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# The calculation of gut metabolic modules from gene profile

Forked from [The calculation of gut metabolic modules form gene profile](#)

In 2 collections

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1 Works for me [dx.doi.org/10.17504/protocols.io.bq6gmzbw](https://dx.doi.org/10.17504/protocols.io.bq6gmzbw)

BGI GIGA 1 more workspace

wangqi

## ABSTRACT

The calculation of gut metabolic modules from gene profile

## DOI

[dx.doi.org/10.17504/protocols.io.bq6gmzbw](https://dx.doi.org/10.17504/protocols.io.bq6gmzbw)

## PROTOCOL CITATION

Qi Wang 2021. The calculation of gut metabolic modules from gene profile. **protocols.io**  
<https://dx.doi.org/10.17504/protocols.io.bq6gmzbw>

## COLLECTIONS ⓘ

**Protocols for &#34;Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss&#34;**

**Protocols for &#34;Linking gut microbiome to bone mineral density: a shotgun metagenomic study of 361 eldly women&#34;**

## FORK NOTE

## FORK FROM

Forked from [The calculation of gut metabolic modules form gene profile](#), Qi Wang

## KEYWORDS

gut metabolic modules, Metagenomics data, KO profile

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#### OWNERSHIP HISTORY

Jan 05, 2021  Hongling Zhou

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#### PROTOCOL INTEGER ID

45992

#### PARENT PROTOCOLS

Part of collection

[Protocols for &#34;Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss&#34;](#);

[Protocols for &#34;Linking gut microbiome to bone mineral density: a shotgun metagenomic study of 361 elderly women&#34;](#);

#### GUIDELINES

The calculation of gut metabolic modules from gene profile

#### ABSTRACT

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#### BEFORE STARTING

The input is the gene profile

- 1 Step 1: the putative amino acid sequences were translated from the gene catalogues and aligned against the proteins/domains in the KEGG databases (release 79.0, with animal and plant genes removed) using BLASTP (v2.2.26, default parameter except that -e 0.01 -b 100 -K 1 -F T -m 8). Each protein was assigned to the KO group by the highest scoring annotated hit(s) containing at least one HSP scoring >60 bits. The relative abundance profile of KOs was determined by summing the relative abundance of genes from each KO.
- 2 Step 2: The calculation of gut metabolic modules by one command:  
'java -jar gmms.jar -a 2 -d GMMs.v1.07.txt -i input\_KO\_profile -s average -o index'  
You could refer to the <http://www.raeslab.org/companion/gmms/> for 'gmms.jar' and 'GMMs.v1.07.txt'.