

Conformational flexibility of a free and TCR-bound pMHC-I protein investigated by
long-term molecular dynamics simulations

Supplementary Material

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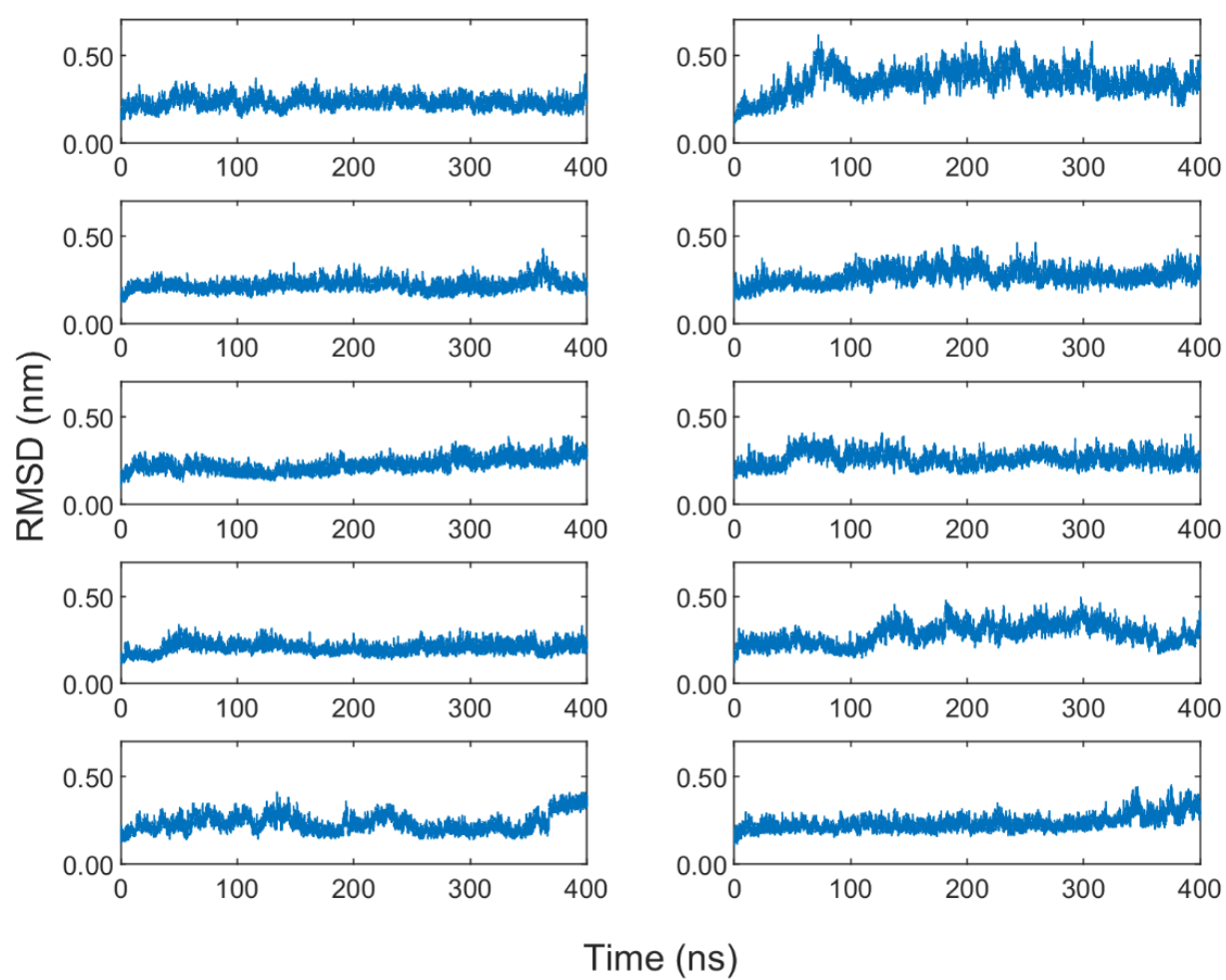


Fig. S1 Time courses of C_{α} RMSD-values of 10 independent MD simulations of the whole pMHC-TCR complex.

