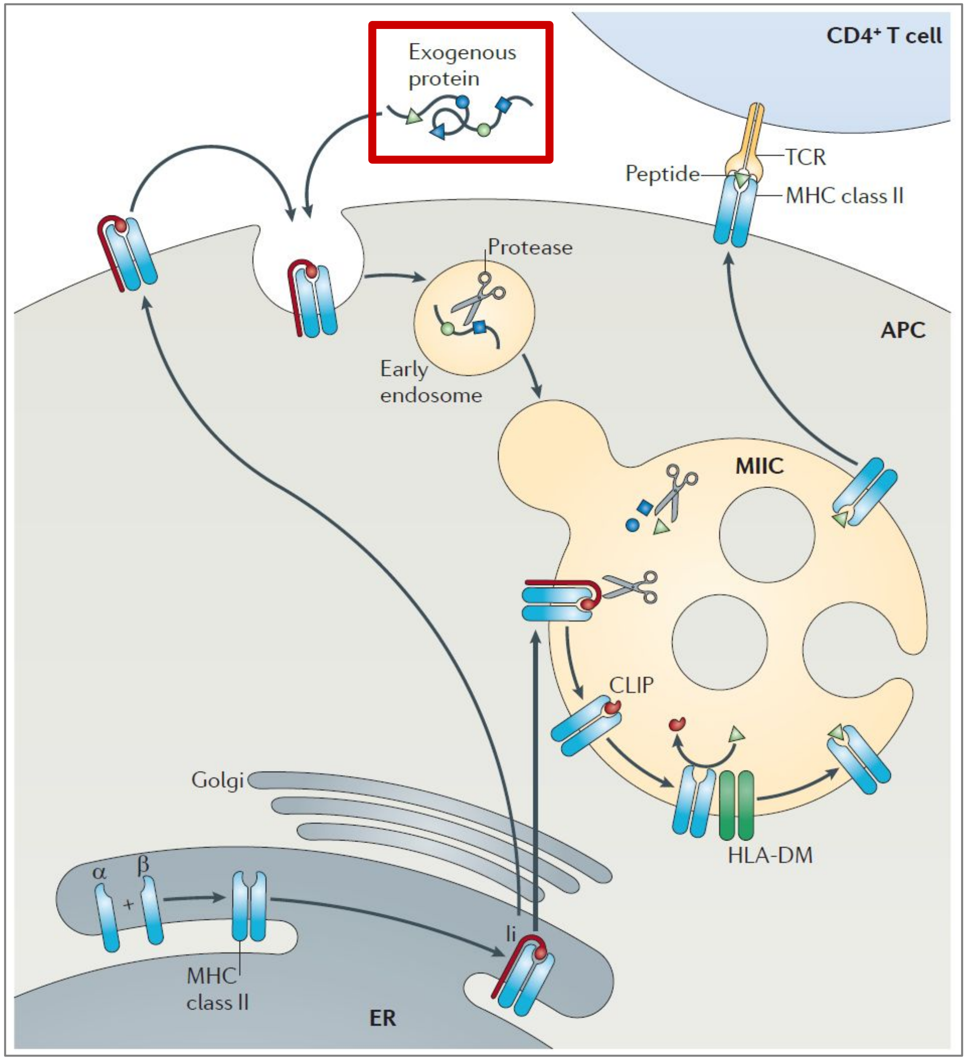
IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

MHC-II Binding Predictions

tools.iedb.org

Presented by:
Raphael Trevizani

Exogenous antigen processing pathway (class II)



- Antigens generated outside the cell
  - Entered through inhalation, ingestion, injection
  - Bacteria, Allergens, Parasites etc.

Nat Rev Immunol. 2011 Nov 11;11(12):823-36. doi: 10.1038/nri3084.

Towards a systems understanding of MHC class I and MHC class II antigen presentation.

Neefjes J[1], Jongsma ML, Paul P, Bakke O.

