

Table 1. Dynamic changes in composition of the DNA repairing protein complex, Uvr, as a response to DNA damages after UV irradiation of the *Mycobacterium bovis* BCG cells. The numbers (intensity) reflect not only presence or absence of the protein but also relative abundance of the protein in that complex (semi-quantitative analysis).

Protein IDs	Description	Mol. weight [kDa]	Intensity				
			UvrA 0'	UvrA 1'	UvrA 5'	UvrA 15'	UvrA 30'
Rv1638/BCG_1676	excinuclease ABC subunit A (UvrA)	106.2	6.98E+08	5.11E+08	6.51E+08	2.21E+09	8.45E+09
BCG_1671	excinuclease ABC subunit B (UvrB)	78.1	1.20E+07	5.97E+06			2.56E+06
BCG_3704c	DNA topoisomerase I	102.4	1.03E+06		2.64E+06		3.08E+06
BCG_3222c	putative DNA helicase II (UvrD2)	75.6	1.58E+06				1.60E+06
BCG_1667	DNA polymerase I	98.5			4.99E+06		

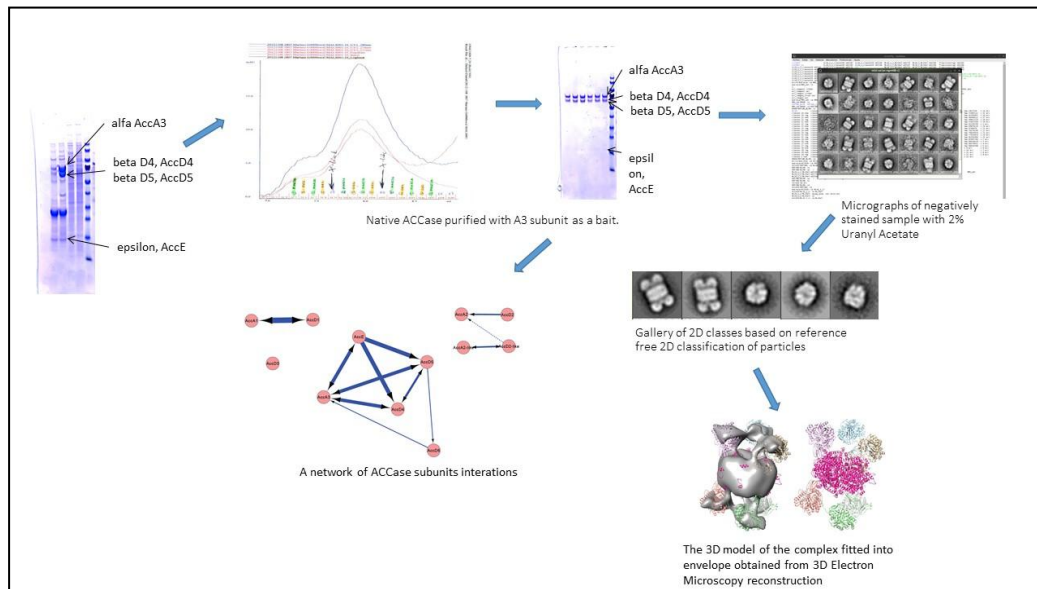


Figure 1 An example of analysis of the ACC protein complex, involved in mycolic acid synthesis, a key component of the bacterial wall. The method developed in this work allowed to purified the ACC complex and visualize it using electron microscopy and reconstruct the 3D structure.

