

Anders Lade L Nielsen

List of Publications by Year in descending order

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109
papers

4,614
citations

134610

34
h-index

134545

62
g-index

111
all docs

111
docs citations

111
times ranked

8066
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide screening for genes involved in the epigenetic basis of fragile X syndrome. <i>Stem Cell Reports</i> , 2022, 17, 1048-1058.	2.3	6
2	Inactivation of the Schizophrenia-associated BRD1 gene in Brain Causes Failure-to-thrive, Seizure Susceptibility and Abnormal Histone H3 Acetylation and N-tail Clipping. <i>Molecular Neurobiology</i> , 2021, 58, 4495-4505.	1.9	9
3	<i>EGFR</i> transcription in non-small cell lung cancer tumours can be revealed in ctDNA by cell-free chromatin immunoprecipitation (cfChIP). <i>Molecular Oncology</i> , 2021, 15, 2868-2876.	2.1	7
4	Assessing the impacts of groundwater abstractions on flow regime and stream biota: Combining SWAT-MODFLOW with flow-biota empirical models. <i>Science of the Total Environment</i> , 2020, 706, 135702.	3.9	23
5	Epithelial-to-mesenchymal transition is a resistance mechanism to sequential MET-TKI treatment of MET-amplified EGFR-TKI resistant non-small cell lung cancer cells. <i>Translational Lung Cancer Research</i> , 2020, 9, 1904-1914.	1.3	13
6	An empirical attack tolerance test alters the structure and species richness of plant-pollinator networks. <i>Functional Ecology</i> , 2020, 34, 2246-2258.	1.7	33
7	Cell-free Chromatin Immunoprecipitation (cfChIP) from blood plasma can determine gene-expression in tumors from non-small-cell lung cancer patients. <i>Lung Cancer</i> , 2020, 147, 244-251.	0.9	12
8	Predicting ecosystem state changes in shallow lakes using an aquatic ecosystem model: Lake Hinge, Denmark, an example. <i>Ecological Applications</i> , 2020, 30, e02160.	1.8	33
9	The <i>IFNL4</i> Gene Is a Noncanonical Interferon Gene with a Unique but Evolutionarily Conserved Regulation. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
10	<i>PD-L1</i> and <i>PD-L2</i> expression correlated genes in non-small cell lung cancer. <i>Cancer Communications</i> , 2019, 39, 1-14.	3.7	66
11	Cause-and-Effect relationship between FGFR1 expression and epithelial-mesenchymal transition in EGFR-mutated non-small cell lung cancer cells. <i>Lung Cancer</i> , 2019, 132, 132-140.	0.9	20
12	Comparison of abstraction scenarios simulated by SWAT and SWAT-MODFLOW. <i>Hydrological Sciences Journal</i> , 2019, 64, 434-454.	1.2	57
13	The influence of paternal diet on sncRNA-mediated epigenetic inheritance. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1-11.	1.0	38
14	Up-Regulated FGFR1 Expression as a Mediator of Intrinsic TKI Resistance in EGFR-Mutated NSCLC. <i>Translational Oncology</i> , 2019, 12, 432-440.	1.7	20
15	Effects of changes in land use and climate on aquatic ecosystems: Coupling of models and decomposition of uncertainties. <i>Science of the Total Environment</i> , 2019, 657, 627-633.	3.9	48
16	A QGIS-based graphical user interface for application and evaluation of SWAT-MODFLOW models. <i>Environmental Modelling and Software</i> , 2019, 111, 493-497.	1.9	48
17	Bee conservation: Inclusive solutions. <i>Science</i> , 2018, 360, 389-390.	6.0	16
18	Genome-wide determination of on-target and off-target characteristics for RNA-guided DNA methylation by dCas9 methyltransferases. <i>GigaScience</i> , 2018, 7, 1-19.	3.3	64

