

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

Migratory Locust EST Database

RRID:SCR_008201

Type: Tool

Proper Citation

Migratory Locust EST Database (RRID:SCR_008201)

Resource Information

URL: <http://locustdb.genomics.org.cn/>

Proper Citation: Migratory Locust EST Database (RRID:SCR_008201)

Description: The migratory locust (*Locusta migratoria*) is an orthopteran pest and a representative member of hemimetabolous insects. Its transcriptomic data provide invaluable information for molecular entomology study of the insect and pave a way for comparative studies of other medically, agronomically, and ecologically relevant insects. This first transcriptomic database of the locust (LocustDB) has been developed, building necessary infrastructures to integrate, organize, and retrieve data that are either currently available or to be acquired in the future. It currently hosts 45,474 high quality EST sequences from the locust, which were assembled into 12,161 unigenes. This database contains original sequence data, including homologous/orthologous sequences, functional annotations, pathway analysis, and codon usage, based on conserved orthologous groups (COG), gene ontology (GO), protein domain (InterPro), and functional pathways (KEGG). It also provides information from comparative analysis based on data from the migratory locust and five other invertebrate species, such as the silkworm, the honeybee, the fruitfly, the mosquito and the nematode. LocustDB also provides information from comparative analysis based on data from the migratory locust and five other invertebrate species, such as the silkworm, the honeybee, the fruitfly, the mosquito and the nematode. It starts with the first transcriptome information for an orthopteran and hemimetabolous insect and will be extended to provide a framework for incorporation of in-coming genomic data of relevant insect groups and a workbench for cross-species comparative studies.

Synonyms: LocustDB

Resource Type: database, data or information resource

Keywords: ecologically, entomology, est, fruitfly, functional, gene, agronomically, analysis, annotation, codon, comparative, data, domain, genomic, hemimetabolous, homologous, honeybee, insect, invertebrate, invertebrate databases, locust, locusta migratoria, medically, migratory, molecular, mosquito, nematode, orthologous,

orthopteran, pathway, pest, protein, sequence, silkworm, specie, transcriptome, transcriptomic, unigene, ontology

Resource Name: Migratory Locust EST Database

Resource ID: SCR_008201

Alternate IDs: nif-0000-21244

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260805T044206+0000

Ratings and Alerts

No rating or validation information has been found for Migratory Locust EST Database.

No alerts have been found for Migratory Locust EST Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Zheng X, et al. (2020) Locust can detect β -1, 3-glucan of the fungal pathogen before penetration and defend infection via the Toll signaling pathway. Developmental and comparative immunology, 106, 103636.

Jiang ZY, et al. (2020) HYD3, a conidial hydrophobin of the fungal entomopathogen *Metarhizium acridum* induces the immunity of its specialist host locust. International journal of biological macromolecules, 165(Pt A), 1303.

Zhang J, et al. (2014) Molecular and functional characterization of cDNAs putatively encoding carboxylesterases from the migratory locust, *Locusta migratoria*. PloS one, 9(4), e94809.

Yang Q, et al. (2014) Selection and assessment of reference genes for quantitative PCR normalization in migratory locust *Locusta migratoria* (Orthoptera: Acrididae). PloS one, 9(6), e98164.

Zheng X, et al. (2012) β -1,3-Glucan recognition protein (β GRP) is essential for resistance against fungal pathogen and opportunistic pathogenic gut bacteria in *Locusta migratoria manilensis*. Developmental and comparative immunology, 36(3), 602.

Robinson KL, et al. (2011) Evidence for widespread genomic methylation in the migratory locust, *Locusta migratoria* (Orthoptera: Acrididae). PloS one, 6(12), e28167.

Wang J, et al. (2010) Construction and preliminary analysis of a normalized cDNA library from *Locusta migratoria manilensis* topically infected with *Metarhizium anisopliae* var. *acridum*. Journal of insect physiology, 56(8), 998.