



# GutUDB: A comprehensive multiomics database for intestinal diseases

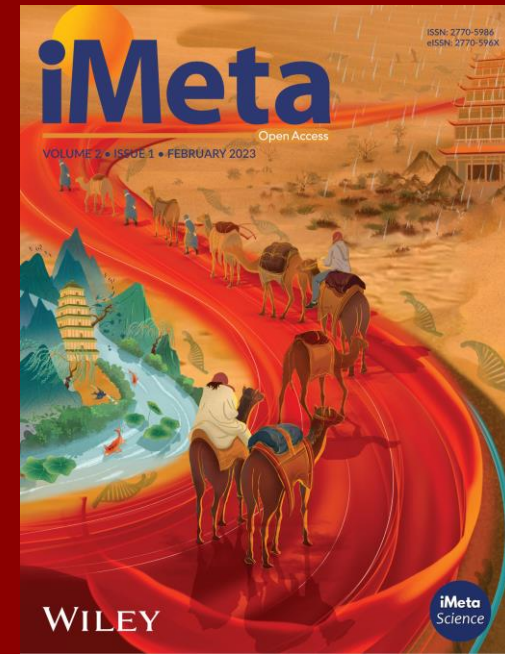
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“GutUDB: A Comprehensive Multiomics Database for Intestinal Diseases.” *iMeta* 3: e195.  
<https://doi.org/10.1002/imt2.195>



# Introduction

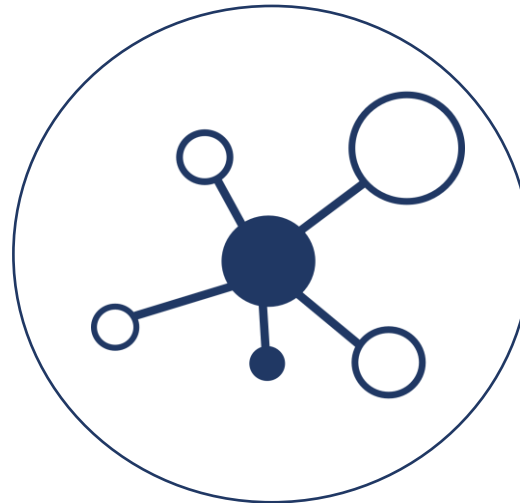
High-throughput  
sequencing:  
RNA-seq  
ChIP-seq  
scRNA-seq  
MeRIP-seq



