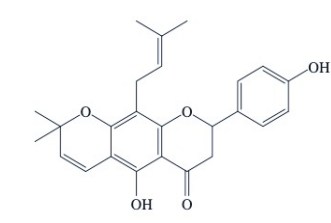


Introduction

Vancomycin-resistant enterococci (VRE) is a major concern of a global public health because it has been a leading cause of healthcare-associated infections. (Selleck *et al.*, 2019). Currently, bioactive compound have gained popularity and played a key role as an alternative treatment against infectious diseases, including antibacterial drugs (Atanasov *et al.*, 2021).



- Lupinifolin is a prenylated flavonoid in Thai traditional herbs.
- The bioactive compound used in this study was isolated from *Albizia myriophylla* Benth. stem.
- Lupinifolin showed the potential antibacterial activity against Gram-positive bacteria including *Enterococcus* (Joycharat *et al.*, 2013; Joycharat *et al.*, 2016; Sianglum *et al.*, 2019).
- Lupinifolin is a promising new antibiotic.
- However, the mechanism of action underlying antibiotic effects of this compound is not yet understood.

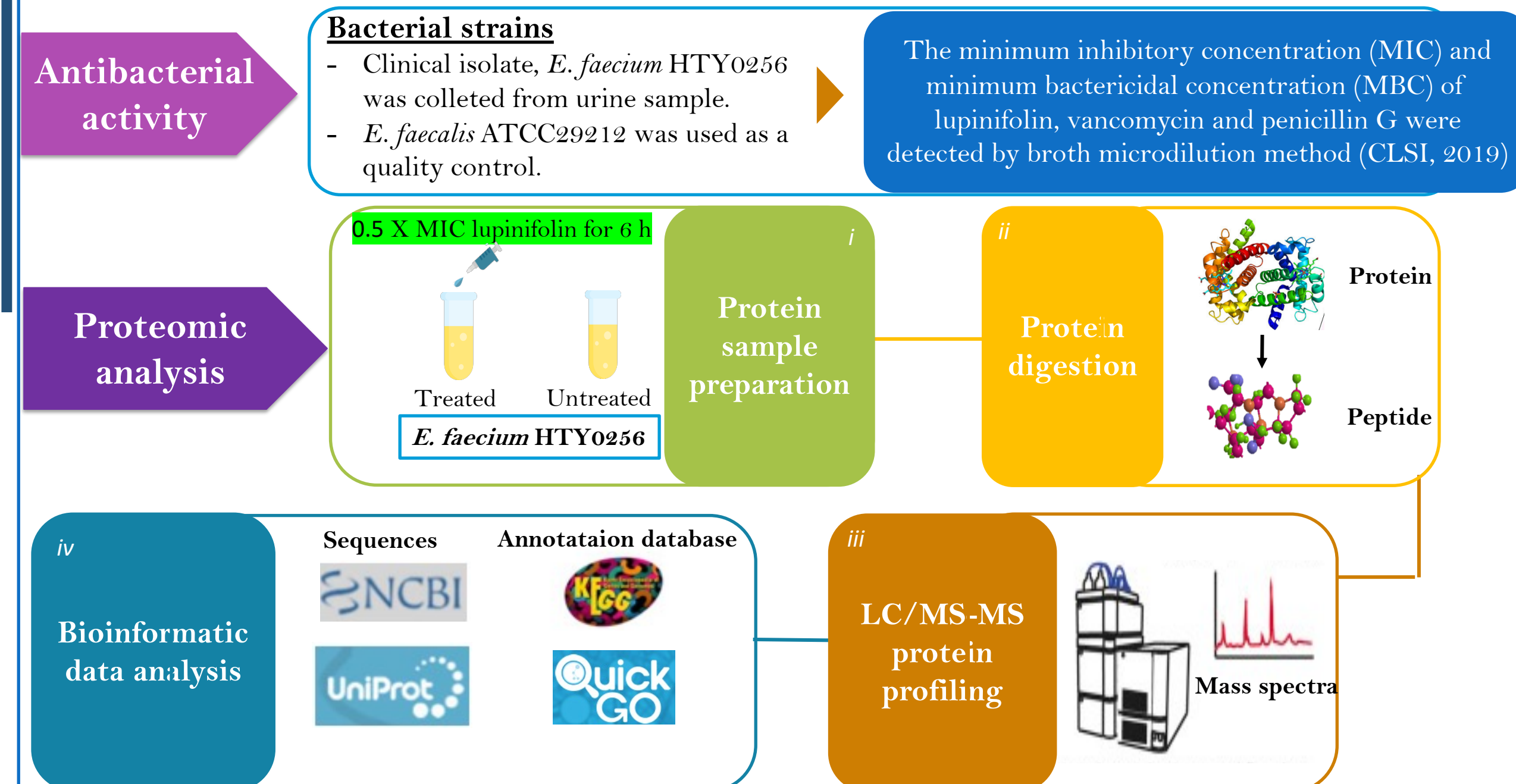


Albizia myriophylla Benth.
(Joycharat *et al.*, 2016)

