

Resource Summary Report

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LAGAN

RRID:SCR_008558

Type: Tool

Proper Citation

LAGAN (RRID:SCR_008558)

Resource Information

URL: <http://lagan.stanford.edu>

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Description: About the LAGAN Toolkit The LAGAN Toolkit consists of four components: CHAOS CHAOS is a pairwise local aligner optimized for non-coding, and other poorly conserved regions of the genome. It uses both exact matching and degenerate seeds, and is able to find homology in the presence of gaps. LAGAN LAGAN is our highly parametrizable pairwise global alignment program. It takes local alignments generated by CHAOS as anchors, and limits the search area of the Needleman-Wunsch algorithm around these anchors; Multi-LAGAN Multi-LAGAN is a generalization of the pairwise algorithm to multiple sequence alignment. M-LAGAN performs progressive pairwise alignments, guided by a user-specified phylogenetic tree. Alignments are aligned to other alignments using the sum-of-pairs metric. Shuffle-LAGAN Shuffle-LAGAN is a novel global alignment algorithm that is able to find rearrangements (inversions, transpositions and some duplications) in a global alignment framework. It uses CHAOS local alignments to build a map of the rearrangements between the sequences, and LAGAN to align the regions of conserved synteny. The website uses scripts written by Alex Poliakov. The website was designed by Marina Sirota.

Synonyms: LAGAN

Resource Type: software resource

Defining Citation: [DOI:10.1101/gr.926603](https://doi.org/10.1101/gr.926603)

Resource Name: LAGAN

Resource ID: SCR_008558

Alternate IDs: OMICS_08469, nif-0000-31432

Alternate URLs: <https://sources.debian.org/src/lagan/>

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260725T190649+0000

Ratings and Alerts

No rating or validation information has been found for LAGAN.

No alerts have been found for LAGAN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 82 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Doh H, et al. (2025) Genomic diversity and comparative phylogenomic analysis of genus Norovirus. Scientific reports, 15(1), 5412.

Treaster MJ, et al. (2025) A Y-linked duplication of anti-Mullerian hormone is the sex determination gene in threespine stickleback. PLoS genetics, 21(11), e1011932.

Shao C, et al. (2025) Integrating phylogenomic and morphological evidence to solve the taxonomy of Phoebe legendrei (Lauraceae) and closely related species. BMC plant biology, 25(1), 1736.

Healey HM, et al. (2025) Single-cell sequencing provides clues about the developmental genetic basis of evolutionary adaptations in syngnathid fishes. eLife, 13.

Desvignes T, et al. (2025) Hemoglobin-Gene Cluster Deletions in Antarctic White-Blooded Icefishes Facilitated by Transposable Elements. Genome biology and evolution, 17(10).

Al-Andal A, et al. (2025) Plastome diversity and phylogenetic insights among modern Egyptian wheat cultivars: Genome-Wide and Gene-Level perspectives. BMC plant biology, 25(1), 1781.

Treaster MJ, et al. (2025) A Y-linked duplication of anti-Mullerian hormone is the sex determination gene in threespine stickleback. bioRxiv : the preprint server for biology.

Hawkins MB, et al. (2025) Establishment, conservation, and innovation of dorsal determination mechanisms during the evolution of vertebrate paired appendages. bioRxiv : the preprint server for biology.

Li X, et al. (2025) Phylogeny and evolutionary dynamics of the Rubia genus based on the chloroplast genome of Rubia tibetica. Scientific reports, 15(1), 14370.

Xiao X, et al. (2025) Comparative Analysis of Complete Chloroplast Genomes and Phylogenetic Relationships of 21 Sect. *Camellia* (*Camellia* L.) Plants. *Genes*, 16(1).

Cheng X, et al. (2024) Unveiling the conserved nature of *Heliconia* chloroplast genomes: insights from the assembly and analysis of four complete chloroplast genomes. *Frontiers in plant science*, 15, 1535549.

Gu J, et al. (2024) Comparative chloroplast genomes analysis of nine *Primulina* (*Gesneriaceae*) rare species, from karst region of southwest China. *Scientific reports*, 14(1), 30256.

Xiang YN, et al. (2024) Deciphering the Plastomic Code of Chinese Hog-Peanut (*Amphicarpaea edgeworthii* Benth., *Leguminosae*): Comparative Genomics and Evolutionary Insights within the Phaseoleae Tribe. *Genes*, 15(1).

Panara V, et al. (2024) Multiple cis-regulatory elements control *prox1a* expression in distinct lymphatic vascular beds. *Development (Cambridge, England)*, 151(9).

Kim JS, et al. (2024) Chloroplast genome sequencing and divergence analysis of 18 *Pyrus* species: insights into intron length polymorphisms and evolutionary processes. *Frontiers in genetics*, 15, 1468596.

Healey HM, et al. (2024) Single Cell Sequencing Provides Clues about the Developmental Genetic Basis of Evolutionary Adaptations in Syngnathid Fishes. *bioRxiv : the preprint server for biology*.

Hao Q, et al. (2024) Monoallelically expressed noncoding RNAs form nucleolar territories on NOR-containing chromosomes and regulate rRNA expression. *eLife*, 13.

Wang T, et al. (2024) Complete chloroplast genomes and phylogenetic relationships of *Pedicularis chinensis* and *Pedicularis kansuensis*. *Scientific reports*, 14(1), 14357.

He L, et al. (2024) Chloroplast genomes in seven *Lagerstroemia* species provide new insights into molecular evolution of photosynthesis genes. *Frontiers in genetics*, 15, 1378403.

Go S, et al. (2024) Pan-chloroplast genomes for accession-specific marker development in *Hibiscus syriacus*. *Scientific data*, 11(1), 246.