

Email	l.a.kelley@imperial.ac.uk
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Figure 1 displays the schematic representation of the protein structure for three proteins: PTL1, PTL2, and PTL3. The figure is organized into three main sections, each corresponding to a protein. Each section contains five rows of information:

- Sequence:** The amino acid sequence of the protein, with residues numbered from 1 to 60 for PTL1 and PTL2, and 1 to 4 for PTL3.
- Secondary structure:** A diagram showing the predicted secondary structure elements (alpha-helices and beta-strands) as blue arrows.
- SS confidence:** A bar chart representing the confidence in the secondary structure prediction, with colors indicating different confidence levels (red for high, green for medium, yellow for low).
- Disorder:** A bar chart representing the predicted disorder of the protein, with colors indicating different confidence levels (red for high, green for medium, yellow for low).
- Disorder confidence:** A bar chart representing the confidence in the disorder prediction, with colors indicating different confidence levels (red for high, green for medium, yellow for low).

The proteins are shown as follows:

- PTL1 (top):** A full-length protein of 60 residues. The sequence is MI NSPRVCI QVQS VYI EAQS SP DNERY VF AYT VTI RNL GRAP VQL LGRY WLI TNGNGRET. The secondary structure shows several alpha-helices and beta-strands. The SS confidence is high (red) for most of the protein, with some lower confidence (yellow/green) at the N-terminus and C-terminus. The disorder is predicted to be high (red) for most of the protein, with some lower confidence (yellow/green) at the N-terminus and C-terminus.
- PTL2 (middle):** A full-length protein of 120 residues. The sequence is EVQGEGVVG VQPLI APGEEYQYTS GAI I ETPLGTMQGHYEMI DENGVPFSI DIPVFR LAV. The secondary structure shows several alpha-helices and beta-strands. The SS confidence is high (red) for most of the protein, with some lower confidence (yellow/green) at the N-terminus and C-terminus. The disorder is predicted to be high (red) for most of the protein, with some lower confidence (yellow/green) at the N-terminus and C-terminus.
- PTL3 (bottom):** A truncated version of the protein, consisting of the first 4 residues (PTLIH). The secondary structure shows a single alpha-helix. The SS confidence is high (red) for most of the protein, with some lower confidence (yellow/green) at the N-terminus and C-terminus. The disorder is predicted to be high (red) for most of the protein, with some lower confidence (yellow/green) at the N-terminus and C-terminus.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand