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# **In silico epitope mapping and Identification of essential enzymes as potential drug targets in *Mycobacterium tuberculosis* using genome metabolic pathways analysis**

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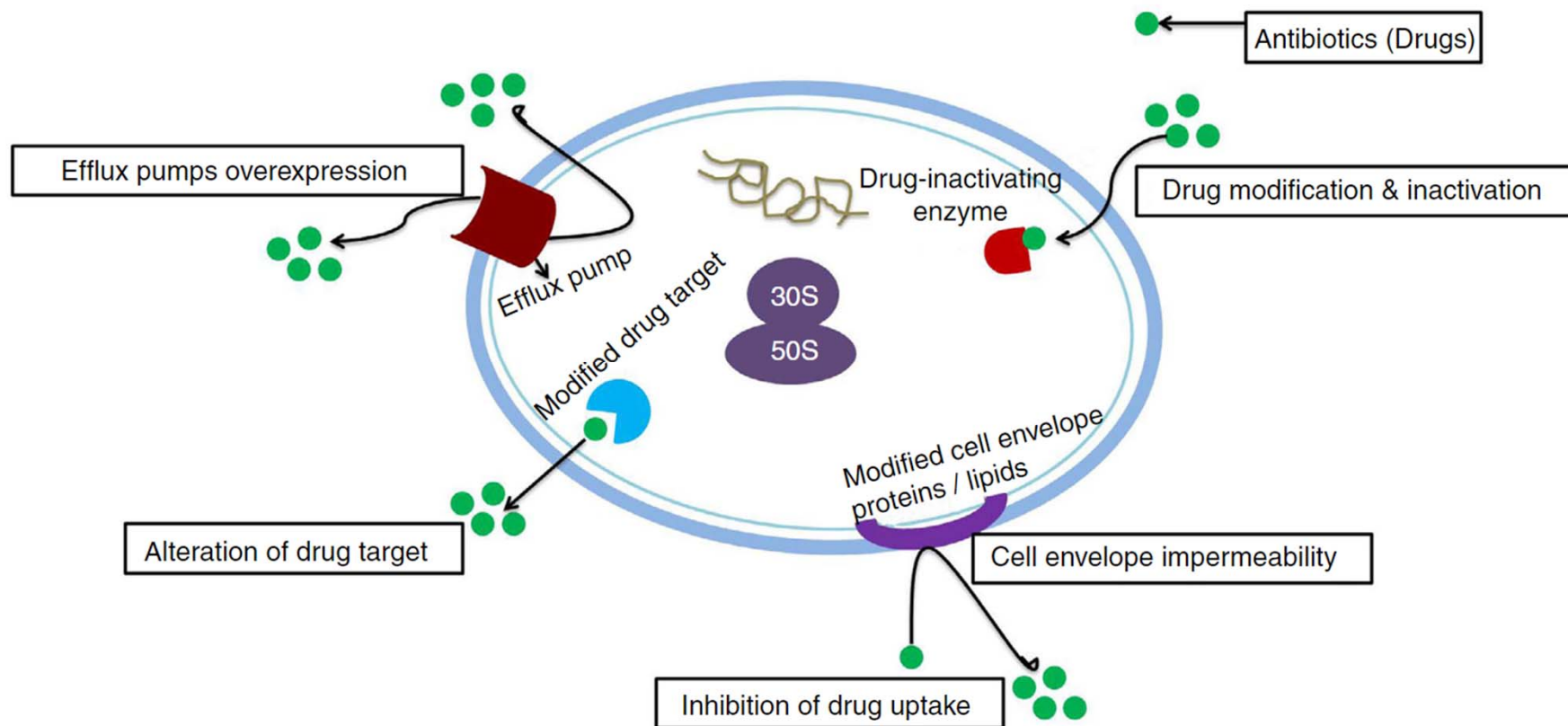
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**From West Java for Indonesia to the World through SDGs**



