

# Resource Summary Report

Generated by [dkNET](#) on Apr 30, 2025

## NGS QC Toolkit

RRID:SCR\_005461

Type: Tool

### Proper Citation

NGS QC Toolkit (RRID:SCR\_005461)

### Resource Information

**URL:** <http://www.nipgr.res.in/ngsqctoolkit.html>

**Proper Citation:** NGS QC Toolkit (RRID:SCR\_005461)

**Description:** A software toolkit for the quality control (QC) of next generation sequencing (NGS) data. The toolkit comprises of user-friendly stand alone tools for quality control of the sequence data generated using Illumina and Roche 454 platforms with detailed results in the form of tables and graphs, and filtering of high-quality sequence data. It also includes few other tools, which are helpful in NGS data quality control and analysis.

**Abbreviations:** NGS QC Toolkit

**Resource Type:** software resource

**Defining Citation:** [PMID:22312429](#)

**Keywords:** next generation sequencing

**Funding:**

**Resource Name:** NGS QC Toolkit

**Resource ID:** SCR\_005461

**Alternate IDs:** OMICS\_01062

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20250420T014252+0000

## Ratings and Alerts

No rating or validation information has been found for NGS QC Toolkit.

No alerts have been found for NGS QC Toolkit.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 268 mentions in open access literature.

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

Lin Y, et al. (2024) Molecular evidence provides new insights into the evolutionary origin of an ancient traditional Chinese medicine, the domesticated "Baizhi". *Frontiers in plant science*, 15, 1388586.

Xia L, et al. (2024) Spatio-temporal expression patterns of glycine-rich beta proteins and cysteine-rich beta proteins in setae development of *Gekko japonicus*. *BMC genomics*, 25(1), 535.

He S, et al. (2024) Genome-wide identification, characterization and expression analysis of the bZIP transcription factors in garlic (*Allium sativum* L.). *Frontiers in plant science*, 15, 1391248.

Chen W, et al. (2024) Mitogenomic phylogeny, biogeography, and cryptic divergence of the genus *Silurus* (Siluriformes: Siluridae). *Zoological research*, 45(4), 711.

Cao S, et al. (2024) Cytoplasmic genome contributions to domestication and improvement of modern maize. *BMC biology*, 22(1), 64.

Guo N, et al. (2024) A graph-based pan-genome of *Brassica oleracea* provides new insights into its domestication and morphotype diversification. *Plant communications*, 5(2), 100791.

Liu B, et al. (2024) Development of a 1-step multiplex PCR assay for the detection of *S. Enteritidis*, *S. Pullorum*, *S. Typhimurium*, and *S. Infantis* associated with poultry production. *Poultry science*, 103(9), 104043.

Pires GP, et al. (2024) Effects of trimer repeats on *Psidium guajava* L. gene expression and prospection of functional microsatellite markers. *Scientific reports*, 14(1), 9811.

Gosain TP, et al. (2024) Mycobacterium tuberculosis strain with deletions in menT3 and menT4 is attenuated and confers protection in mice and guinea pigs. *Nature communications*, 15(1), 5467.

Arunima A, et al. (2024) CYP1B1-AS1 regulates CYP1B1 to promote *Coxiella burnetii* pathogenesis by inhibiting ROS and host cell death. *Research square*.

Chen L, et al. (2024) Comparative transcriptome and methylome of polar bears, giant and red pandas reveal diet-driven adaptive evolution. *Evolutionary applications*, 17(6), e13731.

Dong W, et al. (2024) Flowering-associated gene expression and metabolic characteristics in adzuki bean (*Vigna angularis* L.) with different short-day induction periods. *PeerJ*, 12, e17716.

Xing Y, et al. (2024) The role of RNA epigenetic modification-related genes in the immune response of cattle to mastitis induced by *Staphylococcus aureus*. *Animal bioscience*, 37(7), 1141.

Wang C, et al. (2024) Microbial metabolite deoxycholic acid-mediated ferroptosis exacerbates high-fat diet-induced colonic inflammation. *Molecular metabolism*, 84, 101944.

Yin Y, et al. (2024) The complete chloroplast genome of *Buxus sinica* var. *parvifolia* (Buxaceae) and its phylogenetic analysis. *Mitochondrial DNA. Part B, Resources*, 9(10), 1322.

Chander AM, et al. (2024) Genomic and morphological characterization of *Knufia obscura* isolated from the Mars 2020 spacecraft assembly facility. *Scientific reports*, 14(1), 12249.

Xie Q, et al. (2024) Transcriptome Analysis Reveals Novel Insights into the Hyperaccumulator *Phytolacca acinosa* Roxb. Responses to Cadmium Stress. *Plants (Basel, Switzerland)*, 13(2).

Li C, et al. (2024) Metformin dampens the progression of cholangiofibrosis induced by thioacetamide using deep learning. *Heliyon*, 10(18), e37347.

Zhang B, et al. (2024) Rapid genome-wide profiling of DNA methylation and genetic variation using guide positioning sequencing (GPS). *Frontiers in cell and developmental biology*, 12, 1457387.

Cheng WP, et al. (2024) The complete plastid genome of *Polygonatum gracile* P. Y. Li (Asparagaceae): characterization and phylogeny. *Mitochondrial DNA. Part B, Resources*, 9(11), 1473.