

Supplementary information

The structure of *Legionella pneumophila* LegK4 type four secretion system (T4SS) effector reveals a novel dimeric eukaryotic-like kinase

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Supplementary Figure S1-3

Figure legends

Figure S1

A) Electron density map ($2F_o - F_c$, blue) contoured at 1.3σ of AMP-PNP•LegK4¹⁻⁴⁴⁵ crystal structure. The model is shown as ball and sticks with carbon atoms colored in yellow, oxygen atoms in red and nitrogen atoms in blue. B) $F_o - F_c$ omit map (green) for the AMP-PNP molecule of the crystal structure of AMP-PNP•LegK4¹⁻⁴⁴⁵ represented as in A). The model of AMP-PNP molecule is shown as ball and sticks with carbon atoms colored in magenta, oxygen in red and nitrogen in blue.

Figure S2

Structure-based sequence alignment of LegK1 (Uniprotkb Accession Number Q5WWA8), LegK2 (UAN Q5WUV1), LegK3 (UAN Q5WTP3) and LegK4 (UAN Q5WZW9) from *Legionella pneumophila* strain Lens. For clarity, C-terminal sequences have been truncated. Secondary structure elements corresponding to LegK4¹⁻⁴⁴⁵ are indicated above the sequences. Active sites motifs are indicated below the sequences by colored bar and labeled accordingly. Identical residues are colored in white and shaded in red. Conserved residues are colored in red. Secondary structure predictions of LegK1-3 obtained using the server PSI-pred (<http://bioinf.cs.ucl.ac.uk/psipred/>) are indicated by blue (helices) or yellow (strands) bars on the sequences aligned with the cap and FHB domains.

Figure S3

Saxs data collection analysis and quality assessment. A) Kratky plot SAXS measurement of LegK4¹⁻⁴⁴⁵. The shape of the plot suggests that the protein is a multidomain protein which shows limited flexibility. A P(r) plot for LegK4¹⁻⁴⁴⁵ with Dmax of 111 Å (right) provides an excellent fit to the experimental data (left).

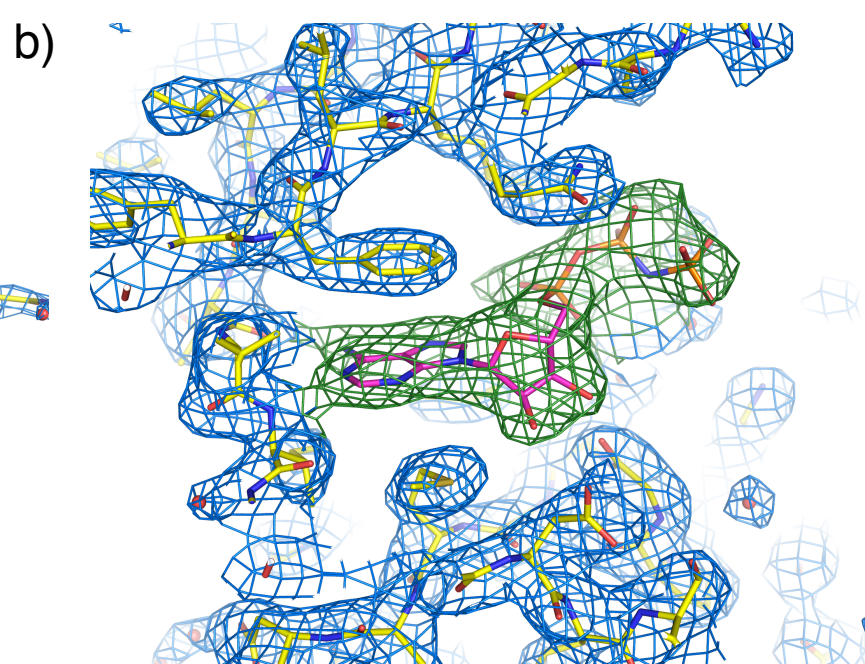
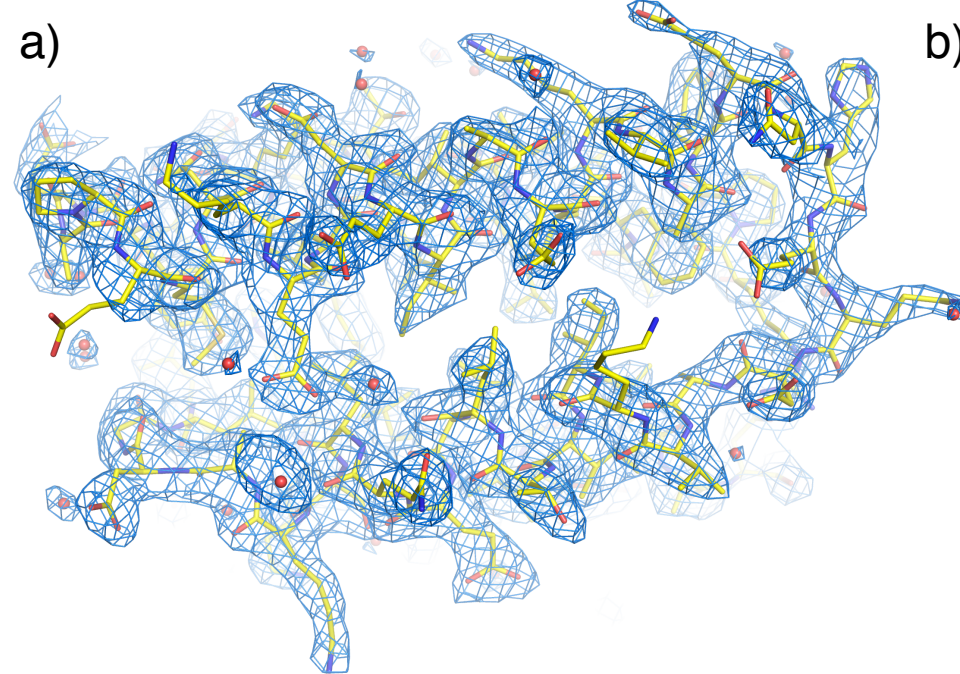


