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*Cover picture:* Transformation of the structure of bacterial adhesin OpcA upon removal of the crystal contacts and crystallization agents. (*Left*) The conformation of OpcA resolved in the crystal structure. Loops 1 (*cyan*) and 2 (*red*) form a crevice that was proposed to harbor a binding site for proteoglycan receptors of host cells. Zinc ions (*orange*), which were required for protein crystallization, are shown as vdW spheres. (*Right*) The conformation of OpcA in a lipid bilayer membrane obtained from a 16-ns molecular dynamics simulation carried out in the absence of the zinc ions and crystal contacts. The crevice between loops 1 and 2 is no longer evident. See article by Luan et al. on page 3058.