

Resource Summary Report

Generated by [NIF](#) on Sep 5, 2026

Gblocks

RRID:SCR_015945

Type: Tool

Proper Citation

Gblocks (RRID:SCR_015945)

Resource Information

URL: http://molevol.cmima.csic.es/castresana/Gblocks_server.html

Proper Citation: Gblocks (RRID:SCR_015945)

Description: Software that eliminates poorly aligned positions and divergent regions of a DNA or protein alignment so that it becomes more suitable for phylogenetic analysis., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: software application, software resource, standalone software, web application

Defining Citation: [PMID:10742046](#), [PMID:17654362](#)

Keywords: position, dna, protein, align, alignment, phylogenetic, analysis, block, ansi c, deletion, removal

Funding: Desarrollo e Innovación Tecnológica ;
Fundación BBVA ;
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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Gblocks

Resource ID: SCR_015945

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260903T235327+0000

Ratings and Alerts

No rating or validation information has been found for Gblocks.

No alerts have been found for Gblocks.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2043 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia* × *blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Garsmeur O, et al. (2025) The genomic footprints of wild *Saccharum* species trace domestication, diversification, and modern breeding of sugarcane. *Cell*, 188(25), 7252.

Penot-Raquin M, et al. (2025) Prevalence and environmental abundance of the TSET complex in cosmopolitan algal groups. *iScience*, 28(6), 112679.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte* (Hong Kong, China), 2025, gigabyte155.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte* (Hong Kong, China), 2025, gigabyte150.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of *Cypriniformes*. *GigaScience*, 14.

Huang J, et al. (2025) Phylogenomic relationships and species delimitation of *Cotoneaster* ser. *Pannosi*, ser. *Buxifolii*, and related taxa. *Frontiers in plant science*, 16, 1575925.

Veríssimo J, et al. (2025) The mitochondrial genomes of Iberian freshwater and diadromous fishes. *Scientific data*, 12(1), 349.

Aleix-Mata G, et al. (2025) Characterizing the complete mitochondrial genome and rDNA of *Oestrus* sp. (Diptera: Oestridae): the bot fly parasitizing the Iberian ibex, *Capra pyrenaica*. *Journal of medical entomology*, 62(4), 808.

Badillo-Viloria M, et al. (2025) *Rickettsia* spp. and Anaplasmataceae in Ticks From Domestic Animals in Northern Colombia. *Zoonoses and public health*, 72(5), 421.

Kon T, et al. (2025) Chromosome-level genome assembly of the doctor fish (*Garra rufa*). *Scientific data*, 12(1), 765.

Tan S, et al. (2025) Comprehensive analysis of 111 Pleuronectiformes mitochondrial genomes: insights into structure, conservation, variation and evolution. *BMC genomics*, 26(1), 50.

Liu Q, et al. (2025) Comparative Mitogenomes and Phylogenetic Analyses of Coccinellidae (Coleoptera: Coccinelloidea). *Ecology and evolution*, 15(3), e71053.

Cadena-Cruz C, et al. (2025) Respiratory syncytial virus fuses with plasma membrane to infect primary cultures of bronchial epithelial cells. *Frontiers in microbiology*, 16, 1498955.

Otero CE, et al. (2025) Rhesus Cytomegalovirus-encoded Fc γ -binding glycoproteins facilitate viral evasion from IgG-mediated humoral immunity. *Nature communications*, 16(1), 1200.

Trojanovsky RB, et al. (2025) Actin-dependent γ -catenin oligomerization contributes to adherens junction assembly. *Nature communications*, 16(1), 1801.

Sato S, et al. (2025) Phylogenomics of the rarest animals: a second species of Micrognathozoa identified by machine learning. *Proceedings. Biological sciences*, 292(2041), 20242867.