# Introduction



**Figure 1.** Schematic diagram showing the drug resistance mechanisms in *Mycobacterium tuberculosis*

Singh et al. 2019



# Purposes of the study

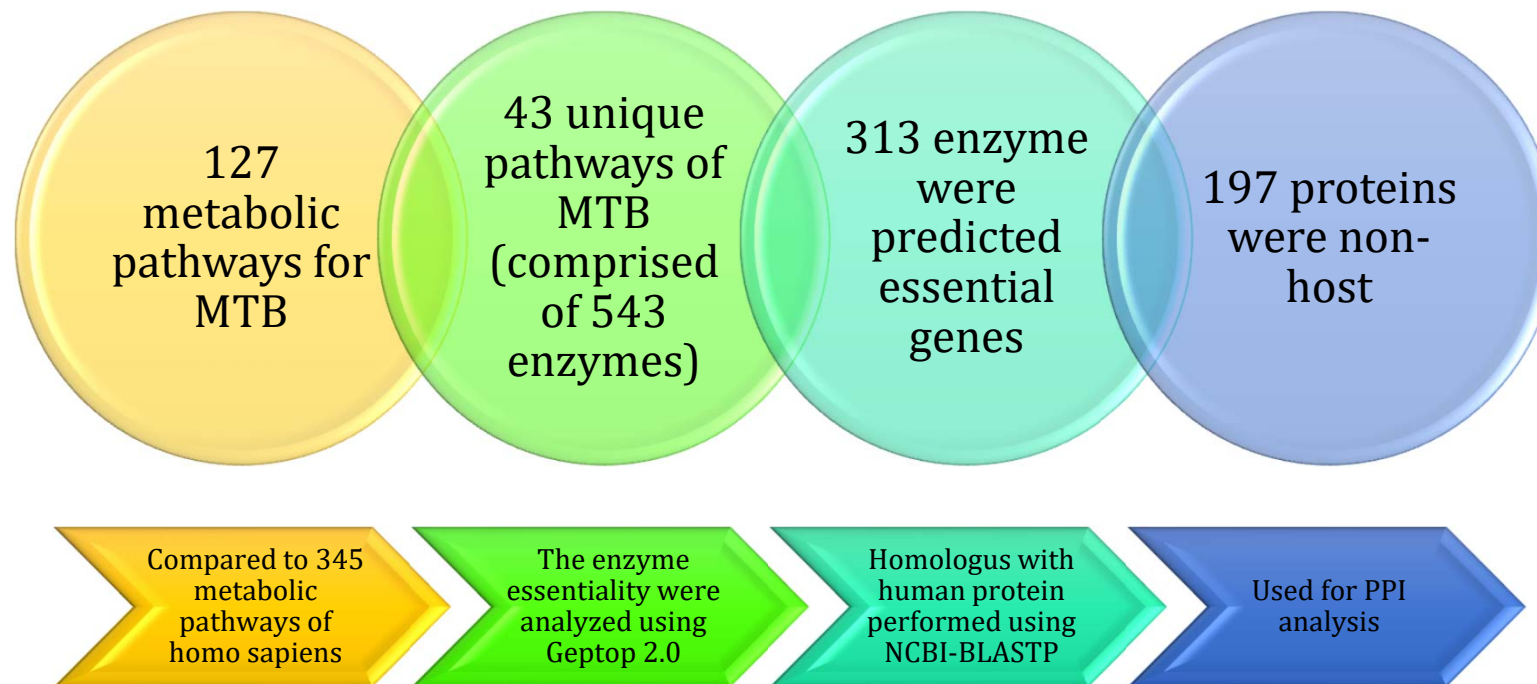
to identify essential enzymes of MTB for survival and potential drug targets using a comparative analysis of the metabolic pathways of the host and pathogen

to identify the potential epitopes from peptidoglycan binding protein ompA Rv0899 MTB for vaccine-peptide candidate using an epitope mapping analysis



# Results

(Metabolic pathways analysis and identification of essential genes)

