Maurizio D'esposito

List of Publications by Year
in descending order

69	3,827	136740	123241
papers	citations	32 h-index	61 g-index

69	69	69	3950
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Transcriptomic and Epigenomic Landscape in Rett Syndrome. Biomolecules, 2021, 11, 967.	1.8	10
2	MeCP2 and Major Satellite Forward RNA Cooperate for Pericentric Heterochromatin Organization. Stem Cell Reports, 2020, 15, 1317-1332.	2.3	13
3	Epigenetic Factors that Control Pericentric Heterochromatin Organization in Mammals. Genes, 2020, 11, 595.	1.0	20
4	Interpretation of the Epigenetic Signature of Facioscapulohumeral Muscular Dystrophy in Light of Genotype-Phenotype Studies. International Journal of Molecular Sciences, 2020, 21, 2635.	1.8	18
5	ATRX Contributes to MeCP2-Mediated Pericentric Heterochromatin Organization during Neural Differentiation. International Journal of Molecular Sciences, 2019, 20, 5371.	1.8	19
6	Glycosphingolipid metabolic reprogramming drives neural differentiation. EMBO Journal, 2018, 37, .	3.5	56
7	ICF-specific DNMT3B dysfunction interferes with intragenic regulation of mRNA transcription and alternative splicing. Nucleic Acids Research, 2017, 45, 5739-5756.	6.5	42
8	Retention of Mitochondria in Mature Human Red Blood Cells as the Result of Autophagy Impairment in Rett Syndrome. Scientific Reports, 2017, 7, 12297.	1.6	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. BMC Bioinformatics, 2016, 17, 14.	1.2	10
10	MECP2, a multi-talented modulator of chromatin architecture. Briefings in Functional Genomics, 2016, 15, elw023.	1.3	59
11	X inactivation and reactivation in X-linked diseases. Seminars in Cell and Developmental Biology, 2016, 56, 78-87.	2.3	43
12	Abnormal N-glycosylation pattern for brain nucleotide pyrophosphatase-5 (NPP-5) in Mecp2-mutant murine models of Rett syndrome. Neuroscience Research, 2016, 105, 28-34.	1.0	7
13	MECP2 Duplication Syndrome: Evidence of Enhanced Oxidative Stress. A Comparison with Rett Syndrome. PLoS ONE, 2016, 11, e0150101.	1.1	22
14	Exploring the possible link between MeCP2 and oxidative stress in Rett syndrome. Free Radical Biology and Medicine, 2015, 88, 81-90.	1.3	53
15	Non-coding RNAs in chromatin disease involving neurological defects. Frontiers in Cellular Neuroscience, 2014, 8, 54.	1.8	13
16	Epigenetic control of hypoxia inducible factor-1Î±-dependent expression of placental growth factor in hypoxic conditions. Epigenetics, 2014, 9, 600-610.	1.3	36
17	Oxidative brain damage in Mecp2-mutant murine models of Rett syndrome. Neurobiology of Disease, 2014, 68, 66-77.	2.1	118
18	Global Transcriptome Profiles of Italian Mediterranean Buffalo Embryos with Normal and Retarded Growth. PLoS ONE, 2014, 9, e90027.	1.1	14

