

Lawrence W Stanton

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

10,558
citations

43973

48
h-index

60497

81
g-index

84
all docs

84
docs citations

84
times ranked

14658
citing authors

#	ARTICLE	IF	CITATIONS
1	Upregulation of β -catenin due to loss of miR-139 contributes to motor neuron death in amyotrophic lateral sclerosis. <i>Stem Cell Reports</i> , 2022, , .	2.3	9
2	Single-cell transcriptomics identifies master regulators of neurodegeneration in SOD1 ALS iPSC-derived motor neurons. <i>Stem Cell Reports</i> , 2021, 16, 3020-3035.	2.3	14
3	A Balanced Translocation in Kallmann Syndrome Implicates a Long Noncoding RNA, RMST, as a GnRH Neuronal Regulator. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e231-e244.	1.8	28
4	A genomic biomarker that identifies human bone marrow-derived mesenchymal stem cells with high scalability. <i>Stem Cells</i> , 2020, 38, 1124-1136.	1.4	16
5	In Reply. <i>Stem Cells</i> , 2020, 38, E7-E8.	1.4	0
6	Phenotypic and molecular features underlying neurodegeneration of motor neurons derived from spinal and bulbar muscular atrophy patients. <i>Neurobiology of Disease</i> , 2019, 124, 1-13.	2.1	15
7	APP upregulation contributes to retinal ganglion cell degeneration via JNK3. <i>Cell Death and Differentiation</i> , 2018, 25, 663-678.	5.0	24
8	Cyclin-Dependent Kinase-Dependent Phosphorylation of Sox2 at Serine 39 Regulates Neurogenesis. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	18
9	Genetic Correction of SOD1 Mutant iPSCs Reveals ERK and JNK Activated AP1 as a Driver of Neurodegeneration in Amyotrophic Lateral Sclerosis. <i>Stem Cell Reports</i> , 2017, 8, 856-869.	2.3	108
10	Re-engineered RNA-Guided FokI-Nucleases for Improved Genome Editing in Human Cells. <i>Molecular Therapy</i> , 2017, 25, 342-355.	3.7	25
11	Generation of sibling-matched induced pluripotent stem cell lines from spinal and bulbar muscular atrophy patients. <i>Stem Cell Research</i> , 2017, 20, 30-33.	0.3	7
12	Single-cell gene expression analysis reveals regulators of distinct cell subpopulations among developing human neurons. <i>Genome Research</i> , 2017, 27, 1783-1794.	2.4	39
13	A Role for RE-1-Silencing Transcription Factor in Embryonic Stem Cells Cardiac Lineage Specification. <i>Stem Cells</i> , 2016, 34, 860-872.	1.4	7
14	MiR-375 is Essential for Human Spinal Motor Neuron Development and May Be Involved in Motor Neuron Degeneration. <i>Stem Cells</i> , 2016, 34, 124-134.	1.4	64
15	Molecular Features Underlying Neurodegeneration Identified through In Vitro Modeling of Genetically Diverse Parkinson's Disease Patients. <i>Cell Reports</i> , 2016, 15, 2411-2426.	2.9	76
16	Chromatin and RNA Maps Reveal Regulatory Long Noncoding RNAs in Mouse. <i>Molecular and Cellular Biology</i> , 2016, 36, 809-819.	1.1	75
17	The Neurogenic Potential of Astrocytes Is Regulated by Inflammatory Signals. <i>Molecular Neurobiology</i> , 2016, 53, 3724-3739.	1.9	36
18	NeuO: a Fluorescent Chemical Probe for Live Neuron Labeling. <i>Angewandte Chemie</i> , 2015, 127, 2472-2476.	1.6	12

