Resource Summary Report

Generated by dkNET on May 21, 2025

Gmove

RRID:SCR_019132
Type: Tool

Proper Citation

Gmove (RRID:SCR_019132)

Resource Information

URL: http://www.genoscope.cns.fr/gmove

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Description: Software tool for genome annotation. Eukaryotic gene prediction tool focused on evidence supported by expressed sequences like transcripts and conserved proteins alignments. Can be used to reannotate genomes, to do comparative gene prediction and improve existing genome annotation. Can predict gene models with canonical and non-canonical splice sites.

Synonyms: Gene MOdeling using Various Evidence

Resource Type: simulation software, software resource, software application

Keywords: Expressed sequences, RNAseq, conserved proteins, conserved proteins alignment, genome annotation, Eukaryotic gene prediction, gene prediction, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Gmove

Resource ID: SCR_019132

Alternate IDs: biotools:gmove

Alternate URLs: https://github.com/institut-de-genomique/gmove, https://bio.tools/gmove

License: CeCILL

Record Creation Time: 20220129T080343+0000

Record Last Update: 20250521T061805+0000

Ratings and Alerts

No rating or validation information has been found for Gmove.

No alerts have been found for Gmove.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943.

Eleftheriou E, et al. (2021) Chromosome-scale assembly of the yellow mealworm genome. Open research Europe, 1, 94.

Rousseau-Gueutin M, et al. (2020) Long-read assembly of the Brassica napus reference genome Darmor-bzh. GigaScience, 9(12).