

Resource Summary Report

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[jMHC](#)

RRID:SCR_005605

Type: Tool

Proper Citation

jMHC (RRID:SCR_005605)

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: 20260725T190606+0000

Ratings and Alerts

No rating or validation information has been found for jMHC.

No alerts have been found for jMHC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

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.