

# Gary J Latham

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6828011/publications.pdf>

Version: 2024-02-01

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