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19	Quantifying the combined effects of land use and climate changes on stream flow and nutrient loads: A modelling approach in the Odense Fjord catchment (Denmark). <i>Science of the Total Environment</i> , 2018, 621, 253-264.	3.9	79
20	Simple method for assembly of CRISPR synergistic activation mediator gRNA expression array. <i>Journal of Biotechnology</i> , 2018, 274, 54-57.	1.9	3
21	Voluntary Physical Exercise Induces Expression and Epigenetic Remodeling of VegfA in the Rat Hippocampus. <i>Molecular Neurobiology</i> , 2018, 55, 567-582.	1.9	35
22	Evaluating the Feasibility of DNA Methylation Analyses Using Long-Term Archived Brain Formalin-Fixed Paraffin-Embedded Samples. <i>Molecular Neurobiology</i> , 2018, 55, 668-681.	1.9	6
23	Changes in first trimester fetal CYP1A1 and AHRR DNA methylation and mRNA expression in response to exposure to maternal cigarette smoking. <i>Environmental Toxicology and Pharmacology</i> , 2018, 57, 19-27.	2.0	16
24	A QGIS plugin to tailor SWAT watershed delineations to lake and reservoir waterbodies. <i>Environmental Modelling and Software</i> , 2018, 108, 67-71.	1.9	18
25	DNA methylation in epigenetic inheritance of metabolic diseases through the male germ line. <i>Journal of Molecular Endocrinology</i> , 2018, 60, R39-R56.	1.1	47
26	The Effects of Voluntary Physical Exercise-Activated Neurotrophic Signaling in Rat Hippocampus on mRNA Levels of Downstream Signaling Molecules. <i>Journal of Molecular Neuroscience</i> , 2017, 62, 142-153.	1.1	9
27	Effects of competition and climate on a crop pollinator community. <i>Agriculture, Ecosystems and Environment</i> , 2017, 246, 253-260.	2.5	38
28	The impact of the objective function in multi-site and multi-variable calibration of the SWAT model. <i>Environmental Modelling and Software</i> , 2017, 93, 255-267.	1.9	75
29	MET amplification and epithelial-to-mesenchymal transition exist as parallel resistance mechanisms in erlotinib-resistant, EGFR-mutated, NSCLC HCC827 cells. <i>Oncogenesis</i> , 2017, 6, e307-e307.	2.1	42
30	An open source QGIS-based workflow for model application and experimentation with aquatic ecosystems. <i>Environmental Modelling and Software</i> , 2017, 95, 358-364.	1.9	36
31	Saliva as a Blood Alternative for Genome-Wide DNA Methylation Profiling by Methylated DNA Immunoprecipitation (MeDIP) Sequencing. <i>Epigenomes</i> , 2017, 1, 14.	0.8	8
32	The Genome-Wide DNA Methylation Profile of Peripheral Blood Is Not Systematically Changed by Short-Time Storage at Room Temperature. <i>Epigenomes</i> , 2017, 1, 23.	0.8	0
33	IGF1R depletion facilitates MET amplification as mechanism of acquired resistance to erlotinib in HCC827 NSCLC cells. <i>Oncotarget</i> , 2017, 8, 33300-33315.	0.8	23
34	The role of epithelial to mesenchymal transition in resistance to epidermal growth factor receptor tyrosine kinase inhibitors in non-small cell lung cancer. <i>Translational Lung Cancer Research</i> , 2016, 5, 172-182.	1.3	80
35	Expression of the Alzheimer's Disease Mutations A β PP695sw and PSEN1M146I in Double-Transgenic CA τ tggingen Mice. <i>Journal of Alzheimer's Disease</i> , 2016, 53, 1617-1630.	1.2	35
36	Assessment of global DNA methylation in the first trimester fetal tissues exposed to maternal cigarette smoking. <i>Clinical Epigenetics</i> , 2016, 8, 128.	1.8	17

