Research Introduction & Interest

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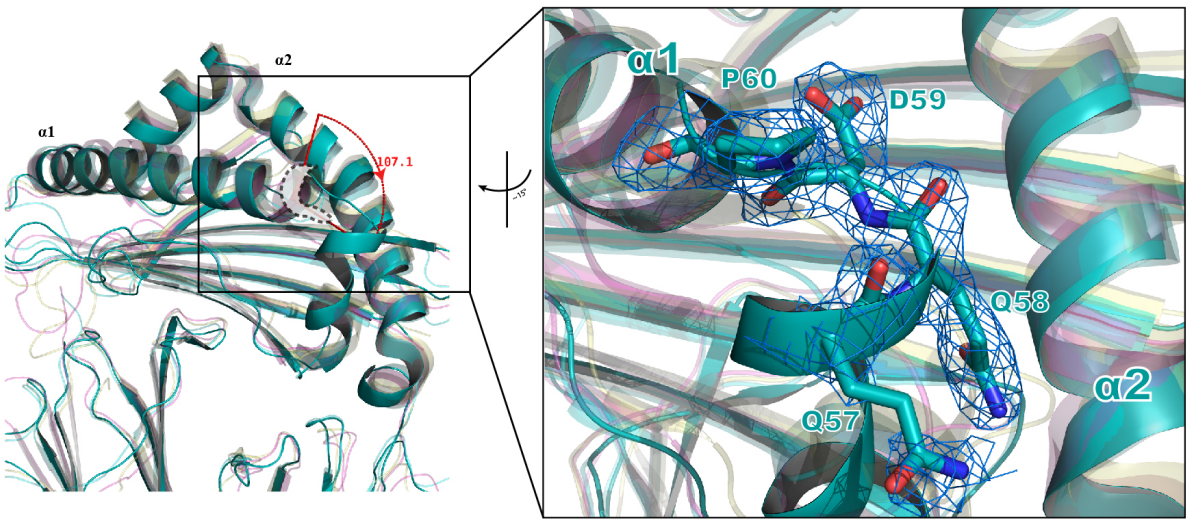
Research Introduction

Presentation characteristic of bat MHC I

The Bat is related to many lethal viruses spread, and therefore becomes more and more important for public health security. To understand why bat can tolerate infection without apparent symptoms, study on immune system of bat is necessary. MHC I molecules play a pivot role to activate anti-viral cellular immune reaction, through presenting antigenic peptides on cell surface to be recognized by TCR receptor. By determining the crystal structure of Ptal-N*01:01 peptide complex, we find that there is a special ‘flip down’ on its peptide binding groove which is leaded by the 3 or 5 amino acids insertion. Interestingly, this insertion is conserved in almost all kinds of bats.

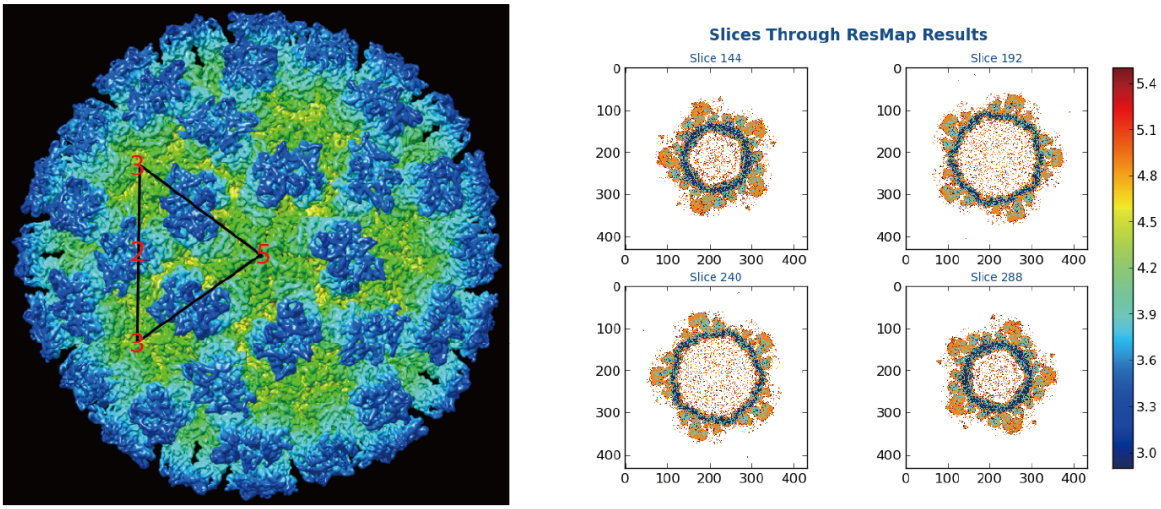


The different conformations with other reported mammals’ MHC I molecules

We design and build the random peptide library de novo MS (RPLD-MS) analysis work flow to try to get the peptidome information totally out of cellular environment. Through the comparison between the peptidome from cell and out of cell, we find this special 'flip down' can help to increase binding peptide N-terminal Asp ratio during peptide exchange process in the cell and further increase the affinity of the presentation polypeptide. Related work has been published on the journal cover of **the Journal of Immunology** (*https://doi.org/10.4049/jimmunol.1900001*).

