

Article

# Tristetraprolin/ZFP36 Regulates the Turnover of Autoimmune-Associated HLA-DQ mRNAs

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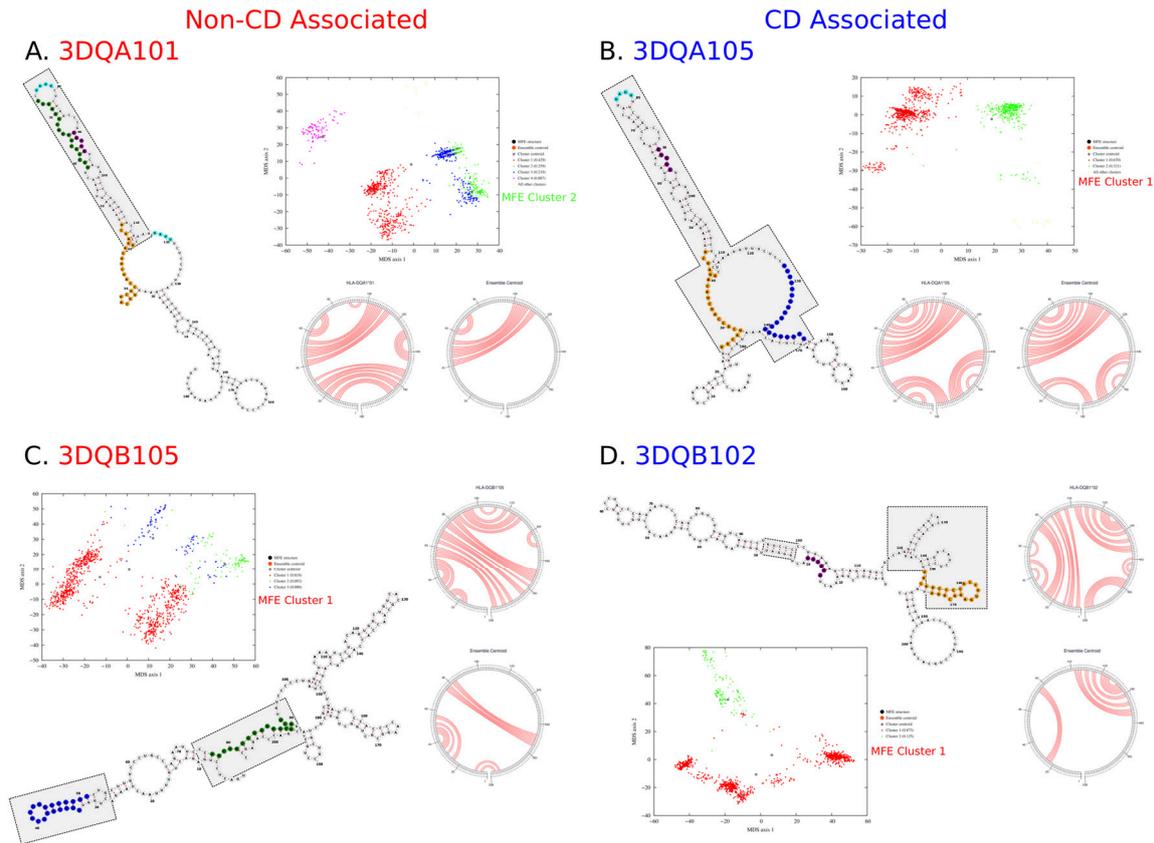
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**Figure S1.** Sfold Structure Comparison of 3'UTR of DQA1\* and DQB1\*. Each of the riboprobe sequences was analysed with Sfold to predict statistical ensembles of structures. The ensembles permit many different conformations of the structures and clustering indicating the most likely conformations adopted by each sequence. The minimum-free energy (MFE) structure is also predicted and its parent cluster identified. **A.** 3DQA101, **B.** 3DQA105, **C.** 3DQB105 and **D.** 3DQB102 show the ensemble structures to contain fewer conserved base pairings (grey boxes) than the MFE structure indicating the structure is more dynamic/flexible outside of these regions. This is particularly evident in **D.** 3DQB102 where there is little conservation of base pairings in the large stem as seen in the other structures.

