David Monk

List of Publications by Year in descending order

83 papers	5,139 citations	81900 39 h-index	95266 68 g-index
85 all docs	85 docs citations	85 times ranked	7169 citing authors

#	Article	IF	Citations
1	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	5.5	341
2	Diagnosis and management of Silverâ€“Russell syndrome: first international consensus statement. Nature Reviews Endocrinology, 2017, 13, 105-124.	9.6	336
3	Genome-wide parent-of-origin DNA methylation analysis reveals the intricacies of human imprinting and suggests a germline methylation-independent mechanism of establishment. Genome Research, 2014, 24, 554-569.	5.5	311
4	Genomic imprinting disorders: lessons on how genome, epigenome and environment interact. Nature Reviews Genetics, 2019, 20, 235-248.	16.3	291
5	Diagnosis and management of pseudohypoparathyroidism and related disorders: first international Consensus Statement. Nature Reviews Endocrinology, 2018, 14, 476-500.	9.6	224
6	Imprinting disorders: a group of congenital disorders with overlapping patterns of molecular changes affecting imprinted loci. Clinical Epigenetics, 2015, 7, 123.	4.1	174
7	Duplication of 7p11.2-p13, Including GRB10, in Silver-Russell Syndrome. American Journal of Human Genetics, 2000, 66, 36-46.	6.2	148
8	Conserved methylation imprints in the human and mouse GRB10 genes with divergent allelic expression suggests differential reading of the same mark. Human Molecular Genetics, 2003, 12, 1005-1019.	2.9	141
9	The role and interaction of imprinted genes in human fetal growth. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140074.	4.0	113
10	Epigenetic Allele Silencing Unveils Recessive RYR1 Mutations in Core Myopathies. American Journal of Human Genetics, 2006, 79, 859-868.	6.2	111
11	Genomic imprinting in the human placenta. American Journal of Obstetrics and Gynecology, 2015, 213, S152-S162.	1.3	107
12	A Screen for Retrotransposed Imprinted Genes Reveals an Association between X Chromosome Homology and Maternal Germ-Line Methylation. PLoS Genetics, 2007, 3, e20.	3.5	103
13	Genome-Wide Allelic Methylation Analysis Reveals Disease-Specific Susceptibility to Multiple Methylation Defects in Imprinting Syndromes. Human Mutation, 2013, 34, n/a-n/a.	2.5	96
14	Human Oocyte-Derived Methylation Differences Persist in the Placenta Revealing Widespread Transient Imprinting. PLoS Genetics, 2016, 12, e1006427.	3.5	94
15	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrettâ€™s Esophagus. Gastroenterology, 2015, 148, 367-378.	1.3	93
16	Reciprocal imprinting of human GRB10 in placental trophoblast and brain: evolutionary conservation of reversed allelic expression. Human Molecular Genetics, 2009, 18, 3066-3074.	2.9	92
17	Causes and Consequences of Multi-Locus Imprinting Disturbances in Humans. Trends in Genetics, 2016, 32, 444-455.	6.7	81
18	Germline-derived DNA methylation and early embryo epigenetic reprogramming: The selected survival of imprints. International Journal of Biochemistry and Cell Biology, 2015, 67, 128-138.	2.8	80

