HLA-EMMA – Epitope Mismatch Algorithm version 1.06

March 2022

HLA-EMMA is a free software package for registered users and is developed at the Laboratory for Transplantation Immunology, department of Immunohematology and Blood transfusion, LUMC Leiden. HLA-EMMA can be used to compute recipient and donor HLA compatibility at the amino acid level.

This software package is only available for Windows OS.

System requirements

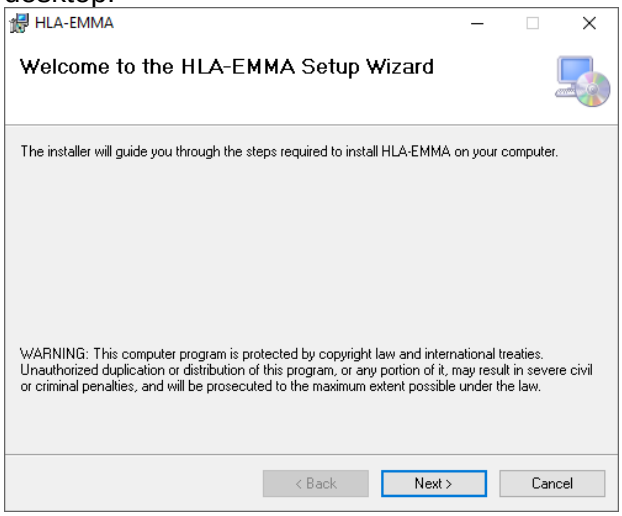
The minimal system requirements for HLA-EMMA are:

Operating system	Microsoft Windows 10
Processor	1GHz
RAM	512 MB
Screen resolution	1920 x1080
Additional software	.NET Framework 4.6.1 Microsoft Excel

Download and Install

HLA-EMMA is available by download only. Please register your account and login to www.HLA-EMMA.com and use the link on the download page to download the setup file.

Run the setup file to install HLA-EMMA on your Pc. After installing, you will find the shortcuts to HLA-EMMA in your Windows menu and on your desktop.

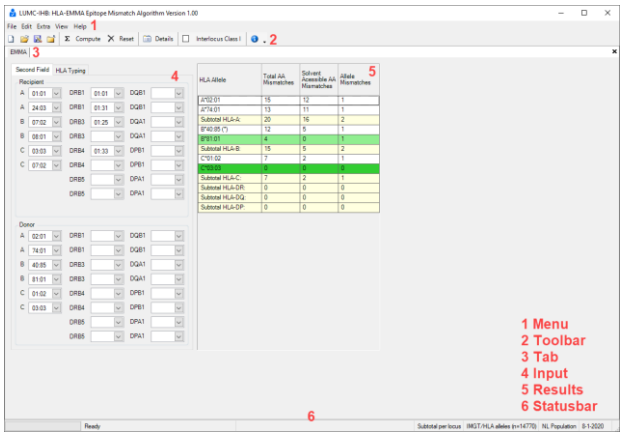


You can repair and uninstall HLA-EMMA by executing the setup or via Windows Settings.

Licence activation

When you start HLA-EMMA for the first time, you will be prompted for a licence. Please send an email to info@HLA-EMMA.com with the generated key to obtain a licence to activate your copy of HLA-EMMA.
To activate HLA-EMMA you have to copy the licence file into the installation folder of the program or paste the key from the activation email into the licence activation screen.

HLA-EMMA



When HLA-EMMA is started, you will see the following view, after clicking menu item New on the toolbar, or file New on the menu.

1. Menu

The main menu contains items to work with the program or change the appearance of HLA-EMMA.

2. Toolbar

In the toolbar you will find the primary functions for HLA-EMMA. Here you will find shortcuts to open or save a document.

3. Tab

Each document will open in a new tab. To track your documents, the tab header will display the path to the document on your Pc.

4. Input

Select the HLA allele by dropdown for each locus or copy and paste the donor and recipient typing in the HLA Typing tab to complete your case.

Second field HLA typing data is preferred, but first field HLA typing data can be entered. The most likely second field HLA typing will be used, based on the population setting in the option screen.

5. Results

The table contains the result of the comparison between the donor and recipient. It is an overview of all amino acid mismatches and those that are solvent accessible. By clicking on details, you will find more information.

6. Status bar

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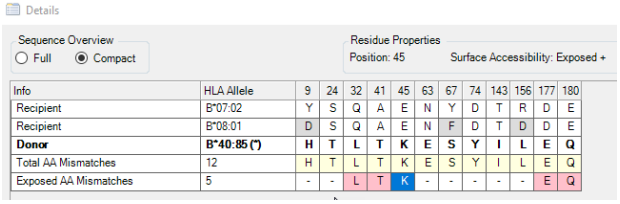
To track the progress of the comparison, the status bar will provide information on the selected options and the current step in de comparison process.