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19	RE1 silencing transcription factor/neuronâ€restrictive silencing factor regulates expansion of adult mouse subventricular zoneâ€derived neural stem/progenitor cells in vitro. Journal of Neuroscience Research, 2015, 93, 1203-1214.	1.3	13
20	Establishing Criteria for Human Mesenchymal Stem Cell Potency. Stem Cells, 2015, 33, 1878-1891.	1.4	163
21	PDX1 Binds and Represses Hepatic Genes to Ensure Robust Pancreatic Commitment in Differentiating Human Embryonic Stem Cells. Stem Cell Reports, 2015, 4, 578-590.	2.3	44
22	NeuO: a Fluorescent Chemical Probe for Live Neuron Labeling. Angewandte Chemie - International Edition, 2015, 54, 2442-2446.	7.2	73
23	Pluripotency Activity of Nanog Requires Biochemical Stabilization by Variant Histone Protein H2A.Z. Stem Cells, 2015, 33, 2126-2134.	1.4	10
24	Pleiotropic Functions for Transcription Factor Zscan10. PLoS ONE, 2014, 9, e104568.	1.1	16
25	Mi<sc>R</sc>â€135b is a direct <sc>PAX</sc>6 target and specifies human neuroectoderm by inhibiting <sc>TGF</sc>â€2/<sc>BMP</sc> signaling. EMBO Journal, 2014, 33, 1271-1283.	3.5	53
26	Transcription Factor-Induced Lineage Programming of Noradrenaline and Motor Neurons from Embryonic Stem Cells. Stem Cells, 2014, 32, 609-622.	1.4	25
27	Klf4 and Klf5 differentially inhibit mesoderm and endoderm differentiation in embryonic stem cells. Nature Communications, 2014, 5, 3719.	5.8	94
28	Sox Transcription Factors Require Selective Interactions with Oct4 and Specific Transactivation Functions to Mediate Reprogramming. Stem Cells, 2013, 31, 2632-2646.	1.4	60
29	Nanofibrous scaffold-mediated REST knockdown to enhance neuronal differentiation of stem cells. Biomaterials, 2013, 34, 3581-3590.	5.7	90
30	The Long Noncoding RNA RMST Interacts with SOX2 to Regulate Neurogenesis. Molecular Cell, 2013, 51, 349-359.	4.5	378
31	An epigenetic signature of developmental potential in neural stem cells and early neurons. Stem Cells, 2013, 31, 1868-1880.	1.4	41
32	Long nonâ€coding RNAs in stem cell pluripotency. Wiley Interdisciplinary Reviews RNA, 2013, 4, 121-128.	3.2	29
33	Dysregulation of <sc>REST</sc>â€regulated coding and nonâ€coding <sc>RNA</sc>s in a cellular model of Huntington's disease. Journal of Neurochemistry, 2013, 124, 418-430.	2.1	64
34	Oct4 switches partnering from Sox2 to Sox17 to reinterpret the enhancer code and specify endoderm. EMBO Journal, 2013, 32, 938-953.	3.5	161
35	Long noncoding RNAs in development and disease of the central nervous system. Trends in Genetics, 2013, 29, 461-468.	2.9	319
36	Genome Wide Analysis Reveals Zic3 Interaction with Distal Regulatory Elements of Stage Specific Developmental Genes in Zebrafish. PLoS Genetics, 2013, 9, e1003852.	1.5	35

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37	A Genome-Wide Screen for Genetic Variants That Modify the Recruitment of REST to Its Target Genes. <i>PLoS Genetics</i> , 2012, 8, e1002624.	1.5	17
38	Neural stem cell specific fluorescent chemical probe binding to FABP7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10214-10217.	3.3	70
39	Structural analysis and dimerization profile of the SCAN domain of the pluripotency factor Zfp206. <i>Nucleic Acids Research</i> , 2012, 40, 8721-8732.	6.5	21
40	Human long non-coding RNAs promote pluripotency and neuronal differentiation by association with chromatin modifiers and transcription factors. <i>EMBO Journal</i> , 2012, 31, 522-533.	3.5	461
41	Directing Neuronal Differentiation of Primary Neural Progenitor Cells by Gene Knockdown Approach. <i>DNA and Cell Biology</i> , 2012, 31, 1148-1160.	0.9	17
42	Repressor Element 1 Silencing Transcription Factor Couples Loss of Pluripotency with Neural Induction and Neural Differentiation. <i>Stem Cells</i> , 2012, 30, 425-434.	1.4	34
43	Activin and BMP4 Synergistically Promote Formation of Definitive Endoderm in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2012, 30, 631-642.	1.4	97
44	Nanofiber topography and sustained biochemical signaling enhance human mesenchymal stem cell neural commitment. <i>Acta Biomaterialia</i> , 2012, 8, 1290-1302.	4.1	111
45	Transcription Factor-Induced Lineage Selection of Stem-Cell-Derived Neural Progenitor Cells. <i>Cell Stem Cell</i> , 2011, 8, 663-675.	5.2	65
46	Conversion of Sox17 into a Pluripotency Reprogramming Factor by Reengineering Its Association with Oct4 on DNA. <i>Stem Cells</i> , 2011, 29, 940-951.	1.4	92
47	Coassembly of REST and its cofactors at sites of gene repression in embryonic stem cells. <i>Genome Research</i> , 2011, 21, 1284-1293.	2.4	46
48	Human accelerated region 1 noncoding RNA is repressed by REST in Huntington's disease. <i>Physiological Genomics</i> , 2010, 41, 269-274.	1.0	97
49	The Pluripotency Regulator Zic3 Is a Direct Activator of the <i>Nanog</i> Promoter in ESCs. <i>Stem Cells</i> , 2010, 28, 1961-1969.	1.4	67
50	Genome-wide computational identification and manual annotation of human long noncoding RNA genes. <i>Rna</i> , 2010, 16, 1478-1487.	1.6	354
51	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96.	1.6	90
52	Evolution of the Vertebrate Gene Regulatory Network Controlled by the Transcriptional Repressor REST. <i>Molecular Biology and Evolution</i> , 2009, 26, 1491-1507.	3.5	36
53	Zfp206, Oct4, and Sox2 Are Integrated Components of a Transcriptional Regulatory Network in Embryonic Stem Cells. <i>Journal of Biological Chemistry</i> , 2009, 284, 31327-31335.	1.6	65
54	Is REST a regulator of pluripotency?. <i>Nature</i> , 2009, 457, E5-E6.	13.7	51

