

Resource Summary Report

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[omegaMap](#)

RRID:SCR_024143

Type: Tool

Proper Citation

omegaMap (RRID:SCR_024143)

Resource Information

URL: <http://www.danielwilson.me.uk/omegaMap.html>

Proper Citation: omegaMap (RRID:SCR_024143)

Description: Software tool for detecting natural selection and recombination in DNA or RNA sequences.

Synonyms: omegamap

Resource Type: software resource, software application, data processing software, data analysis software

Defining Citation: [DOI:10.1534/genetics.105.044917](https://doi.org/10.1534/genetics.105.044917)

Keywords: detecting natural selection and recombination, DNA sequences, RNA sequences

Availability: Free, Available for download, Freely available,

Resource Name: omegaMap

Resource ID: SCR_024143

Alternate IDs: OMICS_31719

Old URLs: <https://sources.debian.org/src/omegamap/>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260817T040705+0000

Ratings and Alerts

No rating or validation information has been found for omegaMap.

No alerts have been found for omegaMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Marcuzzi O, et al. (2025) Genetic diversity of BoLA-DRB3 in Latin American Creole cattle: an update of the state of the art. *Immunogenetics*, 77(1), 28.

Stefanovi? M, et al. (2021) Positive selection on the MHC class II DLA-DQA1 gene in golden jackals (*Canis aureus*) from their recent expansion range in Europe and its effect on their body mass index. *BMC ecology and evolution*, 21(1), 122.

Bletsa M, et al. (2021) Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. *Virus evolution*, 7(1), veab036.

Rocha RG, et al. (2019) Alternated selection mechanisms maintain adaptive diversity in different demographic scenarios of a large carnivore. *BMC evolutionary biology*, 19(1), 90.

Awadi A, et al. (2018) Positive selection and climatic effects on MHC class II gene diversity in hares (*Lepus capensis*) from a steep ecological gradient. *Scientific reports*, 8(1), 11514.

Hart MW, et al. (2018) Positive selection on human gamete-recognition genes. *PeerJ*, 6, e4259.

Li Y, et al. (2017) Contrasting patterns of nucleotide polymorphism suggest different selective regimes within different parts of the PgiC1 gene in *Festuca ovina* L. *Hereditas*, 154, 11.

Crispo E, et al. (2017) The evolution of the major histocompatibility complex in upstream versus downstream river populations of the longnose dace. *Ecology and evolution*, 7(10), 3297.

Zeng QQ, et al. (2016) Balancing selection and recombination as evolutionary forces caused population genetic variations in golden pheasant MHC class I genes. *BMC evolutionary biology*, 16, 42.

Joshi A, et al. (2015) Structures of the Ultra-High-Affinity Protein-Protein Complexes of Pyocins S2 and AP41 and Their Cognate Immunity Proteins from *Pseudomonas aeruginosa*. *Journal of molecular biology*, 427(17), 2852.

Maddamsetti R, et al. (2015) Synonymous Genetic Variation in Natural Isolates of *Escherichia coli* Does Not Predict Where Synonymous Substitutions Occur in a Long-Term Experiment. *Molecular biology and evolution*, 32(11), 2897.

Kohyama TI, et al. (2015) Spatial and temporal variation at major histocompatibility complex class IIB genes in the endangered Blakiston's fish owl. *Zoological letters*, 1, 13.

Jaratlerdsiri W, et al. (2014) Selection and trans-species polymorphism of major histocompatibility complex class II genes in the order Crocodylia. *PloS one*, 9(2), e87534.

Golubchik T, et al. (2013) Within-host evolution of *Staphylococcus aureus* during asymptomatic carriage. *PloS one*, 8(5), e61319.

Nydam ML, et al. (2012) The fester locus in *Botryllus schlosseri* experiences selection. *BMC evolutionary biology*, 12, 249.

Thomé MT, et al. (2012) Delimiting genetic units in Neotropical toads under incomplete lineage sorting and hybridization. *BMC evolutionary biology*, 12, 242.

Yasukochi Y, et al. (2012) MHC class II DQB diversity in the Japanese black bear, *Ursus thibetanus japonicus*. *BMC evolutionary biology*, 12, 230.

MacManes MD, et al. (2012) Is promiscuity associated with enhanced selection on MHC-DQ? in mice (genus *Peromyscus*)? *PloS one*, 7(5), e37562.

Kent BN, et al. (2011) Evolutionary genomics of a temperate bacteriophage in an obligate intracellular bacteria (*Wolbachia*). *PloS one*, 6(9), e24984.

Pérez-Losada M, et al. (2011) Phylodynamics of HIV-1 from a phase III AIDS vaccine trial in Bangkok, Thailand. *PloS one*, 6(3), e16902.