DNA level processes



Transcriptional dynamics



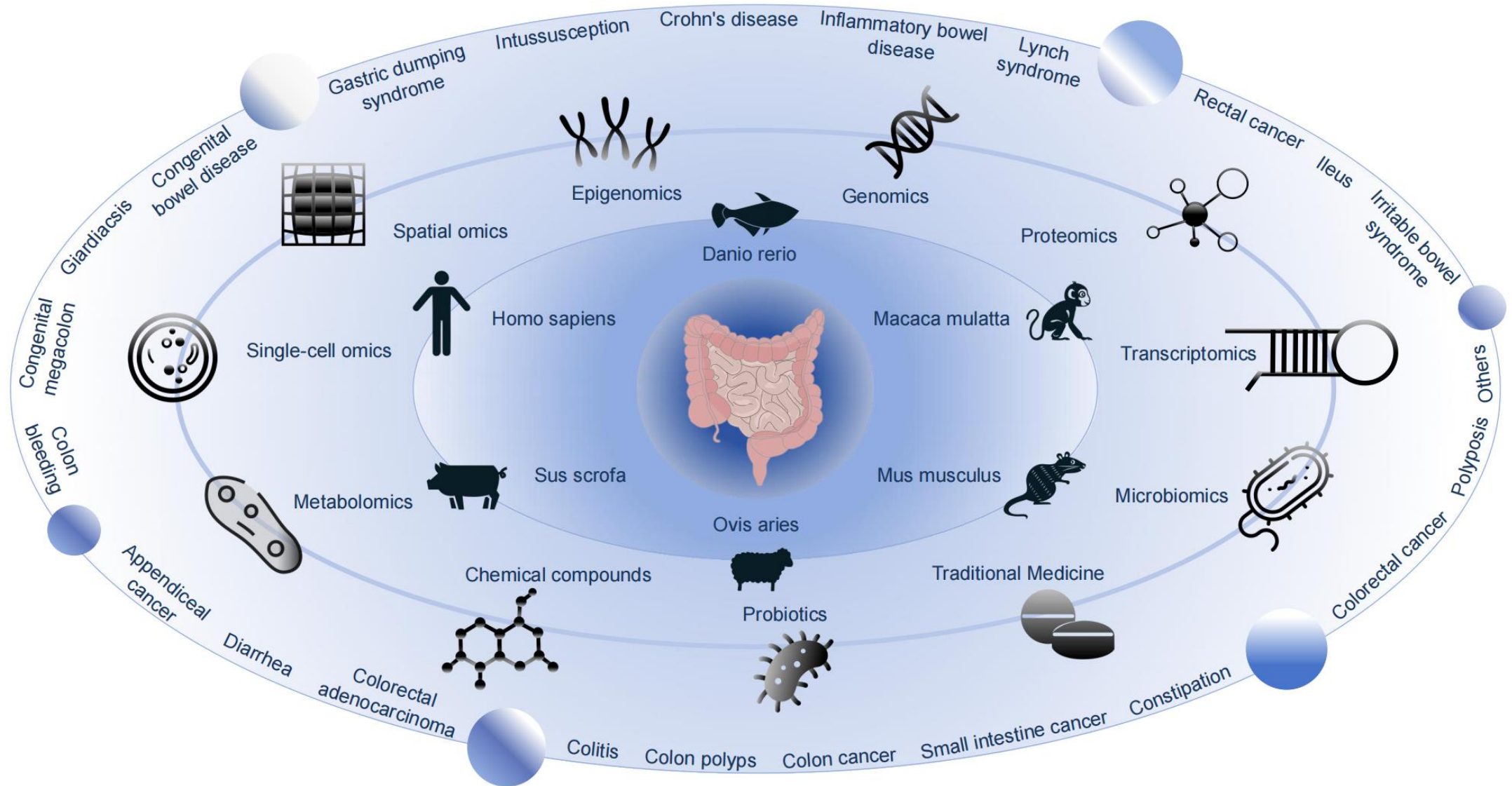
Protein-related activities



Epigenetic modifications



# Introduction

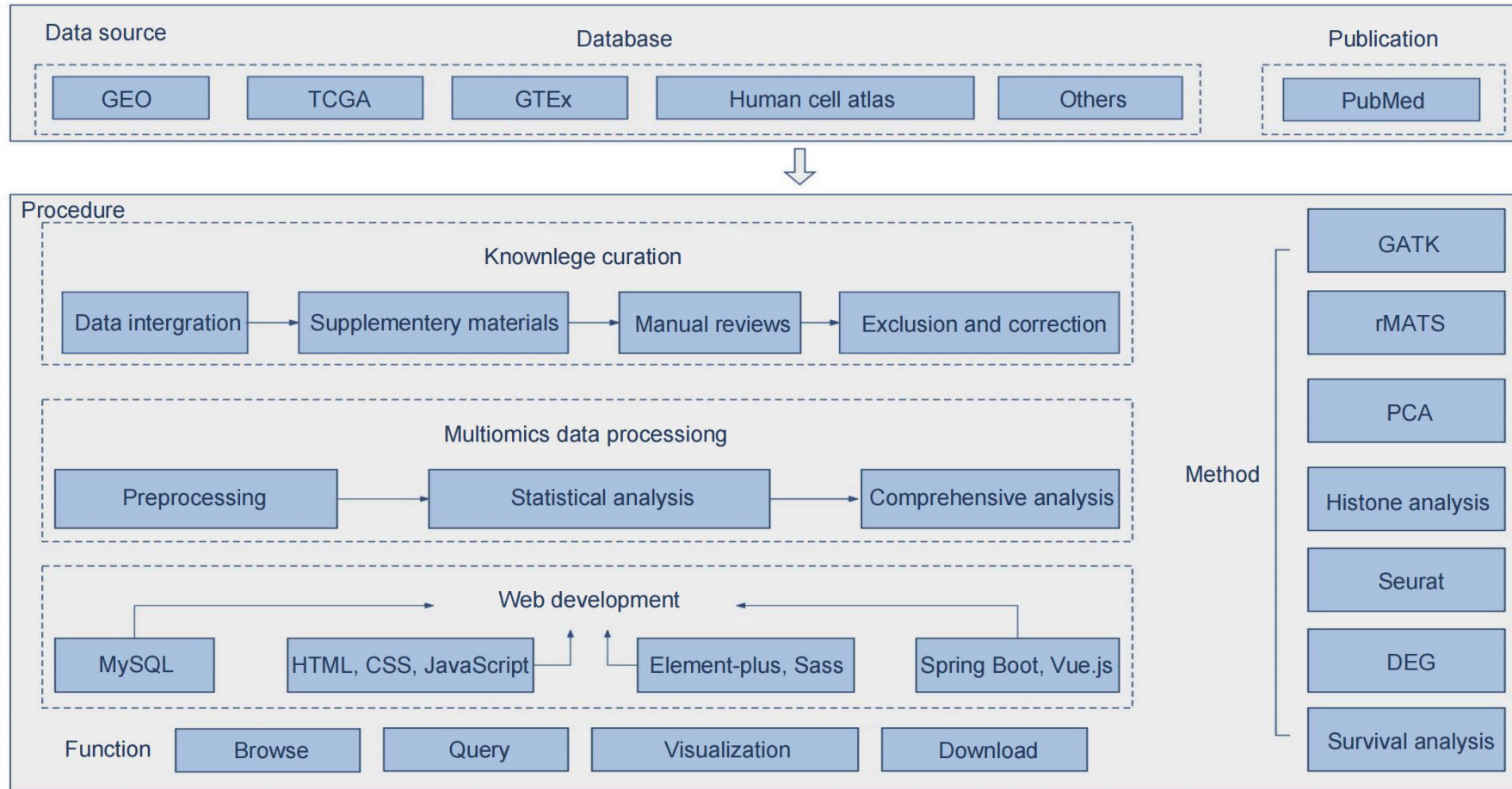


GutUDB: A comprehensive multiomics database for intestinal diseases



# Result: Overview of GutUDB

(A)



- 8 types of omics
- 6 types of species
- 56 types of intestinal diseases
- 11 types of intestinal tissues
- 63 types of intestinal cell lines
- 58970 genes

FIGURE 1 (A) The process of data collection and processing, as well as the construction procedure of the database website, incorporating four core functions (browsing, querying, visualizing, and downloading).

