Marcel Mam Mannens

List of Publications by Year
in descending order

67	6,482	76196	106150
papers	citations	40 h-index	65 g-index

70	70	70	7424
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prenatal NeuN+ neurons of Down syndrome display aberrant integrative DNA methylation and gene expression profiles. Epigenomics, 2022, 14, 375-390.	1.0	1
2	DNA methylation as the link between migration and theÂmajor noncommunicable diseases: the RODAM study. Epigenomics, 2021, 13, 653-666.	1.0	5
3	Differential DNA Methylation Is Associated With Hippocampal Abnormalities in Pediatric Posttraumatic Stress Disorder. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2021, 6, 1063-1070.	1.1	8
4	Genome-wide DNA methylation analysis on C-reactive protein among Ghanaians suggests molecular links to the emerging risk of cardiovascular diseases. Npj Genomic Medicine, 2021, 6, 46.	1.7	4
5	Screening for inborn errors of metabolism in psychotic patients using Next Generation Sequencing. Journal of Psychiatric Research, 2021, 138, 125-129.	1.5	1
6	Evaluation of DNA Methylation Episignatures for Diagnosis and Phenotype Correlations in 42 Mendelian Neurodevelopmental Disorders. American Journal of Human Genetics, 2020, 106, 356-370.	2.6	171
7	Prevalence and determinants of type 2 diabetes among lean African migrants and non-migrants: the RODAM study. Journal of Global Health, 2019, 9, 020426.	1.2	20
8	Perceived discrimination and stressful life events are associated with cardiovascular risk score in migrant and non-migrant populations: The RODAM study. International Journal of Cardiology, 2019, 286, 169-174.	0.8	21
9	An inactivating mutation in the histone deacetylase SIRT6 causes human perinatal lethality. Genes and Development, 2018, 32, 373-388.	2.7	41
10	NTCP deficiency and persistently raised bile salts: an adult case. Journal of Inherited Metabolic Disease, 2017, 40, 313-315.	1.7	27
11	Truncating titin mutations are associated with a mild and treatable form of dilated cardiomyopathy. European Journal of Heart Failure, 2017, 19, 512-521.	2.9	127
12	An epigenome-wide association study in whole blood of measures of adiposity among Ghanaians: the RODAM study. Clinical Epigenetics, 2017, 9, 103.	1.8	55
13	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.	1.4	68
14	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.	1.4	44
15	The idiopathic preterm delivery methylation profile in umbilical cord blood DNA. BMC Genomics, 2015, 16, 736.	1.2	33
16	Prevalence of type 2 diabetes and its association with measures of body composition among African residents in the Netherlands â€“ The HELIUS study. Diabetes Research and Clinical Practice, 2015, 110, 137-146.	1.1	20
17	Next-generation sequencing-based genome diagnostics across clinical genetics centers: implementation choices and their effects. European Journal of Human Genetics, 2015, 23, 1142-1150.	1.4	56
18	Clinical utility gene card for: Beckwithâ€“Wiedemann Syndrome. European Journal of Human Genetics, 2014, 22, 435-435.	1.4	50

