



Analysis Tools

tools.iedb.org

Presented by: Alessandro Sette, IEDB Principal Investigator

Analysis tools with broad applications

<http://tools.iedb.org/main/analysis-tools/>

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Datasets](#) [Contribute Tools](#) [References](#)

Analysis Tools

Analysis Tools

The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

[Population Coverage](#)

This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

[Epitope Conservancy Analysis](#)

This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

[Epitope Cluster Analysis](#)

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

[Computational Methods for Mapping Mimotopes to Protein Antigens](#)

This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.

[RATE \(Restrictor Analysis Tool for Epitopes\)](#)

The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.

[ImmunomeBrowser](#)


The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.

[PepSySco](#)

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully.

[PepX \(Peptide Expression Annotation\)](#)

This tool identifies from which proteins a list of peptides can be derived, and returns an estimate of the expression level of those peptides from selected public databases.

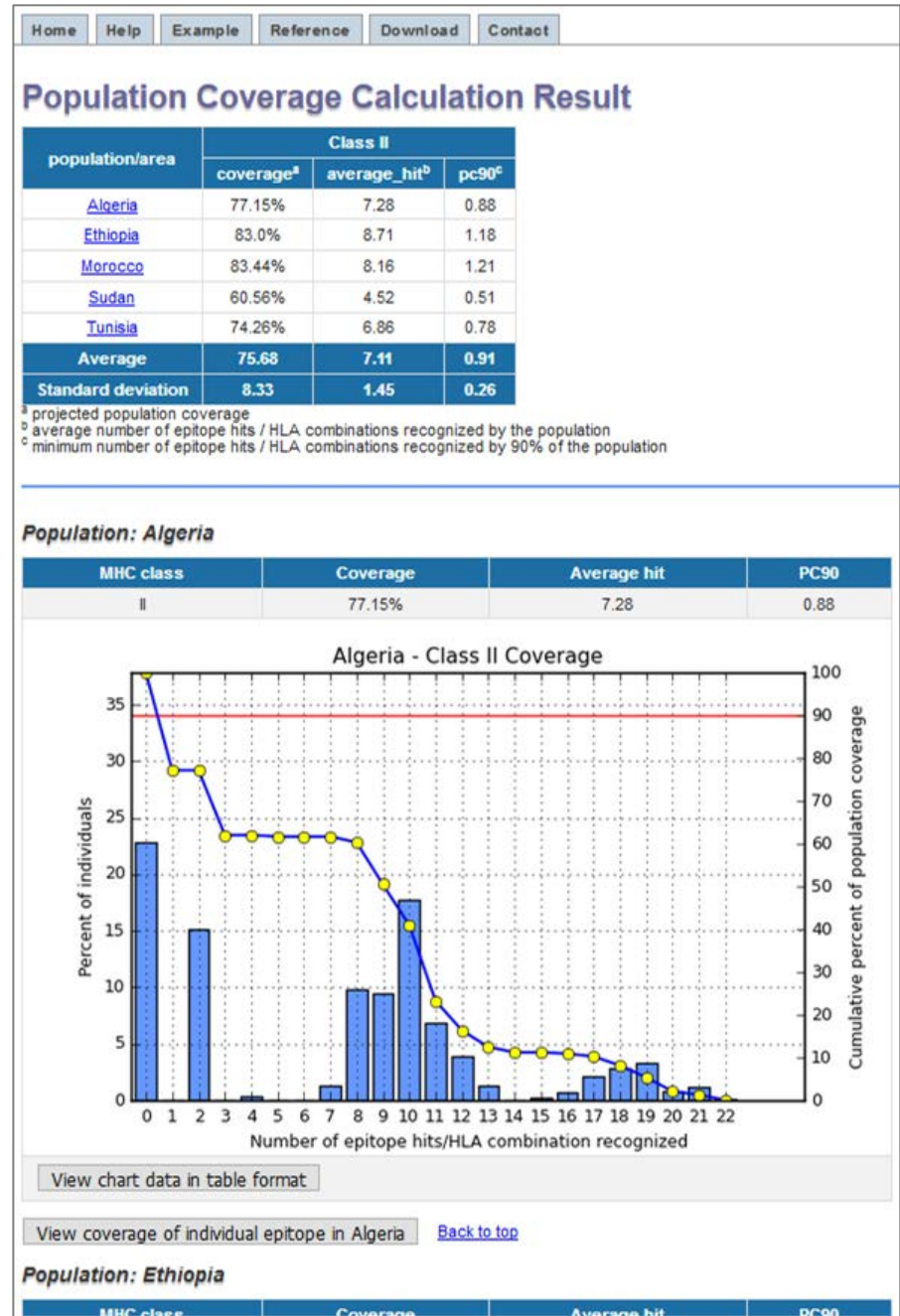
 : Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.



