## Membrane protein mobility depends on the length of extra-membrane domains and on protein concentration - Supplementary Information

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FIG. 1: Representative time-averaged mean square displacement (MSD) obtained for a single anchored protein (left panel) and a single transmembrane proteins (right panel) within one simulation run (i.e. no ensemble averaging was applied). Shown are four different conditions with the indicated extra-membrane domain lengths, L, and area fractions,  $\phi$ , occupied by the proteins. At small times DPD-typical remnants of an initially ballistic motion can be seen while for intermediate and long times a linear scaling is observed (indicated by dotted lines). Protein diffusion coefficients D were determined in the linear regime by fitting the data with a function MSD = 4Dt.



FIG. 2: Normalized friction coefficent  $\gamma/\gamma_0$  for anchored proteins (left panel) and for transmembrane proteins (right panel) plotted against the extra-membrane domain's length, L, for protein densities  $\phi=0.0594$ , 0.1188, 0.1782, 0.2376, 0.2970, 0.3564 (shown as red, blue, grey, orange, green, magenta symbols). Data and color-coding are identical to Fig. 2a and Fig. 3a of the main manuscript, but are displayed here individually without shift and with error bars; lines again represent global fits according to Eq. (2). Error bars are only shown when being larger than the symbol size.



FIG. 3: Normalized friction coefficient  $\gamma/\gamma_0$  for anchored proteins (left panel) and for transmembrane proteins (right panel) plotted against the protein occupancy,  $\phi$ , for domain lengths L=1.45nm, 2.35nm, 3.25nm, 5.05nm, 7.3000nm (shown as red, blue, grey, orange, green symbols). Data and color-coding are identical to Fig. 2b and Fig. 3b of the main manuscript, but are displayed here individually without shift and with error bars; lines again represent global fits according to Eq. (2). Error bars are only shown when being larger than the symbol size.