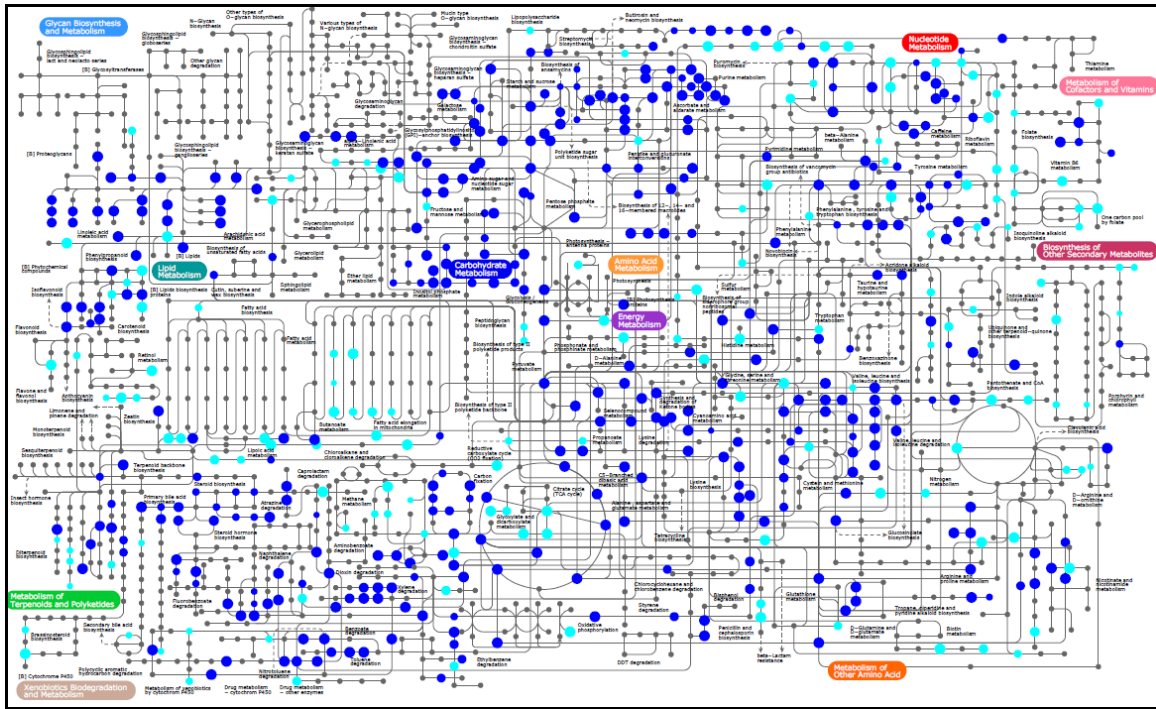
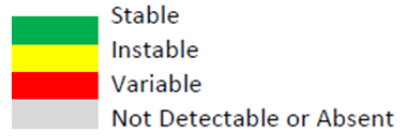
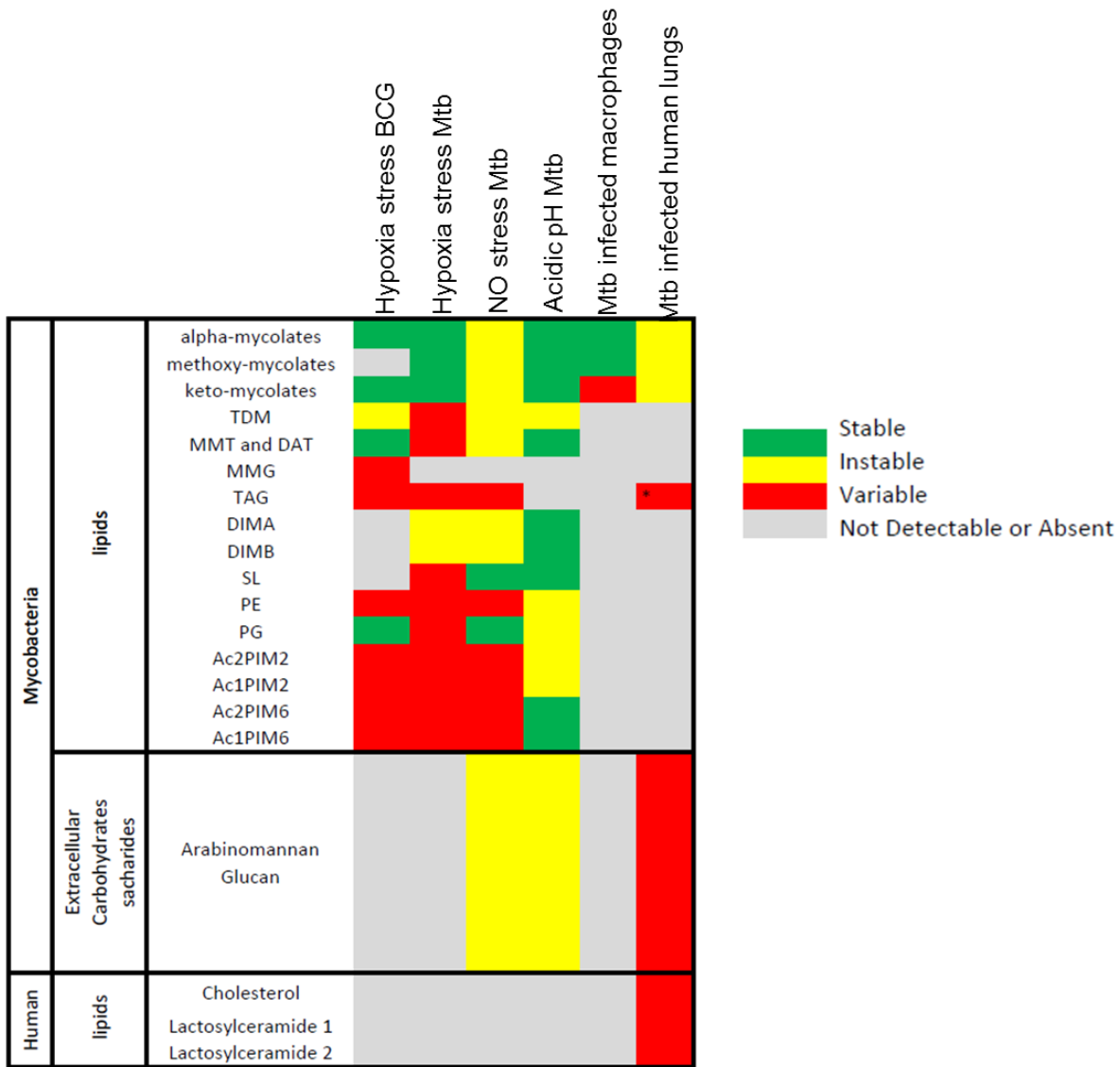


