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## Mechanism Of Ubiquitin-Dependent Phospholipase Activity By The L. Pneumophila Effector Vpdc

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## Keywords

Legionella, Pneumophila, VpdC, Structure, Protein, Ubiquitin, Pathogen, Vacuole, LCV, Legionnaire's, Mechanism, Infection, Vector, Function, Phospholipase, Eukaryotic, Bacteria

## Abstract

Legionella pneumophila is a pathogenic organism ubiquitous in aqueous environments and the causative agent of Legionnaire's disease, a severe infection affecting the lungs. L. pneumophila is found in waterways, stagnant pipes, showerheads, sprinkler systems, and faucets, increasing the likelihood of human infection and disease to those with weaker immune systems. A major component of the success of L. pneumophila as a pathogen is the Legionella-containing vacuole (LCV), a membrane-bound organelle that shields the bacteria from immune defenses. The LCV is established through the action of virulence factors secreted by L. pneumophila through the IVB Dot/Icm type 4 secretion system (T4SS), a protein channel that injects bacterial proteins directly into the host cell. Among them is the family of Vpd/Vip phospholipase proteins that regulate the size of the LCV. Previous research has credited VpdC as a primary contributor in vacuole expansion. Interestingly, the function of VpdC is reportedly regulated by interaction with the eukaryotic post-translational modifier ubiquitin (Ub), although the true structure and mechanism of this process are unknown. Using structural models generated by AlphaFold, we have predicted regions of VpdC that are important for function. Through cloning these regions into vectors for a bacterial expression system, we established a system for the recombinant production of VpdC. With this system in hand, further research with VpdC will enable us to understand the mechanism this effector protein uses for virulence through vacuole expansion and may explain how other species use Ub binding as an efficient method of host infection.

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