Population Coverage

<http://tools.iedb.org/population/>

- Calculates the fraction of individuals projected to bind and/or respond to a given set of epitopes with defined reactivity
- Based on
 - Epitope known HLA binding/restrictions
 - HLA genotypic frequencies
- HLA genotypic frequencies vary in different ethnicities
 - <http://allelefreqencies.net>
 - Focused more on worldwide migration patterns/based on ancestral studies



Updated Population Coverage Tool

New Data Source (In Progress)

- National Marrow Donor Program (NMDP) Database



High Resolution HLA Alleles and Haplotypes in the US Population

	A	C	B	DRB345	DRB1	DQB1
1	A*26:01g	C*07:02g	B*39:06	DRB3*01:01	DRB1*03:01	DQB1*02:01g
2	A*02:01g	C*02:02g	B*27:05g	DRB5*01:01	DRB1*15:01	DQB1*05:02
3	A*11:01g	C*16:01	B*44:03	DRB4*01:01g	DRB1*04:07g	DQB1*03:02g
4	A*01:01g	C*05:01g	B*18:01g	DRB3*02:02g	DRB1*03:01	DQB1*02:01g
5	A*02:11g	C*07:01g	B*44:03	DRB3*02:02g	DRB1*03:01	DQB1*02:01g
6	A*01:01g	C*06:02g	B*35:02	DRB3*02:02g	DRB1*13:01	DQB1*06:03g
7	A*01:01g	C*07:01g	B*57:01g	DRB4*01:01g	DRB1*04:02	DQB1*03:02g
8	A*32:01	C*04:01g	B*35:02	DRB5*02:02	DRB1*16:01	DQB1*05:02
9	A*74:01g	C*06:02g	B*58:02	DRB3*01:01	DRB1*03:02	DQB1*04:02
10	A*26:01g	C*03:02	B*58:01g	DRB3*02:02g	DRB1*14:01g	DQB1*05:03g
11	A*29:01	C*04:01g	B*35:08	DRB4*01:01g	DRB1*07:01	DQB1*03:03g
12	A*32:01	C*07:02g	B*39:06	DRB4*01:01g	DRB1*04:04	DQB1*03:02g
13	A*02:06g	C*06:02g	B*13:02g	DRB4*01:01g	DRB1*04:05	DQB1*04:01g
14	A*01:01g	C*04:01g	B*35:08	DRB5*02:02	DRB1*16:01	DQB1*05:02
15	A*02:01g	C*15:02g	B*40:06	DRB3*NNNN	DRB1*10:01	DQB1*05:01
16	A*30:02g	C*07:01g	B*57:03	DRB3*03:01	DRB1*13:02	DQB1*05:01

Gragert, L., Madbouly, A., Freeman, J., & Maiers, M. (2013). Six-locus high resolution HLA haplotype frequencies derived from mixed-resolution DNA typing for the entire US donor registry. *Human Immunology*, 74(10), 1313–1320. <http://dx.doi.org/10.1016/j.humimm.2013.06.025>.