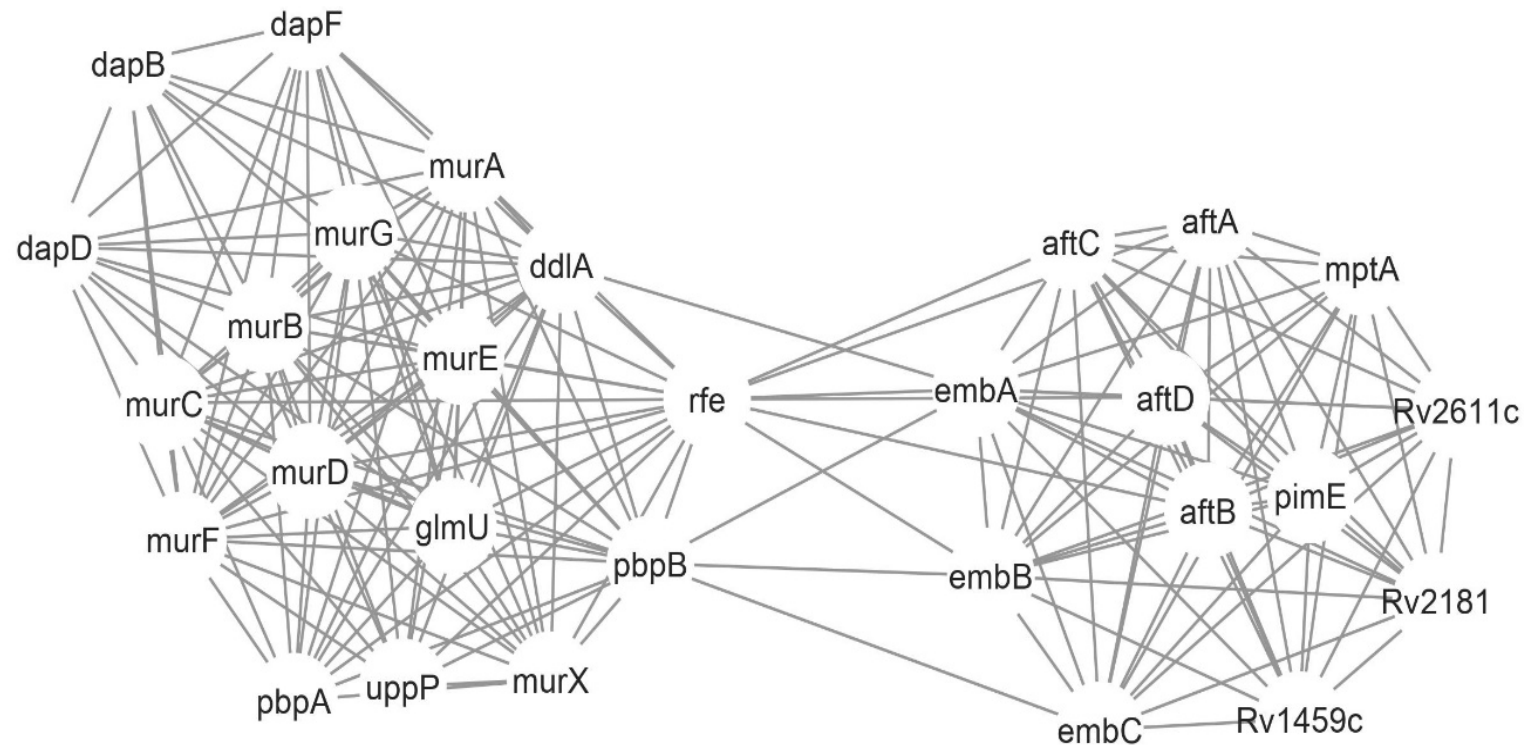


**Figure 2.** Extraction of essential proteins of MTB from metabolic comparison between homo sapiens and MTB



# Results

## (Protein-protein interaction (PPI) analysis)

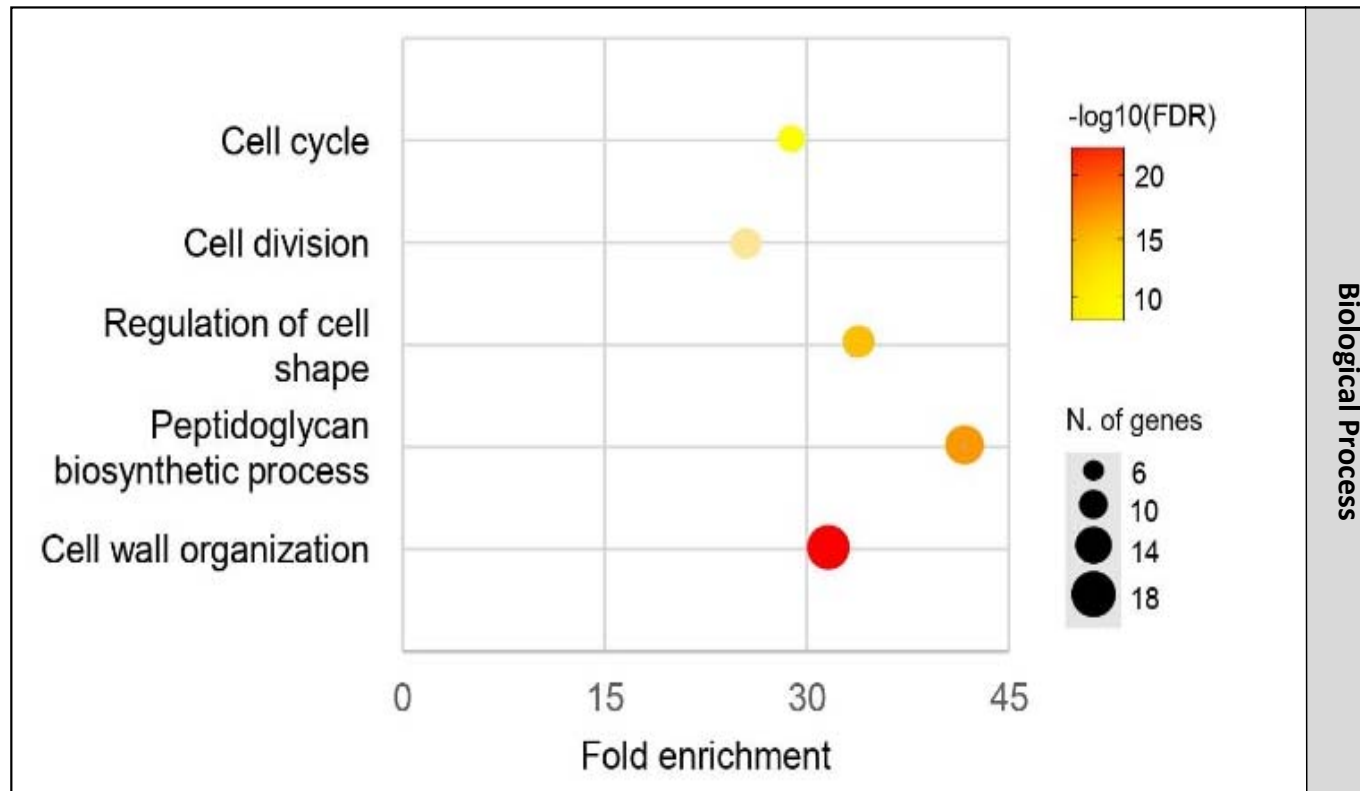


**Figure 3.