



Corrigendum: Correction of Table

# Identification of Maturity-Onset Diabetes of the Young Caused by Glucokinase Mutations Detected Using Whole-Exome Sequencing

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In the published article, there was an incorrect amino acid change in Table 1. The “p.Ser383Pro” should be changed to “p.Ser383Leu.” The corrected table is shown below.

**Table 1.** Bioinformatics Analysis of *GCK* Mutations

Case	<i>GCK</i> exon	PolyPhen-2/SIFT prediction	Amino acid change	DUET predicted stability changes ( $\Delta\Delta G$ )	Reference
Family 1	2	1/Damaging	c.92T>C, p.Leu30Pro	-2.175 Kcal/mol (Destabilizing)	[6]
Family 2	9	1/Damaging	c.1151C>T, p.Ser383Leu	-0.465 Kcal/mol (Destabilizing)	[6]

Two mutations were predicted to be deleterious using online prediction tools. DUET is a web server that uses an integrated computational approach to study missense mutations in proteins; it is available at <http://structure.bioc.cam.ac.uk/duet>.

*GCK*, glucokinase; PolyPhen-2, polymorphism phenotyping v2.

We would like to apologize for any inconvenience or misunderstanding.

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