

# Resource Summary Report

Generated by [ASWG](#) on Aug 1, 2026

## [jMHC](#)

RRID:SCR\_005605

Type: Tool

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### Proper Citation

jMHC (RRID:SCR\_005605)

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### Resource Information

**URL:** <https://code.google.com/p/jmhc/>

**Proper Citation:** jMHC (RRID:SCR\_005605)

**Description:** Software for analyzing and visualization of the results of deep amplicon sequencing.

**Abbreviations:** jMHC

**Synonyms:** jmhc - software for analyzing and visualization of the results of deep amplicon sequencing

**Resource Type:** software resource

**Defining Citation:** [PMID:21676201](#)

**Keywords:** matlab

**Availability:** GNU General Public License, v3, Acknowledgement requested

**Resource Name:** jMHC

**Resource ID:** SCR\_005605

**Alternate IDs:** OMICS\_00300

**Record Creation Time:** 20220129T080231+0000

**Record Last Update:** 20260801T190256+0000

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### Ratings and Alerts

No rating or validation information has been found for jMHC.

No alerts have been found for jMHC.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Cortázar-Chinarro M, et al. (2020) Antimicrobial peptide and sequence variation along a latitudinal gradient in two anurans. *BMC genetics*, 21(1), 38.

Baltrušis P, et al. (2018) Exploring benzimidazole resistance in *Haemonchus contortus* by next generation sequencing and droplet digital PCR. *International journal for parasitology. Drugs and drug resistance*, 8(3), 411.

Cortázar-Chinarro M, et al. (2017) Drift, selection, or migration? Processes affecting genetic differentiation and variation along a latitudinal gradient in an amphibian. *BMC evolutionary biology*, 17(1), 189.

Mulder KP, et al. (2017) Evolutionary dynamics of an expressed MHC class II? locus in the Ranidae (Anura) uncovered by genome walking and high-throughput amplicon sequencing. *Developmental and comparative immunology*, 76, 177.

Razali H, et al. (2017) A quantitative and qualitative comparison of illumina MiSeq and 454 amplicon sequencing for genotyping the highly polymorphic major histocompatibility complex (MHC) in a non-model species. *BMC research notes*, 10(1), 346.

Biedrzycka A, et al. (2017) Extreme MHC class I diversity in the sedge warbler (*Acrocephalus schoenobaenus*); selection patterns and allelic divergence suggest that different genes have different functions. *BMC evolutionary biology*, 17(1), 159.

Eimes JA, et al. (2016) Early Duplication of a Single MHC IIB Locus Prior to the Passerine Radiations. *PloS one*, 11(9), e0163456.

Balasubramaniam S, et al. (2016) New data from basal Australian songbird lineages show that complex structure of MHC class II ? genes has early evolutionary origins within passerines. *BMC evolutionary biology*, 16(1), 112.

Grogan KE, et al. (2016) Next-generation genotyping of hypervariable loci in many individuals of a non-model species: technical and theoretical implications. *BMC genomics*, 17, 204.

Rico Y, et al. (2015) Lack of Spatial Immunogenetic Structure among Wolverine (*Gulo gulo*) Populations Suggestive of Broad Scale Balancing Selection. *PloS one*, 10(10), e0140170.