

Resource Summary Report

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SEQtools

RRID:SCR_008579

Type: Tool

Proper Citation

SEQtools (RRID:SCR_008579)

Resource Information

URL: <http://www.seqtools.dk/>

Proper Citation: SEQtools (RRID:SCR_008579)

Description: A large collection of tools for basic and advanced analyses of nucleotide and protein sequences. The tools are wrapped into a common user interface making handling, storage, retrieval and viewing the results easy and logical. A seqtools project can accommodate many thousand sequences making unattended batch analyses like database searching at NCBI painless with the robust search engine included in seqtools.

Synonyms: SEQtools

Resource Type: software resource

Keywords: software, sequence analysis, FASEB list

Availability: Free for students; senior scientists are expected to pay to help cover costs

Resource Name: SEQtools

Resource ID: SCR_008579

Alternate IDs: nif-0000-31491

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260801T190348+0000

Ratings and Alerts

No rating or validation information has been found for SEQtools.

No alerts have been found for SEQtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Norton AM, et al. (2025) Deformed wing virus genotypes A and B do not elicit immunologically different responses in naïve honey bee hosts. *Insect molecular biology*, 34(1), 33.

Torma G, et al. (2025) Long-read transcriptomics of caviid gammaherpesvirus 1: compiling a comprehensive RNA atlas. *mSystems*, 10(3), e0167824.

Yamaura K, et al. (2025) Chromosomal domain formation by archaeal SMC, a roadblock protein, and DNA structure. *Nature communications*, 16(1), 1312.

Zhang J, et al. (2024) ?Clarifying the phylogenetic placement of Eupoinae Maddison, 2015 (Araneae, Salticidae) with ultra-conserved element data. *ZooKeys*, 1217, 343.

Prazsák I, et al. (2024) KSHV 3.0: a state-of-the-art annotation of the Kaposi's sarcoma-associated herpesvirus transcriptome using cross-platform sequencing. *mSystems*, 9(2), e0100723.

Torma G, et al. (2024) Long-read Transcriptomics of Caviid Gammaherpesvirus 1: Compiling a Comprehensive RNA Atlas. *bioRxiv : the preprint server for biology*.

Guinet B, et al. (2023) Endoparasitoid lifestyle promotes endogenization and domestication of dsDNA viruses. *eLife*, 12.

Zhou Z, et al. (2023) Sulfur cycling connects microbiomes and biogeochemistry in deep-sea hydrothermal plumes. *The ISME journal*, 17(8), 1194.

Gyenis A, et al. (2023) Genome-wide RNA polymerase stalling shapes the transcriptome during aging. *Nature genetics*, 55(2), 268.

Prazsák I, et al. (2023) KSHV 3.0: A State-of-the-Art Annotation of the Kaposi's Sarcoma-Associated Herpesvirus Transcriptome Using Cross-Platform Sequencing. *bioRxiv : the preprint server for biology*.

Torma G, et al. (2022) Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. *Scientific reports*, 12(1), 1291.

Torma G, et al. (2021) An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome. *Pathogens (Basel, Switzerland)*, 10(2).

Scieuzo C, et al. (2021) *Hermetia illucens* (L.) (Diptera: Stratiomyidae) Odorant Binding Proteins and Their Interactions with Selected Volatile Organic Compounds: An In Silico

Approach. *Insects*, 12(9).

Bertini L, et al. (2021) What Antarctic Plants Can Tell Us about Climate Changes: Temperature as a Driver for Metabolic Reprogramming. *Biomolecules*, 11(8).

Scieuzo C, et al. (2021) An integrated transcriptomic and proteomic approach to identify the main *Torymus sinensis* venom components. *Scientific reports*, 11(1), 5032.

Trauelsén M, et al. (2021) Extracellular succinate hyperpolarizes M2 macrophages through SUCNR1/GPR91-mediated Gq signaling. *Cell reports*, 35(11), 109246.

Tombácz D, et al. (2021) Dynamic Transcriptome Sequencing of Bovine Alphaherpesvirus Type 1 and Host Cells Carried Out by a Multi-Technique Approach. *Frontiers in genetics*, 12, 619056.

Merski M, et al. (2020) Self-analysis of repeat proteins reveals evolutionarily conserved patterns. *BMC bioinformatics*, 21(1), 179.

Olasz F, et al. (2020) Short and Long-Read Sequencing Survey of the Dynamic Transcriptomes of African Swine Fever Virus and the Host Cells. *Frontiers in genetics*, 11, 758.

Becchimanzi A, et al. (2020) Venomics of the ectoparasitoid wasp *Bracon nigricans*. *BMC genomics*, 21(1), 34.