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19	Absence of Maternal Methylation in Biparental Hydatidiform Moles from Women with NLRP7 Maternal-Effect Mutations Reveals Widespread Placenta-Specific Imprinting. PLoS Genetics, 2015, 11, e1005644.	3.5	80
20	Chromosome 7p disruptions in Silver Russell syndrome: delineating an imprinted candidate gene region.. Human Genetics, 2002, 111, 376-387.	3.8	79
21	Intrauterine growth restrictionâ€"genetic causes and consequences. Seminars in Fetal and Neonatal Medicine, 2004, 9, 371-378.	2.3	77
22	Maternal repression of the human GRB10 gene in the developing central nervous system; evaluation of the role for GRB10 in Silver-Russell syndrome. European Journal of Human Genetics, 2001, 9, 82-90.	2.8	76
23	PM20D1 is aÂquantitative trait locus associated with Alzheimerâ€™s disease. Nature Medicine, 2018, 24, 598-603.	30.7	73
24	Comparative analysis of human chromosome 7q21 and mouse proximal chromosome 6 reveals a placental-specific imprinted gene, TFPI2/Tfpi2, which requires EHMT2 and EED for allelic-silencing. Genome Research, 2008, 18, 1270-1281.	5.5	72
25	Recommendations for a nomenclature system for reporting methylation aberrations in imprinted domains. Epigenetics, 2018, 13, 117-121.	2.7	70
26	The consequences of uniparental disomy and copy number neutral loss-of-heterozygosity during human development and cancer. Biology of the Cell, 2011, 103, 303-317.	2.0	68
27	EMQN best practice guidelines for the molecular genetic testing and reporting of chromosome 11p15 imprinting disorders: Silverâ€"Russell and Beckwithâ€"Wiedemann syndrome. European Journal of Human Genetics, 2016, 24, 1377-1387.	2.8	68
28	Altered expression of the imprinted transcription factor PLAGL1 deregulates a network of genes in the human IUGR placenta. Human Molecular Genetics, 2014, 23, 6275-6285.	2.9	66
29	Combined epigenetic and intraspecific variation of theDRD4andSERTgenes influence novelty seeking behavior in great titParus major. Epigenetics, 2015, 10, 516-525.	2.7	65
30	NLRPs, the subcortical maternal complex and genomic imprinting. Reproduction, 2017, 154, R161-R170.	2.6	58
31	Methylation screening of reciprocal genome-wide UPDs identifies novel human-specific imprinted genesâ€. Human Molecular Genetics, 2011, 20, 3188-3197.	2.9	55
32	Transcript- and tissue-specific imprinting of a tumour suppressor gene. Human Molecular Genetics, 2009, 18, 118-127.	2.9	54
33	Variable maternal methylation overlapping thenc886/vtRNA2-1locus is locked between hypermethylated repeats and is frequently altered in cancer. Epigenetics, 2014, 9, 783-790.	2.7	54
34	Genome-wide DNA methylation analysis of pseudohypoparathyroidism patients with GNAS imprinting defects. Clinical Epigenetics, 2016, 8, 10.	4.1	53
35	Stability of Genomic Imprinting and Gestational-Age Dynamic Methylation in Complicated Pregnancies Conceived Following Assisted Reproductive Technologies1. Biology of Reproduction, 2013, 89, 50.	2.7	49
36	The PEG13-DMR and brain-specific enhancers dictate imprinted expression within the 8q24 intellectual disability risk locus. Epigenetics and Chromatin, 2014, 7, 5.	3.9	46