Race Code	Detailed Race/Ethnic Description	Broad Race Group
AAFA	African American	AFA
AFB	African	AFA
AINDI	South Asian Indian	API
AISC	American Indian - South or Central Am.	NAM
ALANAM	Alaska Native or Aleut	NAM
AMIND	North American Indian	NAM
CARB	Caribbean Black	AFA
CARHIS	Caribbean Hispanic	HIS
CARIBI	Caribbean Indian	NAM
EURCAU	European Caucasian	CAU
FILII	Filipino	API
HAWI	Hawaiian or other Pacific Islander	API
JAPI	Japanese	API
KORI	Korean	API
MENAF	Middle Eastern or N. Coast of Africa	CAU
MSWHIS	Mexican or Chicano	HIS
NCHI	Chinese	API
SCAHIS	Hispanic – South or Central American	HIS
SCAMB	Black - South or Central American	AFA
SCSEAI	Southeast Asian	API
VIET	Vietnamese	API

- Newer data (includes DRB345)
- Uniform, high resolution HLA typing
- Better reflection of HLA allele diversity/linkage patterns
- Populations all screened within US

Analysis tools with broad applications

<http://tools.iedb.org/main/analysis-tools/>

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Datasets](#) [Contribute Tools](#) [References](#)

Analysis Tools

Analysis Tools

The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

[Population Coverage](#)

This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

[Epitope Conservancy Analysis](#)

This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

[Epitope Cluster Analysis](#)

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

[Computational Methods for Mapping Mimotopes to Protein Antigens](#)

This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.



[RATE \(Restrictor Analysis Tool for Epitopes\)](#)

The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.



[ImmunomeBrowser](#)

The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.



[PepSySco](#)

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully.



[PepX \(Peptide Expression Annotation\)](#)

This tool identifies from which proteins a list of peptides can be derived, and returns an estimate of the expression level of those peptides from selected public databases.



: Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.



Epitope Conservancy Analysis

<http://tools.iedb.org/conservancy/>

- Calculates the degrees of conservancy of one or more epitopes, within a given set of protein sequences
- Adjustable sequence identity threshold

“Degree of conservation” = the fraction of protein sequences containing the epitope at a given identity level

The screenshot shows the web interface for Epitope Conservancy Analysis. It is divided into three main steps:

- Step 1. Epitope Sequence(s)**: A text input field for entering epitope sequences in PLAIN or FASTA format. A red arrow points to this field, which contains several known epitope sequences in FASTA format, such as >NP 1 MSASKEVRSFLWTQS and >NP 21 SGYCSNIKLVVVKDA. Below the input field is a "Browse..." button and the text "No file selected."
- Step 2. Protein Sequence(s)**: A text input field for entering protein sequences in PLAIN or FASTA format. A red arrow points to this field, which contains a large protein sequence in FASTA format starting with >58643 Lassa NP. Below the input field is a "Browse..." button and the text "No file selected."
- Step 3. Calculation option(s)**: A section for selecting analysis options. It includes a radio button for "Epitope linear sequence conservancy" (which is selected), a radio button for "Epitope discontinuous sequence conservancy", a dropdown menu for "Sequence identity threshold" set to "100%", and a checkbox for "Remove duplicated protein sequences?".

At the bottom right of the interface are "Submit" and "Reset" buttons.

Known epitopes

Protein sequences

Analysis tools with broad applications

<http://tools.iedb.org/main/analysis-tools/>

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Datasets](#) [Contribute Tools](#) [References](#)

Analysis Tools

Analysis Tools

The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

[Population Coverage](#)

This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

[Epitope Conservancy Analysis](#)

This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

[Epitope Cluster Analysis](#)

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

[Computational Methods for Mapping Mimotopes to Protein Antigens](#)

This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.

[RATE \(Restrictor Analysis Tool for Epitopes\)](#)

The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.

[ImmunomeBrowser](#)


The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.

