

Maurizio D'esposito

List of Publications by Year in descending order

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69
papers

3,827
citations

136950

32
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123424

61
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69
all docs

69
docs citations

69
times ranked

3950
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic and Epigenomic Landscape in Rett Syndrome. <i>Biomolecules</i> , 2021, 11, 967.	4.0	10
2	MeCP2 and Major Satellite Forward RNA Cooperate for Pericentric Heterochromatin Organization. <i>Stem Cell Reports</i> , 2020, 15, 1317-1332.	4.8	13
3	Epigenetic Factors that Control Pericentric Heterochromatin Organization in Mammals. <i>Genes</i> , 2020, 11, 595.	2.4	20
4	Interpretation of the Epigenetic Signature of Facioscapulohumeral Muscular Dystrophy in Light of Genotype-Phenotype Studies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2635.	4.1	18
5	ATRX Contributes to MeCP2-Mediated Pericentric Heterochromatin Organization during Neural Differentiation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5371.	4.1	19
6	Glycosphingolipid metabolic reprogramming drives neural differentiation. <i>EMBO Journal</i> , 2018, 37, .	7.8	56
7	ICF-specific DNMT3B dysfunction interferes with intragenic regulation of mRNA transcription and alternative splicing. <i>Nucleic Acids Research</i> , 2017, 45, 5739-5756.	14.5	42
8	Retention of Mitochondria in Mature Human Red Blood Cells as the Result of Autophagy Impairment in Rett Syndrome. <i>Scientific Reports</i> , 2017, 7, 12297.	3.3	28
9	Effects of Mecp2 loss of function in embryonic cortical neurons: a bioinformatics strategy to sort out non-neuronal cells variability from transcriptome profiling. <i>BMC Bioinformatics</i> , 2016, 17, 14.	2.6	10
10	MECP2, a multi-talented modulator of chromatin architecture. <i>Briefings in Functional Genomics</i> , 2016, 15, elw023.	2.7	59
11	X inactivation and reactivation in X-linked diseases. <i>Seminars in Cell and Developmental Biology</i> , 2016, 56, 78-87.	5.0	43
12	Abnormal N-glycosylation pattern for brain nucleotide pyrophosphatase-5 (NPP-5) in Mecp2-mutant murine models of Rett syndrome. <i>Neuroscience Research</i> , 2016, 105, 28-34.	1.9	7
13	MECP2 Duplication Syndrome: Evidence of Enhanced Oxidative Stress. A Comparison with Rett Syndrome. <i>PLoS ONE</i> , 2016, 11, e0150101.	2.5	22
14	Exploring the possible link between MeCP2 and oxidative stress in Rett syndrome. <i>Free Radical Biology and Medicine</i> , 2015, 88, 81-90.	2.9	53
15	Non-coding RNAs in chromatin disease involving neurological defects. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 54.	3.7	13
16	Epigenetic control of hypoxia inducible factor-1 α -dependent expression of placental growth factor in hypoxic conditions. <i>Epigenetics</i> , 2014, 9, 600-610.	2.7	36
17	Oxidative brain damage in Mecp2-mutant murine models of Rett syndrome. <i>Neurobiology of Disease</i> , 2014, 68, 66-77.	4.4	118
18	Global Transcriptome Profiles of Italian Mediterranean Buffalo Embryos with Normal and Retarded Growth. <i>PLoS ONE</i> , 2014, 9, e90027.	2.5	14

