

Mutation sequence analysis

Contributed by : CHU Lyon

HGVS nomenclature (NM_000295.4)

Nomenclature including the signal peptide

c.839A>T

Type of variation	Mutation Location	Genetic background	ACMG classification
AAT variant	Exon 3	M1 Val	Pathogenic

Comments

AAT variant and Q0 alleles

Variant name	Also Known as	Pathogenicity	HGVS nomenclature protéine
P _{lowell}		Deficient	p.Asp280Val

3D position of aa affected	Mobility on polyacrylamide gel	Mobility on agarose gel
The aa residue at position 280 corresponds to a point where a bêta-sheet strand (B3) undergoes a sharp turn to become an alpha-helix (G)	P	P

AATserum level (g/L)		Anti-elastolytic activity (IU/L)	
Heterozygous	Homozygous	Heterozygous	Homozygous
0.75		6688	

Comments

The Plowell variant corresponds to the Pcardiff variant with a M1Val genetic background This variant was identified at heterozygous status Plowells in a 62 year-old smoking man with emphysema. Also his brother received a liver transplant for cirrhosis.

Occurrence

Ethnic background without frequency range :

Ethnic background and frequency

Frequency range

Group tested

from (%)

To (%)

Size

Description (who was tested)

0.01

0.34

Occurrence comments

from gnomAD (2.1)

Overall comments

Occurrence comments

This variant was also identified at a heterozygous status M1Plowell in a 77-year old man presenting with liver cirrhosis of unknown etiology.

References

Medline ID

Authors

Title

2240842

Holmes MD,Brantly
ML,Crystal RG

Molecular analysis of the heterogeneity among the
P-family of alpha-1-antitrypsin alleles.

Journal

Year

Volume

Num

Pp

The American review of respiratory
disease

1990

142

5

1185-92

Last Update

First publication : 07-04-2020 22:33 Last update : 08-10-2020 17:23 by Pr Curateur test