

## Supplemental Information

### <sup>13</sup>C-Flux Spectral Analysis of Host-Pathogen

#### Metabolism Reveals a Mixed Diet for Intracellular

#### *Mycobacterium tuberculosis*

Dany J.V. Beste, Katharina Nöh, Sebastian Niedenführ, Tom A. Mendum, Nathaniel D. Hawkins, Jane L. Ward, Michael H. Beale, Wolfgang Wiechert, and Johnjoe McFadden

#### Inventory of Supplemental Information

Table S1, Related to Figure 1. <sup>13</sup>C isotopomer abundance of protein amino acids extracted from *Mycobacterium tuberculosis* after 24, 48 and 72 hours growth in <sup>13</sup>C pre-labelled THP-1 macrophages demonstrating isotopic steady state after 48 hours of the infection.

Table S2, Related to Figure 4. Experimental (GC-MS) mass distributions in the amino acid derivatives of [U-<sup>13</sup>C<sub>6</sub>] glucose RPMI grown *Mycobacterium tuberculosis* H37Rv (MTB), intracellular MTB (extracted from THP-1 macrophages pre-labelled with [U-<sup>13</sup>C<sub>6</sub>] glucose), infected and uninfected THP-1 macrophages pre-labelled with [U-<sup>13</sup>C<sub>6</sub>] glucose after 48 hours of infection/growth.

Table S3, Related to Figure 6. Experimental (GC-MS) mass distributions in the amino acid derivatives of RPMI grown wild type *Mycobacterium tuberculosis*

**(MTB), intracellular MTB, intracellular PEPCK KO and infected THP-1 macrophages cultivated with sodium [<sup>13</sup>C] bicarbonate.**

**Table S4, Related to Figure 5. Experimental (GC-MS) mass distributions in the amino acid derivatives extracted from  $\Delta$ PEPCK KO cultivated in [U<sup>13</sup>-C<sub>6</sub>] glucose RPMI and intracellular  $\Delta$ PEPCK grown inside THP-1 macrophages which were pre-labelled with [U-<sup>13</sup>C<sub>6</sub>] glucose.**

**Table S5, Related to Experimental Procedures. Network reference model of the central metabolism of *Mycobacterium tuberculosis*.**

**Table S6, Related to Experimental Procedures. Experimental (GC-MS) and calculated mass distributions in the amino acid derivatives of *Mycobacterium tuberculosis* (MTB) residing in the macrophage environment (MAC) .**

**Table S5: Network reference model of the central metabolism of *Mycobacterium tuberculosis***

Reaction	Stoichiometry and C-atom transitions
GlcUptake(_0/_1)	GLC(#ABCDEF) → G6P(#ABCDEF)
GlycUptake(_0/_1)	GLYC_IN (#ABC) → GAP (#ABC)
OLACUptake(_0/_1)	OLAC (#AB) → ACE (#AB)
aceProd	ACE (#AB) ⇌ ACCOA (#AB)
AlaUptake	ALA_IN (#ABC) → ALA (#ABC)
AspUptake	ASP (#ABC) → ASP (#ABC)
CO2out	CO <sub>2</sub> (#A) → CO <sub>2ex</sub> (#A)
GluUptake	GLU_IN (#ABCDE) → GLU (#ABCDE)
GlycUptake	GLYC (#ABC) → GAP (#ABC)
HisUptake	HIS_IN (#ABCDEF) → HIS (#ABCDEF)
IsoUptake	ISO_IN (#ABCDEF) → ISO (#ABCDEF)
LeuUptake	LEU_IN (#ABCDEF) → LEU (#ABCDEF)
LysUptake	LYS_IN (#ABCDEF) → LYS (#ABCDEF)
SerUptake	SER_IN (#ABC) → SER (#ABC)
ThrUptake	THR_IN (#ABCD) → THR (#ABCD)
TyrUptake	TYR_IN (#ABCDEFGHI) → TYR (#ABCDEFGHI)
ValUptake	VAL_IN (#ABCDE) → VAL (#ABCDE)
pgi	G6P (#ABCDEF) ↔ FBP (#ABCDEF)
fba	GAP (#CBA) + GAP (#DEF) ↔ FBP (#ABCDEF)
gapA	GAP (#ABC) ↔ PGA (#ABC)
pykeno	PGA (#ABC) ↔ PYRPEP (#ABC)
gnd	G6P (#ABCDEF) → P5P (#BCDEF) + CO <sub>2</sub> (#A)
tkt1	GAP (#CDE) + G6P (#ABabcd) ↔ P5P (#ABCDE) + E4P (#abcd)
tkt2	S7P (#ABabcde) + GAP (#CDE) ↔ P5P (#ABCDE) + P5P (#abcde)
tal	E4P (#defg) + G6P (#abcABC) ↔ GAP (#ABC) + S7P (#abcdefg)
pdh	PYRPEP (#ABC) → ACCOA (#BC) + CO <sub>2</sub> (#A)
cs	MALOOA (#ABCD) + ACCOA (#ab) ⇌ ICIT (#DCBbaA)
icdh	ICIT (#ABCDEF) ⇌ OXG (#ABCDE) + CO <sub>2</sub> (#F)
kor	OXG (#ABCDE) ⇌ SUCCOA (#BCDE) + CO <sub>2</sub> (#A)
scs	SUCCOA (#ABCD) ↔ SUC (#ABCD)
sdh	SUC (#ABCD) ↔ FUM (#ABCD)
fum(a/b)	FUM (#ABCD) ↔ MALOOA (0.5 #ABCD + 0.5 #DCBA)
icl	ICIT (#ABCDEF) ⇌ GLX (#AB) + SUC (#FCDE)
ms	GLX (#AB) + ACCOA (#ab) → MALOOA (#ABba)
pckmez	PYRPEP (#ABC) + CO <sub>2</sub> (#a) ↔ MALOOA (#ABCa)
alaProd	PYRPEP (#ABC) ⇌ ALA (#ABC)
kivProd	PYR (#ABC) + PYR (#abc) → KIV (#ABCbc) + CO <sub>2</sub> (#a)
valProd	KIV (#ABCDE) ⇌ VAL (#ABCDE)
leuProd	KIV (#ABCDE) + ACCOA (#ab) ⇌ LEU (#BCDEab) + CO <sub>2</sub> (#A)
serProd	GAP (#ABC) ⇌ SER (#ABC)
gl1	SER (#ABC) ⇌ GLY (#AB) + MTHF (#C)
hisProd	P5P (#ABCDE) + MTHF (#F) ⇌ HIS (#FEDCBA)
gl2	GLY (#AB) ⇌ MTHF (#B) + CO <sub>2</sub> (#A)
aspProd	MALOOA (#ABCD) ⇌ ASP (#ABCD)

