

# Carbon-Phosphorus Lyase Complex Structures Reveal the Binding Mode of the NBD-like PhnK

– Junjie Zhang, et al.

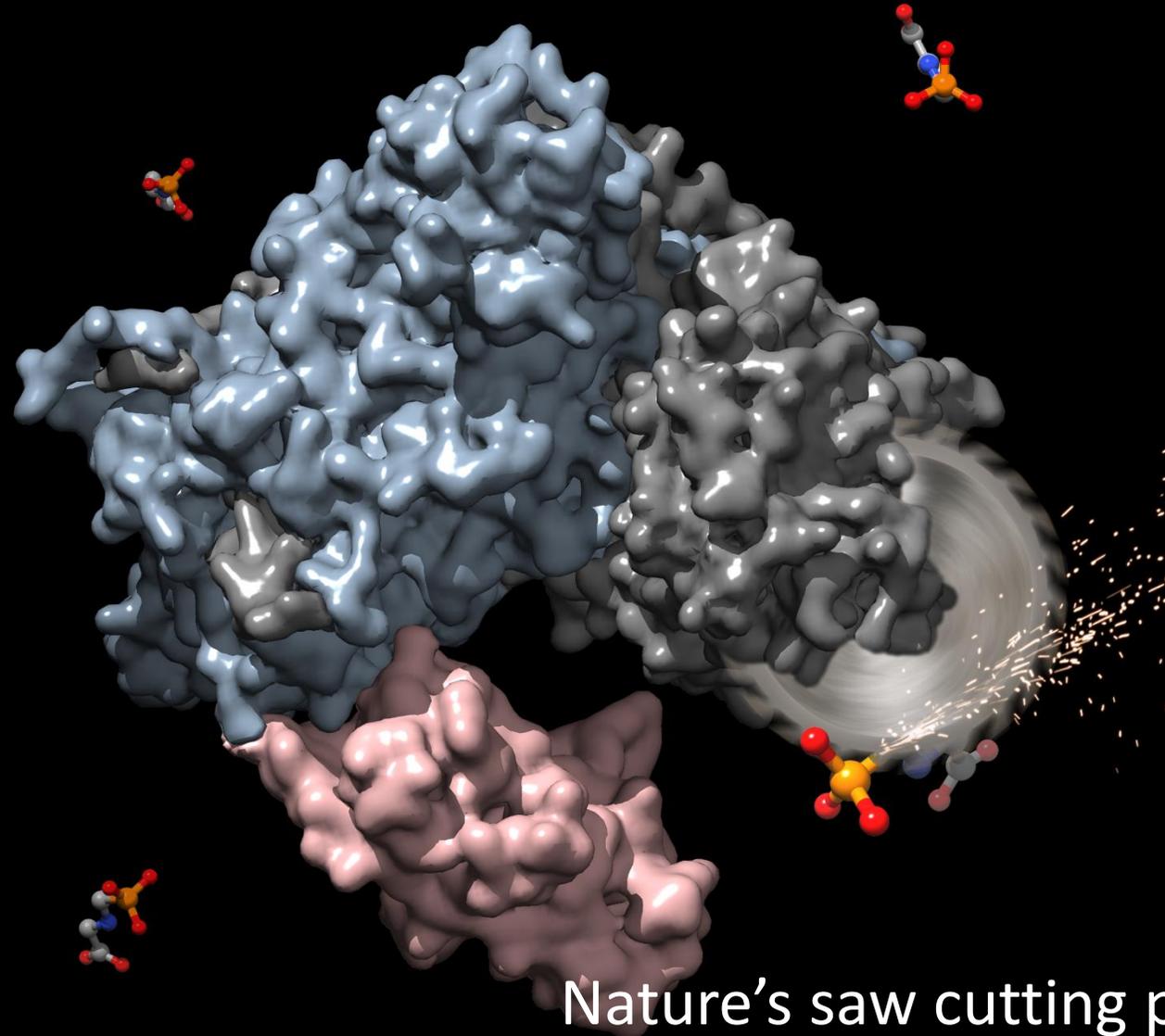




# Structures of the Carbon-Phosphorus Lyase Complex Reveal the Binding Mode of the NBD-like PhnK

Kailu Yang, Zhongjie Ren, Frank M. Raushel, Junjie Zhang  
Department of Biochemistry & Biophysics, Texas A&M University

