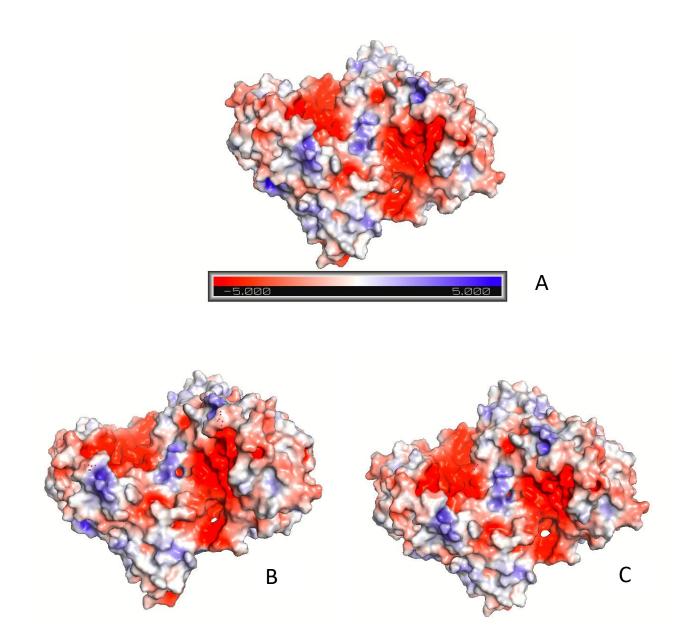


Fig 1.  $\alpha$ -Gal A three-dimensional structural map of the two novel amino acid substitutions together with the two active sites (spheres) in the A and B chains of the enzyme. Pymol



Fig. 2. Alignment of wild-type human  $\alpha$ -Gal A amino acids with other organisms sequences. The rectangles indicates the amino acids at position 211 and 360 that we found mutated in the index cases.



**Fig 3.** Electrostatic Surface potencial of the mutant proteins, products of the novel missense variants. The color scale ranges from -5KT/e (red) to 5 KT/e (blue). A) Wild type protein; B) p.Phe211Ser; C) p. Gly360Ala. Alterations in the potential of the electrostatic surface in the mutant proteins are observed.

Variant	Tool	p.Phe211Ser	p.Gly360Ala
		(c.632T>C)	(c.1079G>C)
SIFT		Tolerated	Deleterious
Poly-Phen2		Benign	Probably damaging
FATHMM		Harmful	Harmful
M-CAP		Harmful	Harmful
MetaLR		Harmful	Harmful
MetaSVM		Harmful	Harmful
<b>Mutation Assessor</b>		Moderate	Moderate
Mutation Taster		Neutral	Harmful
PROVEAN		Neutral	Harmful
SNP & GO		Disease causing	Disease causing
SAAP		No effects	Pathogenic
PhD - SNP		Benign	Benign

Table 1. Predictions of the effect of novel variants on  $\alpha\textsc{-}\mathsf{Gal}\textsc{-}\mathsf{A}$  protein.