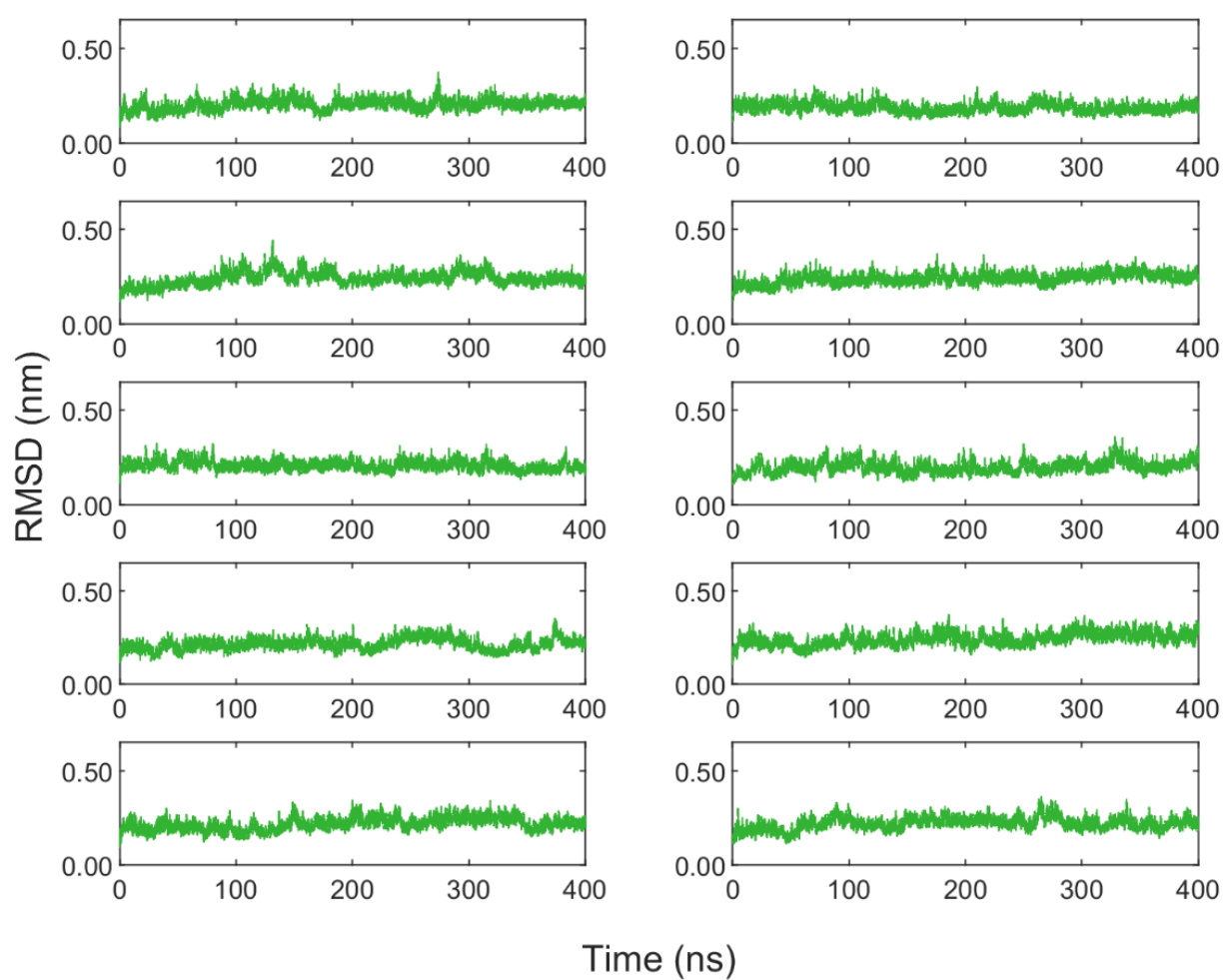


Fig. S2 Time courses of C_{α} RMSD-values of 10 independent MD simulations of the free pMHC system.