Michael A Levy

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11214460/publications.pdf

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20	874	686830 13	713013 21
papers	citations	h-index	g-index

22	22	22	1242
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Reducing cytogenetic testing in the era of next generation sequencing: Are we choosing wisely?. International Journal of Laboratory Hematology, 2022, 44, 333-341.	0.7	3
2	DNA methylation episignature testing improves molecular diagnosis of Mendelian chromatinopathies. Genetics in Medicine, 2022, 24, 51-60.	1.1	24
3	Novel diagnostic DNA methylation episignatures expand and refine the epigenetic landscapes of Mendelian disorders. Human Genetics and Genomics Advances, 2022, 3, 100075.	1.0	42
4	Clinical Utility of a Unique Genome-Wide DNA Methylation Signature for KMT2A-Related Syndrome. International Journal of Molecular Sciences, 2022, 23, 1815.	1.8	8
5	Clinical Utility of Implementing a Frontline NGS-Based DNA and RNA Fusion Panel Test for Patients with Suspected Myeloid Malignancies. Molecular Diagnosis and Therapy, 2022, 26, 333-343.	1.6	8
6	Detection of a DNA Methylation Signature for the Intellectual Developmental Disorder, X-Linked, Syndromic, Armfield Type. International Journal of Molecular Sciences, 2021, 22, 1111.	1.8	10
7	Clinical epigenomics: genome-wide DNA methylation analysis for the diagnosis of Mendelian disorders. Genetics in Medicine, 2021, 23, 1065-1074.	1.1	88
8	SPEN haploinsufficiency causes a neurodevelopmental disorder overlapping proximal 1p36 deletion syndrome with an episignature of X chromosomes in females. American Journal of Human Genetics, 2021, 108, 502-516.	2.6	48
9	Analysis of Sequence and Copy Number Variants in Canadian Patient Cohort With Familial Cancer Syndromes Using a Unique Next Generation Sequencing Based Approach. Frontiers in Genetics, 2021, 12, 698595.	1.1	2
10	Identification of a DNA Methylation Episignature in the 22q11.2 Deletion Syndrome. International Journal of Molecular Sciences, 2021, 22, 8611.	1.8	15
11	Deficiency of TET3 leads to a genome-wide DNA hypermethylation episignature in human whole blood. Npj Genomic Medicine, 2021, 6, 92.	1.7	11
12	Functional annotation of genomic variation: DNA methylation episignatures in neurodevelopmental Mendelian disorders. Human Molecular Genetics, 2020, 29, R27-R32.	1.4	23
13	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
14	Implementation of an NGSâ€based sequencing and gene fusion panel for clinical screening of patients with suspected hematologic malignancies. European Journal of Haematology, 2019, 103, 178-189.	1.1	21
15	Gene domain-specific DNA methylation episignatures highlight distinct molecular entities of ADNP syndrome. Clinical Epigenetics, 2019, 11, 64.	1.8	71
16	DNA methylation signatures in mendelian developmental disorders as a diagnostic bridge between genotype and phenotype. Epigenomics, 2019, 11, 563-575.	1.0	42
17	Diagnostic Utility of Genome-wide DNA Methylation Testing in Genetically Unsolved Individuals with Suspected Hereditary Conditions. American Journal of Human Genetics, 2019, 104, 685-700.	2.6	125
18	ATRX promotes gene expression by facilitating transcriptional elongation through guanine-rich coding regions. Human Molecular Genetics, 2015, 24, 1824-1835.	1.4	71

#	Article	IF	Citations
19	The SWI/SNF protein ATRX co-regulates pseudoautosomal genes that have translocated to autosomes in the mouse genome. BMC Genomics, 2008, 9, 468.	1.2	26
20	Neuronal Death Resulting from Targeted Disruption of the Snf2 Protein ATRX Is Mediated by p53. Journal of Neuroscience, 2008, 28, 12570-12580.	1.7	61