of Hypothalamic RNA Methylation and Risk of Obesity in Offspring. Molecular Nutrition and Food Research, 2018, 62, e1800134.	1.5	12
148	Chinese Famine and the diabetes mellitus epidemic. Nature Reviews Endocrinology, 2020, 16, 123-123.	4.3	12
149	Molecular model of naphthalene-induced DNA damage in the murine lung. Human and Experimental Toxicology, 2012, 31, 42-50.	1.1	11
150	DNA damage detection and repair, and the involvement of epigenetic states. Human Mutation, 2005, 25, 101-109.	1.1	10
151	DNA methylation regulates hypothalamic gene expression linking parental diet during pregnancy to the offspringâ€™s risk of obesity in Psammomys obesus. International Journal of Obesity, 2016, 40, 1079-1088.	1.6	10
152	Epigenomic changes associated with impaired norepinephrine transporter function in postural tachycardia syndrome. Neuroscience and Biobehavioral Reviews, 2017, 74, 342-355.	2.9	10
153	Epigenetic Contribution to the Development and Progression of Vascular Diabetic Complications. Antioxidants and Redox Signaling, 2018, 29, 1074-1091.	2.5	10
154	Pharmacological Histone Deacetylation Distinguishes Transcriptional Regulators. Current Topics in Medicinal Chemistry, 2017, 17, 1611-1622.	1.0	9
155	On the use of DNA methylation inhibitors and the reversal of transcriptional silencing. Blood, 2003, 101, 1656-1657.	0.6	8
156	Introduction: Understanding the consequences of epigenetic mechanisms and its effects on transcription in health and disease. Cancer Biology and Therapy, 2004, 3, 816-818.	1.5	8
157	Endothelial Transcriptome in Response to Pharmacological Methyltransferase Inhibition. ChemMedChem, 2014, 9, 1755-1762.	1.6	8
158	RNA sequencing supports distinct reactive oxygen species-mediated pathways of apoptosis by high and low size mass fractions of Bay leaf (Lauris nobilis) in HT-29 cells. Food and Function, 2015, 6, 2507-2524.	2.1	8
159	Sex-Based Mhrt Methylation Chromatinizes MeCP2 in the Heart. IScience, 2019, 17, 288-301.	1.9	8
160	Absolute Quantitation of MDR1 Transcripts Using Heterologous DNA Standardsâ€”Validation of the Competitive RT-PCR (CRT-PCR) Approach. BioTechniques, 1999, 26, 1114-1124.	0.8	7
161	Epigenetic changes activate widespread signals in response to doublestrand breaks. Cancer Biology and Therapy, 2004, 3, 617-623.	1.5	7
162	Dysregulation of the cohesin subunit RAD21 by Hepatitis C virus mediates hostâ€“virus interactions. Nucleic Acids Research, 2019, 47, 2455-2471.	6.5	7

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163	Evaluation of the Spatial Distribution of γH2AX following Ionizing Radiation. Journal of Visualized Experiments, 2010, , .	0.2	6
164	A pipeline for the identification and characterization of chromatin modifications derived from ChIP-Seq datasets. Biochimie, 2012, 94, 2353-2359.	1.3	6
165	Age-Related Differential Structural and Transcriptomic Responses in the Hypertensive Heart. Frontiers in Physiology, 2018, 9, 817.	1.3	6
166	Microencapsulation-based cell therapies. Cellular and Molecular Life Sciences, 2022, 79, .	2.4	6
167	RNA-seq-based identification of Star upregulation by islet amyloid formation. Protein Engineering, Design and Selection, 2019, 32, 67-76.	1.0	5
168	Targeting Treatment Refractory NET by EZH2 Inhibition in Postural Tachycardia Syndrome. Circulation Research, 2020, 126, 1058-1060.	2.0	5
169	DNA methylation status correlates with adult Î²-cell regeneration capacity. Npj Regenerative Medicine, 2021, 6, 7.	2.5	5
170	Metaboloepigenetics in cancer, immunity, and cardiovascular disease. Cardiovascular Research, 2023, 119, 357-370.	1.8	5
171	Quantitation of γH2AX Foci in Tissue Samples. Journal of Visualized Experiments, 2010, , .	0.2	4
172	Remodeling is at the heart of chromatin. Epigenetics, 2011, 6, 884-887.	1.3	4
173	Pathological hypertrophy reverses Î² ₂ -adrenergic receptor-induced angiogenesis in mouse heart. Physiological Reports, 2015, 3, e12340.	0.7	4
174	Mechanisms of abnormal gene expression in tumor cells. , 2006, , 351-361.		4
175	Non-referenced genome assembly from epigenomic short-read data. Epigenetics, 2014, 9, 1329-1338.	1.3	3
176	The diabetes epidemic in China is a public health emergency: the potential role of prenatal exposure. Journal of Public Health and Emergency, 2017, 1, 80-80.	4.4	3
177	Targeting Methylglyoxal in Diabetic Kidney Disease Using the Mitochondria-Targeted Compound MitoGamide. Nutrients, 2021, 13, 1457.	1.7	3
178	Prolonged Honeymoon Period in a Thai Patient with Adult-Onset Type 1 Diabetes Mellitus. Case Reports in Endocrinology, 2021, 2021, 1-6.	0.2	3
179	Epigenetics of Diabetic Nephropathy: From Biology to Therapeutics. European Medical Journal (Chelmsford, England), 0, , 48-57.	3.0	3
180	DNA damage repair and transcription. Cellular and Molecular Life Sciences, 2004, 61, 2135-6.	2.4	2

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181	Epigenetic-Mediated Reprogramming of Pancreatic Endocrine Cells. Antioxidants and Redox Signaling, 2015, 22, 1483-1495.	2.5	2
182	Current perspectives in Set7 mediated stem cell differentiation. Non-coding RNA, 2016, 2, 14.	1.3	2
183	Improving understanding of chromatin regulatory proteins and potential implications for drug discovery. Expert Review of Proteomics, 2016, 13, 435-445.	1.3	2
184	Contemporary Trends Emerging in Epigenomics and Metabolism. Antioxidants and Redox Signaling, 2018, 29, 1019-1022.	2.5	2
185	Distinguishable DNA methylation defines disease susceptibility influenced by race and ethnicity. Clinical Epigenetics, 2021, 13, 189.	1.8	2
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