Supplementary Information

Molecular and Structural Parallels Between Gluten Pathogenic Peptides and Bacterial-derived Proteins by Bioinformatics Analysis

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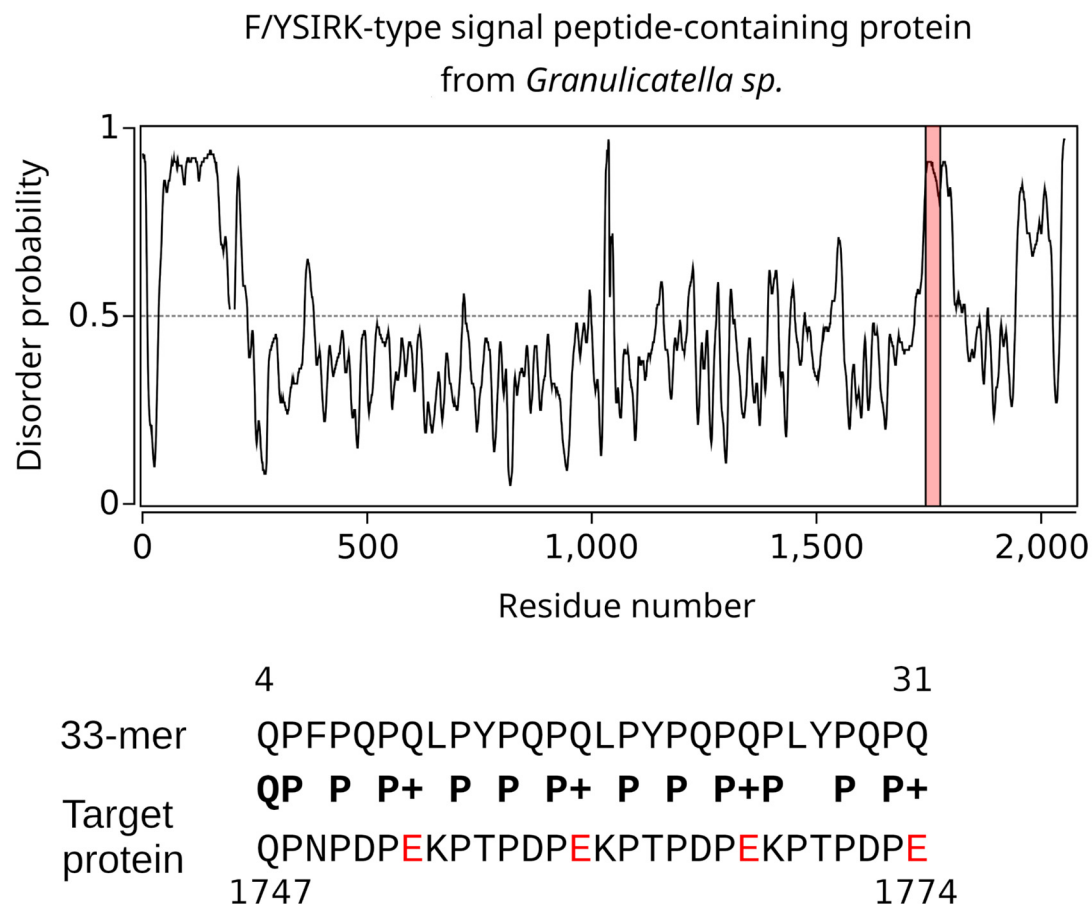
Fig S1

Fig S1. Intrinsic disorder profile of the F/YSIRK-type signal peptide-containing protein from *Granulicatella sp*. HMSC31F03 calculated using PrDOS [1]. The region sharing high sequence similarity with the 33-mer sequence is shown in a red box. In addition, the sequence alignment between the 33-mer sequence and the high similarity region of the target protein is shown at the bottom.

Bibliography

1. Ishida T, Kinoshita K. PrDOS: prediction of disordered protein regions from amino acid sequence. Nucleic Acids Res. 2007;35: W460-4. doi:10.1093/nar/gkm363