Resource Summary Report

Generated by dkNET on Apr 29, 2025

SEER

RRID:SCR_015499
Type: Tool

Proper Citation

SEER (RRID:SCR_015499)

Resource Information

URL: https://github.com/johnlees/seer

Proper Citation: SEER (RRID:SCR_015499)

Description: Sequence element enrichment analysis tool to perform pan-genome-wide association studies in bacteria.

Resource Type: source code, data processing software, sequence analysis software, data analysis software, software resource, software application

Defining Citation: DOI:10.1038/ncomms12797, DOI:10.1101/038463

Keywords: bacterial genome association, sequence element enrichment analysis, kmer enrichment analysis

Funding:

Availability: Available for download

Resource Name: SEER

Resource ID: SCR_015499

Alternate IDs: OMICS_21699

Alternate URLs: https://sources.debian.org/src/seer/

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250429T055743+0000

Ratings and Alerts

No rating or validation information has been found for SEER.

No alerts have been found for SEER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Houerbi N, et al. (2024) Secretome profiling reveals acute changes in oxidative stress, brain homeostasis, and coagulation following short-duration spaceflight. Nature communications, 15(1), 4862.

Roberts MD, et al. (2024) A novel deep proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training. Aging, 16(8), 6631.

Roberts MD, et al. (2023) A novel deep proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training. bioRxiv : the preprint server for biology.

Wang J, et al. (2023) The Impact of a History of Different Other Cancers on the Long-Term Outcomes of Patients with Gallbladder Cancer: A Propensity Score-Adjusted, Population-Based Study. Technology in cancer research & treatment, 22, 15330338231183937.

McElderry RM, et al. (2022) Predation thresholds for reintroduction of native avifauna following suppression of invasive Brown Treesnakes on Guam. Ecological applications : a publication of the Ecological Society of America, 32(8), e2716.

Lees JA, et al. (2017) Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. eLife, 6.