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CM2D3

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Supplementary material to:

CM2D3: Furnishing the human interactome with structural models of protein complexes derived by comparative modeling and docking.

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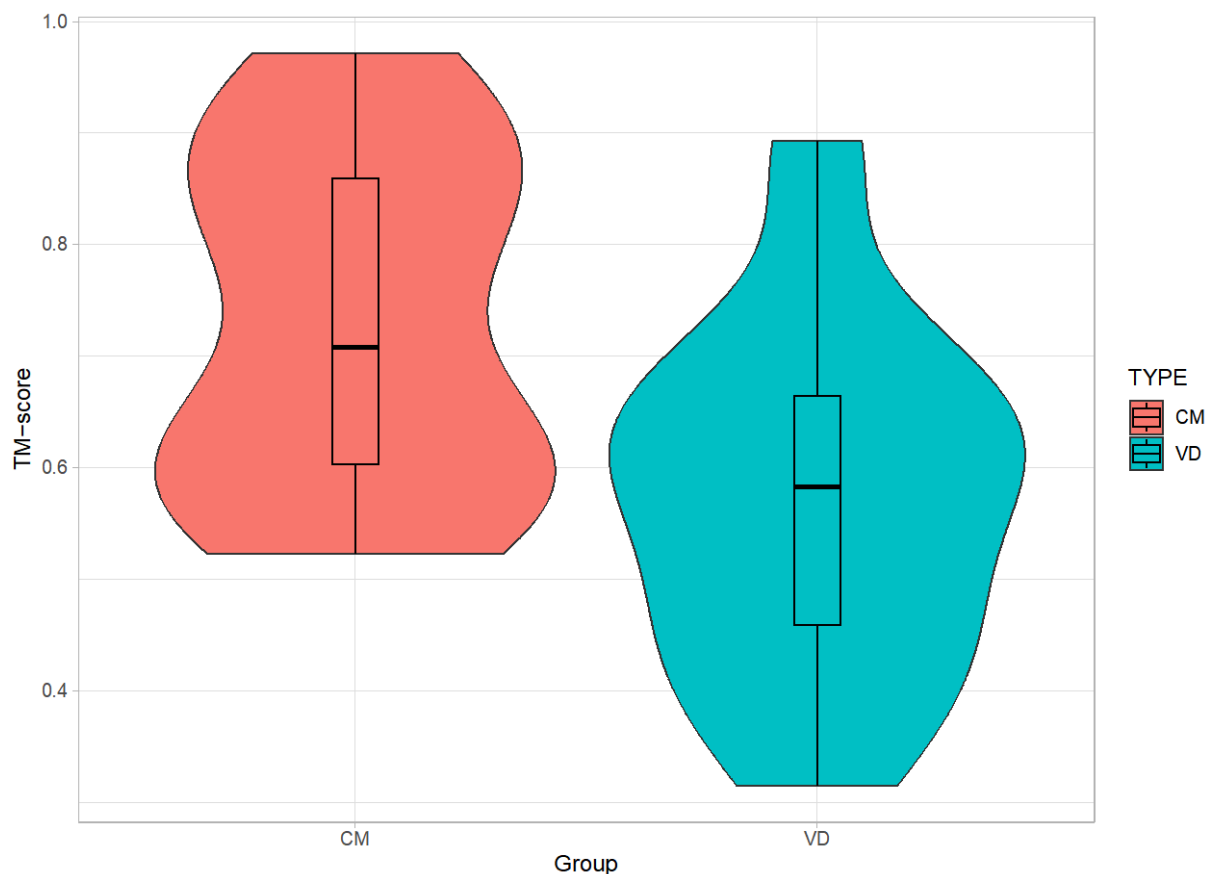


Figure 1. Violin plots of TM-Scores. Distribution of TM-scores comparing AF2[1] and MODPIN models (CM)[2] and AF2[1] and V2DOCK (VD)[3]. The TM-scores were obtained using MM-align[4].

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