** Protein-protein interaction of 29 proteins from non-host essential protein from MTB



# Results

## (Gene enrichment analysis)

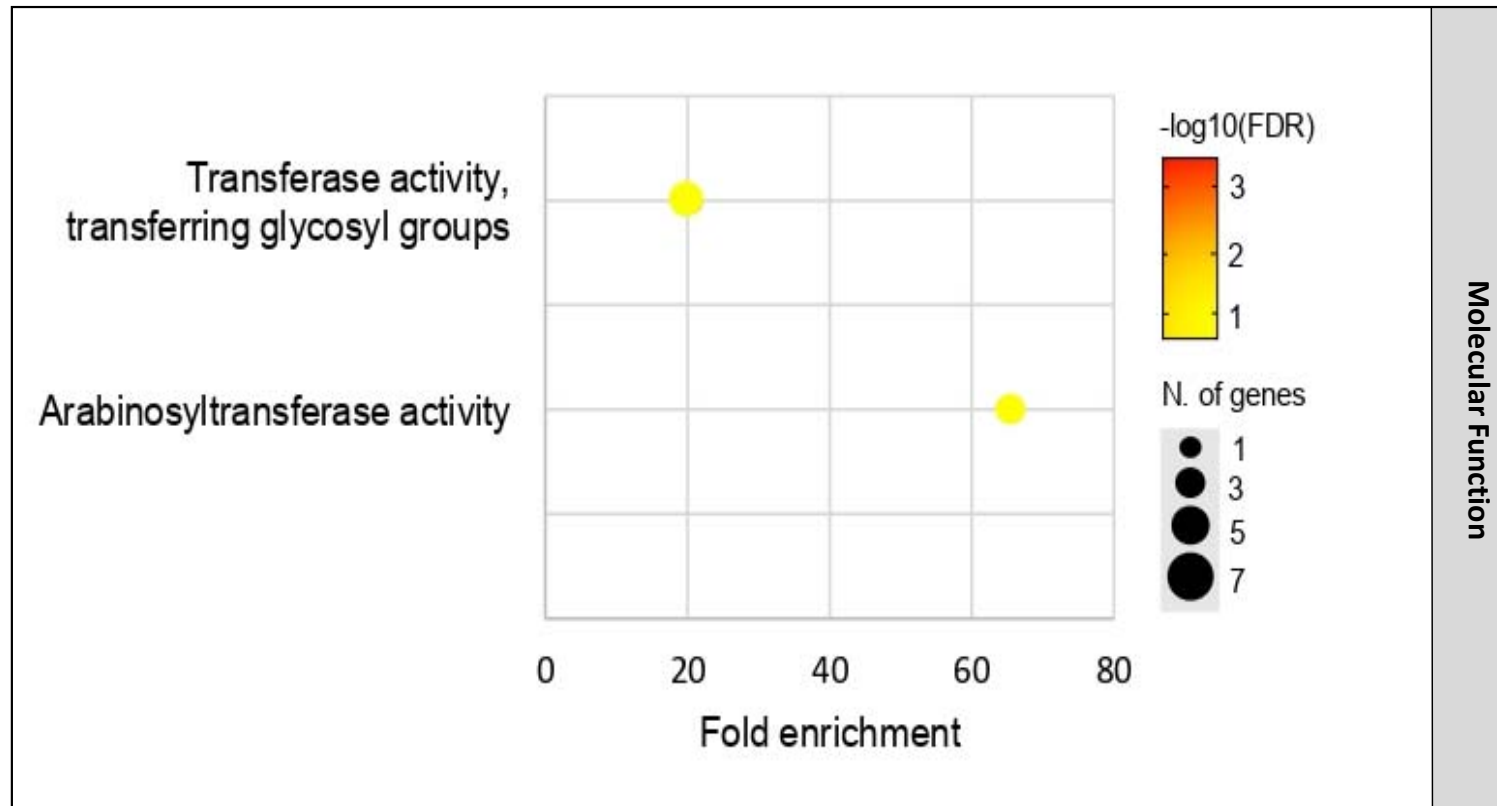


**Figure 4.** Gene ontology analysis of 29 proteins from non-host essential protein from MTB. Biological Process (A)



# Results

(Gene enrichment analysis) – cont.