PMID: 22076556 DOI: 10.1038/nri3084

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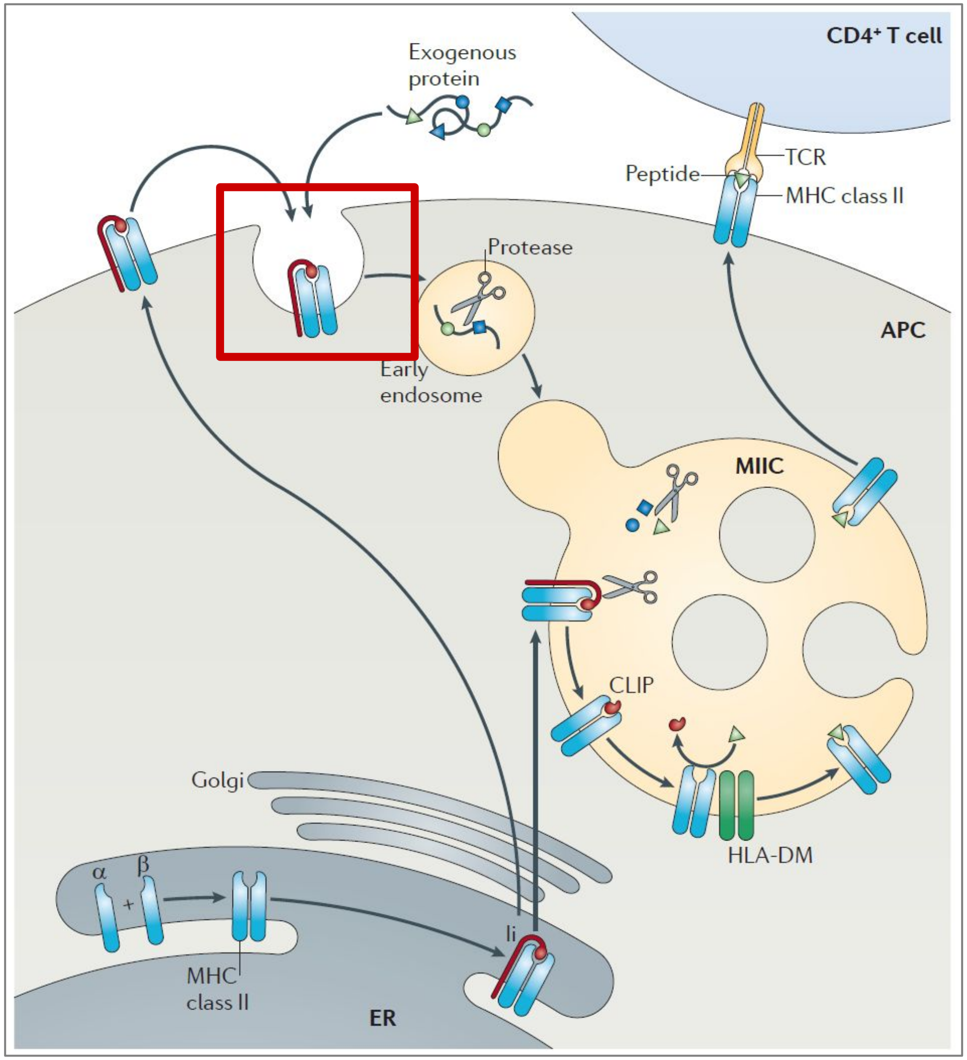

