S1 Table Diffusion coefficients

System	**Diffusion coefficient** in 10^{-7} cm^2/s		
	CXCR4	**CCR5**	**CCR2**
POPC (monomer)	0.44±0.14	0.37±0.11	0.36±0.10
POPC (homodimerization)	0.51±0.13	0.48±0.13	0.47±0.13
POPC/10% chol (monomer)	0.33±0.03	0.25±0.05	0.29±0.09
POPC/30% chol (homodimerization)	0.26±0.06	0.23±0.06	0.23±0.06

Protein self-diffusion coefficients. According to the Einstein relation:

$$D_s = \lim_{t\to\infty} \frac{\langle \Delta r(t)^2 \rangle}{4t},$$

the lateral self-diffusion of proteins was calculated from the slope of the mean square displacement (MSD) averaged over all beads of each protein. Here, $\Delta r(t)$ denotes the distance a bead moved in time t. The MSD was calculated for the inital 200 ns of the simulations. In case of dimerization simulations, the MSD was calculated for simulations that did not show interaction energies between the monomers until 250 ns. For calculations of the MSD, the center of mass motion of the protein-membrane system was substracted. The slope of MSD curves was fitted on the time window between 5-20 ns. Data for CXCR4 was taken from Pluhackova *et al.*, PLoS Comput Biol, 2016;12(11):e1005169.