# Result: Disease-gene associations across distinct intestinal diseases

260,790 disease gene associations

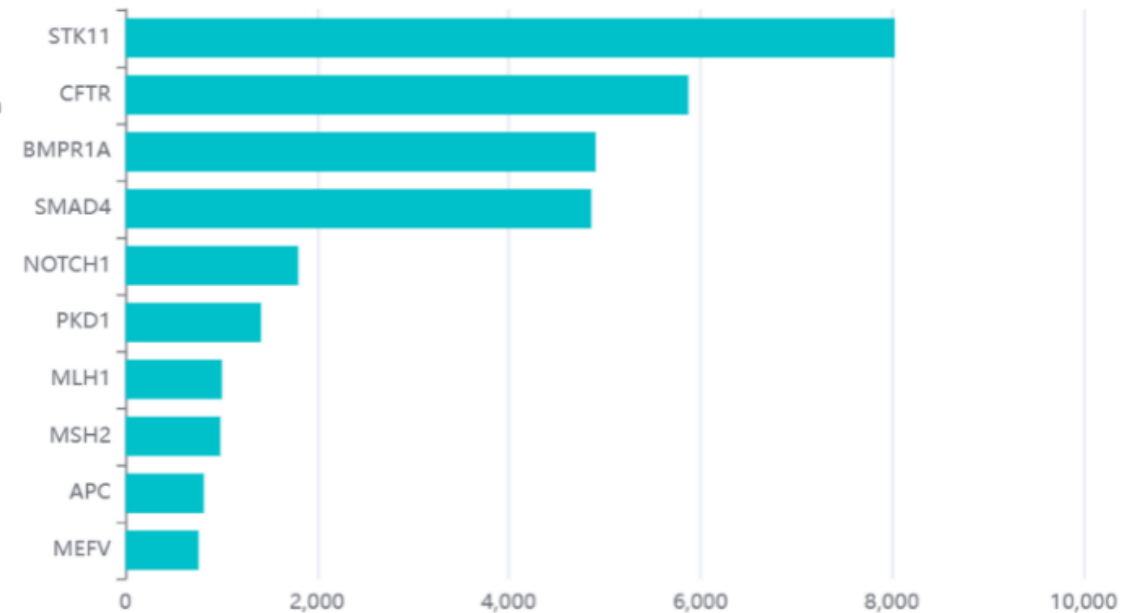
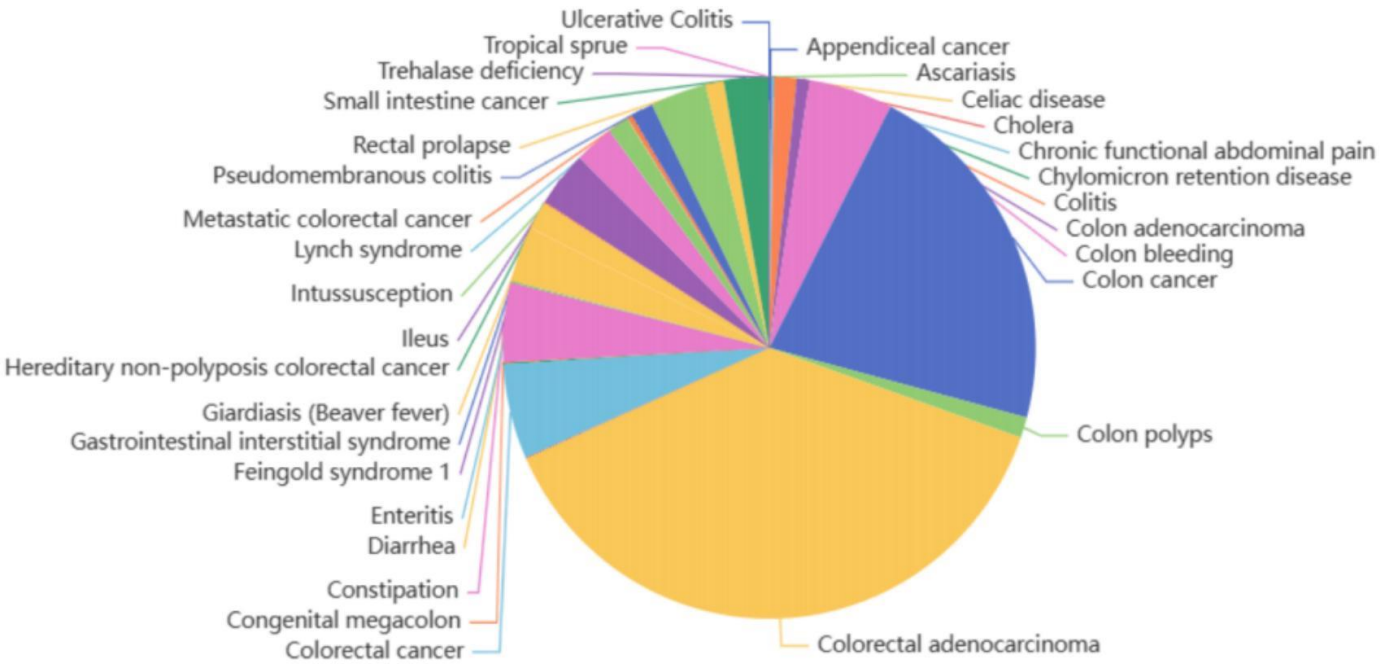


Figure S1 (A) The proportion of various intestinal diseases.