thrProd	ASP (#ABCD) ⇌ THR (#ABCD)
metProd	ASP (#ABCD) → MET (#ABCD)
lysProd(1/2)	PYRPEP (#ABC) + ASP (#ABCD) ⇌ LYS (0.5 #BCabcd + 0.5 #ABCbcd) + CO <sub>2</sub> (0.5 #A + 0.5 #a)
isoProd	THR (#ABCD) + PYRPEP (#abc) ⇌ ISO (#ABCDbc) + CO <sub>2</sub> (#a)
gluProd	OXG (#ABCDE) ⇌ GLU (#ABCDE)
proProd	GLU (#ABCDE) → PRO (#ABCDE)
ornProd	GLU (#ABCDE) → ORN (#ABCDE)
pheProd1	E4P (#ABCD) + PYRPEP (#abc) → CHO (#bcABCDa)
pheProd2	CHO (#ABCDEFG) + PYRPEP (#abc) → PHE (#abcABCDEF) + CO <sub>2</sub> (#G)
tyrProd	CHO (#ABCDEFG) + PYRPEP (#abc) ⇌ TYR (#abcABCDEF) + CO <sub>2</sub> (#G)
Bio	0.046 ALA + 0.009 LEU + 0.006 SER + 0.012 GLY + 0.012 LYS + 0.005 ISO + 0.017 HIS + 0.026 ASP + 0.007 THR + 0.002 MET + 0.007 PRO + 0.018 GLU + 0.002 TYR + 0.003 PHE + 0.026 VAL + 0.018 G6P + 0.041 F6P (taken from G6P pool) + 0.065 P5P + 0.001 GAP + 0.005 PGA + 0.015 PEP (taken from PYRPEP pool) + 0.015 PYR (taken from PYRPEP pool) + 0.589 ACCOA + 0.022 MALOAA + 0.015 OXG [all in mmol g <sub>DW</sub> <sup>-1</sup> ] → 1 BIO [in g <sub>DW</sub> ]

**Legend:**

⇌: net fluxes possible in both directions, zero exchange flux

→: net flux in specified direction, zero exchange flux

↔: net flux possible in both directions, exchange flux present

**Model assumptions and simplifications:**

Linear reaction sequences without carbon cleavage were condensed for simplification. Metabolite pools F6P and G6P are lumped to one pool (G6P), as the interconverting phosphoglucose isomerase reaction has usually a high exchange rate. Pyruvate and PEP, malate and oxaloacetate were lumped to one pool PYRPEP and MALOAA, respectively. Irreversibility assumptions are due to thermodynamic considerations and indicated by directed arrows.