## Maria Pettersson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Integration of whole genome sequencing into a healthcare setting: high diagnostic rates across multiple clinical entities in 3219 rare disease patients. Genome Medicine, 2021, 13, 40.	8.2	116
2	From cytogenetics to cytogenomics: whole-genome sequencing as a first-line test comprehensively captures the diverse spectrum of disease-causing genetic variation underlying intellectual disability. Genome Medicine, 2019, 11, 68.	8.2	88
3	Low Copy Number of the AMY1 Locus Is Associated with Early-Onset Female Obesity in Finland. PLoS ONE, 2015, 10, e0131883.	2.5	70
4	Whole-Genome Sequencing of Cytogenetically Balanced Chromosome Translocations Identifies Potentially Pathological Gene Disruptions and Highlights the Importance of Microhomology in the Mechanism of Formation. Human Mutation, 2017, 38, 180-192.	2.5	58
5	Different mutations in <i>PDE4D</i> associated with developmental disorders with mirror phenotypes. Journal of Medical Genetics, 2014, 51, 45-54.	3.2	57
6	Copy Number Variants Are Enriched in Individuals With Early-Onset Obesity and Highlight Novel Pathogenic Pathways. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 3029-3039.	3.6	39
7	Comprehensive structural variation genome map of individuals carrying complex chromosomal rearrangements. PLoS Genetics, 2019, 15, e1007858.	3.5	36
8	Further evidence for specific <i>IFIH1</i> mutation as a cause of Singleton–Merten syndrome with phenotypic heterogeneity. American Journal of Medical Genetics, Part A, 2017, 173, 1396-1399.	1.2	28
9	Replicative and non-replicative mechanisms in the formation of clustered CNVs are indicated by whole genome characterization. PLoS Genetics, 2018, 14, e1007780.	3.5	28
10	Lissencephaly in an epilepsy cohort: Molecular, radiological and clinical aspects. European Journal of Paediatric Neurology, 2021, 30, 71-81.	1.6	22
11	Recombinant FVIIa in children with liver disease. Thrombosis Research, 2005, 116, 185-197.	1.7	21
12	Rare Copy Number Variants in Array-Based Comparative Genomic Hybridization in Early-Onset Skeletal Fragility. Frontiers in Endocrinology, 2018, 9, 380.	3.5	20
13	High diagnostic yield in skeletal ciliopathies using massively parallel genome sequencing, structural variant screening and RNA analyses. Journal of Human Genetics, 2021, 66, 995-1008.	2.3	19
14	Identification of three novel <i>FGF16</i> mutations in Xâ€linked recessive fusion of the fourth and fifth metacarpals and possible correlation with heart disease. Molecular Genetics & Genomic Medicine, 2014, 2, 402-411.	1.2	17
15	Targeted copy number screening highlights an intragenic deletion of <i>WDR63</i> as the likely cause of human occipital encephalocele and abnormal CNS development in zebrafish. Human Mutation, 2018, 39, 495-505.	2.5	17
16	Wholeâ€genome sequencing reveals complex chromosome rearrangement disrupting <scp><i>NIPBL</i></scp> in infant with Cornelia de Lange syndrome. American Journal of Medical Genetics, Part A, 2020, 182, 1143-1151.	1.2	17
17	<i>Alu-Alu</i> mediated intragenic duplications in <i>IFT81</i> and <i>MATN3</i> are associated with skeletal dysplasias. Human Mutation, 2018, 39, 1456-1467.	2.5	16
18	Rare copy number variants contribute pathogenic alleles in patients with intestinal malrotation. Molecular Genetics & Genomic Medicine, 2019, 7, e549.	1.2	12

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19	Cytogenetically visible inversions are formed by multiple molecular mechanisms. Human Mutation, 2020, 41, 1979-1998.	2.5	12
20	Hybrid sequencing resolves two germline ultra-complex chromosomal rearrangements consisting of 137 breakpoint junctions in a single carrier. Human Genetics, 2021, 140, 775-790.	3.8	9
21	Flanking complex copy number variants in the same family formed through unequal crossing-over during meiosis. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2018, 812, 1-4.	1.0	6
22	Whole genome sequencing unveils genetic heterogeneity in optic nerve hypoplasia. PLoS ONE, 2020, 15, e0228622.	2.5	6
23	Multiâ€omics analysis reveals multiple mechanisms causing Prader–Willi like syndrome in a family with a X;15 translocation. Human Mutation, 2022, 43, 1567-1575.	2.5	3
24	Confined placental mosaicism of Duchenne muscular dystrophy: a case report. Molecular Cytogenetics, 2020, 13, 51.	0.9	2
25	Discordant structural chromosomal aberrations in chorionic villi and amniotic fluid leading to a formation of an isochromosome 21: a case report. Molecular Cytogenetics, 2021, 14, 30.	0.9	1
26	Partial Monosomy 21 Mirrors Gene Expression of Trisomy 21 in a Patient-Derived Neuroepithelial Stem Cell Model. Frontiers in Genetics, 2021, 12, 803683.	2.3	1