

# Pathogenic variants of DNAJC12 and evaluation of the encoded cochaperone as a genetic modifier of hyperphenylalaninemia

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## HUMAN MUTATION

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## Abstract

Biallelic variants of the gene DNAJC12, which encodes a cochaperone, were recently described in patients with hyperphenylalaninemia (HPA). This paper reports the retrospective genetic analysis of a cohort of unsolved cases of HPA. Biallelic variants of DNAJC12 were identified in 20 patients (generally neurologically asymptomatic) previously diagnosed with phenylalanine hydroxylase (PAH) deficiency (phenylketonuria [PKU]). Further, mutations of DNAJC12 were identified in four carriers of a pathogenic variant of PAH. The genetic spectrum of DNAJC12 in the present patients included four new variants, two intronic changes c.298-2A>C and c.502+1G>C, presumably affecting the splicing process, and two exonic changes c.309G>T (p.Trp103Cys) and c.524G>A (p.Trp175Ter), classified as variants of unknown clinical significance (VUS). The variant p.Trp175Ter was detected in 83% of the mutant alleles, with 14 cases homozygous, and was present in 0.3% of a Spanish control population. Functional analysis indicated a significant reduction in PAH and its activity, reduced tyrosine hydroxylase stability, but no effect on tryptophan hydroxylase 2 stability, classifying the two VUS as pathogenic variants. Additionally, the effect of the overexpression of DNAJC12 on some destabilizing PAH mutations was examined and a mutation-specific effect on stabilization was detected suggesting that the proteostasis network could be a genetic modifier of PAH deficiency and a potential target for developing mutation-specific treatments for PKU.

## Keywords

**Author Keywords:** [DNAJC12](#); [hyperphenylalaninemia](#); [molecular chaperones](#); [phenylketonuria](#); [proteostasis network](#)

## KeyWords

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