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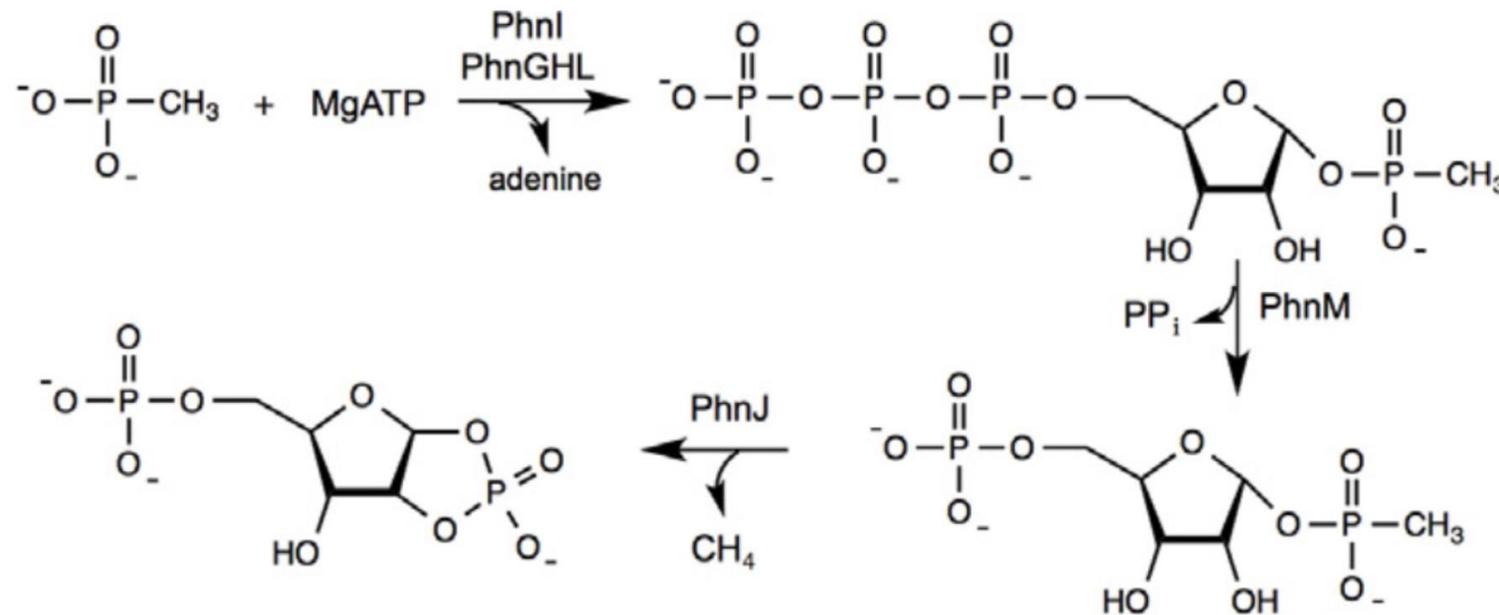


Nature's saw cutting phosphonates



## Background

- The carbon-phosphorus (C-P) lyase complex, which is encoded by the 7 essential genes (*phnGHIJKLM*) within the *phn* operon, is essential for the metabolism of unactivated phosphonates to phosphate in bacteria.
- PhnK is homologous to the nucleotide-binding domain (NBD) of ATP-binding cassette (ABC) transporters. PhnK has all the NBD motifs.





## Problems to be solved

- Why is there only one copy of PhnK bound to a dimeric  $\text{phnG}_2\text{H}_2\text{I}_2\text{J}_2$  core complex?
- How does PhnK bind to the core complex?
- What is the effect on the core complex after PhnK binds?



## Data processing details

- Software: EMAN2, Relion1.4, Unblur, PRIME, B-soft
- Cluster: Ada
- Typical job size: 140 hours
- 200 cores with a total of 1 million SUs.





## Conclusion

- PhnJ subunits in  $\text{PhnG}_2\text{H}_2\text{I}_2\text{J}_2$  provide two identical binding sites for PhnK. Only one PhnK binds to  $\text{PhnG}_2\text{H}_2\text{I}_2\text{J}_2$  due to steric hindrance.
- The NBD-like PhnK binds to a cytoplasmic protein, distinct from NBD-TMD interaction
- Binding of PhnK exposes the active site residue, Gly32 of PhnJ, located near the interface between PhnJ and PhnH.