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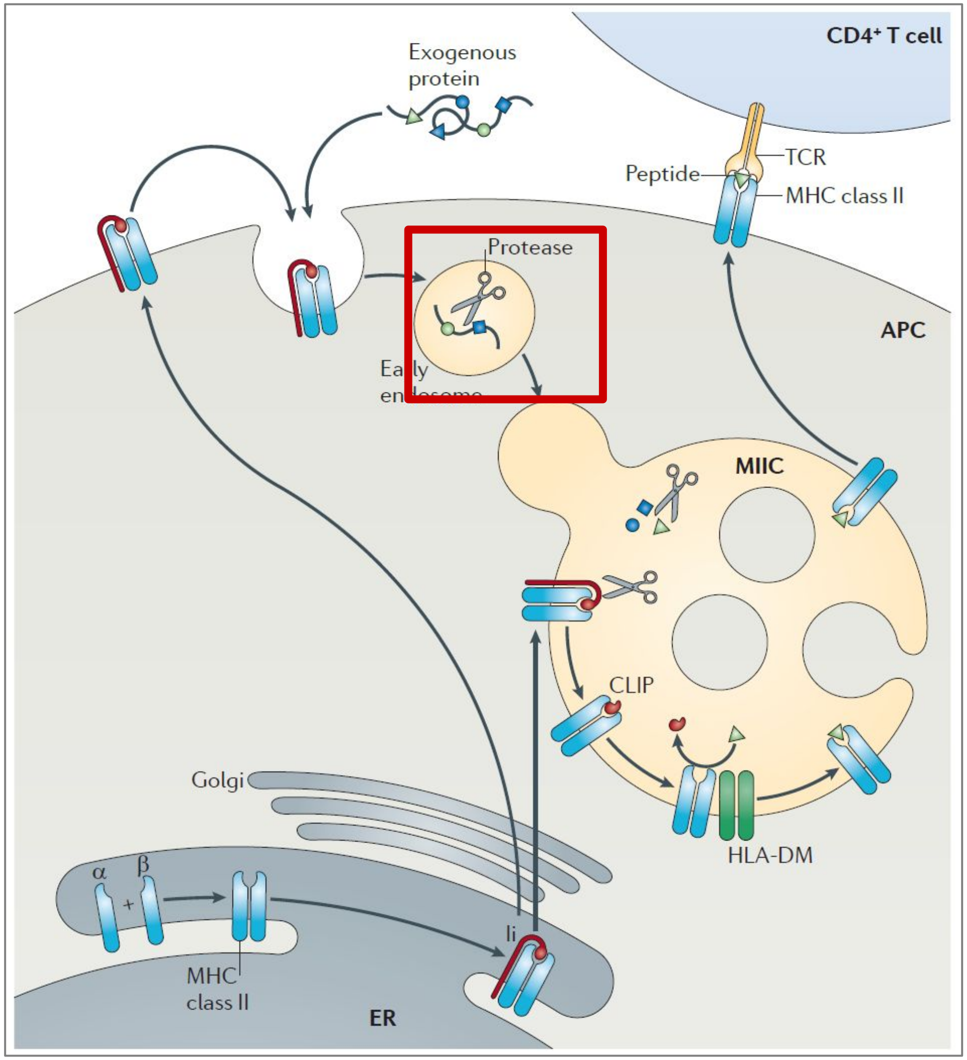

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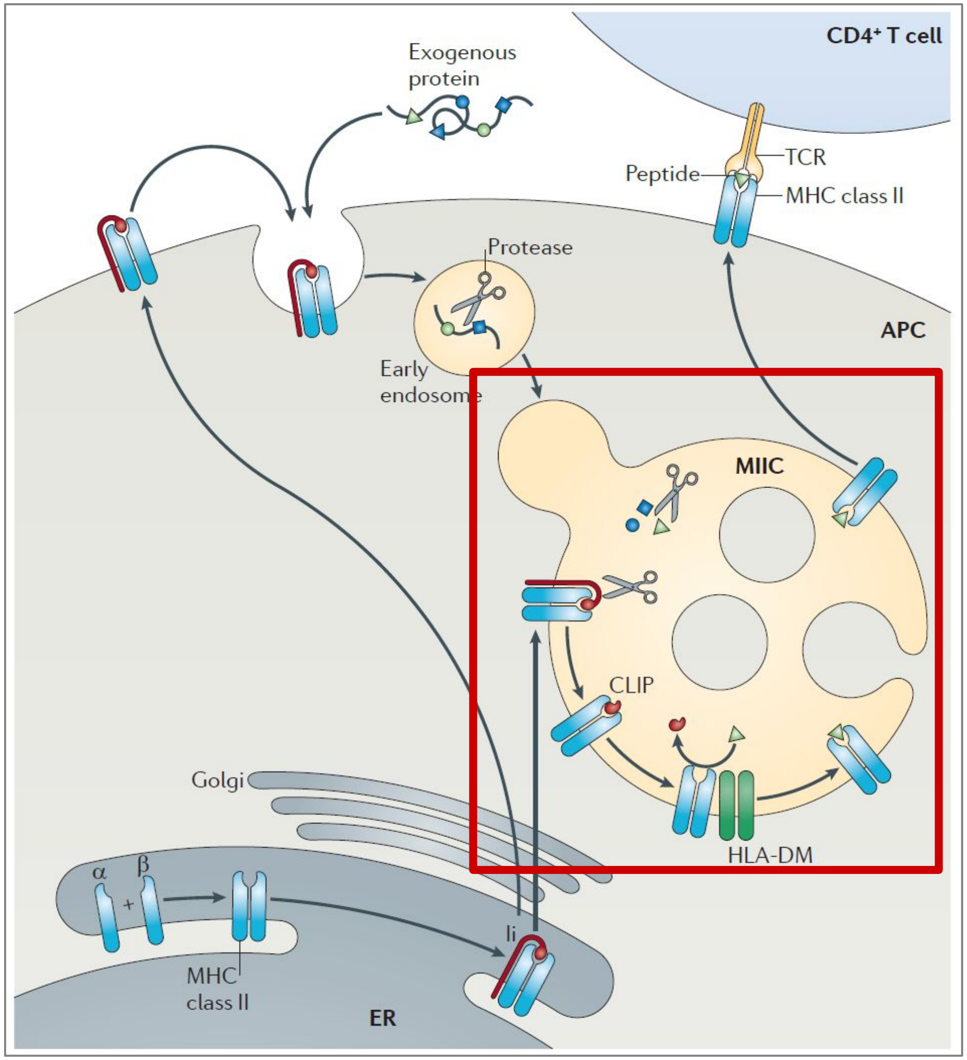