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37	Hypomethylation of FAM63B in bipolar disorder patients. <i>Clinical Epigenetics</i> , 2016, 8, 52.	1.8	24
38	Golden Gate Assembly of CRISPR gRNA expression array for simultaneously targeting multiple genes. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 4315-4325.	2.4	52
39	Genome-wide DNA methylation profiling with MeDIP-seq using archived dried blood spots. <i>Clinical Epigenetics</i> , 2016, 8, 81.	1.8	36
40	Quantitative assessment of methyl-esterification and other side reactions in a standard propionylation protocol for detection of histone modifications. <i>Proteomics</i> , 2016, 16, 2059-2063.	1.3	12
41	CACNA1C hypermethylation is associated with bipolar disorder. <i>Translational Psychiatry</i> , 2016, 6, e831-e831.	2.4	39
42	Regulatory dissection of the CBX5 and hnRNPA1 bi-directional promoter in human breast cancer cells reveals novel transcript variants differentially associated with HP1± down-regulation in metastatic cells. <i>BMC Cancer</i> , 2016, 16, 32.	1.1	13
43	Identification of the BRD1 interaction network and its impact on mental disorder risk. <i>Genome Medicine</i> , 2016, 8, 53.	3.6	29
44	DNA methylation alterations in response to prenatal exposure of maternal cigarette smoking: A persistent epigenetic impact on health from maternal lifestyle?. <i>Archives of Toxicology</i> , 2016, 90, 231-245.	1.9	86
45	Enhanced genome editing in mammalian cells with a modified dual-fluorescent surrogate system. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2543-2563.	2.4	39
46	A Golden Gate-based Protocol for Assembly of Multiplexed gRNA Expression Arrays for CRISPR/Cas9. <i>Bio-protocol</i> , 2016, 6, .	0.2	3
47	EWS and FUS bind a subset of transcribed genes encoding proteins enriched in RNA regulatory functions. <i>BMC Genomics</i> , 2015, 16, 929.	1.2	21
48	Beyond the histone tale: HP1± deregulation in breast cancer epigenetics. <i>Cancer Biology and Therapy</i> , 2015, 16, 189-200.	1.5	35
49	The KRAB zinc finger protein ZFP809 is required to initiate epigenetic silencing of endogenous retroviruses. <i>Genes and Development</i> , 2015, 29, 538-554.	2.7	146
50	Abstract 339: Different receptor tyrosine kinases mediate EMT and erlotinib-resistance in NSCLC cell lines through bypass signalling. , 2015, , .		0
51	Generation of minipigs with targeted transgene insertion by recombinase-mediated cassette exchange (RMCE) and somatic cell nuclear transfer (SCNT). <i>Transgenic Research</i> , 2013, 22, 709-723.	1.3	34
52	Direct RNA sequencing mediated identification of mRNA localized in protrusions of human MDA-MB-231 metastatic breast cancer cells. <i>Journal of Molecular Signaling</i> , 2013, 8, 9.	0.5	23
53	Epigenetic marking and repression of porcine endogenous retroviruses. <i>Journal of General Virology</i> , 2013, 94, 960-970.	1.3	13
54	Assessing ways to combat eutrophication in a Chinese drinking water reservoir using SWAT. <i>Marine and Freshwater Research</i> , 2013, 64, 475.	0.7	33

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55	Genome wide assessment of mRNA in astrocyte protrusions by direct RNA sequencing reveals mRNA localization for the intermediate filament protein nestin. <i>Glia</i> , 2013, 61, 1922-1937.	2.5	31
56	Daily net ecosystem production in lakes predicted from midday dissolved oxygen saturation: analysis of a five-year high frequency dataset from 24 mesocosms with contrasting trophic states and temperatures. <i>Limnology and Oceanography: Methods</i> , 2013, 11, 202-212.	1.0	8
57	Alternative mRNA Splicing from the Glial Fibrillary Acidic Protein (GFAP) Gene Generates Isoforms with Distinct Subcellular mRNA Localization Patterns in Astrocytes. <i>PLoS ONE</i> , 2013, 8, e72110.	1.1	29
58	The Schizophrenia and Bipolar Disorder associated BRD1 gene is regulated upon chronic restraint stress. <i>European Neuropsychopharmacology</i> , 2012, 22, 651-656.	0.3	22
59	Characterization and expression analysis in the developing embryonic brain of the porcine FET family: FUS, EWS, and TAF15. <i>Gene</i> , 2012, 493, 27-35.	1.0	11
60	Identification of catechols as histone lysine demethylase inhibitors. <i>FEBS Letters</i> , 2012, 586, 1190-1194.	1.3	34
61	Gene Expression Responses to FUS, EWS, and TAF15 Reduction and Stress Granule Sequestration Analyses Identifies FET-Protein Non-Redundant Functions. <i>PLoS ONE</i> , 2012, 7, e46251.	1.1	38
62	FMR1 CCG repeat lengths mediate different regulation of reporter gene expression in comparative transient and locus specific integration assays. <i>Gene</i> , 2011, 486, 15-22.	1.0	11
63	Enzyme kinetic studies of histone demethylases KDM4C and KDM6A: Towards understanding selectivity of inhibitors targeting oncogenic histone demethylases. <i>FEBS Letters</i> , 2011, 585, 1951-1956.	1.3	17
64	Establishment of a pig fibroblast-derived cell line for locus-directed transgene expression in cell cultures and blastocysts. <i>Molecular Biology Reports</i> , 2011, 38, 151-161.	1.0	6
65	Pig transgenesis by Sleeping Beauty DNA transposition. <i>Transgenic Research</i> , 2011, 20, 533-545.	1.3	59
66	Analysis of HP1 \pm regulation in human breast cancer cells. <i>Molecular Carcinogenesis</i> , 2011, 50, 601-613.	1.3	17
67	A Boyden chamber-based method for characterization of astrocyte protrusion localized RNA and protein. <i>Glia</i> , 2011, 59, 1782-1792.	2.5	26
68	Targeting Histone Lysine Demethylases by Truncating the Histone...3 Tail to Obtain Selective Substrate-Based Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 9100-9103.	7.2	39
69	DNA Methylation in Peripheral Blood Cells of Pigs Cloned by Somatic Cell Nuclear Transfer. <i>Cellular Reprogramming</i> , 2011, 13, 307-314.	0.5	2
70	The Etiology of Multiple Sclerosis: Genetic Evidence for the Involvement of the Human Endogenous Retrovirus HERV-Fc1. <i>PLoS ONE</i> , 2011, 6, e16652.	1.1	66
71	Comparison of Gene Expression and Genome-Wide DNA Methylation Profiling between Phenotypically Normal Cloned Pigs and Conventionally Bred Controls. <i>PLoS ONE</i> , 2011, 6, e25901.	1.1	22
72	Identification of a novel vimentin promoter and mRNA isoform. <i>Molecular Biology Reports</i> , 2010, 37, 2407-2413.	1.0	16

