

# Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

## MetaPGN

RRID:SCR\_016472

Type: Tool

### Proper Citation

MetaPGN (RRID:SCR\_016472)

### Resource Information

**URL:** <https://pan.genomics.cn/ucdisk/s/VjuIRb&code=877833>

**Proper Citation:** MetaPGN (RRID:SCR\_016472)

**Description:** Pipeline for construction and graphical visualization of annotated pangenome networks from microbial genomes. With the ability to extract and visualize gene contents and gene-gene physical adjacencies of a specific taxon from large-scale metagenomic data provides pangenome analysis to uncultured microbial taxa., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** MetaPGN

**Synonyms:** Meta PanGeNome

**Resource Type:** software toolkit, data processing software, software application, data analysis software, network graph visualization software, software resource, data visualization software

**Defining Citation:** [PMID:30277499](#)

**Keywords:** construct, graphical, visualization, annotated, pangenome, network, microbial, genome, metagenome

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** MetaPGN

**Resource ID:** SCR\_016472

**Alternate URLs:** <https://github.com/peng-ye/MetaPGN>

**License:** GNU GPL

**Record Creation Time:** 20220129T080330+0000

**Record Last Update:** 20260815T182527+0000

---

## Ratings and Alerts

No rating or validation information has been found for MetaPGN.

No alerts have been found for MetaPGN.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

Krisna MA, et al. (2024) Development and implementation of a core genome multilocus sequence typing scheme for Haemophilus influenzae. Microbial genomics, 10(8).

Peng Y, et al. (2018) MetaPGN: a pipeline for construction and graphical visualization of annotated pangenome networks. GigaScience, 7(11).