Resource Summary Report

Generated by dkNET on Apr 22, 2025

Gemi

RRID:SCR_003211
Type: Tool

Proper Citation

Gemi (RRID:SCR_003211)

Resource Information

URL: http://sourceforge.net/projects/gemi/

Proper Citation: Gemi (RRID:SCR_003211)

Description: Automated software tool to design polymerase chain reaction (PCR) primers. It accepts multiple aligned and long sequences with degenerated nucleotides. It can be used for quantitative/real-time PCR, conventional and Sanger sequencing. Gemi accepts DNA and RNA sequences with degenerate nucleotide (non-A/C/G/T bases). The programs are as the following: # The first program is to design PCR primers from multiple sequence alignment. # Program to convert ClustalW format (.aln), Phylip (.phy) and (.gde) formats to Fasta format. # Reverse and/or complement program is to find the reverse and complement counterpart of single or multiple sequences.

Abbreviations: Gemi

Synonyms: Gemi - PCR oligos / primers design from multiple sequence alignments

Resource Type: software resource

Defining Citation: PMID:23316117

Keywords: polymerase chain reaction, primer, pcr primer design, pcr primer, dna sequence, rna sequence, c#, .net/mono, windows, probe, multiple aligned sequence

Funding:

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: Gemi

Resource ID: SCR_003211

Alternate IDs: OMICS_02332

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250420T014137+0000

Ratings and Alerts

No rating or validation information has been found for Gemi.

No alerts have been found for Gemi.

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 dkNET.

Serna Garcia G, et al. (2022) GeMI: interactive interface for transformer-based Genomic Metadata Integration. Database : the journal of biological databases and curation, 2022.

Zhao Y, et al. (2021) Detecting Sorghum Plant and Head Features from Multispectral UAV Imagery. Plant phenomics (Washington, D.C.), 2021, 9874650.

Chiquito-Almanza E, et al. (2021) Diversity and Distribution of Viruses Infecting Wild and Domesticated Phaseolus spp. in the Mesoamerican Center of Domestication. Viruses, 13(6).

Xin H, et al. (2020) GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. Genome biology, 21(1), 188.

Schemmerer M, et al. (2019) Isolation of Subtype 3c, 3e and 3f-Like Hepatitis E Virus Strains Stably Replicating to High Viral Loads in an Optimized Cell Culture System. Viruses, 11(6).

Nguyen TV, et al. (2019) Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. Genome biology and evolution, 11(8), 2273.

Burns JA, et al. (2017) Transcriptome analysis illuminates the nature of the intracellular interaction in a vertebrate-algal symbiosis. eLife, 6.

Tarimo B, et al. (2015) Spatial distribution of temporal dynamics in anthropogenic fires in miombo savanna woodlands of Tanzania. Carbon balance and management, 10, 18.

Sobhy H, et al. (2015) Identification of giant Mimivirus protein functions using RNA interference. Frontiers in microbiology, 6, 345.