Figure 2 Metabolites detected in *M. tuberculosis* with untargeted mass spectrometry. Dark blue dots are annotated with high confidence. Light blue dots cannot be uniquely assigned to a single metabolite.

	Mycobacteria																	
	lipids	Extracellular Carbohydrates sacharides	alpha-mycolates	methoxy-mycolates	keto-mycolates	TDM	MMT and DAT	MMG	TAG	DIMA	DIMB	SL	PE	PG	Ac2PIM2	Ac1PIM2	Ac2PIM6	Ac1PIM6
Human	lipids	Cholesterol Lactosylceramide 1 Lactosylceramide 2	Hypoxia stress BCG		Hypoxia stress Mtb		NO stress Mtb		Acidic pH Mtb		Mtb infected macrophages		Mtb infected human lungs					
			Hypoxia stress BCG		Hypoxia stress Mtb		NO stress Mtb		Acidic pH Mtb		Mtb infected macrophages		Mtb infected human lungs					





BCG : *Mycobacterium bovis* BCG ; Mtb : *Mycobacterium tuberculosis* ; NO: Nitric Oxide, Hypoxia: Hypoxia followed by reeration, TDM: Trehalose DiMycolate, TMM: Trehalose MonoMycolate, DAT: DiAcylTrehalose, MMG: Glucose MonoMycolate, TAG: TriAcylGlycerol, DIM:DiMycocerosate, SL: SulfoLipid, PE: Phosphatidyl Ethanolamine, PG: PhosphatidylGlycerol, PIM: Phosphatidyl mono (1) or diacylated (2) Inositol containing two (2) or six (6) mannosides.