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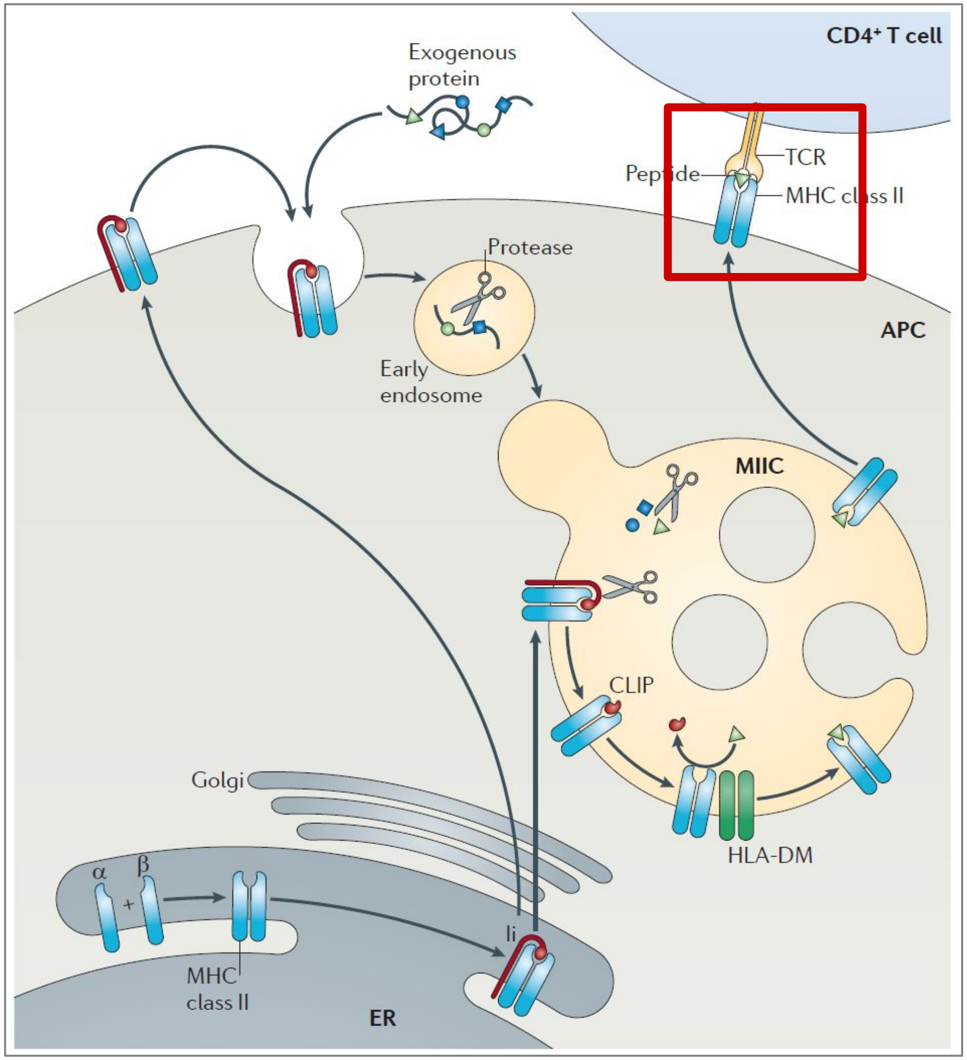

