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Supplemental Data

Mutations in *LARS2*, Encoding Mitochondrial

Leucyl-tRNA Synthetase, Lead to Premature

Ovarian Failure and Hearing Loss in Perrault Syndrome

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Figure S1. Alignments to Human and *E. coli* Leucine-Specific Domains

The HHblits algorithm was used to generate alignments to the human LARS2 (A) and *E. coli* LeuRS (B) leucine-specific domains. The query sequences (top line of each alignment) were anchored by conserved sequences QG at the N-terminal end and by the KMSKS motif at the C-terminal end. Columns for which no residue was present in the query sequence were removed and the alignments were displayed with Jalview.¹ The consensus sequences for the region including HARS2 p.Thr522 and LeuRS p.Ala508 (indicated by asterisk) are identical (underlined).

Reference

1. Waterhouse, A.M., Procter, J.B., Martin, D.M., Clamp, M., and Barton, G.J. (2009) Jalview Version 2 - a multiple sequence alignment editor and analysis workbench. *Bioinformatics*. 25, 1189-1191.