# 通用框架(General framework)

数据库(database)

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## 工具平台(software)

Trinity RNA-Seq, v. r2013-02-25

Bowtie, v. 0.12.9 (not Bowtie2)

Samtools, v. 0.1.18

Blast+, v. 2.2.27

Trimmomatic

## 语言(scripts)

## 分析流程(pipeline or protocol)

## 资源(resources)

### **most comprehensive sources >** [**https://omictools.com/metatranscriptomics-category**](https://omictools.com/metatranscriptomics-category)

https://github.com/liupfskygre

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# **领域(research field)**

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# 序列前处理Reads preprocessing

## 工具平台(software)

Trimmomatic

## Metagenomics

数据库(database)

工具平台(software)

语言(scripts)

分析流程(pipeline or protocol)

## 资源(resources)

综合平台> <http://merenlab.org/software/anvio/>, more on metagenomics

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# Metatranscriptomics

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## 数据库(database)

MG-RAST

NCBI Reference Database (RefSeq)

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## 工具平台(software)

MG-RAST

MEGAN

组装工具(assemble): Trinity RNA-Seq

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## 语言(scripts)

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## 分析流程(pipeline or protocol)

Reads processing

Annotation

Aggregation

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## 资源(resources)

**SAMSA**: a comprehensive metatranscriptome analysis pipeline: <https://github.com/liupfskygre/SAMSA>

**MetaTrans**: an open-source pipeline for metatranscriptomics: <http://www.metatrans.org/>

COMAN: a web server for comprehensive metatranscriptomics analysis> <http://sbb.hku.hk/COMAN/>

Metatranscriptome Pipeline > <http://richardcaseyhpc.com/metatranscriptomics-pipeline/>

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# PCR based Metagenomics

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## 数据库(database)

## 工具平台(software)

**STAMP**> statistics

语言(scripts)

分析流程(pipeline or protocol)

资源(resources)

microbiome\_helper : <https://github.com/LangilleLab/microbiome_helper/wiki>

# transcriptomics

# Genomic and comparative genomics

# Evolutionary