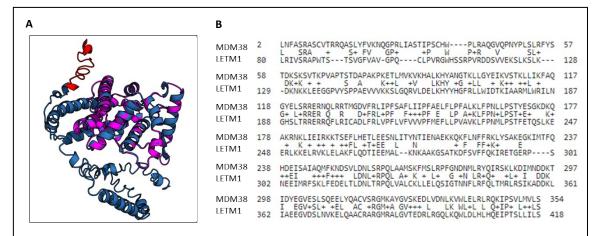
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Supplementary figure. 1 A mammalian homolog Letm1p of Mdm38p and a 3-D model of mdm38p

A, An alignment with MDM38 ribosomal binding domain (PDB:3SKQ). The model (Blue) aligned with the solved structure of the ribosomal binding domain (magenta) the predicted TM domain is in red (aa136-157). This model indicates that the majority of the protein resides in the matrix and its function may be linked to its ribosomal binding activity; B, A protein alignment between mammalian homolog LETM1. I-tasser was used for the model and Blast for the alignment.