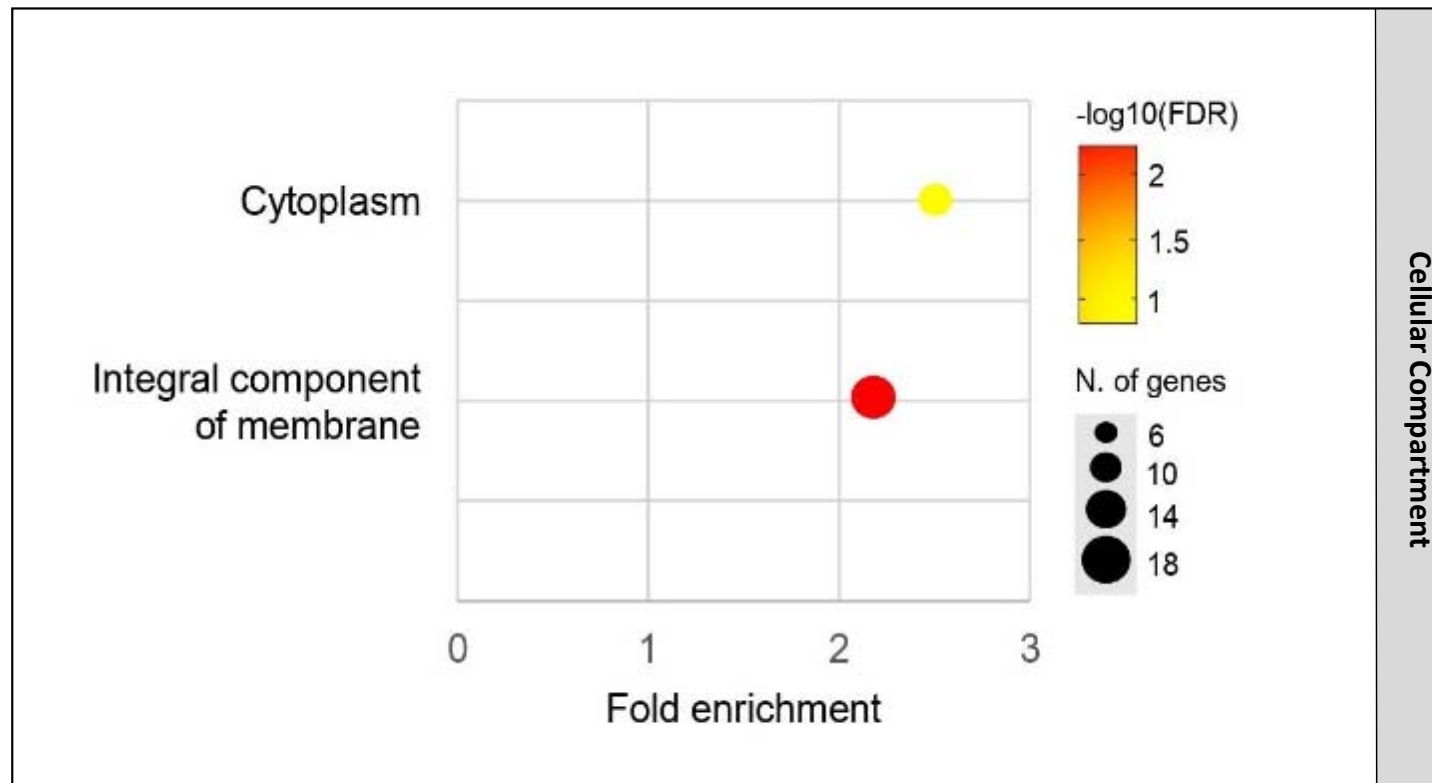


**Figure 5.** Gene ontology analysis of 29 proteins from non-host essential protein from MTB. Molecular function (B)



# Results

(Gene enrichment analysis) – cont.