Figure S1 (B) The top 10 genes associated with gene-disease.



# Result: Homepage

**GutUDB**  
Gut Universe Database

Search all genes

Home Omics ChatDoc Statistics FAQ Contact

APC TP53 KRAS BRAF SMAD4 MLH1 MSH2 MSH6 PMS2 PTEN

**Click to browse**

**SPECIES**  
INTESTINAL MULTISPECIES DATA IN DIFFERENT ANIMALS

**DISEASES**  
DIFFERENT INTESTINAL DISEASES

**Therapy**  
DIFFERENT THERAPY

**OMICS**  
DIFFERENT OMICS

**TESTINES**

**DATABASE**

Gene	58970
Tissue/Cell line	74
Project	2150
Sample	1500
Profile	8997005

**NEWS AND UPDATE**

**Website maintenance**  
We reorganized and uploaded the omics data ensure its accurate presentation.  
Published | 20 January 2

**Website maintenance**  
We resolved the user usage problems discover during the website launch and corrected and optimized various website functions.  
Published | 12 March 2

**External links**  
CASA

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**Navigation**

Home Omics ChatDoc Statistics FAQ Contact

**GutUDB**  
Gut Universe Database

Search all genes

**Search for genes**

Hot search APC TP53 KRAS BRAF SMAD4 MLH1 MSH2 MSH6 PMS2 PTEN

**Click to browse**

**SPECIES**  
INTESTINAL MULTISPECIES DATA IN DIFFERENT ANIMALS

**DISEASES**  
DIFFERENT INTESTINAL DISEASES

**Therapy**  
DIFFERENT THERAPY

**OMICS**  
DIFFERENT OMICS

**TESTINES**

Four modules: omics, species, diseases, therapy

# Result: Overview of GutUDB

Gene Name: **METTL3**

Start: 21498133

🔍 RBP: Yes

🔍 RNA editing: NO

🔍 Therapeutic targets: Yes

Ensemble ID: ENSG00000165819

End: 21511342

🔍 m6A: YES

🔍 TF: Yes

🔍 Diagnostic targets:

Seqnames: chr14

Strand: -

🔍 AS: NO

Motif: NA

[NCBI](#)

