## Suzanne Me Lewis

## List of Publications by Year

 in descending orderSource: https:/|exaly.com/author-pdf/5411029/publications.pdf
Version: 2024-02-01


Novel diagnostic DNA methylation episignatures expand and refine the epigenetic landscapes of
Mendelian disorders. Human Genetics and Genomics Advances, 2022, 3, 100075.

Genome-wide sequencing and the clinical diagnosis of genetic disease: The CAUSES study. Human Genetics and Genomics Advances, 2022, 3, 100108.

Contribution of Multiple Inherited Variants to Autism Spectrum Disorder (ASD) in a Family with 3
Affected Siblings. Genes, 2021, 12, 1053.

Exome sequencing identified a de novo mutation of PURA gene in a patient with familial Xp22.31 microduplication. European Journal of Medical Genetics, 2019, 62, 103-108.

RAPIDOMICS: rapid genome-wide sequencing in a neonatal intensive care unitấ"successes and challenges. European Journal of Pediatrics, 2019, 178, 1207-1218.
1.3

Whole genome sequencing and variant discovery in the ASPIRE autism spectrum disorder cohort.
Clinical Genetics, 2019, 96, 199-206.

Blood Mitochondrial DNA Content in HIV-Exposed Uninfected Children with Autism Spectrum
$7 \quad$ Bisorder. Viruses, 2018, 10, 77.

The phenotypic spectrum of Schaaf-Yang syndrome: 18 new affected individuals from 14 families.
Genetics in Medicine, 2017, 19, 45-52.

Exome Sequencing and the Management of Neurometabolic Disorders. New England Journal of
Medicine, 2016, 374, 2246-2255.

Exome sequencing identifies pathogenic variants of VPS13B in a patient with familial 16p11.2
duplication. BMC Medical Genetics, 2016, 17, 78.
11 Loss-of-function mutations in<i>SCN4A</i>cause severe foetal hypokinesia or â $€^{\sim}$ classicalâ $\epsilon^{\mathrm{TM}}$ congenital
myopathy. Brain, 2016, 139, 674-691.

Identifying candidate genes for 2p15p16.1 microdeletion syndrome using clinical, genomic, and functional analysis. JCI Insight, 2016, 1, e85461.

MG-118â€...Towards understanding phenotypic variability using exome sequencing. Journal of Medical
Genetics, 2015, 52, A4.3-A5.

Functional consequences of copy number variants in miscarriage. Molecular Cytogenetics, 2015, 8, 6 .
0.4

16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. Human Molecular Genetics, 2014, 23, 6069-6080.

Copy number variants (CNVs) analysis in a deeply phenotyped cohort of individuals with intellectual disability (ID). BMC Medical Genetics, 2014, 15, 82.

Opposite effects on facial morphology due to gene dosage sensitivity. Human Genetics, 2014, 133,
1117-1125.

Phenotypic and functional consequences of haploinsufficiency of genes from exocyst and retinoic acid pathway due to a recurrent microdeletion of 2p13.2. Orphanet Journal of Rare Diseases, 2013, 8, 100.

DRD2 and PPP1R1B (DARPP-32) polymorphisms independently confer increased risk for autism spectrum
20 disorders and additively predict affected status in male-only affected sib-pair families. Behavioral and

