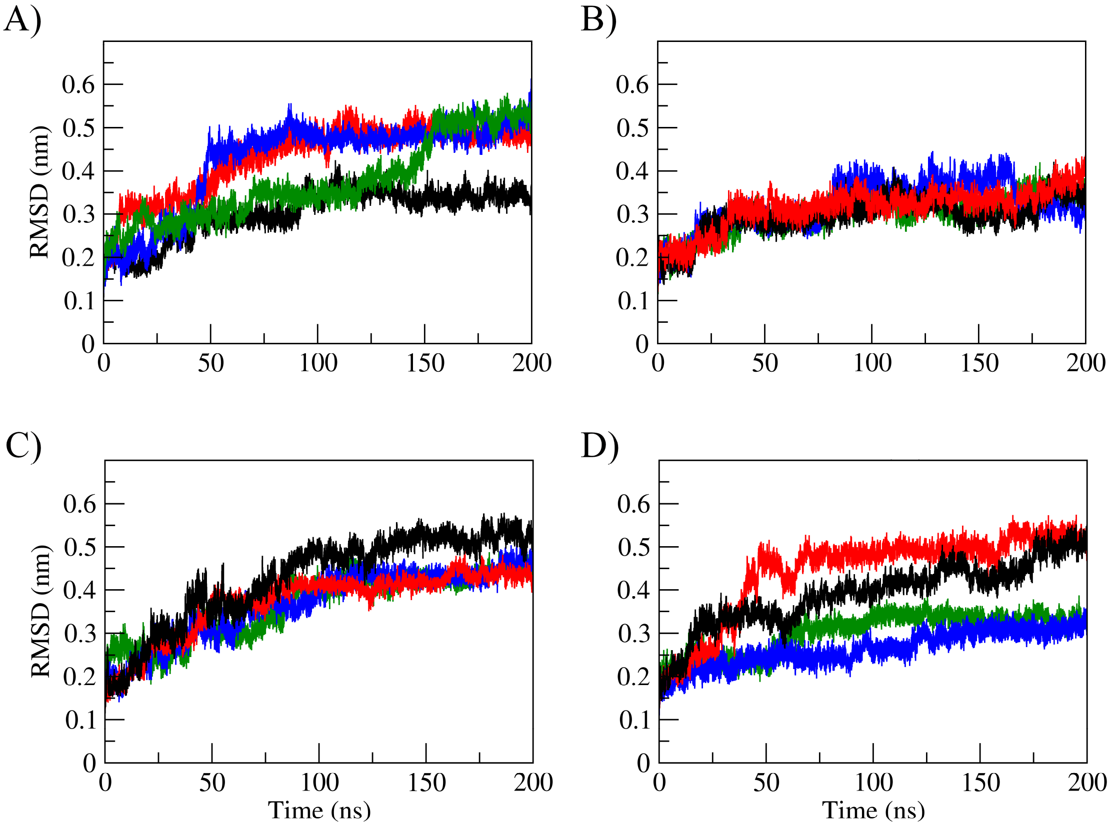

Fig. S5. All-atom root mean square deviation (RMSD) measured for Fel d 1 segments corresponding to the original chain regions (fused in the crystallized protein). (A) Calcium-free system; (B) Calcium-bound system; (C) Minimally glycosylated system; (D) Fully glycosylated system. Region A_1 in black, region A_2 in red, region B_1 in blue, region B_2 in green.