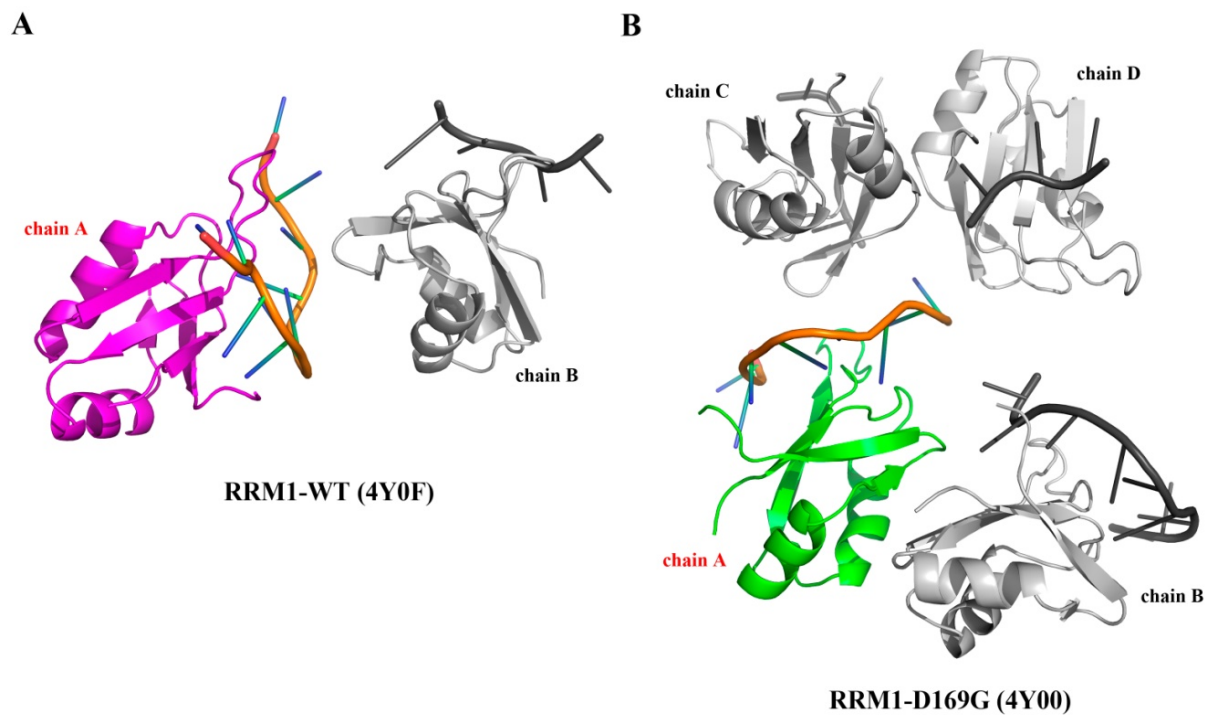


Supplementary Information

Structural analysis of disease-related TDP-43 D169G mutation: linking enhanced stability and caspase cleavage efficiency to protein accumulation

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Supplementary data: Supplementary Figure 1



Supplementary Figure 1. The overall crystal structures of RRM1-WT and RRM1-D169G. (A) The final refined model of RRM1/DNA complex contains two RRM1 polypeptide chains (chain A and B) and two single-stranded DNA per asymmetric unit. The PDB accession code for RRM1/DNA complex is 4Y0F. (B) The final refined model of RRM1-D169G/DNA complex contains four RRM1 polypeptide chains (chain A to D) and four single-stranded DNA per asymmetric unit. The PDB accession code for RRM1-D169G/DNA complex is 4Y00. For clarity, only a single RRM1/DNA (chain A in magenta) and RRM1-D169G/DNA (chain A in green) were used for structural presentation and comparison.