## Gene details

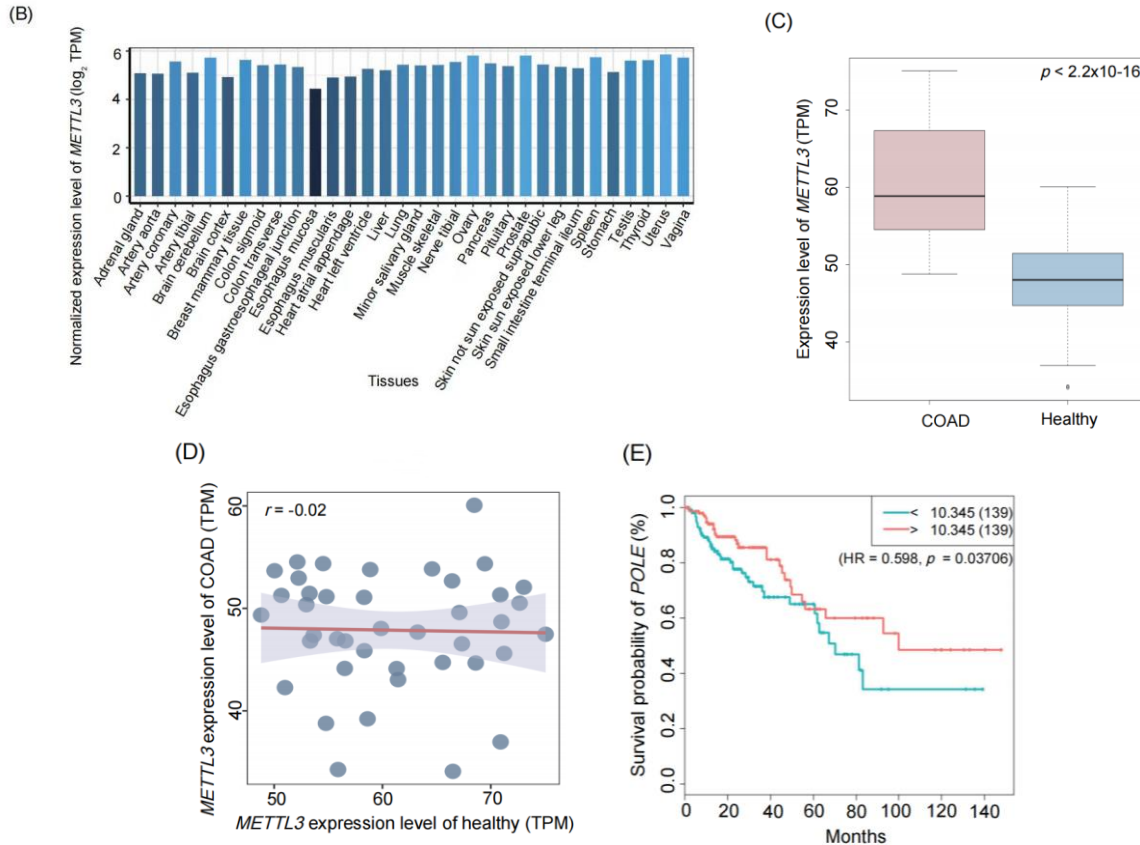


FIGURE 1. (B) The expression levels of the METTL3 in different tissues. The data derived from GTEx. (C) Boxplot displaying gene expression difference between COAD and healthy tissues.  $p < 0.05$  indicated that the expression of METTL3 was significantly different between the two groups. (D) Scatter plot showing the correlation analysis of METTL3 expression between COAD group and healthy group.  $r = -0.02$  indicated that METTL3 expression almost no correlation between the two groups. (E) Survival analysis curve of POLE associated with COAD.



# Result: Overview of GutUDB

profile | omics | drugs

## Epigenomics

DNA Methylation

Epigenomics | Genomics | Transcriptomics | Spatial Omics | Singel Cell Omics | Proteomics | Microbiomics | Metabolomics

DNA Methylation | Genomic Alteration | Non-coding RNA | Gene Expression | Associated Genera

CNA Genes | circRNA | Alternative Splicing

Mutated Genes | Inc RNA

SNP | miRNA

Structural Variant Genes

Virulence Gene

Genomic Alteration: CNA Genes

Disease	Is Cancer Gene (source: On coKB)	Cytoband	CNA	Freq	PMID
Colon Cancer	No	14q11.2	HOMDEL	0.048	<a href="#">31031003</a>

Figure S1 (D) Eight major omics information related to genes.



# Result: THERAPY

Chemical Compounds

Traditional Medicine

Probiotics

## Chemical Compounds

#	Disease related genes	Disease	Species	Direct Evidence
1	ABCC4	Inflammatory Bowel Dis...	Human	NA
2	ABCC4	Colonic Neoplasms	Human	NA
3	ADRA2A	Colonic Neoplasms	Human	NA
4	ABCC4	Intestinal Pseudo-Obstr...	Human	NA
5	ABCC4	Pediatric Crohn's disease	Human	NA
6	ADRA2A	Enteritis	Human	NA

- 6281 types of chemical compounds
- 393 types of traditional medicine
- 22 types of probiotics

Figure S1 (E) The therapy section contains chemical compounds, traditional medicine and probiotics.



# Result: DISEASES

## Intestinal Diseases

**Diseases name :** [All\(24388\)](#) [Colon Adenocarcinoma\(3450\)](#) [Colitis\(2711\)](#) [Intussusception\(2606\)](#) [Colorectal Neoplasms\(1734\)](#)  
[Colonic Neoplasms\(1662\)](#) [Intestinal Neoplasms\(1469\)](#) [Inflammatory Bowel Diseases\(1366\)](#) [Enteritis\(1308\)](#)  
[Duodenal Ulcer\(1175\)](#) [Crohn Disease\(1165\)](#) [Anus Neoplasms\(1164\)](#) [Ileus\(1140\)](#) [Rectal Neoplasms\(950\)](#) [Ileitis\(668\)](#)  
[Megacolon\(522\)](#) [Intestinal obstruction\(483\)](#) [Proctocolitis\(425\)](#) [Duodenal Neoplasms\(390\)](#)

**Omics level:** [All](#) [Genomic](#) [Transcriptomic](#) [Proteomics](#) [Metabolomics](#) [Single cell omics](#) [Spatial omics](#) [Epigenomics](#)  
[Microbiomics](#)

**Hot genes:** [All\(55970\)](#) [APC\(9906\)](#) [STK11\(9471\)](#) [MEN1\(5750\)](#) [SMAD4\(5137\)](#) [BMPR1A\(5048\)](#) [CFTR\(4425\)](#) [PKHD1\(2886\)](#)  
[CDH1\(2650\)](#) [NOTCH1\(2260\)](#) [MLH1\(1568\)](#) [PKD1\(1491\)](#) [KCNT1\(1446\)](#) [AP3B1\(1360\)](#) [MSH2\(1336\)](#) [TP53\(1236\)](#)

#	Disease related genes	Disease	Omics	Source
1	<a href="#">CCND3</a>	Appendiceal Cancer	Genomic	<a href="#">36493333</a>
2	<a href="#">CDKN2A</a>	Appendiceal Cancer	Genomic	<a href="#">36493333</a>
3	<a href="#">TERT</a>	Appendiceal Cancer	Genomic	<a href="#">36493333</a>

Figure S1 (F) Details page of the diseases section.