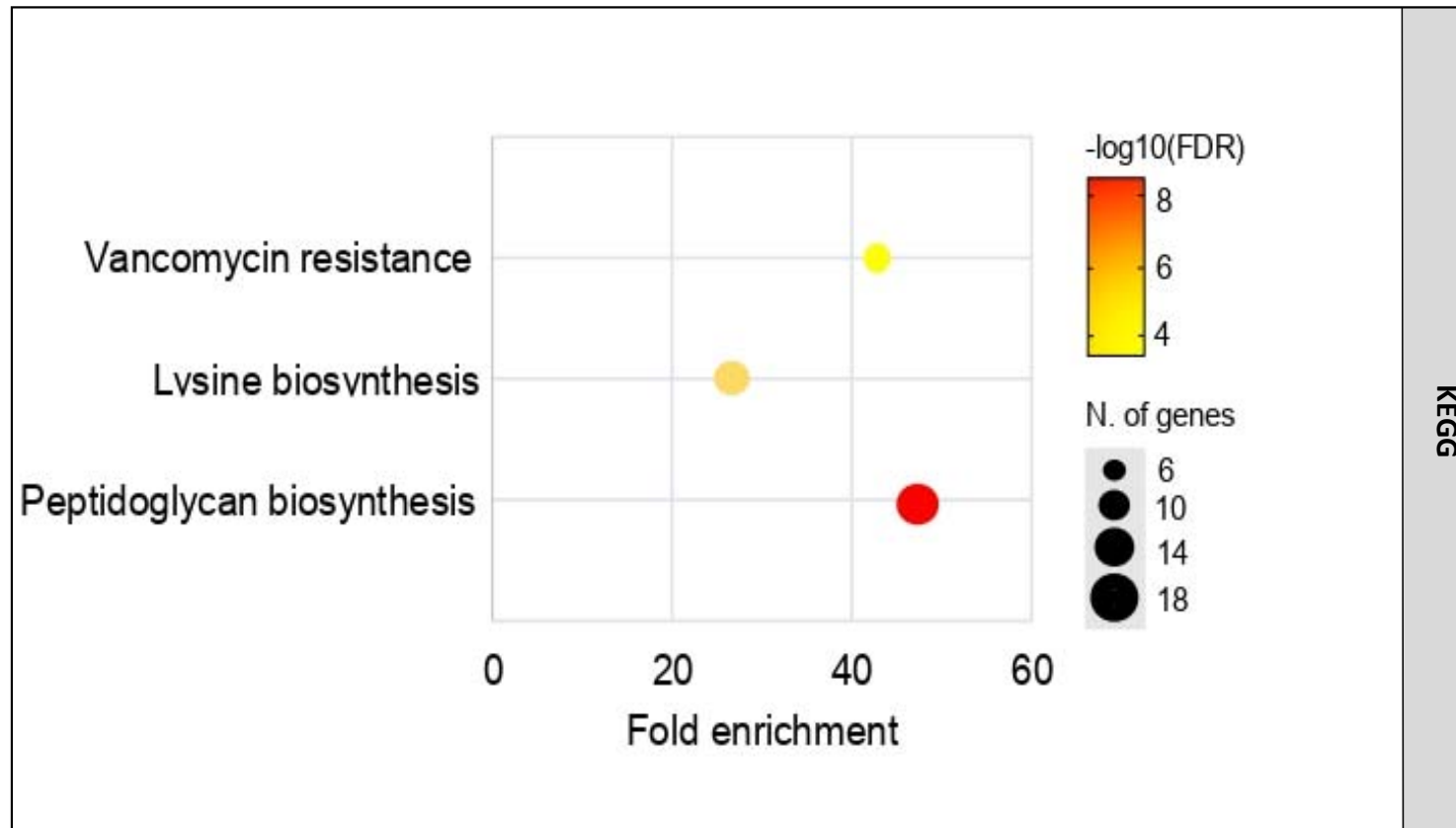
**Figure 6.** Gene ontology analysis of 29 proteins from non-host essential protein from MTB. Cellular compartment (C)





