

Resource Summary Report

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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

Availability: Free, Available for download, Freely available

Resource Name: Gemi

Resource ID: SCR_003211

Alternate IDs: OMICS_02332

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260725T190538+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 13 mentions in open access literature.

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

Hikmat H, et al. (2025) Five-Year (2017-2022) Evolutionary Dynamics of Human Coronavirus HKU1 in Southern France With Emergence of Viruses Harboring Spike H512R Substitution. *Journal of medical virology*, 97(2), e70217.

Houmadi H, et al. (2025) Five-Year (2017-2022) Evolutionary Dynamics of Human Coronavirus OC43 in Southern France Based on Whole Genome Next-Generation Sequencing. *Journal of medical virology*, 97(12), e70726.

Kim S, et al. (2025) Effects of genotype-by-environment and analysis of potential management interaction on vase life in cut lisianthus. *Frontiers in plant science*, 16, 1578100.

Hikmat H, et al. (2025) Implementation of a Multiplex PCR Amplification System Combined With Next-Generation Genome Sequencing to Decipher the Circulation of Human Coronavirus 229E Lineages in Southern France. *Journal of medical virology*, 97(11), e70653.

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.

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.

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).

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.