# Result: SPECIES

## | Species

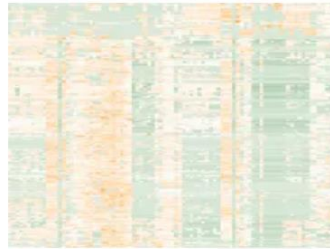
#	Species	Disease	Disease related genes	Direct Evidence	Inference
1	Human	Ileus	<a href="#">ALPI</a>	NA	Methotrex
2	Human	Colitis	<a href="#">ADRA2A</a>	NA	Arsenic Tri
3	Human	Inflammato...	<a href="#">ADRA2A</a>	NA	Dexameth
4	Human	Ileus	<a href="#">ANGPTL4</a>	NA	Cisplatin P
5	Human	Duodenal U...	<a href="#">ADRA2A</a>	NA	Capsaicin
6	Human	Intestinal O...	<a href="#">ABCC4</a>	NA	Carbamaz

Figure S1 (G) Details page of the species section.

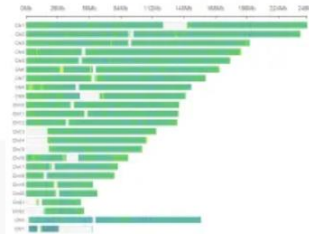


# Result: Omics

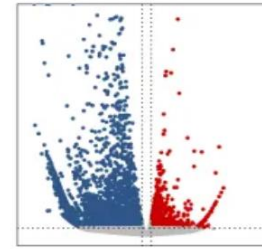
## Omics



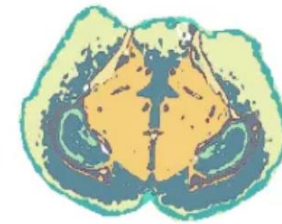
EPIGENOMICS



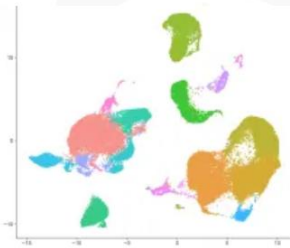
GENOMICS



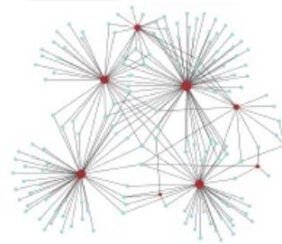
TRANSCRIPTOMICS



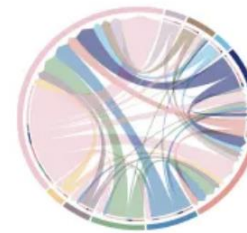
SPATIAL OMICS



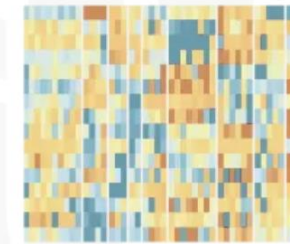
SINGLE CELL OMICS



PROTEOMICS



MICROBIOMICS



METABOLOMICS

Click to view the content of each omic

# Result: Browsing spatial omics and single-cell omics data of intestinal diseases



The page details of spatial omics.

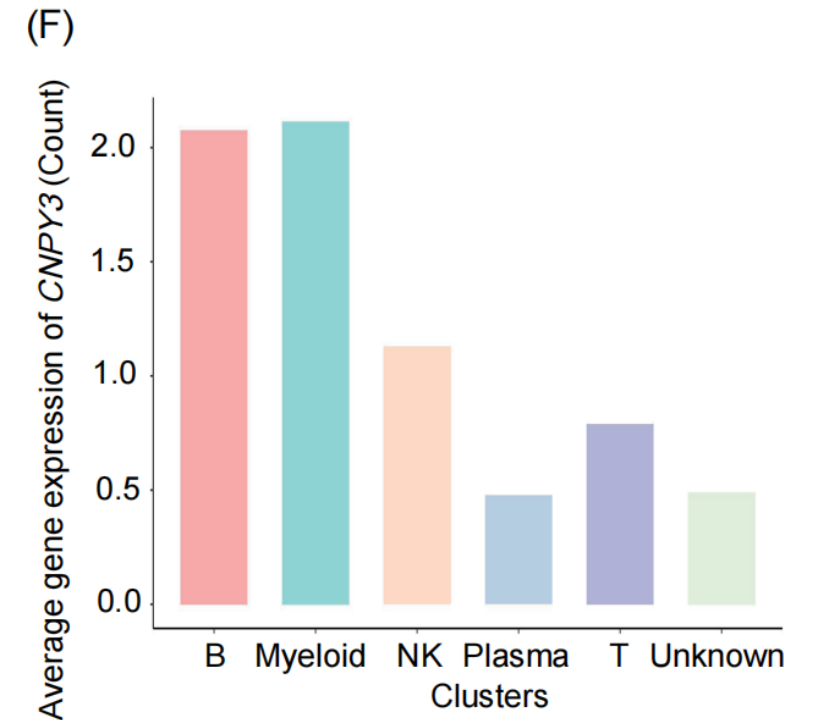


FIGURE 1. (F) The expression levels of CNPY3 in various cells and the presentation of expression maps in scRNA-seq data.