Details

- Check the details for more information on the amino acid mismatches. The compact view shows only the mismatched amino acids. Residue properties are shown by clicking on an amino acid. A summary of the residue properties is shown by clicking on the header position.



Info	HLA Allele	9	24	32	41	45	63	67	74	143	156	177	180
Recipient	B*07:02	Y	S	Q	A	E	N	Y	D	T	R	D	E
Recipient	B*08:01	D	S	Q	A	E	N	F	D	T	D	D	E
Donor	**B*40:85 (*)**	**H**	**T**	**L**	**T**	**K**	**E**	**S**	**Y**	**I**	**L**	**E**	**Q**
Total AA Mismatches	12	H	T	L	T	K	E	S	Y	I	L	E	Q
Exposed AA Mismatches	5	-	-	L	T	K	-	-	-	-	-	E	Q

- Alleles with an (*) like **B*40:85 (*)** are not completely sequenced. The amino acids positions with * are not calculated as a mismatch.

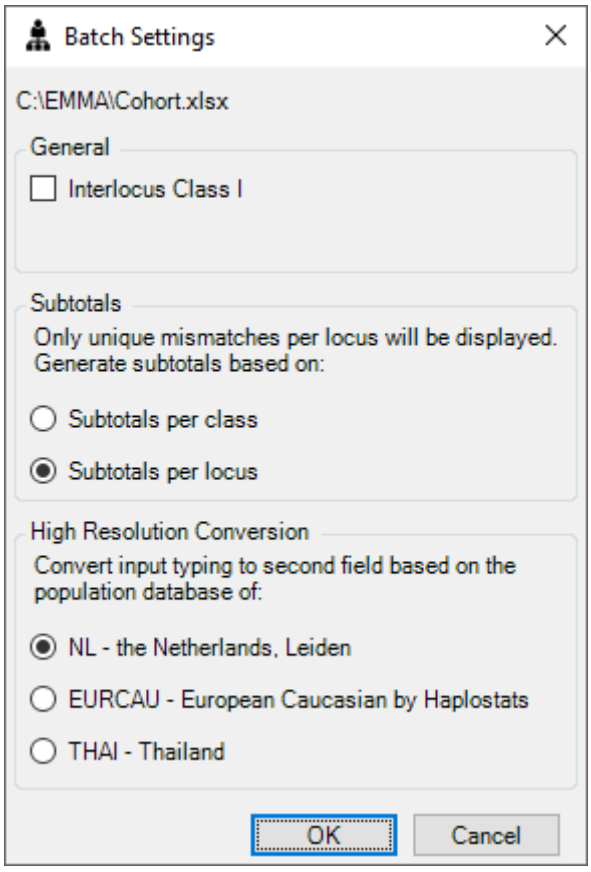
- Null alleles such as **DRB4*01:03N**, are recognised by the program, but are not calculated as a mismatch when present on the donor because the allele is a non-expressed allele.

Save and Export

- With the batch option, an unlimited number of donor and recipient pairs can be analysed at the same time.

- The batch input format is a Microsoft Excel file. This template requires a code for each recipient (R1) and donor pair (D1) and prefers second field typing.

- The batch output is an xml file. Choose the xml file to open in Excel and select the option “open as XML-table” when prompted.

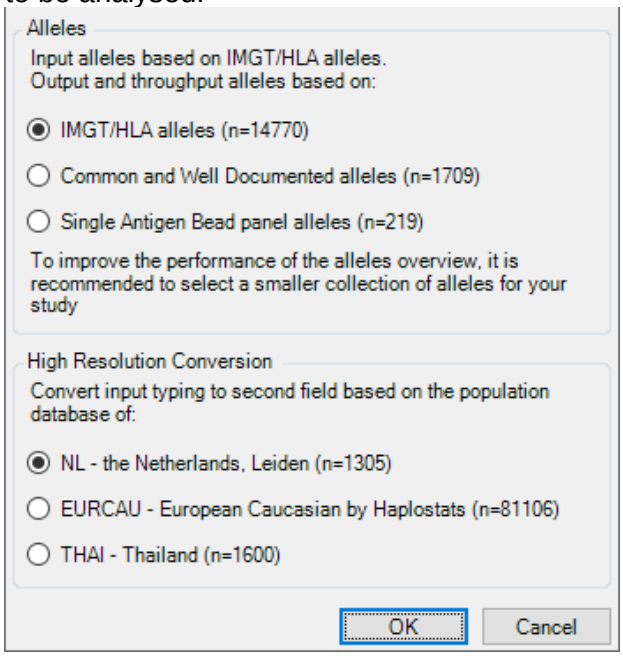


Extra: Options

- Subtotals are generated per HLA locus.

