Resource Summary Report

Generated by NIF on Apr 17, 2025

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 toolkit, software resource

Defining Citation: PMID:23363224, DOI:10.1186/1471-2105-14-33

Keywords: c++, illumina, command-line

Funding:

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: 20250412T055055+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 40 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

Höfurthner 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.

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.

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.

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.

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).

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.

Shang X, et al. (2022) Chromosomal-level genome and multi-omics dataset of Pueraria lobata var. thomsonii provide new insights into legume family and the isoflavone and puerarin biosynthesis pathways. Horticulture research, 9.

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

Feng L, et al. (2022) The highly continuous reference genome of a leaf-chimeric red pineapple (Ananas comosus var. bracteatus f. tricolor) provides insights into elaboration of leaf color. G3 (Bethesda, Md.), 12(2).

Zhang Y, et al. (2021) Comprehensive Analysis of Fecal Microbiome and Metabolomics in Hepatic Fibrosis Rats Reveal Hepatoprotective Effects of Yinchen Wuling Powder From the Host-Microbial Metabolic Axis. Frontiers in pharmacology, 12, 713197.