# Result: Interactive visualization of bulk multiomics profiles related to intestinal diseases



(G)

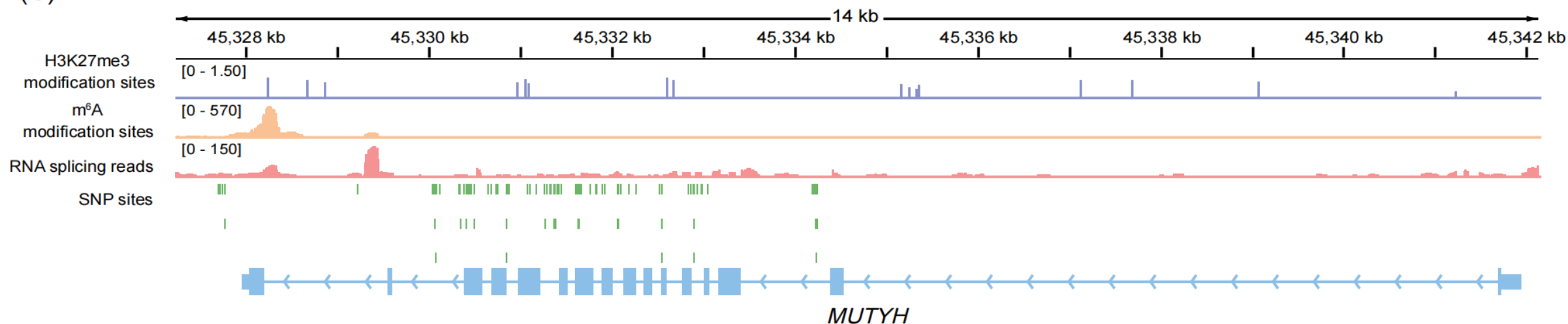


FIGURE 1. (G) Tracks displaying the read coverage of H3k27me3, the m6A sites as well as RNA-seq and SNP data in colorectal cancer on the MUTYH.



# Result: Interactive visualization of bulk multiomics profiles related to intestinal diseases

## Summary

Project: **GSE127938**

Disease: Normal

Species: Homo sapiens

Tissue/Cell line: Pylorus, Duodenum, Jejunum, Ileum, Colon

CASE: Pylorus organoids, Duodenum organoids, Jejunum organoids, Ileum organoids, Colon organoids

Control: Corpus organoids

PMID: 525840

[NCBI](#)

## profile

Sample: **colon** duodenum ileum jejunum pylorus

## Gene expression data

#	Gene Name	Ensemble ID	Mean (Case)	Mean (Control)	Log2(Fold Change)	p.value
1	<a href="#">A1BG</a>	ENSG00000121410	0.0467	0.0074	2.8625	0.0736
2	<a href="#">A1BG-AS1</a>	ENSG00000268895	0.1485	0.1236	0.8733	0.7962
3	<a href="#">A1CF</a>	ENSG00000148584	0.2387	0.0186	0.1082	0.1942
4	<a href="#">A2M</a>	ENSG00000175899	0.0953	0.0383	0.4870	0.5991
5	<a href="#">A2M-AS1</a>	ENSG00000245105	0.3033	0.1406	0.5495	0.2810

< 1 2 3 4 5 6 ... 11343 > 5 1 page


- 137 RNA-seq data sets
- 7.9 million transcriptional profiles

Figure S1 (H) The details page display of each dataset in genomics.



# Result: Chatdoc

## ChatDoc



### ChatDoc

TOP Top 10 key words:

- Temporal and geographical distributi...
- Spatial distribution of data
- Statistical processing of data
- Reliable sources of data
- Openness of data
- Timeliness of datasets
- Biological significance of the data
- Sustainability of data
- Functional classification of disease-a...
- Prognostic markers of disease

#### Single Cell Omics

What is Single Cell Omics?

Single-cell Omics is a field of biology that aims to study and analyse the molecular properties and functions of individual cells within an organism, including the genomes, transcriptomes, proteomes, and metabolomes of individual cells. The field has evolved thanks to high-resolution technologies that allow scientists to delve into cellular diversity, heterogeneity, and interactions at the single-cell level. Below are the main components of Single Cell Omics: (1) Single-cell analysis techniques: Single-cell genomics relies on highly accurate experimental techniques such as single-cell RNA sequencing (scRNA-seq), single-cell mass spectrometry (scMS), single-cell protein mass spectrometry (scPMS), and single-cell metabolomics. These techniques allow the measurement and analysis of biomolecules in individual cells. (2) Studies of cellular heterogeneity: Single-cell histomics can reveal differences and heterogeneity between individual cells within cell populations. This helps to understand the diversity of different cell types, states and functions. (3) Cell development and differentiation: the study of changes in gene expression in individual cells during development and differentiation can help us understand cell fate decisions and tissue development. (4) Disease research: Single-cell genomics can be used to study cellular changes in disease onset and progression, helping to identify potential therapeutic targets and biomarkers. (5) Immunological studies: Single Cell Omics helps to gain insight into the function, interaction and response of various immune cells in the immune system. (6) Drug Screening and Individualised Medicine: Based on the information from single-cell genomics, drug screening experiments can be carried out to find treatments suitable for individual patients.