- High Resolution Conversion based on population of choice.

- Change the alleles to be included in the Overview via options. The performance of HLA-EMMA will improve if less alleles need to be analysed.



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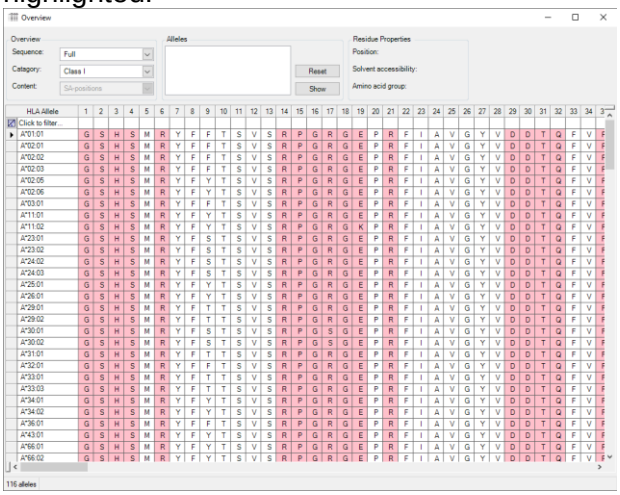
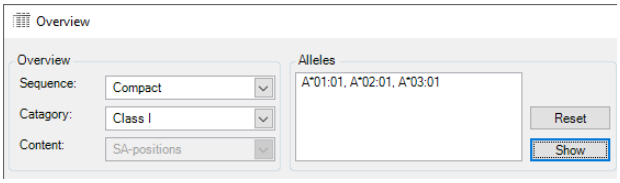
Extra: Overview

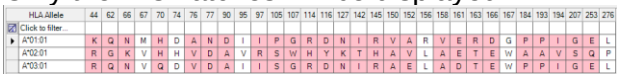
- Amino acid sequence overview with polymorphic solvent accessible positions highlighted.



- Compare HLA in the overview by second field typing and the compact modus of the overview.

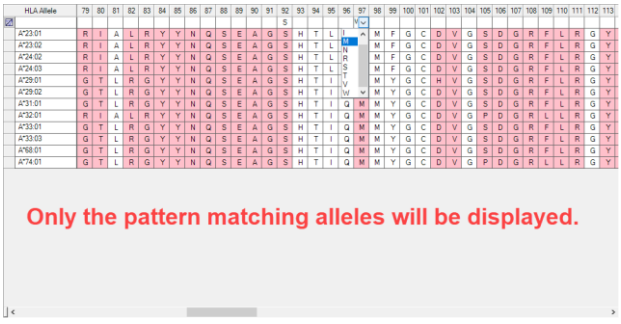


Only the mismatches will be displayed



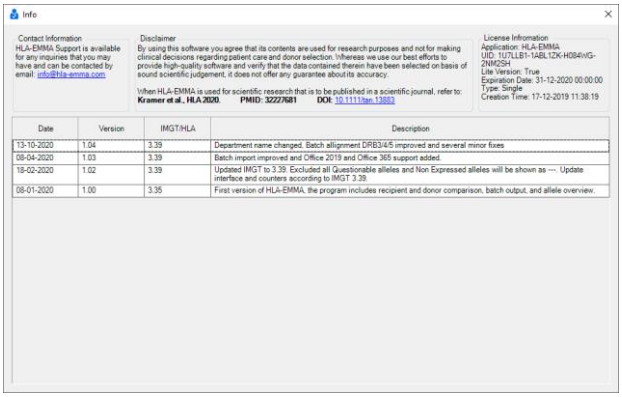
- Use the filter row to select the alleles for your case study.

- Filter alleles on basis of the presence of specific amino acids in their sequence.



Help: Info

- Find the disclaimer, the version and licence information in the info view.



Disclaimer:

By using this software you agree that its contents are used for research purposes and not for making clinical decisions regarding patient care and donor selection. Whereas we use our best efforts to provide high-quality software and verify that the data contained therein have been selected on basis of sound scientific judgement, it does not offer any guarantee about its accuracy.

When HLA-EMMA is used for scientific research that is to be published in a scientific journal, refer to:
Kramer et al, HLA 2020
PMID: 32227681
DOI: [10.1111/tan.13883](https://doi.org/10.1111/tan.13883)