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19	Absence of TI-VAMP/Vamp7 Leads to Increased Anxiety in Mice. <i>Journal of Neuroscience</i> , 2012, 32, 1962-1968.	3.6	63
20	O6-methylguanine-DNA methyltransferase in equine sarcoids: molecular and epigenetic analysis. <i>BMC Veterinary Research</i> , 2012, 8, 218.	1.9	8
21	MeCP2 as a genome-wide modulator: the renewal of an old story. <i>Frontiers in Genetics</i> , 2012, 3, 181.	2.3	20
22	Partial rescue of Rett syndrome by 100% 3 polyunsaturated fatty acids (PUFAs) oil. <i>Genes and Nutrition</i> , 2012, 7, 447-458.	2.5	76
23	MeCP2 Dependent Heterochromatin Reorganization during Neural Differentiation of a Novel Mecp2-Deficient Embryonic Stem Cell Reporter Line. <i>PLoS ONE</i> , 2012, 7, e47848.	2.5	34
24	F4-neuroprostanes mediate neurological severity in Rett syndrome. <i>Clinica Chimica Acta</i> , 2011, 412, 1399-1406.	1.1	68
25	Alternative splicing of the human gene SYBL1 modulates protein domain architecture of longin VAMP7/TI-VAMP, showing both non-SNARE and synaptobrevin-like isoforms. <i>BMC Molecular Biology</i> , 2011, 12, 26.	3.0	10
26	Increased levels of 4HNE-protein plasma adducts in Rett syndrome. <i>Clinical Biochemistry</i> , 2011, 44, 368-371.	1.9	63
27	Variegated silencing through epigenetic modifications of a large Xq region in a case of balanced X;2 translocation with Incontinentia Pigmenti-like phenotype. <i>Epigenetics</i> , 2011, 6, 1242-1247.	2.7	14
28	F2-dihomo-isoprostanes as potential early biomarkers of lipid oxidative damage in Rett syndrome. <i>Journal of Lipid Research</i> , 2011, 52, 2287-2297.	4.2	93
29	Epigenetic alteration of microRNAs in DNMT3B-mutated patients of ICF syndrome. <i>Epigenetics</i> , 2010, 5, 427-443.	2.7	31
30	Differential DNA Methylation as a Tool for Noninvasive Prenatal Diagnosis (NIPD) of X Chromosome Aneuploidies. <i>Journal of Molecular Diagnostics</i> , 2010, 12, 797-807.	2.8	19
31	DDX11L: a novel transcript family emerging from human subtelomeric regions. <i>BMC Genomics</i> , 2009, 10, 250.	2.8	13
32	Chromosome territory reorganization in a human disease with altered DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16546-16551.	7.1	64
33	The X-linked methyl binding protein gene Kaiso is highly expressed in brain but is not mutated in Rett syndrome patients. <i>Gene</i> , 2006, 373, 83-89.	2.2	9
34	DNA methylation 40 years later: Its role in human health and disease. <i>Journal of Cellular Physiology</i> , 2005, 204, 21-35.	4.1	108
35	In vivo analysis of DNA methylation patterns recognized by specific proteins: coupling ChIP and bisulfite analysis. <i>BioTechniques</i> , 2004, 37, 666-673.	1.8	25
36	Human Synaptobrevin-like 1 Gene Basal Transcription Is Regulated through the Interaction of Selenocysteine tRNA Gene Transcription Activating Factor-Zinc Finger 143 Factors with Evolutionary Conserved Cis-elements. <i>Journal of Biological Chemistry</i> , 2004, 279, 7734-7739.	3.4	10

