Resource Summary Report

Generated by RRID on May 8, 2025

seq crumbs

RRID:SCR_006486
Type: Tool

Proper Citation

seq crumbs (RRID:SCR_006486)

Resource Information

URL: http://bioinf.comav.upv.es/seq_crumbs/

Proper Citation: seq crumbs (RRID:SCR_006486)

Description: A collection of small sequence processing utilities that are modeled after the Unix command line text processing utilities so every utility tries to perform a specific task and most of them take a sequence file as input and create a new processed sequence file as output. This design encourages the assembly of the seq_crumbs utilities with Unix pipes to create complex pipelines.

Abbreviations: seq_crumbs

Resource Type: software resource

Funding:

Availability: Mainly under the, GNU General Public License

Resource Name: seq crumbs

Resource ID: SCR_006486

Alternate IDs: OMICS_01075

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250420T014330+0000

Ratings and Alerts

No rating or validation information has been found for seq crumbs.

No alerts have been found for seq crumbs.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Pais Ferreira D, et al. (2020) Central memory CD8+ T cells derive from stem-like Tcf7hi effector cells in the absence of cytotoxic differentiation. Immunity, 53(5), 985.

Zuriaga E, et al. (2018) Resistance to Plum Pox Virus (PPV) in apricot (Prunus armeniaca L.) is associated with down-regulation of two MATHd genes. BMC plant biology, 18(1), 25.

Cui L, et al. (2017) De novo transcriptome and expression profile analyses of the Asian corn borer (Ostrinia furnacalis) reveals relevant flubendiamide response genes. BMC genomics, 18(1), 20.

Kristof A, et al. (2016) A putative species complex in the Sea of Japan revealed by DNA sequence data: a study on Lottia cf. kogamogai (Gastropoda: Patellogastropoda). Journal of zoological systematics and evolutionary research = Zeitschrift fur zoologische Systematik und Evolutionsforschung, 54(3), 177.

De Oliveira AL, et al. (2016) Comparative transcriptomics enlarges the toolkit of known developmental genes in mollusks. BMC genomics, 17(1), 905.

Golanowska M, et al. (2015) Draft Genome Sequence of a Highly Virulent Strain of the Plant Pathogen Dickeya solani, IFB0099. Genome announcements, 3(2).

Kohyama TI, et al. (2015) Spatial and temporal variation at major histocompatibility complex class IIB genes in the endangered Blakiston's fish owl. Zoological letters, 1, 13.

McNulty SN, et al. (2014) Systems biology studies of adult paragonimus lung flukes facilitate the identification of immunodominant parasite antigens. PLoS neglected tropical diseases, 8(10), e3242.

Abubucker S, et al. (2014) Identification and characterization of alternative splicing in parasitic nematode transcriptomes. Parasites & vectors, 7, 151.