Objective:

The aim of this study was to reveal the effect of lupinifolin against vancomycin-resistant *E. faecium* using proteomic analysis.

Material and methodology



Results

Table 1 MIC and MBC of of lupinifolin of *E. faecium* HTY0256 and *E. faecalis* ATCC29212

Bacterial strains	Lupinifolin (µg/ml)		Vancomycin (µg/ml)	
	MIC	MBC	MIC	MBC
<i>E. faecium</i> HTY0256 (<i>vanA</i>)	4	8	256	>1024
<i>E. faecalis</i> ATCC29212	0.5	2	4	128

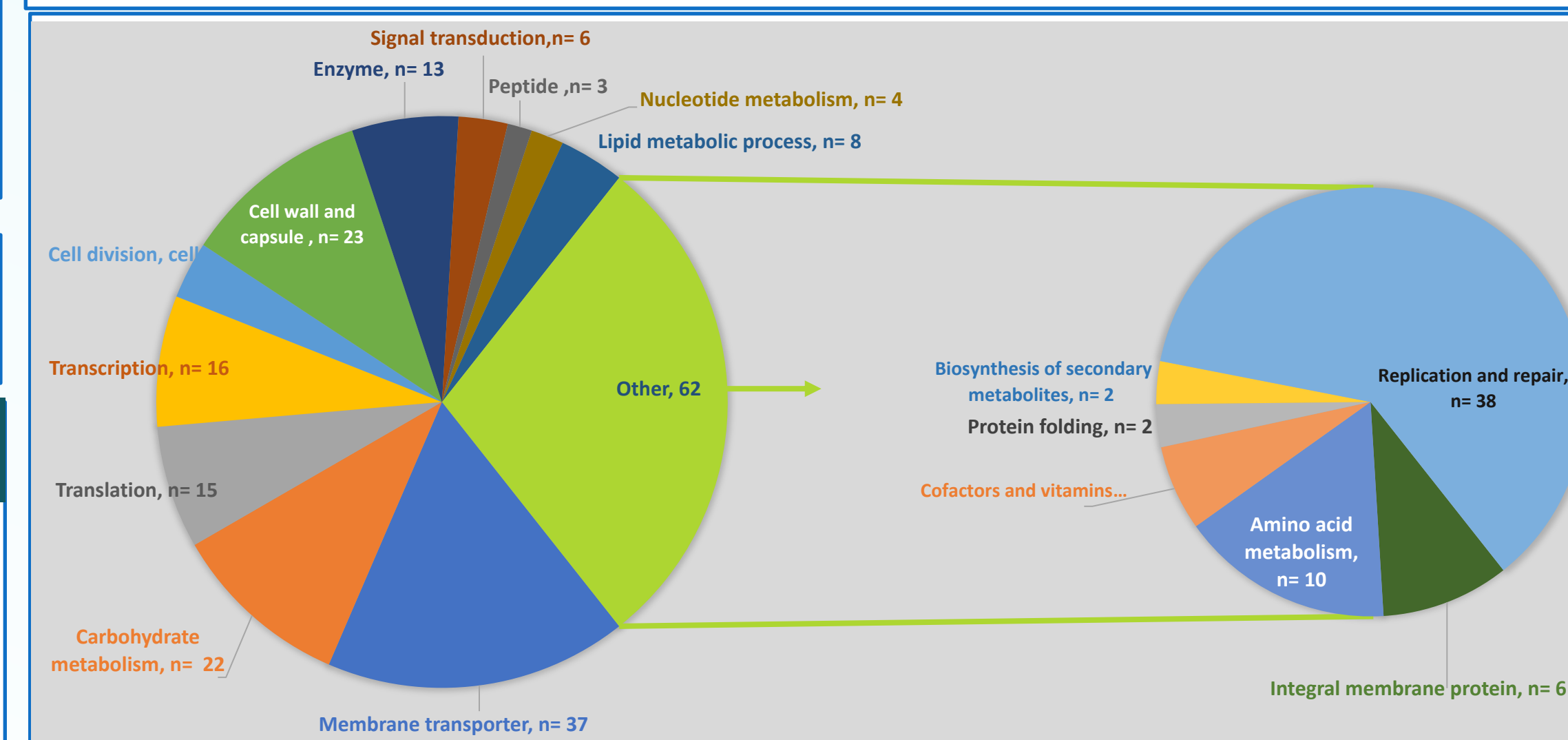


Figure 1. Proteomic profiling of *E. faecium* HTY0256 after lupinifolin exposure. KEGG pathway enrichment analysis of differentially expressed proteins (DEPs). DEPs were functionally sorted into 17 functional categories according to the gene ontology annotation.

- Proteins from same pathway probably carried out their biological function together, KEGG database was applied to analyze the biological pathways of the lupinifolin treatment, DEPs were mapped to KEGG pathway database in control vs treatment group.
