Resource Summary Report

Generated by NIF on Apr 25, 2025

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

Defining Citation: DOI:10.1534/genetics.105.044917

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

Funding:

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: 20250425T060556+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 31 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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.

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.

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

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

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.

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

Smith S, et al. (2011) Evolutionary genetics of MHC class II beta genes in the brown hare, Lepus europaeus. Immunogenetics, 63(11), 743.