λ-Phage Docking Observed at the Single-Particle Level

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We report direct real-time detection of phage lambda docking to its bacterial receptor Maltoporin, a sugar-specific porin of *Escherichia coli* and *Shigella sonnei*, in a planar lipid bilayer. Phage binding affects both ion permeation and sugar molecules' dynamics in a single Maltoporin channel. Added from the *cis*-side, trimeric Maltoporin directionally inserts into a lipid bilayer. In the absence of substrate, the channel is predominantly open, but becomes transiently blocked when maltohexaose is added to the *cis*-, *trans*-, or both sides of the bilayer. Wild type phage lambda, added to the *cis*-side of the bilayer, spontaneously and irreversibly binds to the channel, reducing its ion conductance and completely blocking the *cis*-side sugar entryway of

all three receptor monomers. From the *trans*-side, sugar molecules still have access to the sugar-binding regions of the Maltoporin pores, however, the residence time of maltohexaose is about twice of that in the phage-free channel. The mean time between blockages of a single Maltoporin monomer (with *trans*-side maltohexaose application) is independent of the presence of the phage. This finding suggests that phage docking does not significantly change the structure of Maltoporin, and that the phage-binding regions are close to, but do not overlap with, the sugar-binding domains of the receptor monomers. Our analysis shows, however, that ion fluxes through the pores of Maltoporin share a new common pathway in the phage–receptor complex.