

STRUCTURE AND SPECIFICITY OF BACTERIOPHAGE RECEPTOR-BINDING PROTEINS

MARK VAN RAAIJ

E-mail: mjvanraaij@cnb.csic.es

Affiliation: Centro Nacional de Biotecnología (CNB-CSIC), Lab 20B, calle Darwin 3, 28049 Madrid, Spain

Bacteriophages, the most numerous biological replicating entities in the world, are complicated one-time nano-machines that transfer their genomic material into susceptible host bacteria. They have specialized proteins for initial, reversible, host cell wall recognition. Once a suitable host is found, the phage commits to infection by irreversible attachment via a secondary receptor interaction.

We have solved the detailed structures of several of these receptor-binding proteins and have shown them to be mainly beta-structured, but structurally highly diverse and containing several new protein folds. Structures of the RBPs of the coli-phages T4, T5 and T7, of the Salmonella phage epsilon15 and of the Staphylococcus phages S24-1 and K will be shown. Ongoing structural, mutational and binding analysis of RBPs with receptors and receptor analogues will be discussed.

Bacteriophage receptor-recognizing proteins may be used for bacterial detection, while modification by natural or experimental mutation of bacteriophage receptor-binding domains may allow retargeting of phages to alternative host bacteria.