1.2

1.1

Fold change

Two-component system

0.00

urine m<mark>etabo</mark>lism;Bio<mark>synthe</mark>sis of secondary metabolites;Metabolic pathways;Alanine, aspartate and g icrobial metabolism in diverse environments; Metabolic pathways; Methane metabolism; Carbon fixation

Metabolic pathways; beta-Lactam resistance; Peptidoglycan biosynthesis Purine metabolism: Nucleotide metabolism: Metabolic pathways

late and dicarb<mark>oxyla</mark>te metabolism;Carbon fixation pathways in prokaryotes;Methane metabolism

osynthesis of amino acids;Glycine, serine <mark>and</mark> threonine metabolism;Biosynthesis of secondary metab

biquinone and other terpenoid-quinone biosynthesis; Metabolic pathways; Biosynthesis of cofactors; Bic etabolic pathways;Biosynthesis of secondary metabolites;Glycine, serine and threonine metabolism;Ph of secondary metabolites;Benzoate degradation;Fatty acid metabolism;Ethylbenzene degradati<mark>on</mark> nents;Carbon metabolism;Biosynthesis of secondary metabolites;Exopolysaccharide biosynthesis film formation - Vibrio cholerae; Biosynthesis of amino acids; Sulfur metabolism; Metabolic pathways; Cy Biosynthesis of nucleotide sugars; Metabolic pathways; Lipopolysaccharide biosynthesis

Aminoacy I His NA thie sign of each each continue of the conti beta-Lactam residenticeantimicrobial projetials of CAMAN was is taning. The organization beta-Lactam resistance Metabolic pathways; Valine, leucine and isoleveine degradation lletabblic pathwayenthedeotide metabolism;Antifolate resis<mark>tance;On</mark>e carbon pool by folate;Pyrimidine r Aetaboliceatewayschyckoptideametalealisox:Aatifolate.ceaista.me:Obe.carleoborshby folatesEvrimidine.c pial metabolis<mark>m in</mark> diverse environments:Biosynthesis of secondary metabolites:Metabolic pathways trate cycle (TCA cycle);Pyruvate metabolism;Glycolysis / Gluconeogenesis;Carbon metabolism;Metabo trate cycle (TCA cycle);Pyruvate metabolism;Glycolysis / Gluconeogenesis;Carbon metabolism;Metabo Two-component system

0.05

0.10 0.15 P-value

**Expression** 

1.0

1.5

## Cluster

- Cluster 1
- Cluster 2