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Supporting information for article:

***Legionella* effector LegA15/AnkH contains an unrecognized cysteine protease-like domain and displays structural similarity to LegA3/AnkD, but differs in host cell localization**

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Figure S1. Protein sequence alignment of CPL domains of LegA15 and LegA3 based on structural alignment. The secondary structure elements are shown above and below the protein sequence alignment.

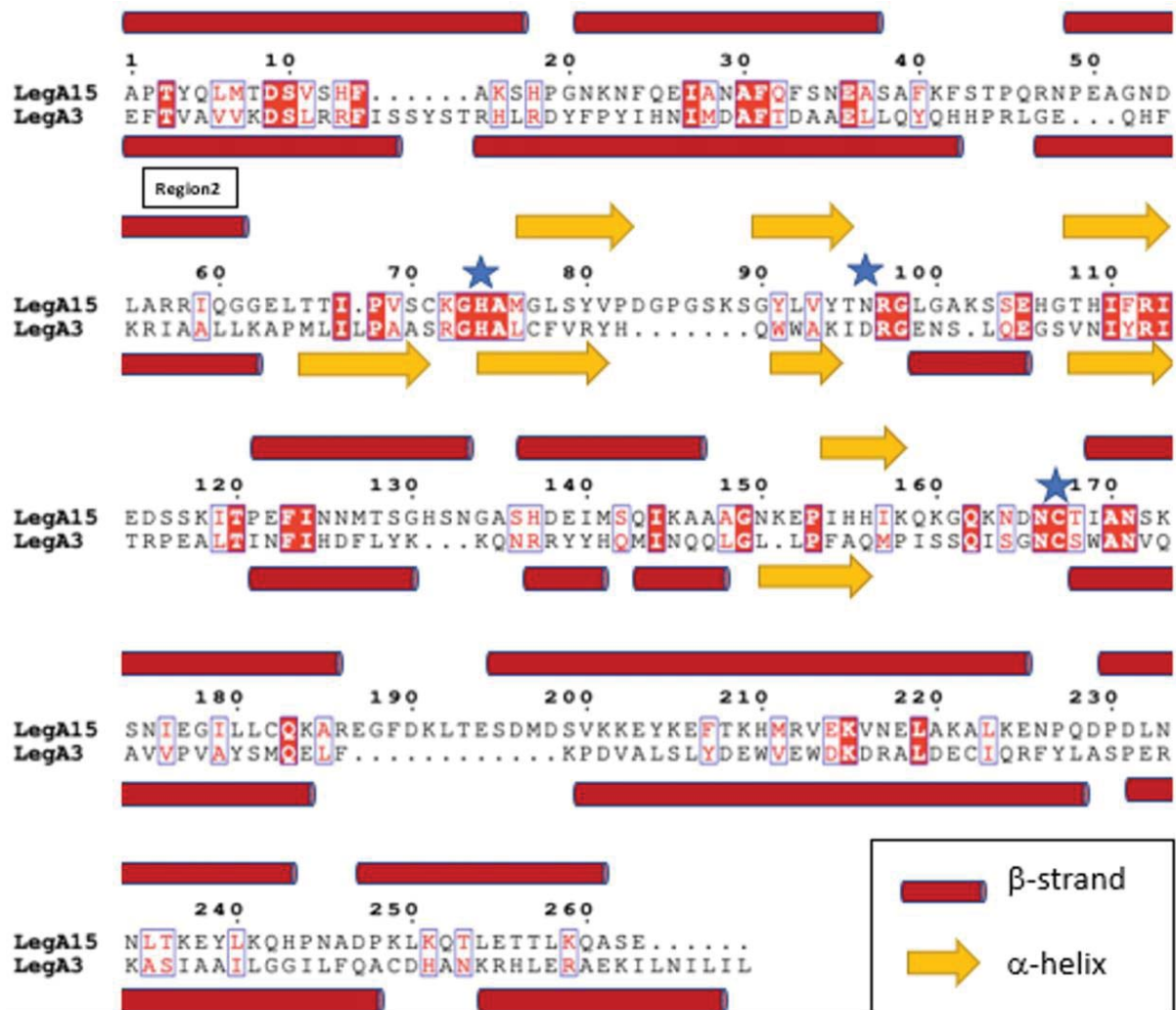


Figure S2. Superposition of LegA15 and LegA3 based on their CPL domains. The ankyrin domain of LegA15 (yellow) is juxtaposed against the catalytic triad obscuring access to this site. The ankyrin domain in LegA3 (orange) assumes a different orientation, interacting with site on CPLD distant from the triad.