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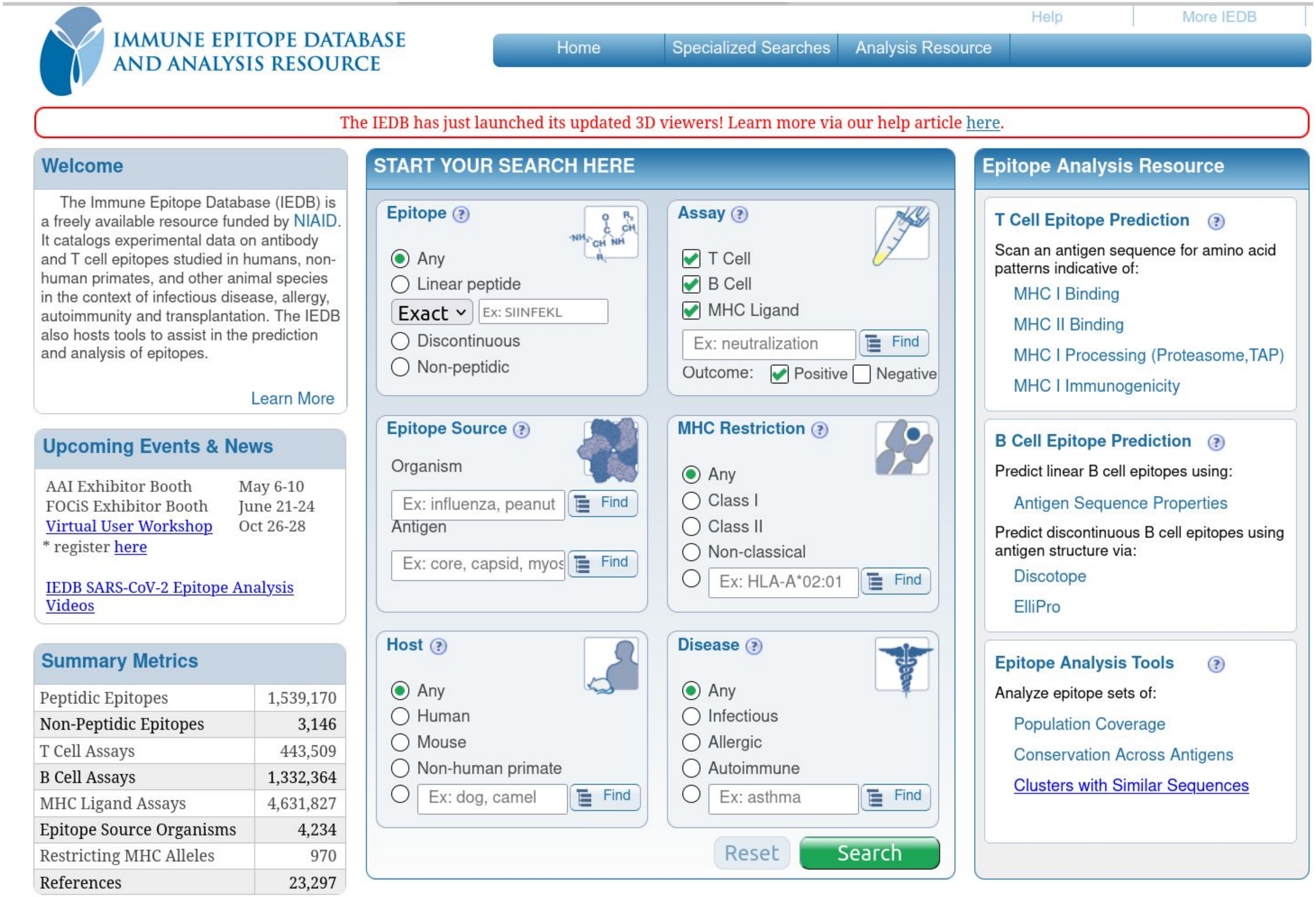


