Supplementary figure legends

S1. Sequence alignment of the BprV, BprB, AprV2 and AprB2 proteases. Secondary structure elements present in BprV are shown above the alignment. Residue numbering is for BprV. The nine amino acid substitutions between BprV and BprB are boxed in cyan. Residues forming the active site are indicated by arrows shown below the alignment. The regions correspond to the I1, I2, I3 and I4 loops are labeled. Residues highlighted in red indicate strictly conserved residues. Residues written in red indicate those with similar physiochemical properties. The alignment was generated using the program Clustal W (1) and ESPript (2). Secondary structure elements were calculated using Stride (3).

S2. Overlay of the BprV and AprV2 structures. AprV2 is shown in blue and BprV is shown in red. Calcium ions are indicated as blue and red spheres for AprV2 and BprV respectively. The figure was prepared using PyMol (4).

S3. $2|F_o|\text{-}|F_c|$ electron density map depicting the residues that form the S1 pocket of BprV (A) and BprB (B). BprV is shown as blue sticks and BprB is shown as orange sticks. The map is contoured at 1 σ. Water molecules have been removed for clarity. The figure was prepared using PyMol (4).

Supplementary references

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