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19	Absence of TI-VAMP/Vamp7 Leads to Increased Anxiety in Mice. Journal of Neuroscience, 2012, 32, 1962-1968.	1.7	63
20	O6-methylguanine-DNA methyltransferase in equine sarcoids: molecular and epigenetic analysis. BMC Veterinary Research, 2012, 8, 218.	0.7	8
21	MeCP2 as a genome-wide modulator: the renewal of an old story. Frontiers in Genetics, 2012, 3, 181.	1.1	20
22	Partial rescue of Rett syndrome by Ï‰-3 polyunsaturated fatty acids (PUFAs) oil. Genes and Nutrition, 2012, 7, 447-458.	1.2	76
23	MeCP2 Dependent Heterochromatin Reorganization during Neural Differentiation of a Novel Mecp2-Deficient Embryonic Stem Cell Reporter Line. PLoS ONE, 2012, 7, e47848.	1.1	34
24	F4-neuroprostanes mediate neurological severity in Rett syndrome. Clinica Chimica Acta, 2011, 412, 1399-1406.	0.5	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. BMC Molecular Biology, 2011, 12, 26.	3.0	10
26	Increased levels of 4HNE-protein plasma adducts in Rett syndrome. Clinical Biochemistry, 2011, 44, 368-371.	0.8	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. Epigenetics, 2011, 6, 1242-1247.	1.3	14
28	F2-dihomo-isoprostanes as potential early biomarkers of lipid oxidative damage in Rett syndrome. Journal of Lipid Research, 2011, 52, 2287-2297.	2.0	93
29	Epigenetic alteration of microRNAs in DNMT3B-mutated patients of ICF syndrome. Epigenetics, 2010, 5, 427-443.	1.3	31
30	Differential DNA Methylation as a Tool for Noninvasive Prenatal Diagnosis (NIPD) of X Chromosome Aneuploidies. Journal of Molecular Diagnostics, 2010, 12, 797-807.	1.2	19
31	DDX11L: a novel transcript family emerging from human subtelomeric regions. BMC Genomics, 2009, 10, 250.	1.2	13
32	Chromosome territory reorganization in a human disease with altered DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16546-16551.	3.3	64
33	The X-linked methyl binding protein gene Kaiso is highly expressed in brain but is not mutated in Rett syndrome patients. Gene, 2006, 373, 83-89.	1.0	9
34	DNA methylation 40 years later: Its role in human health and disease. Journal of Cellular Physiology, 2005, 204, 21-35.	2.0	108
35	In vivo analysis of DNA methylation patterns recognized by specific proteins: coupling ChIP and bisulfite analysis. BioTechniques, 2004, 37, 666-673.	0.8	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. Journal of Biological Chemistry, 2004, 279, 7734-7739.	1.6	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.	3.7	138
38	VAMP subfamilies identified by specific R-SNARE motifs. Biology of the Cell, 2004, 96, 251-256.	0.7	23
39	DNA Methylation in X Inactivation, Imprinting, and Associated Diseases. , 2004, , 27-52.		0
40	High-resolution methylation analysis of thehMLH1 promoter in sporadic endometrial and colorectal carcinomas. Cancer, 2003, 98, 1540-1546.	2.0	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.	6.3	395
42	Complex Events in the Evolution of the Human Pseudoautosomal Region 2 (PAR2). Genome Research, 2003, 13, 281-286.	2.4	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.	3.3	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.	1.4	47
45	The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X-inactivation and contains a non-canonical splice site. Gene, 2001, 273, 285-293.	1.0	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.	0.6	25
47	Mutation analysis of the MECP2 gene in British and Italian Rett syndrome females. Journal of Molecular Medicine, 2001, 78, 648-655.	1.7	51
48	Longins: a new evolutionary conserved VAMP family sharing a novel SNARE domain. Trends in Biochemical Sciences, 2001, 26, 407-409.	3.7	110
49	Human and mouse SYBL1 gene structure and expression. Gene, 1999, 240, 233-238.	1.0	8
50	Evolution of the X-Specific Block Embedded in the Human Xq21.3/Yp11.1 Homology Region. Genomics, 1999, 62, 293-296.	1.3	7
51	Escape from X Inactivation of Two New Genes Associated with DXS6974E and DXS7020E. Genomics, 1997, 43, 183-190.	1.3	17
52	Mapping of 59 EST gene markers in 31 intervals spanning the human X chromosome. Gene, 1997, 187, 179-184.	1.0	14
53	Expressed STSs and transcription of human Xq28. Gene, 1997, 187, 185-191.	1.0	2
54	A synaptobrevinâ€“like gene in the Xq28 pseudoautosomal region undergoes X inactivation. Nature Genetics, 1996, 13, 227-229.	9.4	78

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55	Human protein kinase C iota gene (PRKCI) is closely linked to the BTK gene in Xq21.3. Genomics, 1995, 26, 629-631.	1.3	9
56	PCR-based immortalization and screening of hierarchical pools of cDNAs. Nucleic Acids Research, 1994, 22, 4806-4809.	6.5	16
57	Differential regulation by retinoic acid of the homeobox genes of the four HOX loci in human embryonal carcinoma cells. Mechanisms of Development, 1991, 33, 215-227.	1.7	289
58	EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, is localized at the 5â€² end of HOX4 locus on chromosome 2. Genomics, 1991, 10, 43-50.	1.3	82
59	Isolation and mapping of EVx1, a human homeobox gene homologus toeven-skipped, localized at the 5â€² end of Hox1 locus on chromosome 7. Nucleic Acids Research, 1991, 19, 6541-6545.	6.5	40
60	Expression of HOX homeogenes in human neuroblastoma cell culture lines. Differentiation, 1990, 45, 61-69.	1.0	36
61	Human HOX genes are differentially activated by retinoic acid in embryonal carcinoma cells according to their position within the four loci. Cell Differentiation and Development, 1990, 31, 119-127.	0.4	62
62	Organization of human class I homeobox genes. Genome, 1989, 31, 745-756.	0.9	69
63	Differential expression of human HOX-2 genes along the anterior-posterior axis in embryonic central nervous system. Differentiation, 1989, 40, 191-197.	1.0	61
64	The human HOX gene family. Nucleic Acids Research, 1989, 17, 10385-10402.	6.5	334
65	Posttranscriptional control of human homeobox gene expression in induced NTERA-2 embryonal carcinoma cells. Molecular Reproduction and Development, 1989, 1, 107-115.	1.0	16
66	At least three human homeoboxes on chromosome 12 belong to the same transcription unit. Nucleic Acids Research, 1988, 16, 5379-5390.	6.5	113
67	Organization of human homeobox genes. Human Reproduction, 1988, 3, 880-886.	0.4	130
68	Human homoeobox-containing genes in development. Human Reproduction, 1987, 2, 407-414.	0.4	24
69	Vamp7. The AFCS-nature Molecule Pages, 0, , .	0.2	1