Supplementary Material

Protein Coverage Determination

From the measured refractive indices of the adsorbed protein films, we determined the protein surface density (#/m^2), using one of two different approaches.

Method 1. This approach, which is described in the main text, follows the method described by Vöros (1), and assumes a linear relationship between the protein coverage and refractive index of the adsorbed protein film, according to $n_{meas} = n_b + \left(dn/dc\right)_p dc_p$ where n_b is the refractive index of the buffer, dn/dc is the refractive index increment of the protein, and dc_p is the change in adsorbed protein in mg/m^2. Measured values for the refractive index increment of different adsorbed proteins are between 0.182 and 0.187 for a compact globular protein (1). By solving for dc_p, one determines the mass of protein adsorbed per area. Using the molecular weight of the monomer (or tetramer), one can thus estimate the monomer (or tetramer) density on the bilayer.

Method 2. According to the Cauchy equation, the refractive index is a linear relationship of the volume fractions and refractive indices of the two components in the protein layer (protein and buffer): $n_{meas} = x_p n_p + \left(1 - x_p\right) n_b$ where x_p is the volume fraction of the protein, n_p is the refractive index of the protein, and n_b is the refractive index of the buffer. With refractive indices of 1.46 for the protein (2) and 1.33 for the buffer, x_p is determined from the measured refractive index of the adsorbed protein film.

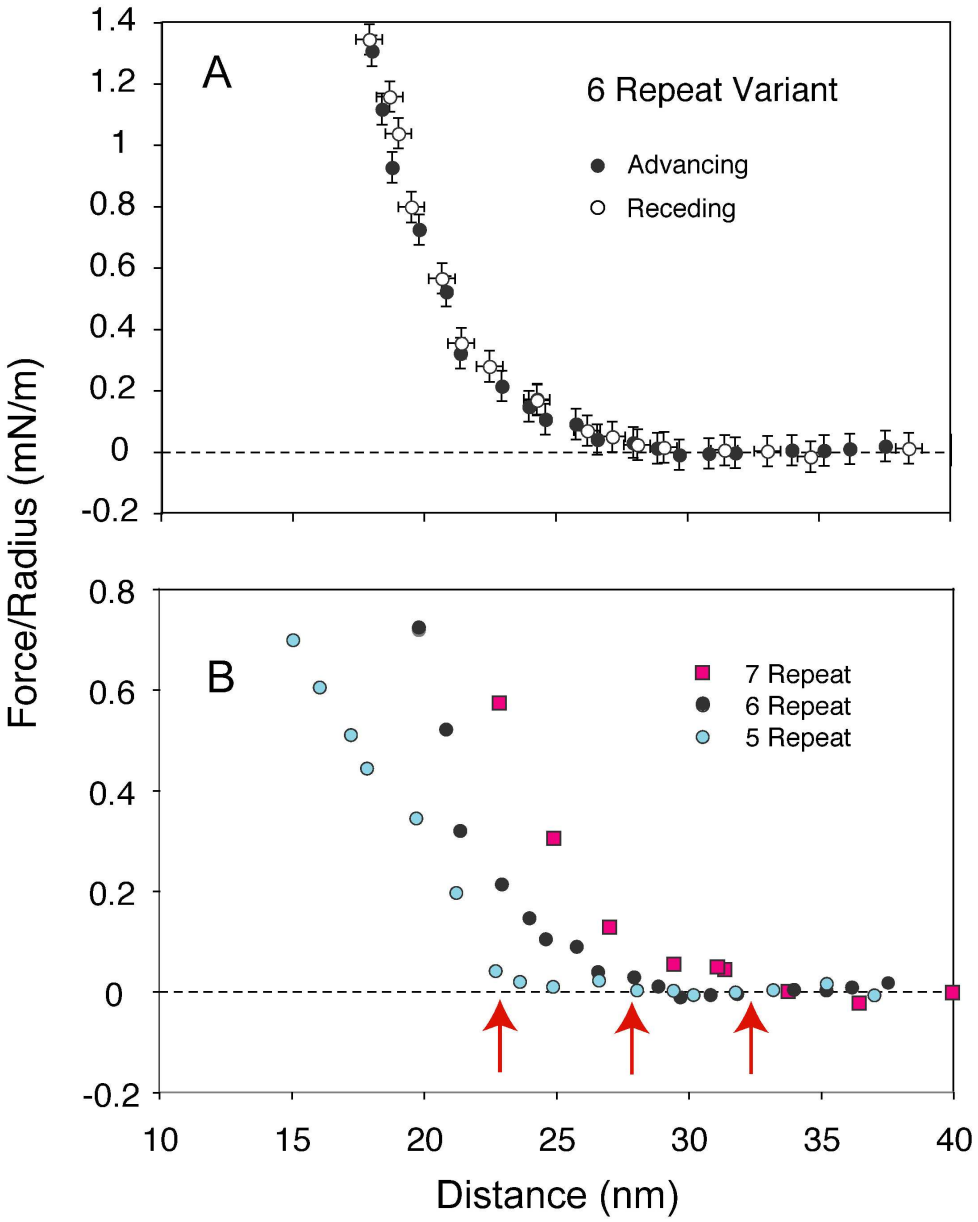
To convert the volume fraction to protein coverage, we use the measured thickness of the protein film l_p, determined from surface force apparatus measurements. The protein volume (nm^3) is estimated, by assuming that the tetramer occupies a cone of length l_p with base area of ~48nm^2. This is used to estimate the protein surface density (proteins/m^2) from the total volume fraction occupied by the protein. Surface densities determined by this method, which was also used to determine the DC-SIGN coverage in a previous publication (3), are summarized in Table S1. The number of monomers per area is the number of tetramers/area multiplied by four (7 repeat and 6 repeat forms).