Asymmetric cryo-EM structure  
of the canonical Allolevivirus Q $\beta$   
reveals a single maturation  
protein and the genomic ssRNA  
in situ

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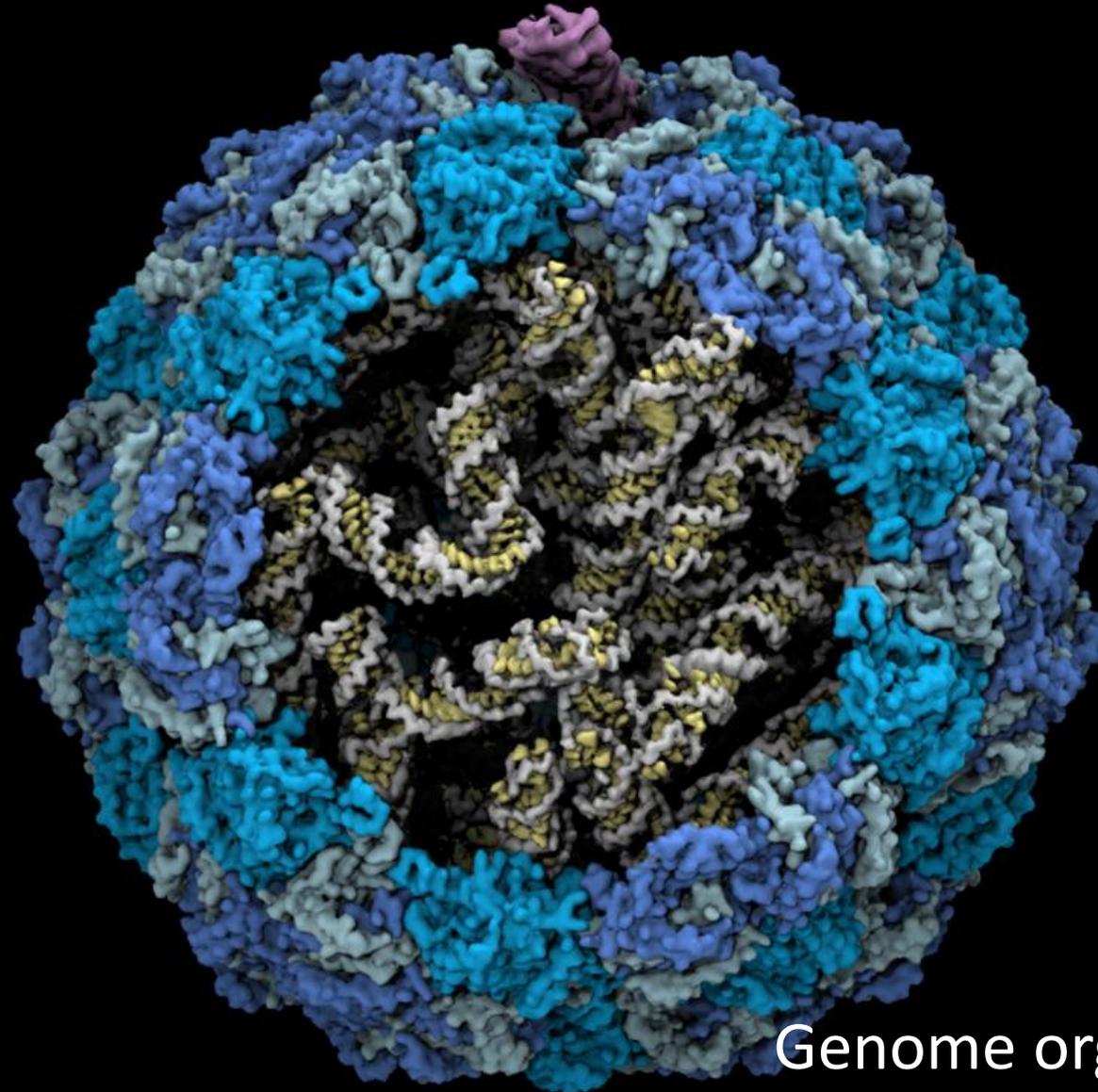




# Asymmetric cryo-EM structure of the canonical Allolevivirus Q $\beta$ reveals a single maturation protein and the genomic ssRNA in situ

Gorzelnik KV, Cui Z, Reed CA, Jakana J, Young R, Zhang J.  
Department of Biochemistry & Biophysics, Texas A&M University

Published in *PNAS*, 2016.



