Table S1. Average Cα-RMSDs and standard deviations (in parenthesis) calculated for whole protein(s) are shown for different simulation systems. The difference from Table 2 is that here not domains but whole protein(s) (*e.g.*, FVIIa, sTF, and sTF:FVIIa) are superimposed and Cα-RMSDs are calculated for the superimposed, whole protein(s), respectively.

The Cα-RMSDs of FVIIa (12.34 Å in solution, 7.11 Å on the membrane, and 2.94 Å on the membrane as the complex) also show clearly that sTF "lock"s FVIIa (cf. *Locking effect of sTF on the rocking motion of FVIIa* in **Results and Discussion**).

System		Environment	Cα-RMSD (Å) Mean (SD)
FVIIa		Solution	12.34 (3.91)
sTF		Solution	3.03 (0.45)
FVIIa		Membrane	7.11 (2.01)
sTF		Membrane	2.37 (0.43)
sTF:FVIIa	of sTF:FVIIa	Membrane	2.94 (0.41)
FIIA	of sTF:FVIIa	Membrane	2.88 (0.43)
sTF	of sTF:FVIIa	Membrane	2.61 (0.45)