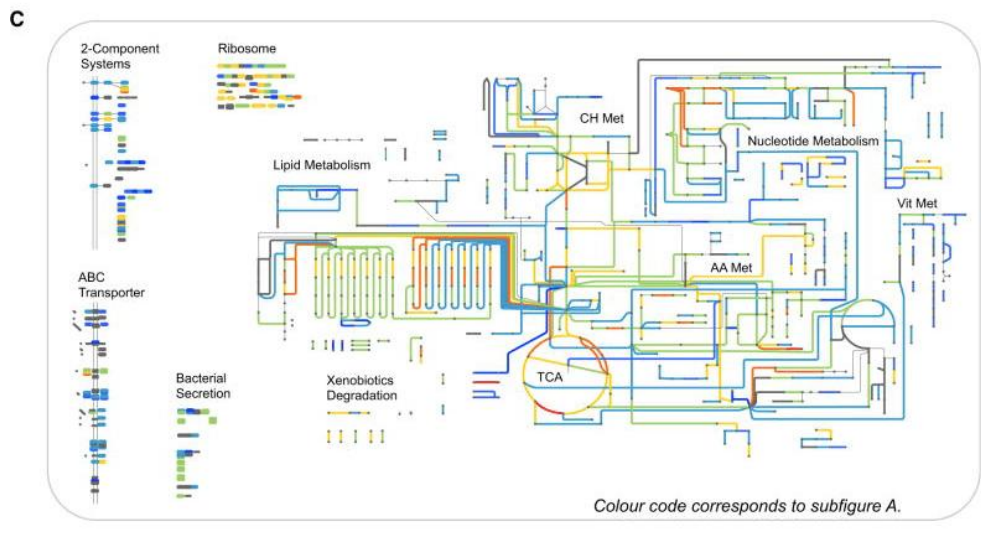


Figure 5 Visualization of Protein abundance data.

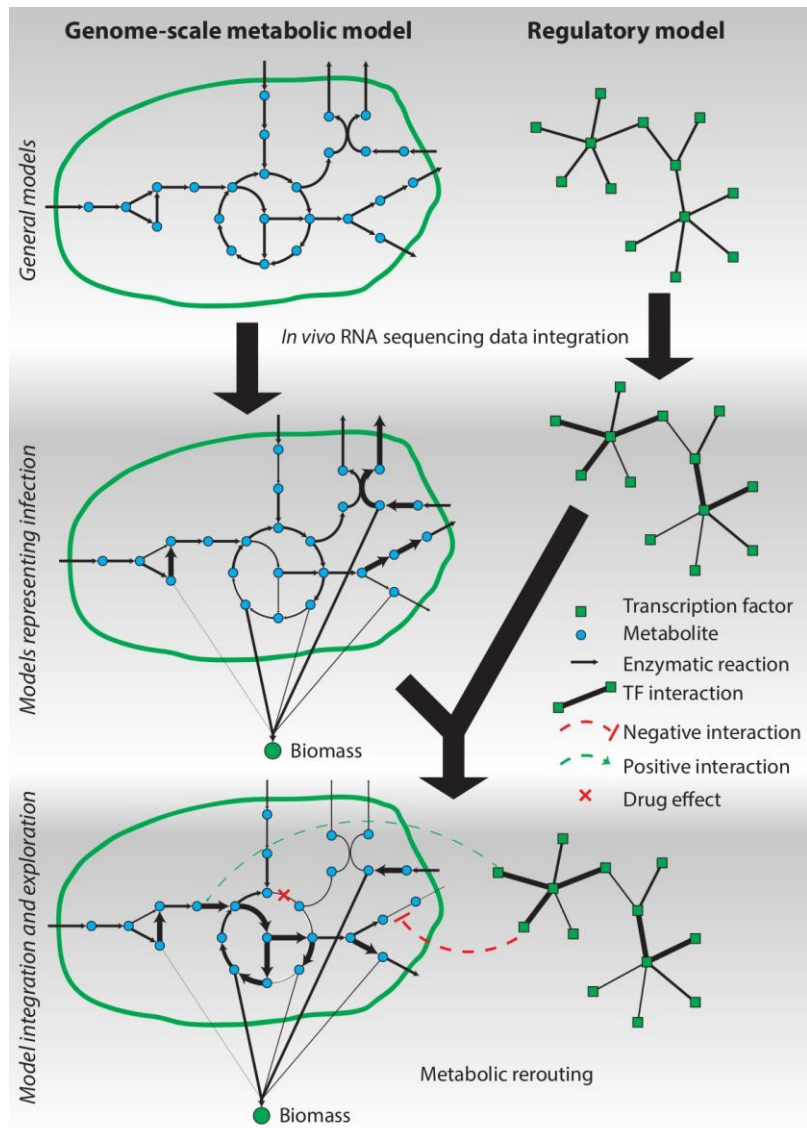


Figure 6 To describe TB infection, general models are created, that are then converted into models representing the infection through the integration of expression data. The final models can be combined and mined to identify new therapeutic strategies.