Genome organization of a virus





## Background and Results

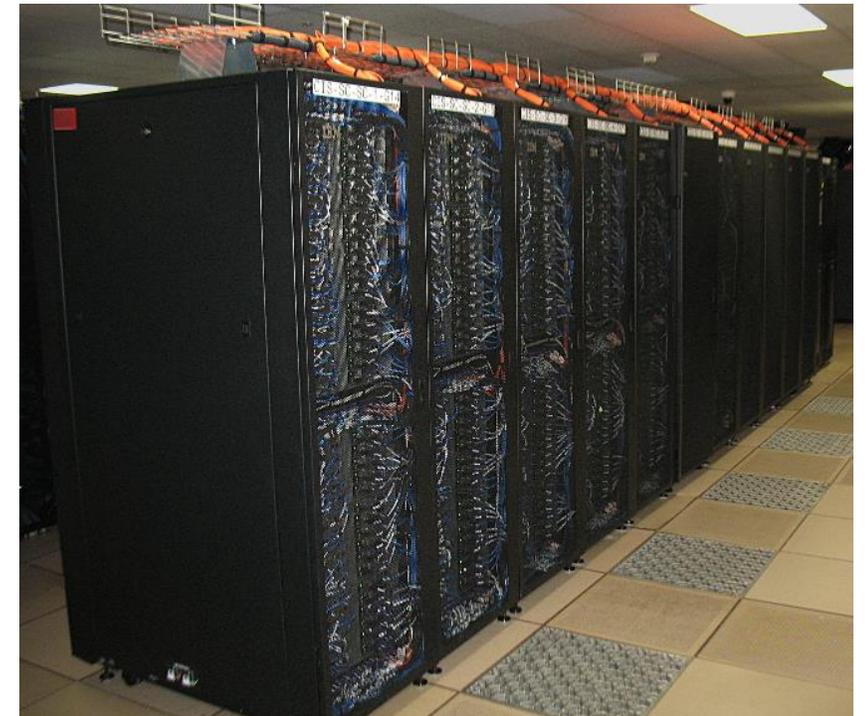
Single-stranded (ss) RNA viruses have ribonucleic acid as their genetic material and infect animals, plants and bacteria. Here we used cryo-electron microscopy to reveal, for the first time, the genomic RNA (gRNA) of the ssRNA virus Q $\beta$ . The asymmetric gRNA adopts a single dominant structure in all virions and binds the capsid of Q $\beta$  at each coat protein. At the same time, we determined the structure of the maturation protein, A2, which functions both as the virion's "tail" and its lysis protein. We see the gRNA is more ordered when interacting with A2. These results provide new structural insights into gRNA packaging and host infection in ssRNA viruses.





## Data processing details

- Software: EMAN2, Relion1.4, Unblur, B-soft
- Cluster: Ada
- Typical job size:
  - 200 Cores with each core of 10GB memory
  - ~1M SUs on Ada.