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19	Methylation analysis in tongue tissue of BWS patients identifies the (EPI)genetic cause in 3 patients with normal methylation levels in blood. European Journal of Medical Genetics, 2014, 57, 293-297.	0.7	27
20	Yield of Molecular and Clinical Testing for Arrhythmia Syndromes. Circulation, 2013, 128, 1513-1521.	1.6	132
21	Postpacing abnormal repolarization in catecholaminergic polymorphic ventricular tachycardia associated with a mutation in the cardiac ryanodine receptor gene. Heart Rhythm, 2011, 8, 1546-1552.	0.3	22
22	Novel tools for extraction and validation of disease-related mutations applied to fabry disease. Human Mutation, 2010, 31, 1026-1032.	1.1	22
23	Desmoglein-2 and Desmocollin-2 Mutations in Dutch Arrhythmogenic Right Ventricular Dysplasia/Cardiomypathy Patients. Circulation: Cardiovascular Genetics, 2009, 2, 418-427.	5.1	77
24	Determination of KCNQ1OT1 and H19 methylation levels in BWS and SRS patients using methylation-sensitive high-resolution melting analysis. European Journal of Human Genetics, 2009, 17, 467-473.	1.4	47
25	Lessons from BWS twins: complex maternal and paternal hypomethylation and a common source of haematopoietic stem cells. European Journal of Human Genetics, 2009, 17, 1625-1634.	1.4	98
26	Haplotype-Sharing Analysis Implicates Chromosome 7q36 Harboring DPP6 in Familial IdiopathicÂVentricular Fibrillation. American Journal of Human Genetics, 2009, 84, 468-476.	2.6	158
27	The RYR2-Encoded Ryanodine Receptor/Calcium Release Channel in Patients Diagnosed Previously With Either Catecholaminergic Polymorphic Ventricular Tachycardia or Genotype Negative, Exercise-Induced Long QT Syndrome. Journal of the American College of Cardiology, 2009, 54, 2065-2074.	1.2	303
28	Identification of copy number variants associated with BPES-like phenotypes. Human Genetics, 2008, 124, 489-498.	1.8	15
29	An intronic mutation leading to incomplete skipping of exon-2 in KCNQ1 rescues hearing in Jervell and Lange-Nielsen syndrome. Progress in Biophysics and Molecular Biology, 2008, 98, 319-327.	1.4	44
30	Recurrent intrauterine fetal loss due to near absence of HERG: Clinical and functional characterization of a homozygous nonsense HERG Q1070X mutation. Heart Rhythm, 2008, 5, 553-561.	0.3	58
31	Expanding Spectrum of Human RYR2 -Related Disease. Circulation, 2007, 116, 1569-1576.	1.6	211
32	Exclusion of multiple candidate genes and large genomic rearrangements in SCN5A in a Dutch Brugada syndrome cohort. Heart Rhythm, 2007, 4, 752-755.	0.3	48
33	A Novel Early Onset Lethal Form of Catecholaminergic Polymorphic Ventricular Tachycardia Maps to Chromosome 7p14-p22. Journal of Cardiovascular Electrophysiology, 2007, 18, 1060-1066.	0.8	74
34	Long QT syndrome caused by a large duplication in the KCNH2 (HERG) gene undetectable by current polymerase chain reaction-based exon-scanning methodologies. Heart Rhythm, 2006, 3, 52-55.	0.3	65
35	Hypomethylation of the H19 Gene Causes Not Only Silver-Russell Syndrome (SRS) but Also Isolated Asymmetry or an SRS-Like Phenotype. American Journal of Human Genetics, 2006, 78, 604-614.	2.6	186
36	Arrhythmogenic right ventricular cardiomyopathy due to a novel plakophilin 2 mutation: Wide spectrum of disease in mutation carriers within a family. Heart Rhythm, 2006, 3, 939-944.	0.3	40