- Among this pathways, the majority of pathways were related to transporter membrane, carbohydrate metabolism, call wall organization and replication, and DNA repair.
- The results suggested that lupinifolin mainly affected the transporter membrane, carbohydrate metabolism, call wall organization and replication, and DNA repair.

Results

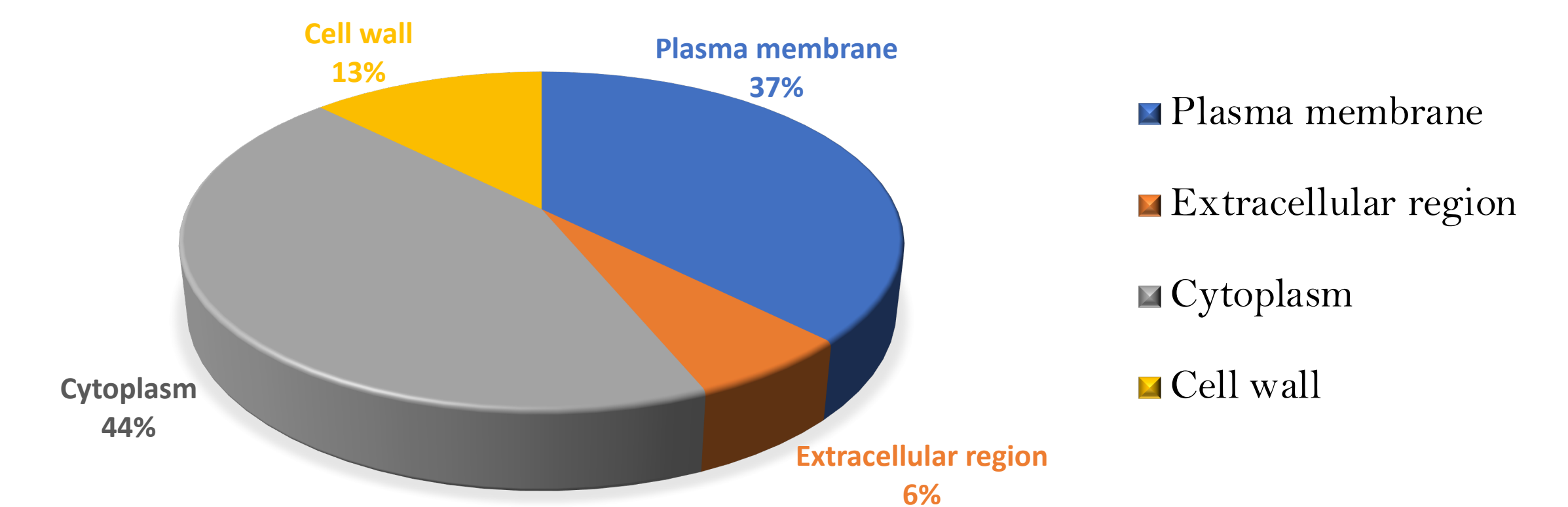


Figure 2. Identification and analysis of differentially expressed proteins (DEPs) between lupinifolin treatment and control. Identified proteins were group based on cellular component in the DEPs.

Conclusions

- These findings mainly suggests the comprehensive proteomic profiling related to action of lupinifolin against vancomycin-resistant *Enterococcus*.
- Our works provide further evidence to support therapeutic efficiency of lupinifolin which could lead to the development of a new effective drug for treatment of multidrug infections.

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Acknowledgments

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