

# Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

## Blocks

RRID:SCR\_007567

Type: Tool

### Proper Citation

Blocks (RRID:SCR\_007567)

### Resource Information

**URL:** <http://blocks.fhcrc.org>

**Proper Citation:** Blocks (RRID:SCR\_007567)

**Description:** Blocks is a database of highly conserved regions of proteins, or Blocks. The database is no longer maintained or updated and some of its tools are no longer functional. However, Blocks does provide Block Searcher, Get Blocks and Block Maker, aids to detection and verification of protein sequence homology. They compare a protein or DNA sequence to a database of protein blocks (current version), retrieve blocks, and create new blocks, respectively. Users can further view blocks by (keyword or number), search a sequence against the database of blocks, search blocks against each other, or make blocks of their own.

**Synonyms:** Blocks

**Resource Type:** data or information resource, database

**Keywords:** block, conserved region, protein, protein conservation, FASEB list

**Resource Name:** Blocks

**Resource ID:** SCR\_007567

**Alternate IDs:** nif-0000-02614

**Record Creation Time:** 20220129T080242+0000

**Record Last Update:** 20260905T133140+0000

### Ratings and Alerts

No rating or validation information has been found for Blocks.

No alerts have been found for Blocks.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 136 mentions in open access literature.

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

Elreify HM, et al. (2026) BiGKbhb: a bi-directional gated recurrent unit model for predicting lysine  $\alpha$ -hydroxybutyrylation sites. BMC genomics, 27(1), 102.

Murtaza G, et al. (2025) GrapHiC: An Integrative Graph Based Approach for Imputing Missing Hi-C Reads. IEEE transactions on computational biology and bioinformatics, 22(2), 409.

Harun-Or-Roshid M, et al. (2025) A genetic algorithm-based ensemble model for efficiently identifying interleukin 6 inducing peptides. Scientific reports, 15(1), 21213.

Elreify HM, et al. (2025) A deep learning framework for lysine 2-hydroxyisobutyrylation site prediction using evolutionary feature representation. Scientific reports, 15(1), 38838.

Fallah Ziarani M, et al. (2023) Evaluation of antibacterial properties of nisin peptide expressed in carrots. Scientific reports, 13(1), 22123.

Klink VP, et al. (2022) The heterologous expression of conserved Glycine max (soybean) mitogen activated protein kinase 3 (MAPK3) paralogs suppresses Meloidogyne incognita parasitism in Gossypium hirsutum (upland cotton). Transgenic research, 31(4-5), 457.

Li X, et al. (2020) ASAP-SML: An antibody sequence analysis pipeline using statistical testing and machine learning. PLoS computational biology, 16(4), e1007779.

Polyanovsky V, et al. (2020) The ranging of amino acids substitution matrices of various types in accordance with the alignment accuracy criterion. BMC bioinformatics, 21(Suppl 11), 294.

Liu B, et al. (2019) BioSeq-Analysis2.0: an updated platform for analyzing DNA, RNA and protein sequences at sequence level and residue level based on machine learning approaches. Nucleic acids research, 47(20), e127.

Ziv Y, et al. (2018) Children and Caregivers' Exposure to Adverse Childhood Experiences (ACES): Association with Children's and Caregivers' Psychological Outcomes in a Therapeutic Preschool Program. International journal of environmental research and public health, 15(4).

Zhang M, et al. (2018) Acid-resistant genes of oral plaque microbiome from the functional metagenomics. Journal of oral microbiology, 10(1), 1424455.

Markovic M, et al. (2018) The clinical relevance of advanced artificial feedback in the control of a multi-functional myoelectric prosthesis. Journal of neuroengineering and

rehabilitation, 15(1), 28.

Murphy C, et al. (2018) Distant from input: Evidence of regions within the default mode network supporting perceptually-decoupled and conceptually-guided cognition. *NeuroImage*, 171, 393.

Alamia A, et al. (2018) Strong Conscious Cues Suppress Preferential Gaze Allocation to Unconscious Cues. *Frontiers in human neuroscience*, 12, 427.

Tang Y, et al. (2018) TRCMGene: A two-step referential compression method for the efficient storage of genetic data. *PloS one*, 13(11), e0206521.

Mistry R, et al. (2018) Longitudinal study of adolescent tobacco use and tobacco control policies in India. *BMC public health*, 18(1), 815.

Wolf C, et al. (2017) The necessity to choose causes the effects of reward on saccade preparation. *Scientific reports*, 7(1), 16966.

Costello JL, et al. (2017) Predicting the targeting of tail-anchored proteins to subcellular compartments in mammalian cells. *Journal of cell science*, 130(9), 1675.

Bradford DE, et al. (2017) Alcohol's effects on emotionally motivated attention, defensive reactivity and subjective anxiety during uncertain threats. *Social cognitive and affective neuroscience*, 12(11), 1823.

Fox OM, et al. (2017) How Configural Is the Configural Superiority Effect? A Neuroimaging Investigation of Emergent Features in Visual Cortex. *Frontiers in psychology*, 8, 32.