

# Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

## MARIA

RRID:SCR\_028673

Type: Tool

### Proper Citation

MARIA (RRID:SCR\_028673)

### Resource Information

**URL:** <https://maria.stanford.edu/index.php>

**Proper Citation:** MARIA (RRID:SCR\_028673)

**Description:** Web multimodal recurrent neural network tool designed to predict HLA-II (Human Leukocyte Antigen class II) peptide ligand presentation. It uses cell HLA alleles, peptide sequences, and source genes to evaluate antigen presentation. Used for predicting the likelihood of antigen presentation from a gene of interest in the context of specific HLA class II alleles.

**Synonyms:** MARIA:Major Histocompatibility Complex Analysis with Recurrent Integrated Architecture

**Resource Type:** software resource, web application

**Defining Citation:** [PMID:31611695](#)

**Keywords:** multimodal recurrent neural network, predicting likelihood of antigen presentation, gene of interest, specific HLA class II alleles,

**Funding:** NCI K08 CA207882;  
NCI U01 CA194389;  
NCRR S10RR027431;  
NIGMS GM 102365

**Availability:** Free, Freely available

**Resource Name:** MARIA

**Resource ID:** SCR\_028673

**Record Creation Time:** 20260714T043827+0000

**Record Last Update:** 20260821T194405+0000

---

## Ratings and Alerts

No rating or validation information has been found for MARIA.

No alerts have been found for MARIA.

---

## Data and Source Information

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

---

## Usage and Citation Metrics

We have not found any literature mentions for this resource.