The IEDB has just launched its updated 3D viewers! Learn more via our help article here.

Welcome

The Immune Epitope Database (IEDB) is a freely available resource funded by NIAID. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of infectious disease, allergy, autoimmunity and transplantation. The IEDB also hosts tools to assist in the prediction and analysis of epitopes.

Learn More

Upcoming Events & News

AAI Exhibitor Booth	May 6-10
FOCiS Exhibitor Booth	June 21-24
Virtual User Workshop	Oct 26-28

* register here

IEDB SARS-CoV-2 Epitope Analysis Videos

Summary Metrics

Peptidic Epitopes	1,539,170
Non-Peptidic Epitopes	3,146
T Cell Assays	443,509
B Cell Assays	1,332,364
MHC Ligand Assays	4,631,827
Epitope Source Organisms	4,234
Restricting MHC Alleles	970
References	23,297

START YOUR SEARCH HERE

Epitope ?

● Any
○ Linear peptide
Exact ⌄ Ex: SIINFEKL
○ Discontinuous
○ Non-peptidic

Assay ?

☑ T Cell
☑ B Cell
☑ MHC Ligand
Ex: neutralization Find
Outcome: ☑ Positive ☐ Negative

Epitope Source ?

Organism
Ex: influenza, peanut Find
Antigen
Ex: core, capsid, myos Find

MHC Restriction ?

● Any
○ Class I
○ Class II
○ Non-classical
○ Ex: HLA-A*02:01 Find

Host ?

● Any
○ Human
○ Mouse
○ Non-human primate
○ Ex: dog, camel Find

Disease ?

● Any
○ Infectious
○ Allergic
○ Autoimmune
○ Ex: asthma Find

Reset Search

Epitope Analysis Resource

T Cell Epitope Prediction ?

Scan an antigen sequence for amino acid patterns indicative of:

- MHC I Binding
- MHC II Binding
- MHC I Processing (Proteasome,TAP)
- MHC I Immunogenicity

B Cell Epitope Prediction ?

Predict linear B cell epitopes using:

