

P04.13.304*Acta Cryst.* (2008). A64, C326**Host recognition of bacteriophage K1F: EndoNF in complex with helical polysialic acid**Eike Ch Schulz¹, Katharina Stummeyer², Achim Dickmanns¹, Rita Gerardy-Schahn², Ralf Ficner¹¹University of Goettingen, Department for molecular structural biology, Justus von Liebig Weg 11, Goettingen, Niedersachsen, D-37077, Germany, ²Hannover Medical School MHH, Department for Cellular Chemistry, OE4330, Carl-Neuberg-Strasse 1, D-30625 Hannover Germany, E-mail: eschulz1@gwdg.de

Alpha-2,8-linked polysialic acid (polySia) is an important mediator of cellular motility and functional plasticity in the vertebrate brain and has implications in tumor metastasis. PolySia is also a common cell wall modification of pathogenic prokaryotes like *Escherichia coli* K1 and *Neisseria meningitidis* serogroup B that cause meningitis and severe sepsis in humans. The only known source for enzymes that specifically degrade polySia are *E. coli* K1 specific bacteriophages. They possess endosialidases as host specificity determining tailspike proteins required to digest the bacterial polySia capsule during infection. We now determined several crystal structures of active site mutants of an endosialidase cloned from bacteriophage K1F (endoNF) in complex with oligomeric sialic acid. The structures have been refined to resolutions up to 1.5 Å. A well defined electron density map of oligomeric sialic acid could be observed for three binding sites, one of which is located in the active site cleft. The complex structure confirms the helical conformation of polySia and supports the model of a substrate assisted catalytic mechanism.

Keywords: bacteriophage, polysialic acid, endoNF

P04.13.305*Acta Cryst.* (2008). A64, C326**Structure of main protease from a global infectious human coronavirus, HCoV-HKU1**

Qi Zhao

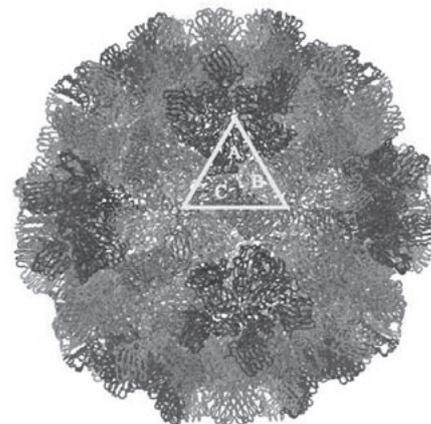
Tsinghua Univ., School of Medicine, new lifescience building 201# Tsinghua Univ Beijing China, Beijing, Beijing, 100089, China, E-mail : zhaqiqi@xtal.tsinghua.edu.cn

Human coronavirus HKU1 (HCoV-HKU1) is a new coronavirus that was first identified in Hong Kong in 2005. Infection by HCoV-HKU1 occurs worldwide and causes syndromes such as common cold, bronchitis and pneumonia. The coronavirus main protease (Mpro), which is a key enzyme in viral replication via a cascade of proteolytic processing of replicase polyproteins, has been identified as an attractive target for rational drug design. In this study, we report the structure of HCoV-HKU1 Mpro in complex with a synthetic compound N3. The structure of HCoV-HKU1 serves as a model for group 2a coronaviruses, which are distinct from group 2b coronaviruses such as SARS-CoV. This structure and enzyme activity assays also support the relative conservation at the P1 position based on genome sequencing. This complex structure also provided clues of substrate binding mode at P3 position which was thought to be solvent-exposed.

Keywords: coronavirus, main protease, HCoV-HKU1

P04.13.306*Acta Cryst.* (2008). A64, C326**The structure of melon necrotic spot virus determined at 2.8Å resolution**Yasunobu Wada¹, Hideaki Tanaka¹, Eiki Yamashita¹, Tamaki Ichiki-Uehara², Toshihiro Omura², Tomitake Tsukihara¹¹Osaka University, Institute for protein research, 3-2, Yamadaoka, Suita, Osaka, Osaka, 565-0871, Japan, ²National Agricultural Research Center, 3-1-1 Kannondai, Tsukuba, Ibaraki 305-8666, Japan, E-mail : nobu-w@eos.ocn.ne.jp

The structure of melon necrotic spot virus (MNSV) was determined at 2.8 Å resolution. Although MNSV is classified into the genus Carmovirus of the family Tombusviridae, the three-dimensional structure of MNSV showed a higher degree of similarity to tomato bushy stunt virus (TBSV), which belongs to the genus Tombusvirus, than to carnation mottle virus (CMtV), turnip crinkle virus (TCV) or cowpea mottle virus (CPMtV) from the genus Carmovirus. Thus, the classification of the family Tombusviridae at the genus level conflicts with the patterns of similarity among coat-protein structures. MNSV is one of the viruses belonging to the genera Tombusvirus or Carmovirus that are naturally transmitted in the soil by zoospores of fungal vectors. The X-ray structure of MNSV provides us with a representative structure of viruses transmitted by fungi.



Keywords: virus, tinbusviridae, coat protein

P04.13.307*Acta Cryst.* (2008). A64, C326-327**Modular structure of receptor binding proteins from *Lactococcus lactis* phages**Christian Cambillau¹, Silvia Spinelli¹, Stephanie Blangy¹, Mariella Tegoni¹, Sylvain Moineau², Denise M Tremblay^{1,2}, Valerie Campanacci¹¹CNRS-Universities of Marseille, AFMB, Campus Luminy, 163 Av de Luminy, case 932, MARSEILLE CEDEX 09, PACA, 13288, France, ²Departement de Biochimie et de Microbiologie, Faculte des Sciences et de Genie, Universite Laval, Quebec City, Quebec, Canada, G1K 7P4, E-mail : christian.cambillau@afmb.univ-mrs.fr

Lactococcus lactis is a Gram positive bacterium, used by the dairy industry for the manufacture of fermented milk products. The double-stranded DNA bacteriophage p2 infects *L. lactis* strains by using a receptor-binding protein (RBP) located at the tip of its tail. The crystal structure of phage p2 RBP, reveals a homo-trimeric protein formed of three domains: the shoulders, a beta-sandwich attached to the phage; the neck, an interlaced beta-prism, and the receptor recognition head, a 7 stranded beta-barrel. The complex of RBP with a neutralizing llama VHH domain identified the area binding to the bacterial receptor. It is able to bind various saccharides present in the bacterial receptor. The structural similarity between the head domain