# Michael A Levy

List of Publications by Year
in descending order

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

Version: 2024-02-01

| 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 | 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 |
| 2 | 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 |
| 3 | Clinical epigenomics: genome-wide DNA methylation analysis for the diagnosis of Mendelian disorders. Genetics in Medicine, 2021, 23, 1065-1074. | 1.1 | 88 |
| 4 | ATRX promotes gene expression by facilitating transcriptional elongation through guanine-rich coding regions. Human Molecular Genetics, 2015, 24, 1824-1835. | 1.4 | 71 |
| 5 | Gene domain-specific DNA methylation episignatures highlight distinct molecular entities of ADNP syndrome. Clinical Epigenetics, 2019, 11, 64. | 1.8 | 71 |
| 6 | 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 |
| 7 | 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 |
| 8 | DNA methylation signatures in mendelian developmental disorders as a diagnostic bridge between genotype and phenotype. Epigenomics, 2019, 11, 563-575. | 1.0 | 42 |
| 9 | 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 |
| 10 | 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 |
| 11 | DNA methylation episignature testing improves molecular diagnosis of Mendelian chromatinopathies. Genetics in Medicine, 2022, 24, 51-60. | 1.1 | 24 |
| 12 | Functional annotation of genomic variation: DNA methylation episignatures in neurodevelopmental Mendelian disorders. Human Molecular Genetics, 2020, 29, R27-R32. | 1.4 | 23 |
| 13 | 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 |
| 14 | Identification of a DNA Methylation Episignature in the 22q11.2 Deletion Syndrome. International Journal of Molecular Sciences, 2021, 22, 8611. | 1.8 | 15 |
| 15 | Deficiency of TET3 leads to a genome-wide DNA hypermethylation episignature in human whole blood. Npj Genomic Medicine, 2021, 6, 92. | 1.7 | 11 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | 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 |