# Results

(Gene enrichment analysis) – cont.



**Figure 7.** Gene ontology analysis of 29 proteins from non-host essential protein from MTB. KEGG; Kyoto Encyclopedia of Genes and Genomes (D)



# Results

## (Novel drug targets)

**Tabel 1.** List of proteins selected as novel drug targets

No	Accession No.	Protein names	Subcellular localization
1	NP_217127.1	Phosphatidylinositol mannoside acyltransferase	Cytoplasm
2	NP_217242.1	Diaminopimelate epimerase	Cytoplasm
3	NP_215534.1	Bifunctional protein GlmU	Cytoplasm
4	NP_215717.1	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	Cytoplasm
5	NP_215675.1	Polyprenol-phosphate-mannose-dependent alpha-(1-2)-phosphatidylinositol pentamannoside	Transmembrane
6	NP_214750.1	Alpha-(1->3)-arabinofuranosyltransferase	Transmembrane
7	NP_216697.1	Polyprenol-phosphate-mannose-dependent alpha-(1-2)-phosphatidylinositol mannoside	Transmembrane
8	NP_216690.1	Alpha-(1->6)-mannopyranosyltransferase A	Transmembrane
9	NP_215975.1	Alpha-(1->6)-mannopyranosyltransferase Rv1459c	Transmembrane
10	NP_218309.1	Galactan 5-O-arabinofuranosyltransferase	Transmembrane
11	NP_218322.1	Terminal beta-(1->2) arabinofuranosyltransferase	Transmembrane
12	NP_215818.1	Decaprenyl-phosphate N-acetylglucosaminephosphotransferase	Transmembrane



# Results

## (Epitope mapping)

**Tabel 2.** Prediction of BepiPred on peptidoglycan of MTB

Label	Start	End	Peptide	Length (mer)
A1	49	74	AFERPQSVTGPTGVLPTLTPT STRGA	26
B1	160	184	VTLTGTAPSSEHKDAVKRAAT STWP	25
C1	193	210	EVTGQAPPGPPASGPCAD	18
D1	216	233	NAVTGGPIAFGNDGASLI	18
E1	258	270	NGYTDNTGSEGIN	13
F1	303	318	VNPIASNATPEGRAKN	16