[PepSySco](#)

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully.

[PepX \(Peptide Expression Annotation\)](#)

This tool identifies from which proteins a list of peptides can be derived, and returns an estimate of the expression level of those peptides from selected public databases.

 : Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.



Epitope Cluster Analysis Tool

<http://tools.iedb.org/cluster/>

- Analyzes how many epitopes in a set have significant sequence homology
- Groups epitopes into clusters based on having sequence identity greater than a specified threshold
- Three different clustering approaches are implemented
- Enables diverse applications such as generating epitope pools, and understanding cross-reactivity

Epitope Cluster Analysis Tool

Clustering Tool Updated! This is an updated version of the IEDB clustering tool that is more robust and has new functionality described in more detail [here](#).

Epitope Cluster Analysis

step 1/3 Specify input peptides

Specify Sequence(s)

Enter epitope sequence(s) in PLAIN or FASTA format

Or upload epitope sequence(s) from a file No file chosen

<http://tools.iedb.org/cluster/>

<https://nextgen-tools.iedb.org/clustering>

Learn more about the new
Cluster Tool **tomorrow!**

Thursday, November 2, 9am PT
Next Generation Tool Pipelines - Cluster & PepMatch

Cluster

Docs API Cite

Input Sequence(s)

Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:

```
> Mus Pep1  
LEQIHVLENSLVL  
> Mus Pep2  
FVEHIHVLENSLAFK  
> Mus Pep3  
GLYGREPDLSDDIKERFA  
> Mus Pep4  
EWFILLSADKREKI  
> Mus Pep5
```

Format: Unknown | 0 characters

Prediction Parameters

Sequence Identity Threshold

Peptide Length(s)

Cluster Method

Analysis tools with broad applications

<http://tools.iedb.org/main/analysis-tools/>

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Datasets](#) [Contribute Tools](#) [References](#)

Analysis Tools

Analysis Tools

The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

[Population Coverage](#)

This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

[Epitope Conservancy Analysis](#)

This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

[Epitope Cluster Analysis](#)

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

[Computational Methods for Mapping Mimotopes to Protein Antigens](#)

This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.

[RATE \(Restrictor Analysis Tool for Epitopes\)](#)

The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.

[ImmunomeBrowser](#)


The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.

[PepSySco](#)

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully.

[PepX \(Peptide Expression Annotation\)](#)

This tool identifies from which proteins a list of peptides can be derived, and returns an estimate of the expression level of those peptides from selected public databases.

 : Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.



Restrictor Analysis Tool for Epitopes (RATE)