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37	STOX1 is not imprinted and is not likely to be involved in preeclampsia. Nature Genetics, 2007, 39, 279-280.	21.4	45
38	A KHDC3L mutation resulting in recurrent hydatidiform mole causes genome-wide DNA methylation loss in oocytes and persistent imprinting defects post-fertilisation. Genome Medicine, 2019, 11, 84.	8.2	45
39	Prenatal molecular testing for Beckwithâ€“Wiedemann and Silverâ€“Russell syndromes: a challenge for molecular analysis and genetic counseling. European Journal of Human Genetics, 2016, 24, 784-793.	2.8	44
40	Recommendations for Diagnosis and Treatment of Pseudohypoparathyroidism and Related Disorders: An Updated Practical Tool for Physicians and Patients. Hormone Research in Paediatrics, 2020, 93, 182-196.	1.8	42
41	Genomic Imprinting of Dopa decarboxylase in Heart and Reciprocal Allelic Expression with Neighboring Grb10. Molecular and Cellular Biology, 2008, 28, 386-396.	2.3	40
42	Maternal Inheritance of a Promoter Variant in the Imprinted PHLDA2 Gene Significantly Increases Birth Weight. American Journal of Human Genetics, 2012, 90, 715-719.	6.2	40
43	Conflicting Reports of Imprinting Status of Human GRB10 in Developing Brain: How Reliable Are Somatic Cell Hybrids for Predicting Allelic Origin of Expression?. American Journal of Human Genetics, 2001, 68, 543-544.	6.2	38
44	Deciphering the cancer imprintome. Briefings in Functional Genomics, 2010, 9, 329-339.	2.7	38
45	A New Overgrowth Syndrome is due to Mutations inRNF125. Human Mutation, 2014, 35, 1436-1441.	2.5	33
46	Constitutional mosaic genome-wide uniparental disomy due to diploidisation: an unusual cancer-predisposing mechanism. Journal of Medical Genetics, 2011, 48, 212-216.	3.2	32
47	The role of ZFP57 and additional KRAB-zinc finger proteins in the maintenance of human imprinted methylation and multi-locus imprinting disturbances. Nucleic Acids Research, 2020, 48, 11394-11407.	14.5	32
48	Characterization of parent-of-origin methylation using the Illumina Infinium MethylationEPIC array platform. Epigenomics, 2018, 10, 941-954.	2.1	31
49	Wnt/Î²-catenin signaling pathway safeguards epigenetic stability and homeostasis of mouse embryonic stem cells. Scientific Reports, 2019, 9, 948.	3.3	31
50	Clinical and molecular analyses of Beckwithâ€“Wiedemann syndrome: Comparison between spontaneous conception and assisted reproduction techniques. American Journal of Medical Genetics, Part A, 2016, 170, 2740-2749.	1.2	30
51	Differences in expression rather than methylation at placenta-specific imprinted loci is associated with intrauterine growth restriction. Clinical Epigenetics, 2019, 11, 35.	4.1	29
52	Uniparental disomy of chromosome 16 unmasks recessive mutations of FA2H /SPG35 in 4 families. Neurology, 2016, 87, 186-191.	1.1	27
53	Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. Nature Communications, 2017, 8, 467.	12.8	27
54	Phenotypic spectrum and extent of DNA methylation defects associated with multilocus imprinting disturbances. Epigenomics, 2016, 8, 801-816.	2.1	26

