Supplementary Materials

CI:Mor interactions in the lysogeny switches of *Lactococcus lactis* TP901-1 and *Staphylococcus aureus* φ13 bacteriophages

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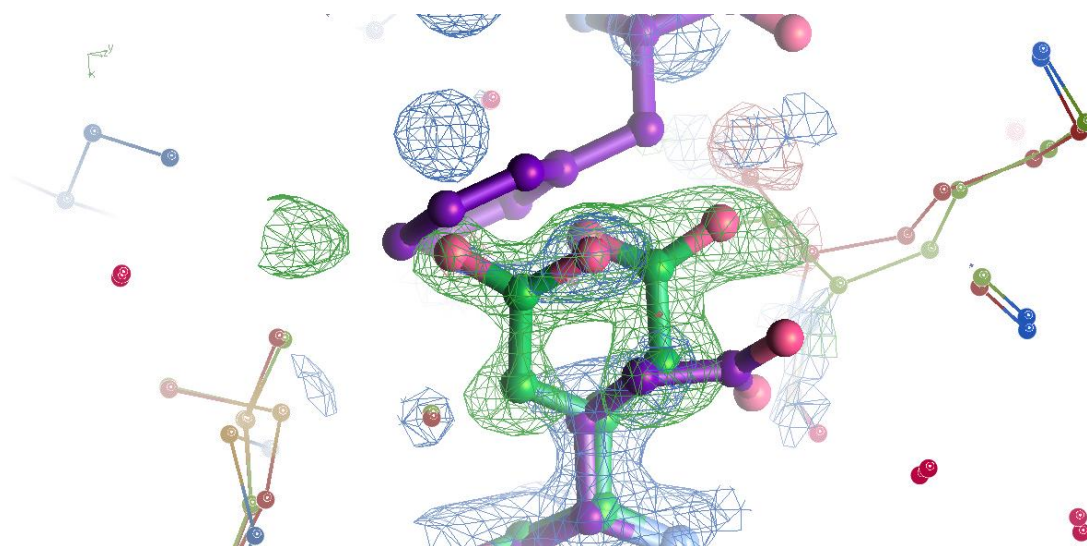[1]Department of Chemistry, University of Copenhagen, Copenhagen DK-2100, Denmark.
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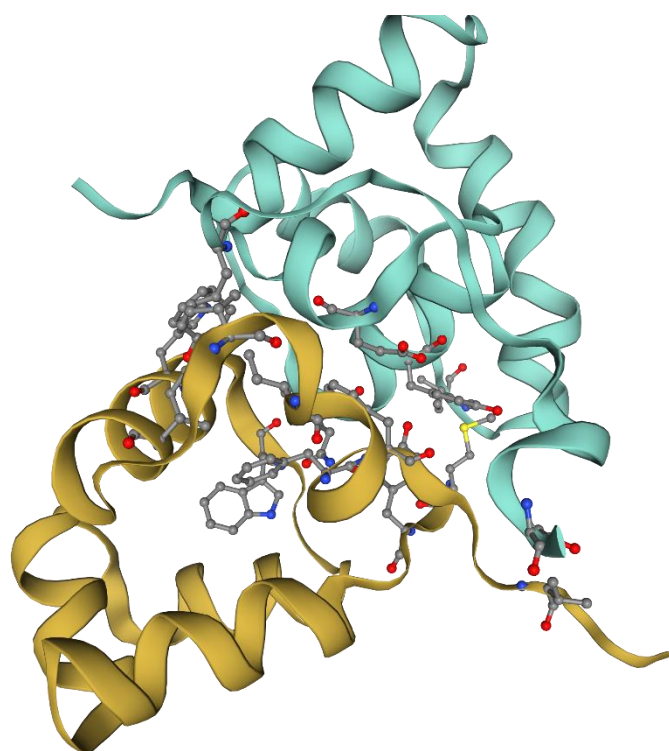
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Supplementary Table 1. Sequences of the φ13 constructs used. His-tag sequences are highlighted in red; TEV protease cleavage sequences are highlighted in green and mutated residues are highlighted in cyan.

CI-WT with TEV cleavage site and His-tag
MKHHHHHHPMSDYDIPTTENLYFQGMREKVSNRLKHIMKIRNLKQVDIINKSKPYQKKLGISLSK STLSQYINDVQSPDQDRIYLLSKTLNVGEAWLMGYDVDSYRVPDEERQDETIMSKINNIFSQLTP PRQENVLNYANEQLEEQNKVTSIDGYKESKLVSYIACGATGAGIGEELYDDILHEEVFFKEDETP SNADFCILVNGDSMEPMLKQGTYAFIKKEDSIKDGTIALVVLDGVSLIKRVDICEDYINLVSLNP KYDDIKVASFSDIKVMGKVVL
Mor with TEV cleavage site and His-tag
MKHHHHHHPMSDYDIPTTENLYFQGMCYDYSRLSGKIVEKYGTQYNFAIAMKLSERSLSLKLNGK VGWKDSEIWKAIQLLDIPVEKIHLYFFKEKVHVI

Supplementary Figure 1. Omit map for Glu69 in the current TP901-1 CI-NTD structure (green) after modeling as Ala. The 2 Fobs-Fcalc electron density map is shown at 1.5σ in blue, while the positive difference electron density is shown in green at 3σ. The structure is superposed on the TP901-1 CI-NTD:Mor complex (PDB 6tri), showing CI-NTD Glu69 and Mor Phe67 in purple.

Supplementary Figure 2. Interface clashes in the initial φ13 CI-NTD:Mor computational model constructed by superposing AF2 models of the individual φ13 proteins onto the experimental TP901-1 complex (PDB code 6TRI). Clashes were detected and visualized at the https://swissmodel.expasy.org/assess.

Supplementary Model. Coordinates of the best final model of φ13 CI-NTD:Mor are available as supplementary material.