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55	The Transcription Factor Zfp281 Controls Embryonic Stem Cell Pluripotency by Direct Activation and Repression of Target Genes. <i>Stem Cells</i> , 2008, 26, 2791-2799.	1.4	67
56	Detailed characterization of the mouse embryonic stem cell transcriptome reveals novel genes and intergenic splicing associated with pluripotency. <i>BMC Genomics</i> , 2008, 9, 155.	1.2	13
57	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	2.6	172
58	Generation of Multipotential Mesendodermal Progenitors from Mouse Embryonic Stem Cells via Sustained Wnt Pathway Activation. <i>Journal of Biological Chemistry</i> , 2007, 282, 31703-31712.	1.6	105
59	Zic3 Is Required for Maintenance of Pluripotency in Embryonic Stem Cells. <i>Molecular Biology of the Cell</i> , 2007, 18, 1348-1358.	0.9	121
60	Oct4 and Sox2 Directly Regulate Expression of Another Pluripotency Transcription Factor, Zfp206, in Embryonic Stem Cells. <i>Journal of Biological Chemistry</i> , 2007, 282, 12822-12830.	1.6	59
61	Genomic and proteomic characterization of embryonic stem cells. <i>Current Opinion in Chemical Biology</i> , 2007, 11, 399-404.	2.8	17
62	Zfp206 Is a Transcription Factor That Controls Pluripotency of Embryonic Stem Cells. <i>Stem Cells</i> , 2007, 25, 2173-2182.	1.4	50
63	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006, 38, 431-440.	9.4	2,162
64	SARS Transmission Pattern in Singapore Reassessed by Viral Sequence Variation Analysis. <i>PLoS Medicine</i> , 2005, 2, e43.	3.9	37
65	Scalable Transcriptional Analysis Routine—Multiplexed Quantitative Real-Time Polymerase Chain Reaction Platform for Gene Expression Analysis and Molecular Diagnostics. <i>Journal of Molecular Diagnostics</i> , 2005, 7, 444-454.	1.2	19
66	Inhibition of SARS Coronavirus Infection In Vitro with Clinically Approved Antiviral Drugs. <i>Emerging Infectious Diseases</i> , 2004, 10, 581-586.	2.0	209
67	Laboratory-Acquired Severe Acute Respiratory Syndrome. <i>New England Journal of Medicine</i> , 2004, 350, 1740-1745.	13.9	137
68	Tracking the Evolution of the SARS Coronavirus Using High-Throughput, High-Density Resequencing Arrays. <i>Genome Research</i> , 2004, 14, 398-405.	2.4	104
69	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation. <i>Nature Biotechnology</i> , 2004, 22, 707-716.	9.4	320
70	Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003. <i>BMC Infectious Diseases</i> , 2004, 4, 32.	1.3	58
71	Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection. <i>Lancet, The</i> , 2003, 361, 1779-1785.	6.3	423
72	Radiation hybrid mapping of 70 rat genes from a data set of differentially expressed genes. <i>Mammalian Genome</i> , 2002, 13, 194-197.	1.0	6

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73	Insulin-Like Growth Factor-Binding Protein-3 Induces Fetalization in Neonatal Rat Cardiomyocytes. <i>DNA and Cell Biology</i> , 2000, 19, 757-763.	0.9	9
74	Host Gene Regulation During Coxsackievirus B3 Infection in Mice. <i>Circulation Research</i> , 2000, 87, 328-334.	2.0	107
75	Altered Patterns of Gene Expression in Response to Myocardial Infarction. <i>Circulation Research</i> , 2000, 86, 939-945.	2.0	353
76	Identification of Cd36 (Fat) as an insulin-resistance gene causing defective fatty acid and glucose metabolism in hypertensive rats. <i>Nature Genetics</i> , 1999, 21, 76-83.	9.4	692
77	Nucleotide sequence comparison of normal and translocated murine c-myc genes. <i>Nature</i> , 1984, 310, 423-425.	13.7	161
78	Rearrangement and Activation of C-MYC Oncogene by Chromosome Translocation in B Cell Neoplasias. , 1984, , 91-116.		2
79	Translocation, breakage and truncated transcripts of c-myc oncogene in murine plasmacytomas. <i>Nature</i> , 1983, 303, 401-406.	13.7	528
80	Nucleotide sequence of cloned cDNA of human c-myc oncogene. <i>Nature</i> , 1983, 303, 725-728.	13.7	324
81	On immunoglobulin heavy chain gene switching: two $\hat{I}32b$ genes are rearranged via switch sequences in MPC-11 cells but only one is expressed. <i>Nucleic Acids Research</i> , 1982, 10, 611-630.	6.5	119
82	Nucleotide sequence and properties of the murine $\hat{I}33$ immunoglobulin heavy chain gene switch region: implications for successive $C\hat{I}3$ gene switching. <i>Nucleic Acids Research</i> , 1982, 10, 5993-6006.	6.5	65
83	A model for the molecular requirements of immunoglobulin heavy chain class switching. <i>Nature</i> , 1982, 298, 87-89.	13.7	85