Gary J Latham

List of Publications by Year
in descending order

13 papers	993 citations	933447 10 h-index	1125743 13 g-index
13 all docs	13 docs citations	13 times ranked	770 citing authors

#	Article	IF	Citations
1	A Novel Triplet-Primed PCR Assay to Detect the Full Range of Trinucleotide CAG Repeats in the Huntingtin Gene (HTT). International Journal of Molecular Sciences, 2021, 22, 1689.	4.1	8
2	A Genotype-Phenotype Study of High-Resolution FMR1 Nucleic Acid and Protein Analyses in Fragile X Patients with Neurobehavioral Assessments. Brain Sciences, 2020, 10, 694.	2.3	54
3	Comprehensive genotyping of the C9orf72 hexanucleotide repeat region in 2095 ALS samples from the NINDS collection using a two-mode, long-read PCR assay. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2019, 20, 107-114.	1.7	12
4	Use of human-derived stem cells to create a novel, in vitro model designed to explore FMR1 CGG repeat instability amongst female premutation carriers. Journal of Assisted Reproduction and Genetics, 2018, 35, 1443-1455.	2.5	1
5	A methylation PCR method determines FMR1 activation ratios and differentiates premutation allele mosaicism in carrier siblings. Clinical Epigenetics, 2016, 8, 130.	4.1	14
6	Fragile X full mutation expansions are inhibited by one or more AGG interruptions in premutation carriers. Genetics in Medicine, 2015, 17, 358-364.	2.4	119
7	The role of AGG interruptions in fragile X repeat expansions: a twenty-year perspective. Frontiers in Genetics, 2014, 5, 244.	2.3	47
8	AGG interruptions and maternal age affect FMR1 CGG repeat allele stability during transmission. Journal of Neurodevelopmental Disorders, 2014, 6, 24.	3.1	94
9	A Novel Methylation PCR that Offers Standardized Determination of FMR1 Methylation and CGG Repeat Length without Southern Blot Analysis. Journal of Molecular Diagnostics, 2014, 16, 23-31.	2.8	38
10	Fragile X AGG analysis provides new risk predictions for 45â€“69 repeat alleles. American Journal of Medical Genetics, Part A, 2013, 161, 771-778.	1.2	110
11	High-resolution methylation polymerase chain reaction for fragile X analysis: Evidence for novel FMR1 methylation patterns undetected in Southern blot analyses. Genetics in Medicine, 2011, 13, 528-538.	2.4	80
12	A Novel FMR1 PCR Method for the Routine Detection of Low Abundance Expanded Alleles and Full Mutations in Fragile X Syndrome. Clinical Chemistry, 2010, 56, 399-408.	3.2	250
13	An Information-Rich CGG Repeat Primed PCR That Detects the Full Range of Fragile X Expanded Alleles and Minimizes the Need for Southern Blot Analysis. Journal of Molecular Diagnostics, 2010, 12, 589-600.	2.8	166