Table 1: Summary of the prediction tools used in this study

Name	Type	Deleterious	Reference
SIFT	Conservation	<0.05	[17]
PolyPhen	Conservation, Protein structure, Protein sequence annotation	>0.15	[18]
SNAP	Conservation, Structural annotation	Non-neutral	[22]
SNPs&GO	Protein sequence, Functional annotation	>0.5	[23]
PANTHER	Protein sequence	<-3	[21]
PhD-SNP	Protein sequence		[19]
FATHMM	Conservation, protein sequence annotation	<-0.75	[20]
I-Mutant	Sequence	<-0.5	[26]