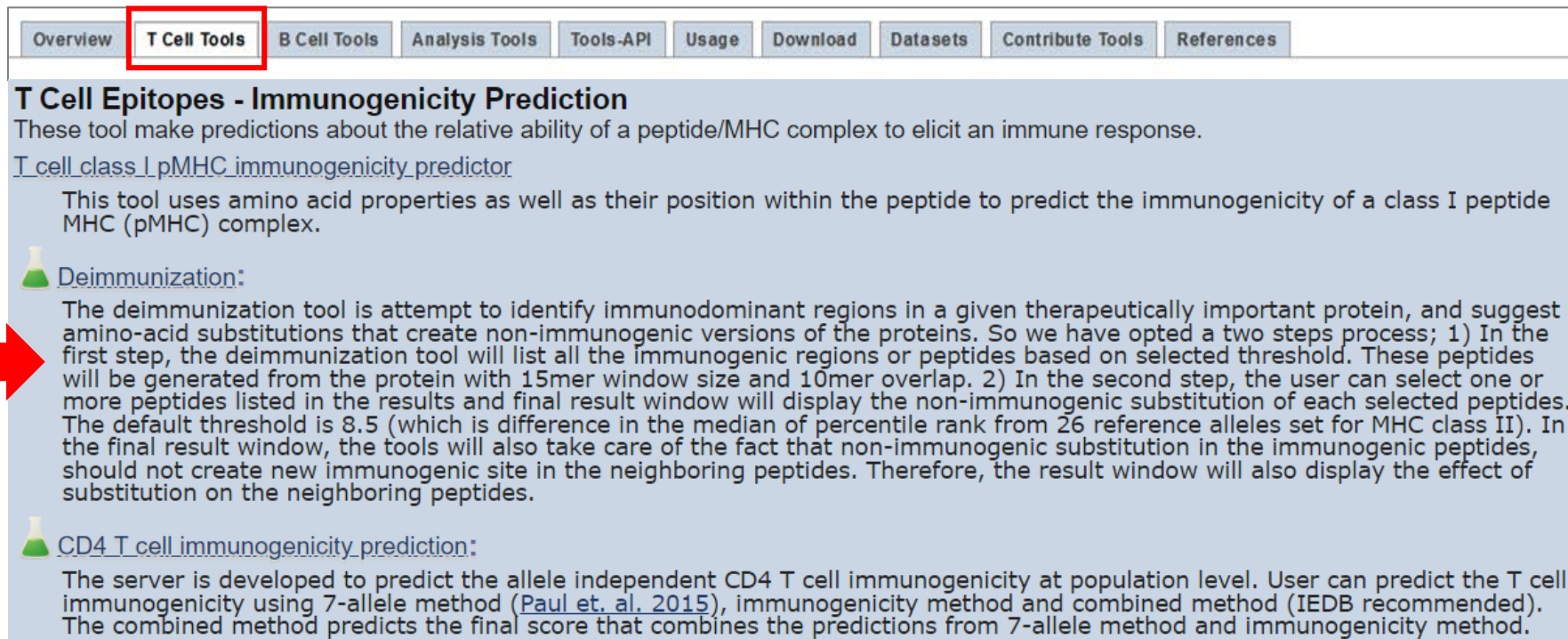
<http://tools.iedb.org/rate/>

- Automated method to infer HLA restriction of a given epitope set, from immune response data of HLA typed subjects
- Based on computing the frequency of alleles expressed in donors who had an immune response to a given epitope
- Compare those frequencies in donors that did not have a response

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Peptide#	Peptide_id	peptide_seq	Allele#	Allele	A+R+	A-R+	A+R-	A-R-	No_of_Donors	Response_n/a	Relative_freq	Odds_ratio	P-value
2	1	3531.0365	GINTIPIAINEAEYV	84	DRB3*02:02	6	0	18	26	50	0	2.08333	inf	0.00847
3	2	3531.0367	AAFQAAHARFVAAAA	54	DRB1*01:01	4	8	0	38	50	0	4.16667	inf	0.00215
4	2	3531.0367	AAFQAAHARFVAAAA	65	DRB1*07:01	5	7	2	36	50	0	2.97619	12.85714	0.00593
5	3	3531.0514	AAVVRFQEAAANKQKQ	89	DRB5*01:01	7	2	8	30	47	3	2.43704	13.125	0.0025
6	5	3531.037	AAGTYVAADAAAAST	54	DRB1*01:01	4	2	0	44	50	0	8.33333	inf	7.00E-05

Deimmunization

<http://tools.iedb.org/deimmunization/>




Overview **T Cell Tools** B Cell Tools Analysis Tools Tools-API Usage Download Datasets Contribute Tools References

T Cell Epitopes - Immunogenicity Prediction


These tool make predictions about the relative ability of a peptide/MHC complex to elicit an immune response.

[T cell class I pMHC immunogenicity predictor](#)

This tool uses amino acid properties as well as their position within the peptide to predict the immunogenicity of a class I peptide MHC (pMHC) complex.