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73	Reelin expression during embryonic development of the pig brain. BMC Neuroscience, 2010, 11, 75.	0.8	15
74	Identification of genes differentially expressed in the embryonic pig cerebral cortex before and after appearance of gyration. BMC Research Notes, 2010, 3, 127.	0.6	8
75	Aromatic l-amino acid decarboxylase expression profiling and isoform detection in the developing porcine brain. Brain Research, 2010, 1308, 1-13.	1.1	15
76	Elimination of the plasmid bacterial backbone in site-directed transgenesis. BioTechniques, 2010, 48, 313-316.	0.8	8
77	Antisense Transcription in Gammaretroviruses as a Mechanism of Insertional Activation of Host Genes. Journal of Virology, 2010, 84, 3780-3788.	1.5	29
78	The NIZP1 KRAB and C2HR domains cross-talk for transcriptional regulation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2010, 1799, 463-468.	0.9	15
79	Nizp1 zinc finger protein localization is determined by SCAN-domain inclusion regulated through alternative splicing. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2010, 1799, 539-545.	0.9	2
80	The NSD3L histone methyltransferase regulates cell cycle and cell invasion in breast cancer cells. Biochemical and Biophysical Research Communications, 2010, 398, 565-570.	1.0	39
81	ANALYSIS OF qPCR DATA BY CONVERTING EXPONENTIALLY RELATED Ct VALUES INTO LINEARLY RELATED X ₀ VALUES. Journal of Bioinformatics and Computational Biology, 2010, 08, 885-900.	0.3	81
82	Activation of alternative Jdp2 promoters and functional protein isoforms in T-cell lymphomas by retroviral insertion mutagenesis. Nucleic Acids Research, 2009, 37, 4657-4671.	6.5	21
83	An improved method for genome wide DNA methylation profiling correlated to transcription and genomic instability in two breast cancer cell lines. BMC Genomics, 2009, 10, 223.	1.2	31
84	Hemizygous minipigs produced by random gene insertion and handmade cloning express the Alzheimer's disease-causing dominant mutation APPsw. Transgenic Research, 2009, 18, 545-558.	1.3	159
85	Identification of novel Bach2 transcripts and protein isoforms through tagging analysis of retroviral integrations in B-cell lymphomas. BMC Molecular Biology, 2009, 10, 2.	3.0	22
86	The coat protein complex II, COPII, protein Sec13 directly interacts with presenilin-1. Biochemical and Biophysical Research Communications, 2009, 388, 571-575.	1.0	3
87	A 5' Splice Site Enhances the Recruitment of Basal Transcription Initiation Factors In Vivo. Molecular Cell, 2008, 29, 271-278.	4.5	156
88	Type III Interferon (IFN) Induces a Type I IFN-Like Response in a Restricted Subset of Cells through Signaling Pathways Involving both the Jak-STAT Pathway and the Mitogen-Activated Protein Kinases. Journal of Virology, 2007, 81, 7749-7758.	1.5	404
89	Regulatory mechanisms for 3'-end alternative splicing and polyadenylation of the Glial Fibrillary Acidic Protein, GFAP, transcript. Nucleic Acids Research, 2007, 35, 7636-7650.	6.5	33
90	Identification and characterization of GFAP ^β , a novel glial fibrillary acidic protein isoform. Glia, 2007, 55, 497-507.	2.5	70