Fig. S1

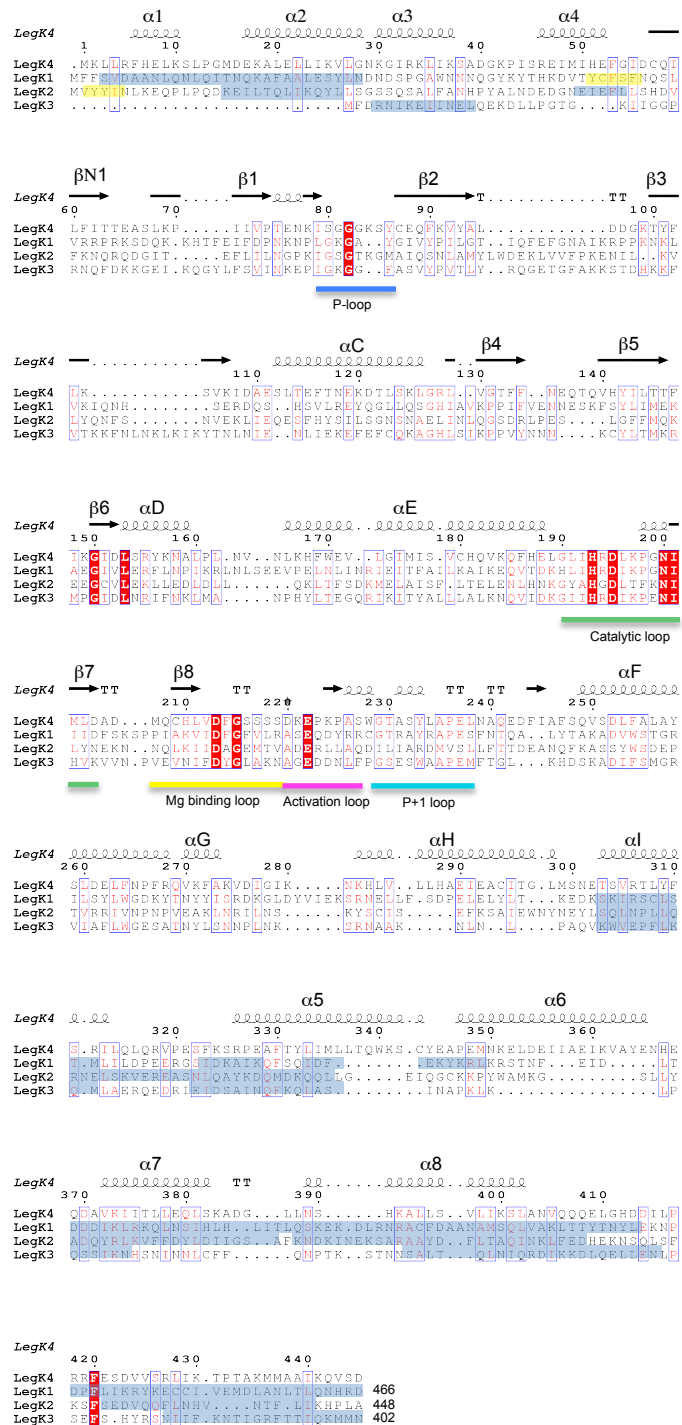


Fig. S2

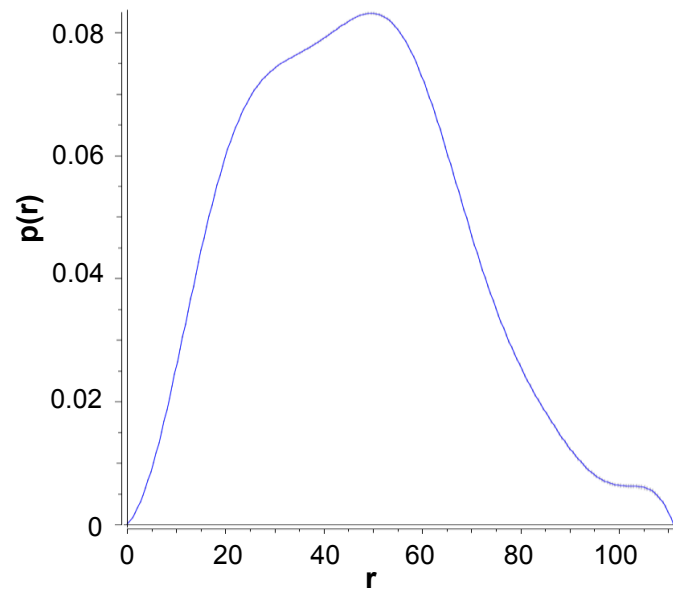