# Results

## (Epitope mapping)

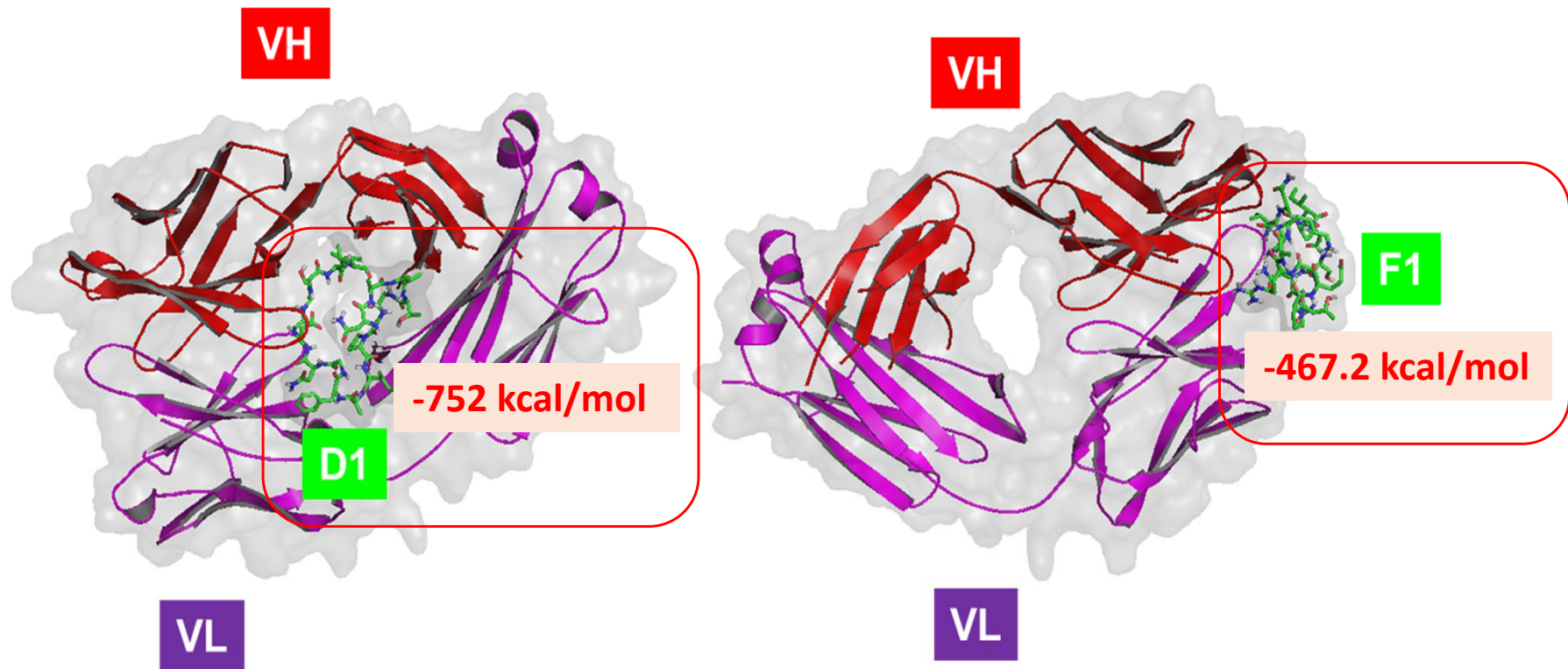
**Tabel 3.** Identification of antigenicity and epitope similarity on peptidoglycan of MTB

Label	Score		Properties	
	Vaxijen	Blastp	Vaxijen	Blastp
A1	-0.862	-	Non-antigen	-
B1	0.238	-	Non-antigen	-
C1	0.226	-	Non-antigen	-
D1	0.733	<20%	Antigen	Non-similar
E1	0.214	-	Non-antigen	
F1	1.011	<20%	Antigen	Non-similar



# Results

## (Epitope mapping)



**Figure 8.** Visualization of peptide-protein docking. BCRs are shown in cartoon with transparent surfaces and sticks for peptides. BCR, B cell receptor; VL, light chain of BCR; VH, heavy chain of BCR



# Conclusion

Twelve proteins were found to be uniquely involved in pathogen-specific unique pathways of MTB. A total of 4 proteins were cytoplasm and 8 proteins were transmembrane proteins.

Two potential epitopes from peptidoglycan binding protein ompA Rv0899 MTB were found with an 18-mer length and a 16-mer length, respectively.



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# ***THANK YOU***

# **TERIMA KASIH**

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