



Group name:

Structural Biology of Viral Fibres

Description:

Some viruses and bacteriophages attach to their host cell via proteins integral to their capsids, for example poliovirus, coxsackievirus and rhinovirus ('common cold virus'). Other viruses bind to their host cell receptors via specialized spike proteins (for example HIV, the AIDS-virus), or via specialized fiber proteins, like adenovirus, reovirus and many bacteriophages. Virus fibers have the same basic architecture: they are trimeric and contain an N-terminal virus or bacteriophage attachment domain, a long, thin, but stable shaft domain and a more globular C-terminal cell attachment domain. Their detailed folds are very diverse and often reveal novel features. These trimeric, fibrous proteins are very stable to denaturation by temperature or detergents. Our goal is to determine the structures of these proteins and thus to make an extensive inventory of stable trimeric folds present in nature. We also want to explain how they bind their receptors and therefore aim to crystallize them with receptor analogues.

Group members:

- Mark Johan van Raaij
- Pablo Soriano Maldonado
- Mateo Seoane Blanco
- Pilar Sánchez Soriano

Research lines:

- Structure determination of bacteriophage tail fibres and tailspikes.
- Structure determination of bacteriophage endolysins.

Articles:

- 1. Seoane-Blanco M, van Raaij MJ*, Granell M: Bacteriophage tail fibers, tailspikes and host cell receptor interaction, Chapter 152 of the Reference Module of Life Sciences 4th Edition (Bamford DN, Zuckermann M, Eds), Academic Press, Volume 4, pp 194-205 (2021).
- 2. Sanz-Gaitero M, Seoane-Blanco M, van Raaij MJ*: Structure and Function of Bacteriophages. Bacteriophages, Biology, Technology, Therapy (Harper D, Abedon S, Burrowes B, McConville M, Eds). Springer, Cham, pp 19-91(2021).-
- 3. Sanz-Gaitero M, van Raaij MJ*: Crystallographic Structure Determination of Bacteriophage Endolysins. *Curr Issues Mol Biol* 40, 165-188 (2020).
- 4. Islam MZ, Fokine A, Mahalingam M, Zhang Z, Garcia-Doval C, van Raaij MJ, Rossmann MG, Rao VB*: Molecular anatomy of the receptor binding module of a bacteriophage long tail fiber. *PLoS Pathog* 15, e1008193 (2019).
- 5. Pennone V, Sanz-Gaitero M, O'Conner P, Coffey A*, Jordan K, van Raaij MJ, McAuliffe O: Inhibition of *L. monocytogenes* biofilm formation by the amidase domain of the phage vB_LmoS_293 endolysin. *Viruses* 11, 722 (2019).
- 6. Korf IHE, Meier-Kolthoff JP, Adriaenssens EM, Kropinski AM, Manfred Nimtz, Rohde M, van Raaij MJ, Wittmann J: Still something to discover – novel insights into *Escherichia coli* phage diversity and taxonomy. *Viruses* 11, 454 (2019).
- 7. San Martín C*, van Raaij MJ*: The so far farthest reaches of the double jelly roll capsid protein fold. *Virology* 15, 181 (2018).
- 8. Taylor NMI*, van Raaij MJ, Leiman PG*: Contractile injection systems of bacteriophages and related systems. *Mol Microbiol* 108, 6-15 (2018).
- 9. Granell M, Namura M, Alvira S, Kanamaru S*, van Raaij MJ*: Crystal structure of the carboxy-terminal region of the bacteriophage T4 proximal long tail fiber protein gp34. *Viruses* 9, 168 (2017).
- 10. Menendez-Conejero R, Nguyen TH, Singh AK, Condezo GN, Marschang RE, van Raaij MJ*, San Martín C*: Structure of a reptilian adenovirus reveals a phage tailspike fold stabilizing a vertebrate virus capsid. *Structure* 25, 1562-1573 (2017).

Projects:

Recent doctoral theses:

- Marta Sanz Gaitero, 07/05/2019: "Crystallographic structure determination of bacteriophage-encoded enzymes that specifically target pathogenic bacteria", Cork Institute of Technology, Cork.
- Antonio Pichel Beleiro, 28/08/2019: "Crystallographic studies on host-interaction proteins of the phage K virion ", Cork Institute of Technology, Cork.
- Mateo Seoane Blanco, 24/05/2021: "Structure and function of Salmonella virus epsilon15 and Campylobacter virus F358 tailspikes", Universidad Autónoma de Madrid.

Weblink:

- <http://www.cnb.csic.es/index.php/en/research/research-departments/macromolecular-structures/structural-biology-of-viral-fibres-2>
- <http://wwwuser.cnb.csic.es/~mjvanraaij/>