

Mutation sequence analysis

Contributed by : CHU Lyon

HGVS nomenclature (NM_000295.4)

Nomenclature including the signal peptide

c.187C>T

Type of variation	Mutation Location	Genetic background	ACMG classification
AAT variant	Exon 2	Unknown	Pathogenic

Comments

rs28931570

AAT variant and Q0 alleles

Variant name	Also Known as	Pathogenicity	HGVS nomenclature protéine
I		Deficient Precipitating Dysfunctional	p.Arg63Cys
3D position of aa affected		Mobility on polyacrylamide gel	Mobility on agarose gel
		I	I
AATserum level (g/L)		Anti-elastolytic activity (IU/L)	
Heterozygous	Homozygous	Heterozygous	Homozygous
0.95-1.82		15140	

Comments

May act indirectly on beta-sheet A stability by perturbing helix A/G-core-packing.

Occurrence

Ethnic background without frequency range :

Ethnic background and frequency				
Frequency range		Group tested		
from (%)	To (%)	Size	Description (who was tested)	
0.30	0.67			
Occurrence comments				
Overall comments				
Occurrence comments				
The polymerization rate of the I variant being very weak, there is no associated hepatic disorder.				
References n°1				
Medline ID	Authors		Title	
10194472	Mahadeva R,Chang WS,Dafforn TR,Oakley DJ,Foreman RC,Calvin J,Wight DG,Lomas DA		Heteropolymerization of S, I, and Z alpha1-antitrypsin and liver cirrhosis.	
Journal	Year	Volume	Num	Pp
The Journal of clinical investigation	1999	103	7	999-1006
References n°2				
Medline ID	Authors		Title	
2606478	Graham A,Kalsheker NA,Newton CR,Bamforth FJ,Powell SJ,Markham AF		Molecular characterisation of three alpha-1-antitrypsin deficiency variants: proteinase inhibitor (Pi) nullcardiff (Asp256----Val); PiMmalton (Phe51----deletion) and PiI (Arg39----Cys).	
Journal	Year	Volume	Num	Pp
Human genetics	1989	84	1	55-8
Last Update				
First publication : 01-19-2020 21:12 Last update : 02-11-2020 20:42 by Pr Curateur test				