- Antigen Sequence Properties

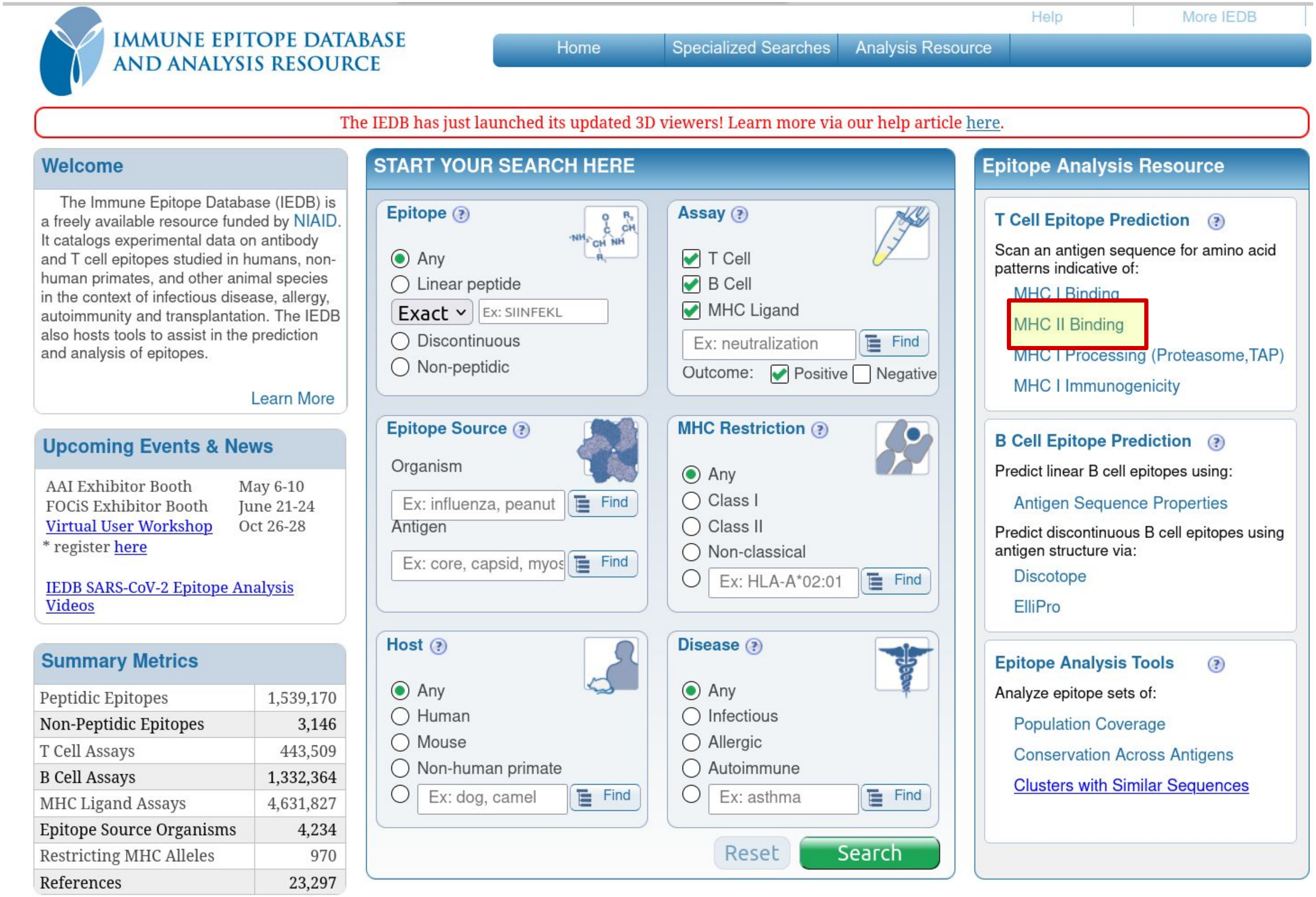
Predict discontinuous B cell epitopes using antigen structure via:

- Discotope
- ElliPro

Epitope Analysis Tools ?

Analyze epitope sets of:

- Population Coverage
- Conservation Across Antigens
- Clusters with Similar Sequences



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Epitope Source Organisms	4,234
Restricting MHC Alleles	970
References	23,297

START YOUR SEARCH HERE

Epitope ?

● Any
○ Linear peptide
Exact ⌄ Ex: SIINFEKL
○ Discontinuous
○ Non-peptidic

Assay ?

☑ T Cell
☑ B Cell
☑ MHC Ligand
Ex: neutralization Find
Outcome: ☑ Positive ☐ Negative

Epitope Source ?

Organism
Ex: influenza, peanut Find
Antigen
Ex: core, capsid, myos Find

MHC Restriction ?

● Any
○ Class I
○ Class II
○ Non-classical
○ Ex: HLA-A*02:01 Find

Host ?

● Any
○ Human
○ Mouse
○ Non-human primate
○ Ex: dog, camel Find

Disease ?

