

Supporting Information

Metabolic Flux Analysis of *Xanthomonas oryzae* Treated with Bismethiazol Revealed Glutathione Oxidoreductase in Glutathione Metabolism Serves as an Effective Target

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Table S1. The information summary of the reactions with metabolic flux upregulation.

ID	Flux	Target name	Formula	Pathway
CYTBO3_4 pp	14.884833	Cytochrome oxidase bo3 (ubiquinol-8: 4 protons) (periplasm)	$4.0 \text{ h_c} + 0.5 \text{ o2_c} + \text{q8h2_c} \rightleftharpoons \text{h2o_c} + \text{q8_c} + 4.0 \text{ h_p}$	Glycolysis / Gluconeogenesis Pyruvate metabolism Metabolic pathways Biosynthesis of secondary metabolites Microbial metabolism in diverse environments
PYK3	8.321336	Pyruvate kinase(3)	$\text{gdp_c} + \text{h_c} + \text{pep_c} \rightleftharpoons \text{gtp_c} + \text{pyr_c}$	Pyruvate metabolism Metabolic pathways Biosynthesis of secondary metabolites Microbial metabolism in diverse environments
TRDR	3.241137	Thioredoxin reductase (NADPH)	$\text{h_c} + \text{nadph_c} + \text{trdox_c} \rightleftharpoons \text{nadp_c} + \text{trdrd_c}$	Selenocompound metabolism
GLUDy	1.907948	Glutamate dehydro- genase (NADP)	$\text{glu_L_c} + \text{h2o_c} + \text{nadp_c} \rightleftharpoons \text{akg_c} + \text{h_c} + \text{nadph_c} + \text{nh4_c}$	Arginine biosynthesis Alanine, aspartate and glutamate metabolism Nitrogen metabolism; Metabolic pathways Microbial metabolism in diverse environments
DCMPDA	1.068792	DCMP deaminase	$\text{dcmp_c} + \text{h_c} + \text{h2o_c} \rightleftharpoons \text{dump_c} + \text{nh4_c}$	Metabolic pathways Pyrimidine metabolism Nucleotide metabolism
CTPS1	1.06577	CTP synthase NH3	$\text{atp_c} + \text{nh4_c} + \text{utp_c} \rightleftharpoons \text{adp_c} + \text{ctp_c} + 2.0 \text{ h_c} + \text{pi_c}$	Pyruvate metabolism Metabolic pathways Nucleotide metabolism Biosynthesis of cofactors
UPPRT	1.063056	Uracil phosphoribosy- ltransferase	$\text{prpp_c} + \text{ura_c} \rightleftharpoons \text{ppi_c} + \text{ump_c}$	Pyrimidine metabolism Metabolic pathways Nucleotide metabolism
UMPK	1.061174	UMP kinase	$\text{atp_c} + \text{ump_c} \rightleftharpoons \text{adp_c} + \text{udp_c}$	Pyrimidine metabolism Metabolic pathways Nucleotide metabolism Biosynthesis of cofactors

PYK2	1.059291	Pyruvate kinase(3)	$h_c + pep_c + udp_c \rightleftharpoons pyr_c + utp_c$	Glycolysis / Gluconeogenesis Pyruvate metabolism Metabolic pathways Biosynthesis of secondary metabolites Microbial metabolism in diverse environments
PRPPS	1.057372	Phosphoribosylpyrophosphate synthetase	$atp_c + r5p_c \rightleftharpoons amp_c + h_c + prpp_c$	Pentose phosphate pathway Purine metabolism Metabolic pathway Biosynthesis of secondary metabolites Microbial metabolism in diverse environments Carbon metabolism; Biosynthesis of amino acids
ACCOAL	0.901765	Acetate-CoA ligase (ADP-forming)	$atp_c + coa_c + ppa_c \rightleftharpoons adp_c + pi_c + ppcoa_c$	Glycolysis / Gluconeogenesis Pyruvate metabolism Metabolic pathways Propanoate metabolism Microbial metabolism in diverse environments
CEPA	0.866570	Cellobiose phosphorylase	$pi_c + cellb_c \rightleftharpoons g1p_c + glc_D_c$	Starch and sucrose metabolism Metabolic pathways

Table S2. The information summary of the reactions with metabolic flux downregulation.