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37	Diagnostic criteria for congenital long QT syndrome in the era of molecular genetics: do we need a scoring system?. European Heart Journal, 2006, 28, 575-580.	1.0	96
38	Plakophilin-2 Mutations Are the Major Determinant of Familial Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy. Circulation, 2006, 113, 1650-1658.	1.6	326
39	Efficient Molecular Diagnostic Strategy for ABCC6 in Pseudoxanthoma Elasticum. Genetic Testing and Molecular Biomarkers, 2004, 8, 292-300.	1.7	19
40	Mutation in the KCNQ1 Gene Leading to the Short QT-Interval Syndrome. Circulation, 2004, 109, 2394-2397.	1.6	603
41	Epigenotyping as a tool for the prediction of tumor risk and tumor type in patients with Beckwith-Wiedemann syndrome (BWS). Journal of Pediatrics, 2004, 145, 796-799.	0.9	93
42	The 2373insG mutation in the MYBPC3 gene is a founder mutation, which accounts for nearly one-fourth of the HCM cases in the Netherlands. European Heart Journal, 2003, 24, 1848-1853.	1.0	127
43	Compound Heterozygosity for Mutations (W156X and R225W) inSCN5AAssociated With Severe Cardiac Conduction Disturbances and Degenerative Changes in the Conduction System. Circulation Research, 2003, 92, 159-168.	2.0	222
44	Absence of Calsequestrin 2 Causes Severe Forms of Catecholaminergic Polymorphic Ventricular Tachycardia. Circulation Research, 2002, 91, e21-6.	2.0	358
45	Genetics of Beckwith-Wiedemann syndrome-associated tumors: Common genetic pathways. Genes Chromosomes and Cancer, 2000, 28, 1-13.	1.5	101
46	A case of methemoglobinemia type II due to NADH-cytochrome b5 reductase deficiency: Determination of the molecular basis. Human Mutation, 2000, 16, 18-22.	1.1	36
47	Molecular genetic testing for familial hypercholesterolemia: spectrum of LDL receptor gene mutations in the Netherlands. Clinical Genetics, 2000, 57, 116-124.	1.0	43
48	Molecular characterisation of 10 Dutch properdin type I deficient families: mutation analysis and X-inactivation studies. European Journal of Human Genetics, 2000, 8, 513-518.	1.4	39
49	Human SCN5A gene mutations alter cardiac sodium channel kinetics and are associated with the Brugada syndrome. Cardiovascular Research, 1999, 44, 507-517.	1.8	181
50	Homozygous Premature Truncation of the HERG Protein. Circulation, 1999, 100, 1264-1267.	1.6	67
51	Cardiac conduction defects associate with mutations in SCN5A. Nature Genetics, 1999, 23, 20-21.	9.4	549
52	Review Article: Genomic imprinting: concept and clinical consequences. Annals of Medicine, 1999, 31, 4-11.	1.5	18
53	Cytogenetic and molecular analysis of cellular atypical mesoblastic nephroma. , 1998, 21, 265-269.		16
54	The Human Chitotriosidase Gene. Journal of Biological Chemistry, 1998, 273, 25680-25685.	1.6	360

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55	A Dominant Negative Isoform of the Long QT Syndrome 1 Gene Product. Journal of Biological Chemistry, 1998, 273, 6837-6843.	1.6	82
56	The Human Achaete-Scute Homologue 2 (ASCL2, HASH2) Maps to Chromosome 11p15.5, Close to IGF2 and is Expressed in Extravillus Trophoblasts. Human Molecular Genetics, 1997, 6, 859-867.	1.4	79
57	KVLQT1, the rhythm of imprinting. Nature Genetics, 1997, 15, 113-115.	9.4	16
58	The human genome project: Deciphering the blueprint of heredity. Trends in Genetics, 1995, 11, 418-419.	2.9	0
59	Characterization of regions of chromosomes 12 and 16 involved in nephroblastoma tumorigenesis. Genes Chromosomes and Cancer, 1995, 14, 285-294.	1.5	50
60	Aniridia-associated cytogenetic rearrangements suggest that a position effect may cause the mutant phenotype. Human Molecular Genetics, 1995, 4, 415-422.	1.4	195
61	A high-resolution integrated physical, cytogenetic, and genetic map of human chromosome 11: distal p13 to proximal p15.1. Genomics, 1995, 25, 447-461.	1.3	58
62	Pericentric intrachromosomal insertion responsible for recurrence of del(11)(p13p14) in a family. Genes Chromosomes and Cancer, 1993, 7, 57-62.	1.5	12
63	Allelic loss of chromosome 1p36 in neuroblastoma is of preferential maternal origin and correlates with Nâ€“myc amplification. Nature Genetics, 1993, 4, 187-190.	9.4	147
64	Detection of a cryptic paracentric inversion within band 11p13 in familial aniridia by fluorescence in situ hybridization. Human Genetics, 1993, 91, 205-9.	1.8	13
65	Evidence that WT1 mutations in Denys â€” Drash syndrome patients may act in a dominant-negative fashion. Human Molecular Genetics, 1993, 2, 259-264.	1.4	158
66	The generation of ordered sets of cosmid DNA clones from human chromosome region 11p. Genomics, 1992, 13, 89-94.	1.3	16
67	Tumor suppressor genes in neuroblastoma. Cancer Genetics and Cytogenetics, 1992, 63, 169.	1.0	0