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37	Longins and their longin domains: regulated SNAREs and multifunctional SNARE regulators. Trends in Biochemical Sciences, 2004, 29, 682-688.	7.5	138
38	VAMP subfamilies identified by specific R-SNARE motifs. Biology of the Cell, 2004, 96, 251-256.	2.0	23
39	DNA Methylation in X Inactivation, Imprinting, and Associated Diseases. , 2004, , 27-52.		0
40	High-resolution methylation analysis of the MLH1 promoter in sporadic endometrial and colorectal carcinomas. Cancer, 2003, 98, 1540-1546.	4.1	31
41	Folate treatment and unbalanced methylation and changes of allelic expression induced by hyperhomocysteinaemia in patients with uraemia. Lancet, The, 2003, 361, 1693-1699.	13.7	395
42	Complex Events in the Evolution of the Human Pseudoautosomal Region 2 (PAR2). Genome Research, 2003, 13, 281-286.	5.5	63
43	A dual mechanism controlling the localization and function of exocytic v-SNAREs. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9011-9016.	7.1	209
44	Allelic inactivation of the pseudoautosomal gene SYBL1 is controlled by epigenetic mechanisms common to the X and Y chromosomes. Human Molecular Genetics, 2002, 11, 3191-3198.	2.9	47
45	The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X-inactivation and contains a non-canonical splice site. Gene, 2001, 273, 285-293.	2.2	18
46	MECP2 gene mutation analysis in the British and Italian Rett Syndrome patients: hot spot map of the most recurrent mutations and bioinformatic analysis of a new MECP2 conserved region. Brain and Development, 2001, 23, S246-S250.	1.1	25
47	Mutation analysis of the MECP2 gene in British and Italian Rett syndrome females. Journal of Molecular Medicine, 2001, 78, 648-655.	3.9	51
48	Longins: a new evolutionary conserved VAMP family sharing a novel SNARE domain. Trends in Biochemical Sciences, 2001, 26, 407-409.	7.5	110
49	Human and mouse SYBL1 gene structure and expression. Gene, 1999, 240, 233-238.	2.2	8
50	Evolution of the X-Specific Block Embedded in the Human Xq21.3/Yp11.1 Homology Region. Genomics, 1999, 62, 293-296.	2.9	7
51	Escape from X Inactivation of Two New Genes Associated with DXS6974E and DXS7020E. Genomics, 1997, 43, 183-190.	2.9	17
52	Mapping of 59 EST gene markers in 31 intervals spanning the human X chromosome. Gene, 1997, 187, 179-184.	2.2	14
53	Expressed STSs and transcription of human Xq28. Gene, 1997, 187, 185-191.	2.2	2
54	A synaptobrevin-like gene in the Xq28 pseudoautosomal region undergoes X inactivation. Nature Genetics, 1996, 13, 227-229.	21.4	78

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55	Human protein kinase C iota gene (PRKCI) is closely linked to the BTK gene in Xq21.3. <i>Genomics</i> , 1995, 26, 629-631.	2.9	9
56	PCR-based immortalization and screening of hierarchical pools of cDNAs. <i>Nucleic Acids Research</i> , 1994, 22, 4806-4809.	14.5	16
57	Differential regulation by retinoic acid of the homeobox genes of the four HOX loci in human embryonal carcinoma cells. <i>Mechanisms of Development</i> , 1991, 33, 215-227.	1.7	289
58	EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, is localized at the 5' end of HOX4 locus on chromosome 2. <i>Genomics</i> , 1991, 10, 43-50.	2.9	82
59	Isolation and mapping of EVx1, a human homeobox gene homologous to even-skipped, localized at the 5' end of Hox1 locus on chromosome 7. <i>Nucleic Acids Research</i> , 1991, 19, 6541-6545.	14.5	40
60	Expression of HOX homeogenes in human neuroblastoma cell culture lines. <i>Differentiation</i> , 1990, 45, 61-69.	1.9	36
61	Human HOX genes are differentially activated by retinoic acid in embryonal carcinoma cells according to their position within the four loci. <i>Cell Differentiation and Development</i> , 1990, 31, 119-127.	0.4	62
62	Organization of human class I homeobox genes. <i>Genome</i> , 1989, 31, 745-756.	2.0	69
63	Differential expression of human HOX-2 genes along the anterior-posterior axis in embryonic central nervous system. <i>Differentiation</i> , 1989, 40, 191-197.	1.9	61
64	The human HOX gene family. <i>Nucleic Acids Research</i> , 1989, 17, 10385-10402.	14.5	334
65	Posttranscriptional control of human homeobox gene expression in induced NTERA-2 embryonal carcinoma cells. <i>Molecular Reproduction and Development</i> , 1989, 1, 107-115.	2.0	16
66	At least three human homeoboxes on chromosome 12 belong to the same transcription unit. <i>Nucleic Acids Research</i> , 1988, 16, 5379-5390.	14.5	113
67	Organization of human homeobox genes. <i>Human Reproduction</i> , 1988, 3, 880-886.	0.9	130
68	Human homeobox-containing genes in development. <i>Human Reproduction</i> , 1987, 2, 407-414.	0.9	24
69	Vamp7. <i>The AFCS-nature Molecule Pages</i> , 0, , .	0.2	1