Maurizio D'esposito

List of Publications by Year
in descending order

69 papers	3,827 citations	136950 32 h-index	123424 61 g-index
69 all docs	69 docs citations	69 times ranked	3950 citing authors

#	Article	IF	Citations
1	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
2	The human HOX gene family. Nucleic Acids Research, 1989, 17, 10385-10402.	14.5	334
3	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
4	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
5	Longins and their longin domains: regulated SNAREs and multifunctional SNARE regulators. Trends in Biochemical Sciences, 2004, 29, 682-688.	7.5	138
6	Organization of human homeobox genes. Human Reproduction, 1988, 3, 880-886.	0.9	130
7	Oxidative brain damage in Mecp2-mutant murine models of Rett syndrome. Neurobiology of Disease, 2014, 68, 66-77.	4.4	118
8	At least three human homeoboxes on chromosome 12 belong to the same transcription unit. Nucleic Acids Research, 1988, 16, 5379-5390.	14.5	113
9	Longins: a new evolutionary conserved VAMP family sharing a novel SNARE domain. Trends in Biochemical Sciences, 2001, 26, 407-409.	7.5	110
10	DNA methylation 40 years later: Its role in human health and disease. Journal of Cellular Physiology, 2005, 204, 21-35.	4.1	108
11	F2-dihomo-isoprostanes as potential early biomarkers of lipid oxidative damage in Rett syndrome. Journal of Lipid Research, 2011, 52, 2287-2297.	4.2	93
12	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.	2.9	82
13	A synaptobrevinâ€“like gene in the Xq28 pseudoautosomal region undergoes X inactivation. Nature Genetics, 1996, 13, 227-229.	21.4	78
14	Partial rescue of Rett syndrome by ï‰-3 polyunsaturated fatty acids (PUFAs) oil. Genes and Nutrition, 2012, 7, 447-458.	2.5	76
15	Organization of human class I homeobox genes. Genome, 1989, 31, 745-756.	2.0	69
16	F4-neuroprostanes mediate neurological severity in Rett syndrome. Clinica Chimica Acta, 2011, 412, 1399-1406.	1.1	68
17	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.	7.1	64
18	Complex Events in the Evolution of the Human Pseudoautosomal Region 2 (PAR2). Genome Research, 2003, 13, 281-286.	5.5	63

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19	Increased levels of 4HNE-protein plasma adducts in Rett syndrome. Clinical Biochemistry, 2011, 44, 368-371.	1.9	63
20	Absence of TI-VAMP/Vamp7 Leads to Increased Anxiety in Mice. Journal of Neuroscience, 2012, 32, 1962-1968.	3.6	63
21	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
22	Differential expression of human HOX-2 genes along the anterior-posterior axis in embryonic central nervous system. Differentiation, 1989, 40, 191-197.	1.9	61
23	MECP2, a multi-talented modulator of chromatin architecture. Briefings in Functional Genomics, 2016, 15, elw023.	2.7	59
24	Glycosphingolipid metabolic reprogramming drives neural differentiation. EMBO Journal, 2018, 37, .	7.8	56
25	Exploring the possible link between MeCP2 and oxidative stress in Rett syndrome. Free Radical Biology and Medicine, 2015, 88, 81-90.	2.9	53
26	Mutation analysis of the MECP2 gene in British and Italian Rett syndrome females. Journal of Molecular Medicine, 2001, 78, 648-655.	3.9	51
27	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
28	X inactivation and reactivation in X-linked diseases. Seminars in Cell and Developmental Biology, 2016, 56, 78-87.	5.0	43
29	ICF-specific DNMT3B dysfunction interferes with intragenic regulation of mRNA transcription and alternative splicing. Nucleic Acids Research, 2017, 45, 5739-5756.	14.5	42
30	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.	14.5	40
31	Expression of HOX homeogenes in human neuroblastoma cell culture lines. Differentiation, 1990, 45, 61-69.	1.9	36
32	Epigenetic control of hypoxia inducible factor-1Î±-dependent expression of placental growth factor in hypoxic conditions. Epigenetics, 2014, 9, 600-610.	2.7	36
33	MeCP2 Dependent Heterochromatin Reorganization during Neural Differentiation of a Novel Mecp2-Deficient Embryonic Stem Cell Reporter Line. PLoS ONE, 2012, 7, e47848.	2.5	34
34	High-resolution methylation analysis of thehMLH1 promoter in sporadic endometrial and colorectal carcinomas. Cancer, 2003, 98, 1540-1546.	4.1	31
35	Epigenetic alteration of microRNAs in DNMT3B-mutated patients of ICF syndrome. Epigenetics, 2010, 5, 427-443.	2.7	31
36	Retention of Mitochondria in Mature Human Red Blood Cells as the Result of Autophagy Impairment in Rett Syndrome. Scientific Reports, 2017, 7, 12297.	3.3	28