#### Metabolomics

What is Metabolomics?

Metabolomics is a subfield of systems biology that studies the composition, structure, quantification and dynamics of all metabolites or small-molecule metabolites in an organism. Metabolomics aims to gain a comprehensive understanding of the metabolic network in organisms to reveal the physiological state of organisms, biochemical processes and the interrelationships between biomolecules. The main components of metabolomics include: (1) Metabolites: Metabolomics studies metabolites, which are the products of metabolic reactions in organisms,

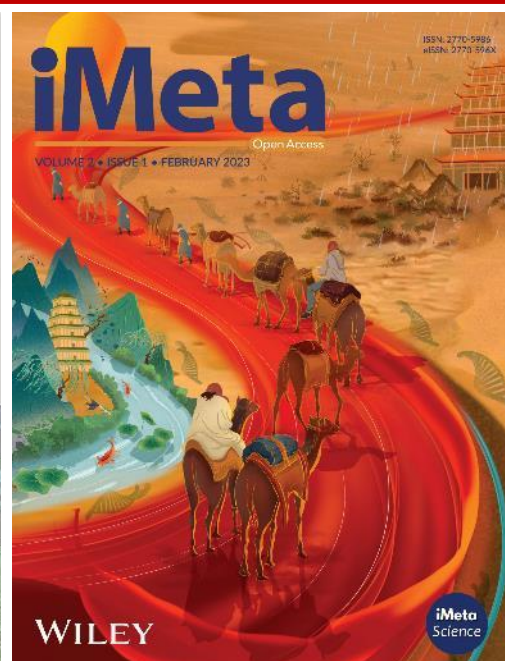
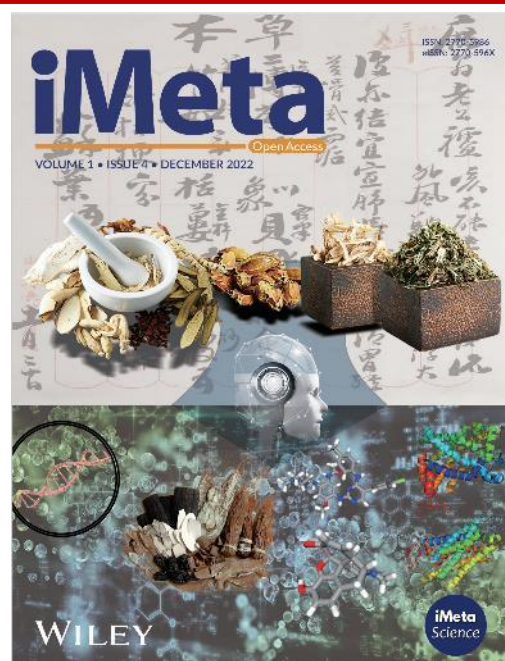
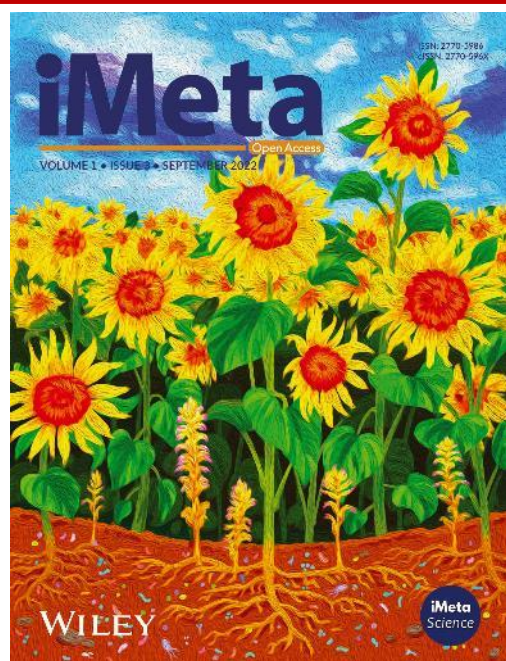
Enter content to start the chat (Ctrl+Enter line wrap) Send clear

Users can enter question keywords to get answers.

# Summary

- ❑ GutUDB is a comprehensive intestinal disease multiomics database. Currently, the database has included 260,790 disease-gene associations, involving eight major omics including epigenomics, genomics, transcriptomics, spatial omics, single-cell omics, proteomics, metabolomics, and microbiomics data, spanning 56 distinct intestinal diseases across six various species. In addition, the database contains a variety of potential clinical treatments.
- ❑ GutUDB integrates four core functions: browse, query, visualization and download, aiming to facilitate user access and use. Based on this database, researchers can conduct various omics data analyzes to explore genes related to certain intestinal diseases.
- ❑ Database website: <https://intestine.splicedb.net>

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<https://doi.org/10.1002/imt2.195>



“**iMeta**”由威立、肠菌分会和华人科学家出版的开放获取期刊，主编由中科院微生物所刘双江和荷兰格罗宁根大学傅静远教授共同担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前10%(IF>20)的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、中英双语、50万用户的社交媒体宣传等。2022年2月发行，相继被**ESCI**、**Google Scholar**、**DOAJ**、**Scopus**等数据库收录，发文161篇，被引2316次([Dimension](#), 2024/2/19)!



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