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91	Molecular characterization and temporal expression profiling of presenilins in the developing porcine brain. <i>BMC Neuroscience</i> , 2007, 8, 72.	0.8	27
92	Identification of the porcine homologous of human disease causing trinucleotide repeat sequences. <i>Neurogenetics</i> , 2007, 8, 207-218.	0.7	7
93	Expression Analysis of cPLA2 Alpha Interacting TIP60 in Diabetic KK ^{AY} and Non-Diabetic C57BL Wild-Type Mice: No Impact of Transient and Stable TIP60 Overexpression on Glucose-Stimulated Insulin Secretion in Pancreatic Beta-Cells. <i>Review of Diabetic Studies</i> , 2007, 4, 147-158.	0.5	0
94	Evidence implicating BRD1 with brain development and susceptibility to both schizophrenia and bipolar affective disorder. <i>Molecular Psychiatry</i> , 2006, 11, 1126-1138.	4.1	77
95	Nizp1, a Novel Multitype Zinc Finger Protein That Interacts with the NSD1 Histone Lysine Methyltransferase through a Unique C2HR Motif. <i>Molecular and Cellular Biology</i> , 2004, 24, 5184-5196.	1.1	44
96	Self-assembly of the Cytoskeletal Glial Fibrillary Acidic Protein Is Inhibited by an Isoform-specific C Terminus. <i>Journal of Biological Chemistry</i> , 2004, 279, 41537-41545.	1.6	30
97	Structural and functional characterization of the zebrafish gene for glial fibrillary acidic protein, GFAP. <i>Gene</i> , 2003, 310, 123-132.	1.0	94
98	Genetic polymorphism and sequence evolution of an alternatively spliced exon of the glial fibrillary acidic protein gene, GFAP α . <i>Genomics</i> , 2003, 82, 185-193.	1.3	18
99	A New Splice Variant of Glial Fibrillary Acidic Protein, GFAP μ , Interacts with the Presenilin Proteins. <i>Journal of Biological Chemistry</i> , 2002, 277, 29983-29991.	1.6	95
100	Short Communication. <i>Journal of Neurogenetics</i> , 2002, 16, 175-179.	0.6	14
101	Selective interaction between the chromatin-remodeling factor BRG1 and the heterochromatin-associated protein HP1 α . <i>EMBO Journal</i> , 2002, 21, 5797-5806.	3.5	81
102	Heterochromatin Formation in Mammalian Cells. <i>Molecular Cell</i> , 2001, 7, 729-739.	4.5	353
103	Interaction with members of the heterochromatin protein 1 (HP1) family and histone deacetylation are differentially involved in transcriptional silencing by members of the TIF1 family. <i>EMBO Journal</i> , 1999, 18, 6385-6395.	3.5	325
104	TIF1 β : A possible link between KRAB zinc finger proteins and nuclear receptors. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 1998, 65, 43-50.	1.2	44
105	TIF1 β : chromatin-specific mediator for the ligand-dependent activation function AF-2 of nuclear receptors?. <i>Biochemical Society Transactions</i> , 1997, 25, 605-612.	1.6	24
106	E-box Sequence and Context-dependent TAL1/SCL Modulation of Basic Helix-Loop-Helix Protein-mediated Transcriptional Activation. <i>Journal of Biological Chemistry</i> , 1996, 271, 31463-31469.	1.6	26
107	Carbon Monoxide in Chronic Uraemia Related to Erythropoietin Treatment and Smoking Habits. <i>Scandinavian Journal of Urology and Nephrology</i> , 1995, 29, 21-25.	1.4	14
108	E-Box Variants Direct Formation of Distinct Complexes with the Basic Helix-Loop-Helix Protein ALF1. <i>Journal of Molecular Biology</i> , 1995, 249, 564-575.	2.0	13

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109	Basic helix-loop-helix proteins in murine type C retrovirus transcriptional regulation. <i>Journal of Virology</i> , 1994, 68, 5638-5647.	1.5	23