Structural basis of FCV 2280 strain with stronger ability of replication and infection

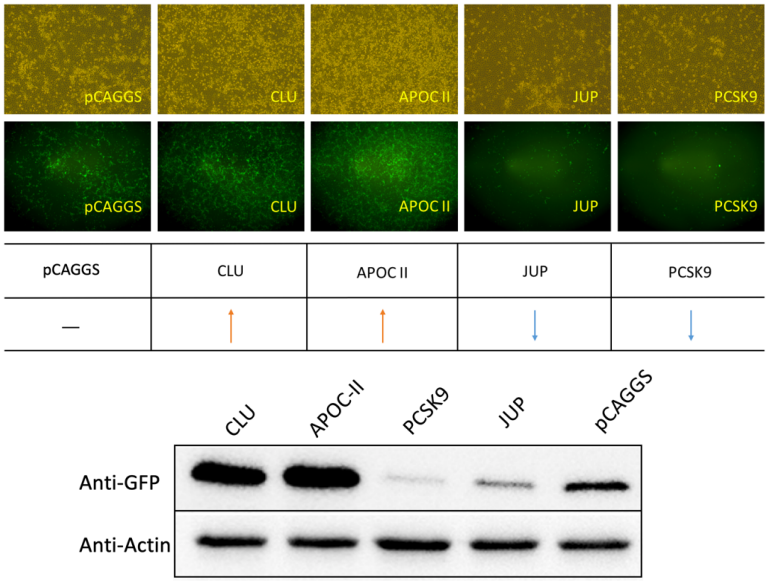
Feline calicivirus (FCV) 2280 strain is a special virulent strain with stronger ability of replication and infection, FCV F9 is a vaccine strain. We analyzed the structure of FCV by cryo-electron microscopy. This study can help understand structural basis of FCV 2280 strain with stronger ability of replication, and the key factors for improving to better vaccine design by comparison with vaccine strains. Related work is preparing to submit.



The resolved structure of FCV 2280 strain

Screening of differentially expressed PRRS virus-entry related proteins

HuN4-F112 is a passaging attenuated pathogenic strain (AP-) of wild type highly pathogenic (HP-) porcine reproductive and respiratory syndrome (PRRS) virus strain HuN4, provides good protection to kinds of PRRSV strains. To explore differentially expressed virus-entry related proteins during HuN4-F112 and HuN4 infection will lay a foundation for understanding the differential infection mechanism. By reverse genetics, we firstly constructed the recombinant EGFP infectious clones of both HuN4-F112 and HuN4 and rescued the recombinant viruses respectively. And then, we sampled these EGFP-recombinant viruses infected cells to the flow sorting by detecting FITC signal for purification. After then, we extracted the membrane proteins and sampled them to Shotgun MS analysis and determined four potential differential proteins which will influence the virus infection efficiency, CLU and APOC-II will up-regulate while JUP and PCSK9 will down-regulate the HP-PRRSV infection. Part of the virus-entry related proteins MS screening work has been published on the **Proteomics** (*https://doi.org/10.1002/pmic.201700101*)



Validated differentially expressed proteins which will influence the virus infection efficiency

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Research Interests

The accurate design of the immunogen based on the structural information

Focus on the relationship between immunogenic structural information and protective immunity induction as well as maintenance, which will help clarify the regulation mechanism and further develop new method to modify immunogen to design more effect vaccine. The clinical proof of the respiratory syncytial virus (RSV) fusion glycoprotein stabilized in its prefusion conformation (DS-Cav1) has been a good example of the concept for how structural biology contribute to precision vaccine design, which portends an era of precision vaccinology.

The structural study of Immune-related protein molecule

I am very interested in solving immune-related protein structure for better understanding the protective functions of the immune system under the help of crystallography and cryo-EM theory exploration and algorithm development. We can get the hidden detail structural information from protein special conformation or complex image data, by specific algorithm aimed at specific protein image data.

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