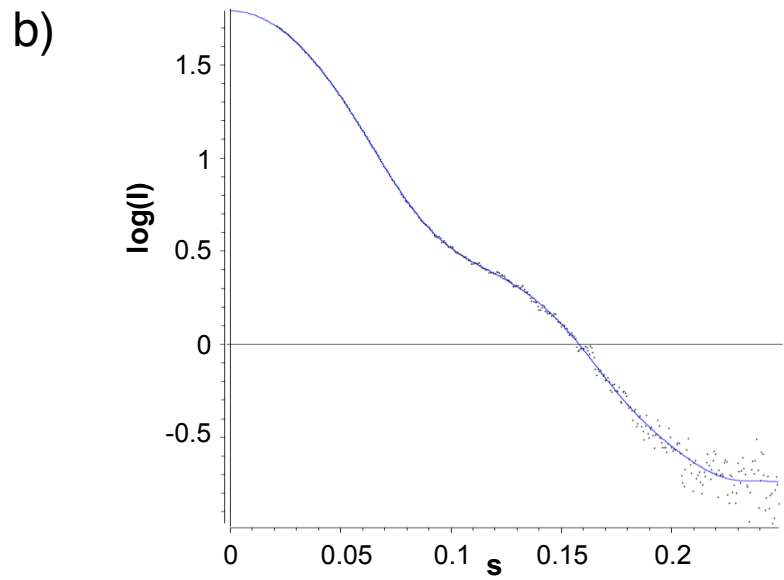
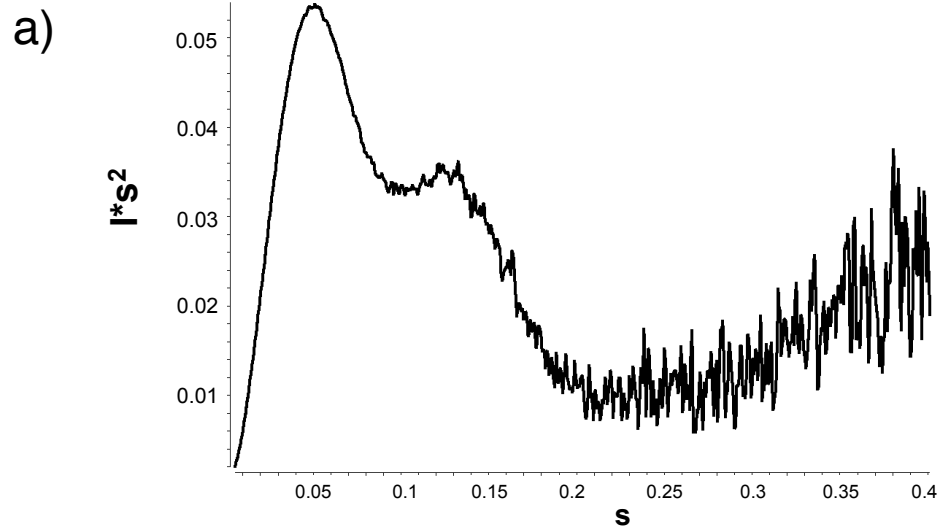


Fig. S3