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55	Imprinting at the PLAGL1 domain is contained within a 70-kb CTCF/cohesin-mediated non-allelic chromatin loop. Nucleic Acids Research, 2013, 41, 2171-2179.	14.5	25
56	DDC and COBL, flanking the imprinted GRB10 gene on 7p12, are biallelically expressed. Mammalian Genome, 2002, 13, 686-691.	2.2	23
57	Congenital imprinting disorders: EUCID.net - a network to decipher their aetiology and to improve the diagnostic and clinical care. Clinical Epigenetics, 2015, 7, 23.	4.1	23
58	Profiling of oxBS-450K 5-hydroxymethylcytosine in human placenta and brain reveals enrichment at imprinted loci. Epigenetics, 2018, 13, 182-191.	2.7	23
59	Human imprinted retrogenes exhibit non-canonical imprint chromatin signatures and reside in non-imprinted host genes. Nucleic Acids Research, 2011, 39, 4577-4586.	14.5	22
60	Characterization of Novel Paternal ncRNAs at the Plagl1 Locus, Including Hymai, Predicted to Interact with Regulators of Active Chromatin. PLoS ONE, 2012, 7, e38907.	2.5	21
61	Hypermethylation of the alternative AWT1 promoter in hematological malignancies is a highly specific marker for acute myeloid leukemias despite high expression levels. Journal of Hematology and Oncology, 2014, 7, 4.	17.0	21
62	Epigenetic Characterization of CDKN1C in Placenta Samples from Non-syndromic Intrauterine Growth Restriction. Frontiers in Genetics, 2016, 7, 62.	2.3	21
63	Genotype of an individual single nucleotide polymorphism regulates DNA methylation at theTRPC3alternative promoter. Epigenetics, 2011, 6, 1236-1241.	2.7	18
64	A case of intraplacental gestational choriocarcinoma; characterised by the methylation pattern of the early placenta and an absence of driver mutations. BMC Cancer, 2019, 19, 744.	2.6	17
65	Comprehensive analysis of PM20D1 QTL in Alzheimerâ€™s disease. Clinical Epigenetics, 2020, 12, 20.	4.1	16
66	Dynamic variation in allele-specific gene expression of Paraoxonase-1 in murine and human tissues. Human Molecular Genetics, 2008, 17, 3263-3270.	2.9	15
67	Tissue-specific DNA methylation profiles regulate liver-specific expression of the APOA1/C3/A4/A5 cluster and can be manipulated with demethylating agents on intestinal cells. Atherosclerosis, 2014, 237, 528-535.	0.8	15
68	APOA5 genetic and epigenetic variability jointly regulate circulating triacylglycerol levels. Clinical Science, 2016, 130, 2053-2059.	4.3	15
69	Environmentally sensitive hotspots in the methylome of the early human embryo. ELife, 2022, 11, .	6.0	15
70	Imprinted methylation profiles for proximal mouse Chromosomes 11 and 7 as revealed by methylation-sensitive representational difference analysis. Mammalian Genome, 2003, 14, 805-816.	2.2	14
71	Trans-acting genetic variants causing multilocus imprinting disturbance (MLID): common mechanisms and consequences. Clinical Epigenetics, 2022, 14, 41.	4.1	14
72	Screening individuals with intellectual disability, autism and Tourette's syndrome for KCNK9 mutations and aberrant DNA methylation within the 8q24 imprinted cluster.. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 472-478.	1.7	13

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73	Maternal mutations ofFOXF1cause alveolar capillary dysplasia despite not being imprinted. Human Mutation, 2017, 38, 615-620.	2.5	13
74	Congenital imprinting disorders: Application of multilocus and high throughput methods to decipher new pathomechanisms and improve their management. Molecular and Cellular Probes, 2015, 29, 282-290.	2.1	12
75	Human Amniocytes Are Receptive to Chemically Induced Reprogramming to Pluripotency. Molecular Therapy, 2017, 25, 427-442.	8.2	10
76	Does Genomic Imprinting Play a Role in Autoimmunity?. Advances in Experimental Medicine and Biology, 2011, 711, 103-116.	1.6	9
77	Distinct promoter methylation and isoform-specific expression of RASFF1A in placental biopsies from complicated pregnancies. Placenta, 2015, 36, 397-402.	1.5	9
78	The hypomethylation of imprinted genes in IVF/ICSI placenta samples is associated with concomitant changes in histone modifications. Epigenetics, 2020, 15, 1386-1395.	2.7	8
79	Novel genetic variants of KHDC3L and other members of the subcortical maternal complex associated with Beckwithâ€“Wiedemann syndrome or Pseudohypoparathyroidism 1B and multi-locus imprinting disturbances. Clinical Epigenetics, 2022, 14, .	4.1	7
80	Preimplantation genetic testing for a chr14q32 microdeletion in a family with Kagami-Ogata syndrome and Temple syndrome. Journal of Medical Genetics, 2022, 59, 253-261.	3.2	5
81	Nongenomic regulation of gene expression. Current Opinion in Pediatrics, 2016, 28, 521-528.	2.0	2
82	The Use of Methylation-Sensitive Multiplex Ligation-Dependent Probe Amplification for Quantification of Imprinted Methylation. Methods in Molecular Biology, 2018, 1766, 109-121.	0.9	2
83	Abstract 4021: Breaking the dogma: AWT1 hypermethylation in myeloid leukemia despite high expression. , 2012, , .		0