 [Deimmunization:](#)

The deimmunization tool is attempt to identify immunodominant regions in a given therapeutically important protein, and suggest amino-acid substitutions that create non-immunogenic versions of the proteins. So we have opted a two steps process; 1) In the first step, the deimmunization tool will list all the Immunogenic regions or peptides based on selected threshold. These peptides will be generated from the protein with 15mer window size and 10mer overlap. 2) In the second step, the user can select one or more peptides listed in the results and final result window will display the non-immunogenic substitution of each selected peptides. The default threshold is 8.5 (which is difference in the median of percentile rank from 26 reference alleles set for MHC class II). In the final result window, the tools will also take care of the fact that non-immunogenic substitution in the immunogenic peptides, should not create new immunogenic site in the neighboring peptides. Therefore, the result window will also display the effect of substitution on the neighboring peptides.

 [CD4 T cell immunogenicity prediction:](#)

The server is developed to predict the allele independent CD4 T cell immunogenicity at population level. User can predict the T cell immunogenicity using 7-allele method ([Paul et. al. 2015](#)), immunogenicity method and combined method (IEDB recommended). The combined method predicts the final score that combines the predictions from 7-allele method and immunogenicity method.

Deimmunization

<http://tools.iedb.org/deimmunization/>

- Generate overlapping peptides from protein sequence
- Predict HLA class II binding binding regions
- Suggest amino acid substitutions that are predicted to decrease binding
 - Also consider the effect of substitutions on neighboring peptides

	A	B	C	D	E	F	G	H	I	J	K	L
	Protein Number	Peptide	Peptide ID	Start Position	End Position	Median Percentile Rank	Median Difference	C terminal Neighbor 1 (Median)	C terminal Neighbor 2 (Median)	N terminal Neighbor 1 (Median)	N terminal Neighbor 2 (Median)	Deimmunization Score
1	1	DTFRKLFVYSNFLR	wild	136	150	10.255	0	14.5	49.75	47	44.25	NA
2	1	DTFRKLFVYSNFDR	L149D	136	150	32	21.745	41	68.5	NA	NA	3
3	1	DTFRKLFVYSNFGR	L149G	136	150	27.5	17.245	31.5	68.75	NA	NA	3
4	1	DTFRKEFRVYSNFLR	L141E	136	150	26.5	16.245	26.5	NA	60.75	NA	3
5	1	DTFRKPFRVYSNFLR	L141P	136	150	26.35	16.095	26.5	NA	52.5	NA	3
6	1	DTFRKQFRVYSNFLR	L141Q	136	150	26	15.745	25.5	NA	53.25	NA	3
7	1	DTFRKLFVYSNFNR	L149N	136	150	26	15.745	21.75	61.75	NA	NA	3
8	1	DTFRKLGRVYSNFLR	F142G	136	150	25.075	14.82	31	NA	50.75	NA	3
9	1	DTFRKLFVYSNFLR	R143D	136	150	24.75	14.495	35.5	NA	49.25	NA	3
10	1	DTFRKKFRVYSNFLR	L141K	136	150	24.525	14.27	23	NA	59	NA	3
11	1	DTFRKLFVYSNFGR	L149C	136	150	24.25	13.995	36	64	NA	NA	3
12	1	DTFRKCFRVYSNFLR	L141C	136	150	23.85	13.595	23.5	NA	73	NA	3
13	1	DTFRKLFVYSNCFR	N147C	136	150	23.75	13.495	39.75	50	NA	NA	3
14	1	DTFRKDFRVYSNFLR	L141D	136	150	23.5	13.245	27.5	NA	62.5	NA	3
15	1	DTFRKGFRVYSNFLR	L141G	136	150	23.5	13.245	27	NA	57.5	NA	3
16	1	DTFRKLFVYSNFKR	L149K	136	150	23.5	13.245	28	59	NA	NA	3
17	1	DTFRKLFVYSNFER	L149E	136	150	22.75	12.495	34	62	NA	NA	3
18	1	DTFRKLERVYSNFLR	F142E	136	150	22.7	12.445	31	NA	48	NA	3
19	1	DTFRKLCRVYSNFLR	F142C	136	150	22.4	12.145	31	NA	50.25	NA	3
20	1	DTFRKLFVYSNFLR	F142T	136	150	22.175	11.92	20	NA	48.75	NA	2

