

Resource Summary Report

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HTQC

RRID:SCR_006448

Type: Tool

Proper Citation

HTQC (RRID:SCR_006448)

Resource Information

URL: <http://sourceforge.net/projects/htqc/>

Proper Citation: HTQC (RRID:SCR_006448)

Description: A software toolkit including statistics tool for illumina high-throughput sequencing data, and filtration tools for sequence quality, length, tail quality, etc..

Abbreviations: HTQC

Synonyms: HTQC - Quality control and filtration for illumina sequencing data

Resource Type: software resource, software toolkit

Defining Citation: [PMID:23363224](#), [DOI:10.1186/1471-2105-14-33](#)

Keywords: c++, illumina, command-line

Availability: GNU General Public License, v3

Resource Name: HTQC

Resource ID: SCR_006448

Alternate IDs: OMICS_01052

Old URLs: <https://sources.debian.org/src/htqc/>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260919T195753+0000

Ratings and Alerts

No rating or validation information has been found for HTQC.

No alerts have been found for HTQC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Zhang Y, et al. (2026) Multi-omics and functional analyses in *Aesculus wilsonii* elucidate the biosynthetic pathways of moretane- and oleanane-type triterpenoids. *Plant communications*, 7(4), 101715.

Liao Y, et al. (2025) Functions of thyroid hormone signaling in regulating melanophore, iridophore, erythrophore, and pigment pattern formation in spotted scat (*Scatophagus argus*). *BMC genomics*, 26(1), 79.

Huang YQ, et al. (2025) Allelic variation and duplication of the *dmrt1* were associated with sex chromosome turnover in three representative Scatophagidae fish species. *Communications biology*, 8(1), 627.

Wei Z, et al. (2025) Chromosome-level genome assembly of *Sambus kanssuensis* (Coleoptera: Buprestidae). *Scientific data*, 12(1), 895.

Li L, et al. (2025) A Chromosomal-level genome assembly and annotation of fat greenling (*Hexagrammos otakii*). *Scientific data*, 12(1), 78.

Zhou S, et al. (2024) A chromosome-level genome assembly of yellow stem borer (*Scirpophaga incertulas*). *Scientific data*, 11(1), 279.

Chang YW, et al. (2024) Chromosome-level genome assembly of the invasive leafminer fly, *Liriomyza trifolii* (Diptera: Agromyzidae). *Scientific data*, 11(1), 1326.

Ji J, et al. (2024) Chromosome-level genome assembly of marmalade hoverfly *Episyrphus balteatus* (Diptera: Syrphidae). *Scientific data*, 11(1), 844.

Liu Y, et al. (2024) Phased chromosome-level genome provides insights into the molecular adaptation for migratory lifestyle and population diversity for Pacific saury, *Cololabis saira*. *Communications biology*, 7(1), 1513.

H??furthner T, et al. (2024) Synthesis of a ¹³C-methylene-labeled isoleucine precursor as a useful tool for studying protein side-chain interactions and dynamics. *Journal of biomolecular NMR*, 78(1), 1.

Liu H, et al. (2024) An omics-based characterization of *Wolfiporia cocos* reveals three CYP450 members involved in the biosynthetic pathway of pachymic acid. *Communications biology*, 7(1), 666.

Wang Y, et al. (2023) Multi-omics of Circular RNAs and Their Responses to Hormones in Moso Bamboo (*Phyllostachys edulis*). *Genomics, proteomics & bioinformatics*, 21(4), 866.

Tian CX, et al. (2023) A chromosome-level genome assembly of Hong Kong catfish (*Clarias fuscus*) uncovers a sex-determining region. *BMC genomics*, 24(1), 291.

Senchenkov VY, et al. (2023) Whole-Genome Sequencing and Biotechnological Potential Assessment of Two Bacterial Strains Isolated from Poultry Farms in Belgorod, Russia. *Microorganisms*, 11(9).

Li G, et al. (2023) A High-Continuity Genome Assembly of Chinese Flowering Cabbage (*Brassica rapa* var. *parachinensis*) Provides New Insights into Brassica Genome Structure Evolution. *Plants (Basel, Switzerland)*, 12(13).

Teng K, et al. (2023) Chromosome-level reference genome assembly provides insights into the evolution of *Pennisetum alopecuroides*. *Frontiers in plant science*, 14, 1195479.

Xu C, et al. (2023) Chromosome level genome assembly of oriental armyworm *Mythimna separata*. *Scientific data*, 10(1), 597.

Li X, et al. (2022) The Manchurian Walnut Genome: Insights into Juglone and Lipid Biosynthesis. *GigaScience*, 11.

Niu J, et al. (2022) Chromosomal-scale genome assembly of the near-extinction big-head schizothorcin (*Aspiorhynchus laticeps*). *Scientific data*, 9(1), 556.

Cai C, et al. (2022) Comparative genomic analysis of high-altitude adaptation for Mongolia Mastiff, Tibetan Mastiff, and *Canis Lupus*. *Genomics*, 114(3), 110359.