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37	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
38	In vivo analysis of DNA methylation patterns recognized by specific proteins: coupling ChIP and bisulfite analysis. BioTechniques, 2004, 37, 666-673.	1.8	25
39	Human homoeobox-containing genes in development. Human Reproduction, 1987, 2, 407-414.	0.9	24
40	VAMP subfamilies identified by specific R-SNARE motifs. Biology of the Cell, 2004, 96, 251-256.	2.0	23
41	MECP2 Duplication Syndrome: Evidence of Enhanced Oxidative Stress. A Comparison with Rett Syndrome. PLoS ONE, 2016, 11, e0150101.	2.5	22
42	MeCP2 as a genome-wide modulator: the renewal of an old story. Frontiers in Genetics, 2012, 3, 181.	2.3	20
43	Epigenetic Factors that Control Pericentric Heterochromatin Organization in Mammals. Genes, 2020, 11, 595.	2.4	20
44	Differential DNA Methylation as a Tool for Noninvasive Prenatal Diagnosis (NIPD) of X Chromosome Aneuploidies. Journal of Molecular Diagnostics, 2010, 12, 797-807.	2.8	19
45	ATRX Contributes to MeCP2-Mediated Pericentric Heterochromatin Organization during Neural Differentiation. International Journal of Molecular Sciences, 2019, 20, 5371.	4.1	19
46	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
47	Interpretation of the Epigenetic Signature of Facioscapulohumeral Muscular Dystrophy in Light of Genotype-Phenotype Studies. International Journal of Molecular Sciences, 2020, 21, 2635.	4.1	18
48	Escape from X Inactivation of Two New Genes Associated with DXS6974E and DXS7020E. Genomics, 1997, 43, 183-190.	2.9	17
49	Posttranscriptional control of human homeobox gene expression in induced NTERA-2 embryonal carcinoma cells. Molecular Reproduction and Development, 1989, 1, 107-115.	2.0	16
50	PCR-based immortalization and screening of hierarchical pools of cDNAs. Nucleic Acids Research, 1994, 22, 4806-4809.	14.5	16
51	Mapping of 59 EST gene markers in 31 intervals spanning the human X chromosome. Gene, 1997, 187, 179-184.	2.2	14
52	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.	2.7	14
53	Global Transcriptome Profiles of Italian Mediterranean Buffalo Embryos with Normal and Retarded Growth. PLoS ONE, 2014, 9, e90027.	2.5	14
54	DDX11L: a novel transcript family emerging from human subtelomeric regions. BMC Genomics, 2009, 10, 250.	2.8	13

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55	Non-coding RNAs in chromatin disease involving neurological defects. Frontiers in Cellular Neuroscience, 2014, 8, 54.	3.7	13
56	MeCP2 and Major Satellite Forward RNA Cooperate for Pericentric Heterochromatin Organization. Stem Cell Reports, 2020, 15, 1317-1332.	4.8	13
57	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.	3.4	10
58	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
59	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.	2.6	10
60	Transcriptomic and Epigenomic Landscape in Rett Syndrome. Biomolecules, 2021, 11, 967.	4.0	10
61	Human protein kinase C iota gene (PRKCI) is closely linked to the BTK gene in Xq21.3. Genomics, 1995, 26, 629-631.	2.9	9
62	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.	2.2	9
63	Human and mouse SYBL1 gene structure and expression. Gene, 1999, 240, 233-238.	2.2	8
64	O6-methylguanine-DNA methyltransferase in equine sarcoids: molecular and epigenetic analysis. BMC Veterinary Research, 2012, 8, 218.	1.9	8
65	Evolution of the X-Specific Block Embedded in the Human Xq21.3/Yp11.1 Homology Region. Genomics, 1999, 62, 293-296.	2.9	7
66	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.	1.9	7
67	Expressed STSs and transcription of human Xq28. Gene, 1997, 187, 185-191.	2.2	2
68	Vamp7. The AFCS-nature Molecule Pages, 0, , .	0.2	1
69	DNA Methylation in X Inactivation, Imprinting, and Associated Diseases. , 2004, , 27-52.		0