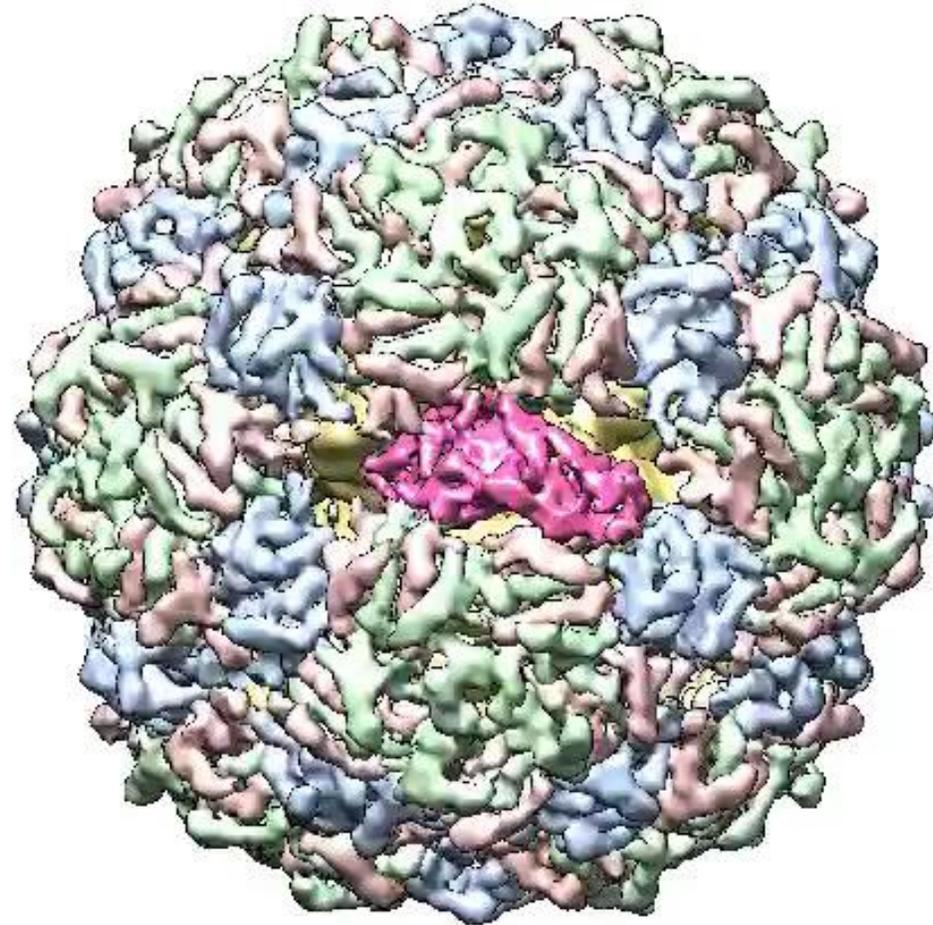




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Asymmetric structure of Q $\beta$ . Coat proteins are in salmon (conformer A), green (conformer B), and blue (conformer C), respectively. A<sub>2</sub> is in hot pink. RNA is in yellow and low-pass-filtered to 10-Å resolution.





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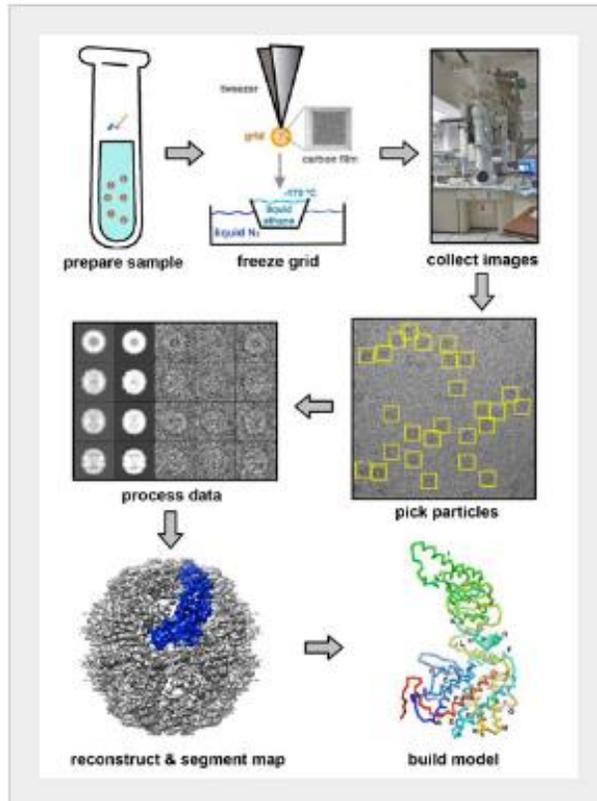
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## Welcome to our Cryo-EM Laboratory



We are part of the [Department of Biochemistry and Biophysics](#) and the [Center for Phage Technology at Texas A&M University](#). Our lab is in the [Interdisciplinary Life Sciences Building](#).

We study the structure and function of macromolecular machines and how they are related to human health.

We develop experimental and computational techniques to understand the mechanism for a variety of macromolecules in the cell, including the viruses, the chaperones, the ribosomes, etc.

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### Latest News:

Paper on christmas eve: "Structures of the Carbon-Phosphorus Lyase Complex Reveal the Binding Mode of the NBD-like PhnK" is online in *Structure*.  
*Dec 24, 2015*

Our new paper "Structure of Ribosomal Filipelese Factor Bound to

<http://cryoem.tamu.edu>