Analysis tools with broad applications

<http://tools.iedb.org/main/analysis-tools/>

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Datasets](#) [Contribute Tools](#) [References](#)

Analysis Tools

Analysis Tools

The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

[Population Coverage](#)

This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

[Epitope Conservancy Analysis](#)

This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

[Epitope Cluster Analysis](#)

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

[Computational Methods for Mapping Mimotopes to Protein Antigens](#)

This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.

[RATE \(Restrictor Analysis Tool for Epitopes\)](#)

The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.

[ImmunomeBrowser](#)


The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.

[PepSySco](#)

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully.

[PepX \(Peptide Expression Annotation\)](#)

This tool identifies from which proteins a list of peptides can be derived, and returns an estimate of the expression level of those peptides from selected public databases.

 : Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.



Peptide Synthesis Score (PepSySco)

<http://tools.iedb.org/pepsysco/>

- Given a set of peptide sequences, PepSySco predicts the likelihood that they can be synthesized successfully.

PepSySco - Peptide Synthesis Score

Specify sequence(s)	
Enter peptide sequence(s)	<input type="text"/>
Or select file containing sequence(s)	<input type="button" value="Choose File"/> No file chosen
<input type="button" value="Submit"/> <input type="button" value="Reset"/>	

Analysis tools with broad applications

<http://tools.iedb.org/main/analysis-tools/>

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Datasets](#) [Contribute Tools](#) [References](#)

Analysis Tools

Analysis Tools

The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

[Population Coverage](#)

This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

[Epitope Conservancy Analysis](#)

This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

[Epitope Cluster Analysis](#)

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

[Computational Methods for Mapping Mimotopes to Protein Antigens](#)

This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.



[RATE \(Restrictor Analysis Tool for Epitopes\)](#)

The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.



[ImmunomeBrowser](#)

The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.



[PepSySco](#)

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully.



[PepX \(Peptide Expression Annotation\)](#)

This tool identifies from which proteins a list of peptides can be derived, and returns an estimate of the expression level of those peptides from selected public databases.



: Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.



Peptide Expression Annotation (PepX)

<http://tools.iedb.org/pepx/>

- PepX identifies from which proteins a list of peptides can be derived
- Returns an estimate of the expression level of those peptides from selected public databases

PepX - Peptide Expression Annotation

Specify Sequence(s)	
Enter peptide sequence(s)	<input type="text" value="Enter peptide sequences here..."/> ADMGHLKY FSDNIEFY HIDFAIQY GLDQPLLK
Or select file containing sequence(s)	<input type="button" value="Choose File"/> No file chosen
Specify Expression Dataset	
Select Quantitation Level	<input checked="" type="radio"/> Gene <input type="radio"/> Transcript
Select Data Source	<input type="text" value="Abelin"/>
Select Dataset	<input type="text" value="abelin-B721.221 RNA expression (n=NA)"/>
<input type="button" value="Submit"/> <input type="button" value="Reset"/>	

Analysis Tools Recap

- Help to examine existing sets of epitopes and gain new knowledge across a broad array of applications

Population Coverage

Analyze T cell epitopes with known HLA restriction that are recognized in a population based on HLA frequencies

Conservancy

Investigate epitope conservancy across different protein sequences.

Cluster

Cluster epitopes on the basis of homology

RATE

Infer HLA restrictions for epitopes of T cell response frequency in HLA typed subjects

Deimmunization

Identify immunodominant regions in a given protein, and suggest amino-acid substitutions that create non-immunogenic versions of the protein

PepSySco

Predict the likelihood that a set of peptides can be synthesized successfully

PepX

Identify peptides that can be derived from which proteins, and estimate the expression level of those peptides from selected public databases