The surface densities estimated by method 2 are ~30% higher than those obtained by using method 1. The differences between methods 1 and 2 lie in the relationships between the refractive index and protein concentration, as well as in the assumed parameters n_p and dn/dc for the protein. Because of the uncertainty in assigning a volume for the dimer of the 5-repeat form of DC-SIGNR, as well as the unknown distribution of dimers and tetramers on the bilayer, this approach was not used to compare the adhesion energies per monomer of the DC-SIGNR variants as in Figure 3A (main text).

Table S1. Protein coverage for the DC-SIGNR variants and DC-SIGN (Method 2)

Protein	Protein molecules per unit area (molecules/m^2)	Monomer per unit area (monomer/m^2)
DC-SIGNR - 7	$8.1 \pm 0.4 \times 10^7$	$5.0 \pm 0.2 \times 10^8$
DC-SIGNR - 6	$3.7 \pm 0.5 \times 10^7$	$2.1 \pm 0.2 \times 10^8$
DC-SIGN	$8.5 \pm 0.2 \times 10^7$	$4.7 \pm 1.0 \times 10^8$

Figure S1. Normalized force (F/R) versus distance curves between the DC-SIGNR and a bare supported bilayer. (A) Advancing (black circles) and receding (white circles) measured between the 6-repeat DC-SIGNR variants and a bare lipid bilayer without ligand. The advancing and receding curves superimpose, and there is no adhesion. (B) Advancing force versus distance curves measured between a bare membrane and the 5-repeat (blue circles), 6-repeat (black circles), and 7-repeat (red squares) DC-SIGNR length variants. The arrows indicate the distances at which the repulsive force exceeded the standard deviation of 0.05mN/m. This defined the thickness D_T in the absence of ligand. The colors of the arrows correspond to the symbols for the corresponding measurements.



References:

1. Vöros, J. (2004) *Biophys. J.* **57**, 553-561
2. Vaknin, D, Als-Nielsen, J, Piepenstock, M, and Lösche, M. (1991) *Biophysical journal* **60**, 1545-1552
3. Menon, S, Rosenberg, K, Graham, SA, Ward, EM, Taylor, ME, Drickamer, K, and Leckband, DE. (2009) *Proc. Natl. Acad. Sci. U S A* **106**, 11524-11529