ID	Flux	Target name	Formula	Pathway
CYTBDt	-20.748077	Cytochrome oxidase bd (ubiquinol-8: 2 protons)	$2.0 \text{ h_c} + 0.5 \text{ o2_c} + \text{q8h2_c} \rightleftharpoons \text{h2o_c} + \text{q8_c} + 2.0 \text{ h_e}$	
ADNK1	-8.329232	Adenosine kinase	$\text{adn_c} + \text{atp_c} \rightleftharpoons \text{adp_c} + \text{amp_c} + \text{h_c}$	Purine metabolism Metabolic pathways Nucleotide metabolism
PYK	-8.283889	Pyruvate kinase	$\text{adp_c} + \text{h_c} + \text{pep_c} \rightleftharpoons \text{atp_c} + \text{pyr_c}$	Glycolysis / Gluconeogenesis Pyruvate metabolism Metabolic pathways Biosynthesis of secondary metabolites Microbial metabolism in diverse environments
NADH16pp	-5.856512	NADH dehydrogenase (ubiquinone-8 & 3 protons) (periplasm)	$4.0 \text{ h_c} + \text{nadh_c} + \text{q8_c} \rightleftharpoons \text{nad_c} + \text{q8h2_c} + 3.0 \text{ h_p}$	Arginine biosynthesis Alanine, aspartate and glutamate metabolism Nitrogen metabolism; Metabolic pathways Microbial metabolism in diverse environments
GRXR	-2.173855	Glutaredoxin reductase	$\text{grxox_c} + 2.0 \text{ gthrd_c} \rightleftharpoons \text{grxrd_c} + \text{gthox_c}$	Glutathione metabolism Metabolic pathways
GTHOr	-2.173855	Glutathione oxidoreductase	$\text{gthox_c} + \text{h_c} + \text{nadph_c} \rightleftharpoons 2.0 \text{ gthrd_c} + \text{nadp_c}$	Glutathione metabolism Metabolic pathways
GLUDxi	-1.885036	Glutamate dehydrogenase NAD	$\text{glu_L_c} + \text{h2o_c} + \text{nad_c} \rightleftharpoons \text{akg_c} + \text{h_c} + \text{nadh_c} + \text{nh4_c}$	Pyrimidine metabolism
PYK4	-1.089009	UMP kinase	$\text{atp_c} + \text{ump_c} \rightleftharpoons \text{adp_c} + \text{udp_c}$	Pyrimidine metabolism Metabolic pathways Nucleotide metabolism Biosynthesis of cofactors

PYK2	-1.059291	Pyruvate kinase(3)	$h_c + pep_c + udp_c \rightleftharpoons pyr_c + utp_c$	Glycolysis / Gluconeogenesis Pyruvate metabolism Metabolic pathways Biosynthesis of secondary metabolites Microbial metabolism in diverse environments
PRPPS	-1.057372	Phosphoribosylpyrophosphate synthetase	$atp_c + r5p_c \rightleftharpoons amp_c + h_c + prpp_c$	Pentose phosphate pathway Purine metabolism Metabolic pathway Biosynthesis of secondary metabolites Microbial metabolism in diverse environments Carbon metabolism; Biosynthesis of amino acids
ACCOAL	-0.901765	Acetate-CoA ligase (ADP-forming)	$atp_c + coa_c + ppa_c \rightleftharpoons adp_c + pi_c + ppcoa_c$	Glycolysis / Gluconeogenesis Pyruvate metabolism Metabolic pathways Propanoate metabolism Microbial metabolism in diverse environments
CEPA	-0.866570	Cellobiose phosphorylase	$pi_c + cellb_c \rightleftharpoons glp_c + glc_D_c$	Starch and sucrose metabolism Metabolic pathways
