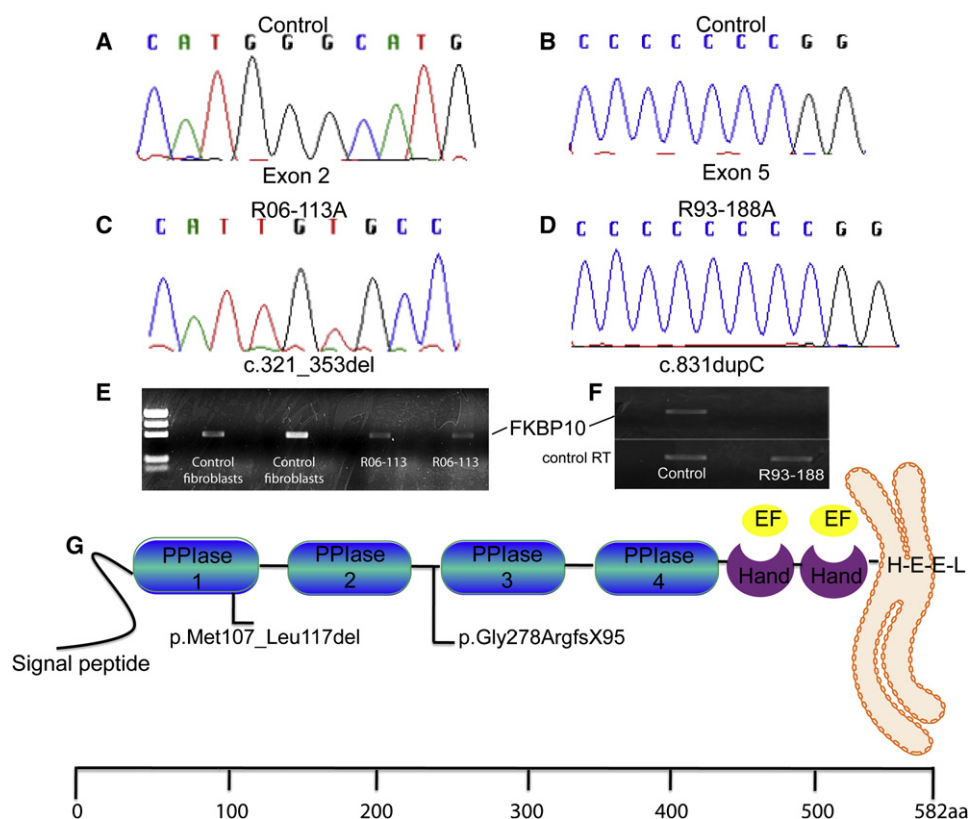


# Mutations in the Gene Encoding the RER Protein FKBP65 Cause Autosomal-Recessive Osteogenesis Imperfecta

Yasemin Alanay, Hrispima Avaygan, Natalia Camacho, G. Eda Utine, Koray Boduroglu, Dilek Aktas, Mehmet Alikasifoglu, Ergul Tuncbilek, Diclehan Orhan, Filiz Tiker Bakar, Bernard Zabel, Andrea Superti-Furga, Leena Bruckner-Tuderman, Cindy J.R. Curry, Shawna Pyott, Peter H. Byers, David R. Eyre, Dustin Baldrige, Brendan Lee, Amy E. Merrill, Elaine C. Davis, Daniel H. Cohn, Nurten Akarsu, and Deborah Krakow\*

(American Journal of Human Genetics, 86, 551–559)

On page 555 under the section titled *Mutations in FKBP10 cause Recessive OI*, there are two errors in the nomenclature for the identified mutations. The *FKBP10* (NM\_021939.3) mutation isolated in the Turkish cases (proband R06-113A) is c.321\_353 del and is predicted to result in the deletion of eleven amino acids in the protein, p.Met107\_Leu117 del. In the second paragraph of the subheading, the mutation in the Mexican-American family (proband R93-188) should be



**Figure 4. FKBP10 Mutation Detection**

(A and B) Sequence analysis of exon 2 in control and a representative affected individual (R06-113A) with the mutation in the Turkish families.

(C and D) Exon 5 sequence analysis in control and a representative affected individual (R93-188A) with the mutation in the Mexican-American family (R93-188A).

(E) RT-PCR of FKBP10 cDNA from control and R06-113A fibroblasts showing that a FKBP10 cDNA is synthesized.

(F) RT-PCR of FKBP10 cDNA from control and R93-188A fibroblasts showing that a FKBP10 cDNA is not synthesized; lower band demonstrates control cDNA synthesis.

(G) Cartoon of the FKBP65 molecule with predicted protein consequences for each mutation. PPIase, peptidyl-prolyl cis-trans isomerase; EF/Hand domain; HEEL, putative ER-retention sequence.

\*Correspondence: [dkrakow@mednet.ucla.edu](mailto:dkrakow@mednet.ucla.edu)

DOI 10.1016/j.ajhg.2010.09.002. ©2010 by The American Society of Human Genetics. All rights reserved.

identified as c.831 dupC, which changes the glycine at position 278 to an arginine, and is predicted to result in a stop codon 94 amino acids downstream, p.Gly278ArgfsX95. The appropriate nomenclature modifications have been made to [Figure 4](#). Note that the change in nomenclature also applies to the *Response to Shaheen et al.*<sup>1</sup> The authors regret the error.

## Reference

1. Alanay, Y., and Krakow, D. (2010). Response to Shaheen et al. *Am. J. Hum. Genet.* 87, 306–308.