● Any
○ Infectious
○ Allergic
○ Autoimmune
○ Ex: asthma Find

Reset Search

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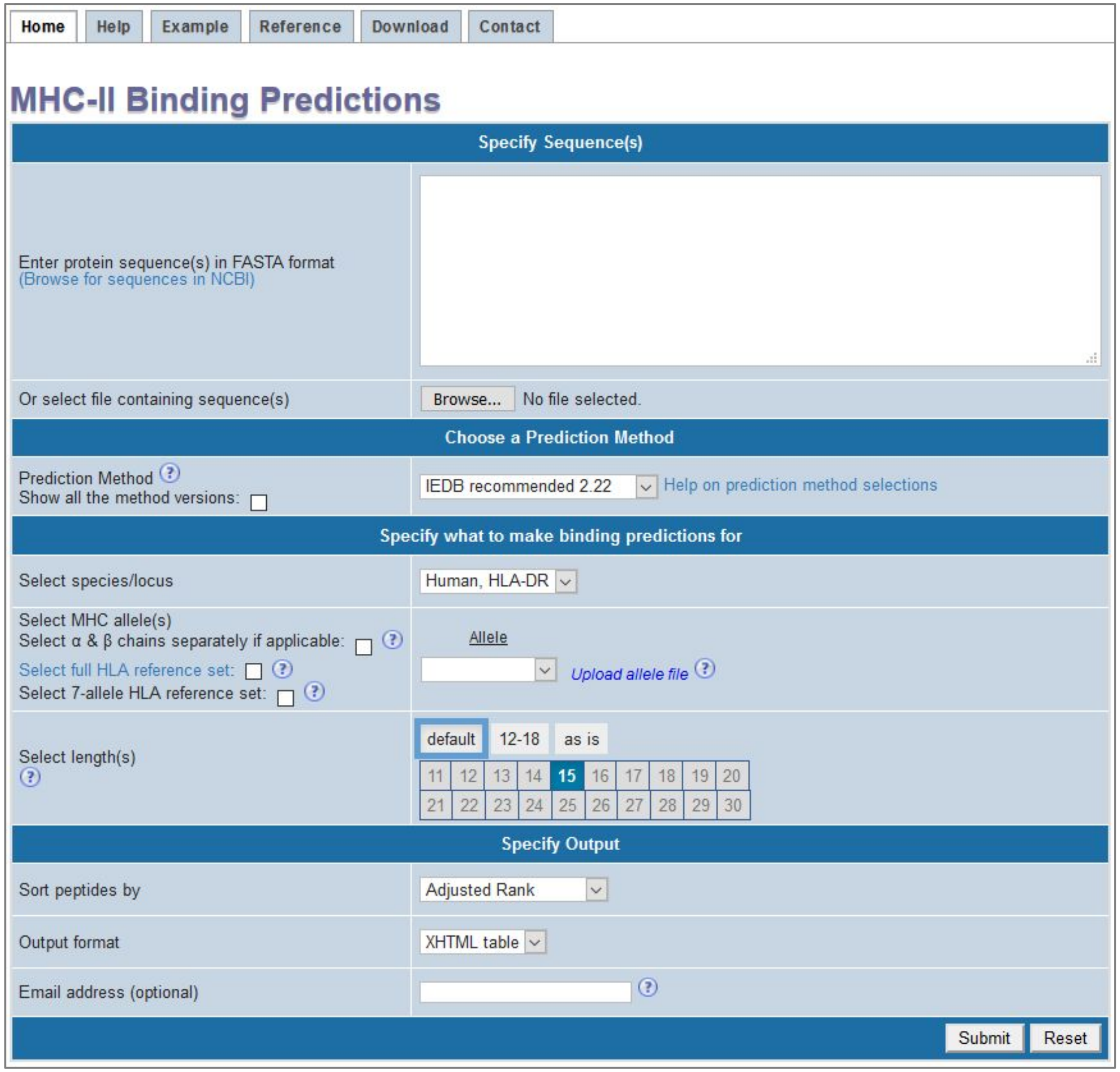
- Clusters with Similar Sequences

MHC-II binding prediction interface

- Tool entry point layout similar to class I



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format (Browse for sequences in NCBI)	
Or select file containing sequence(s)	Browse... No file selected.

Choose a Prediction Method

Prediction Method ? Show all the method versions: ☐	IEDB recommended 2.22 Help on prediction method selections

Specify what to make binding predictions for

Select species/locus	Human, HLA-DR
Select MHC allele(s) Select α & β chains separately if applicable: ☐ ? Select full HLA reference set: ☐ ? Select 7-allele HLA reference set: ☐ ?	Allele Upload allele file ?
Select length(s) ?	default 12-18 as is 11 12 13 14 **15** 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30

Specify Output

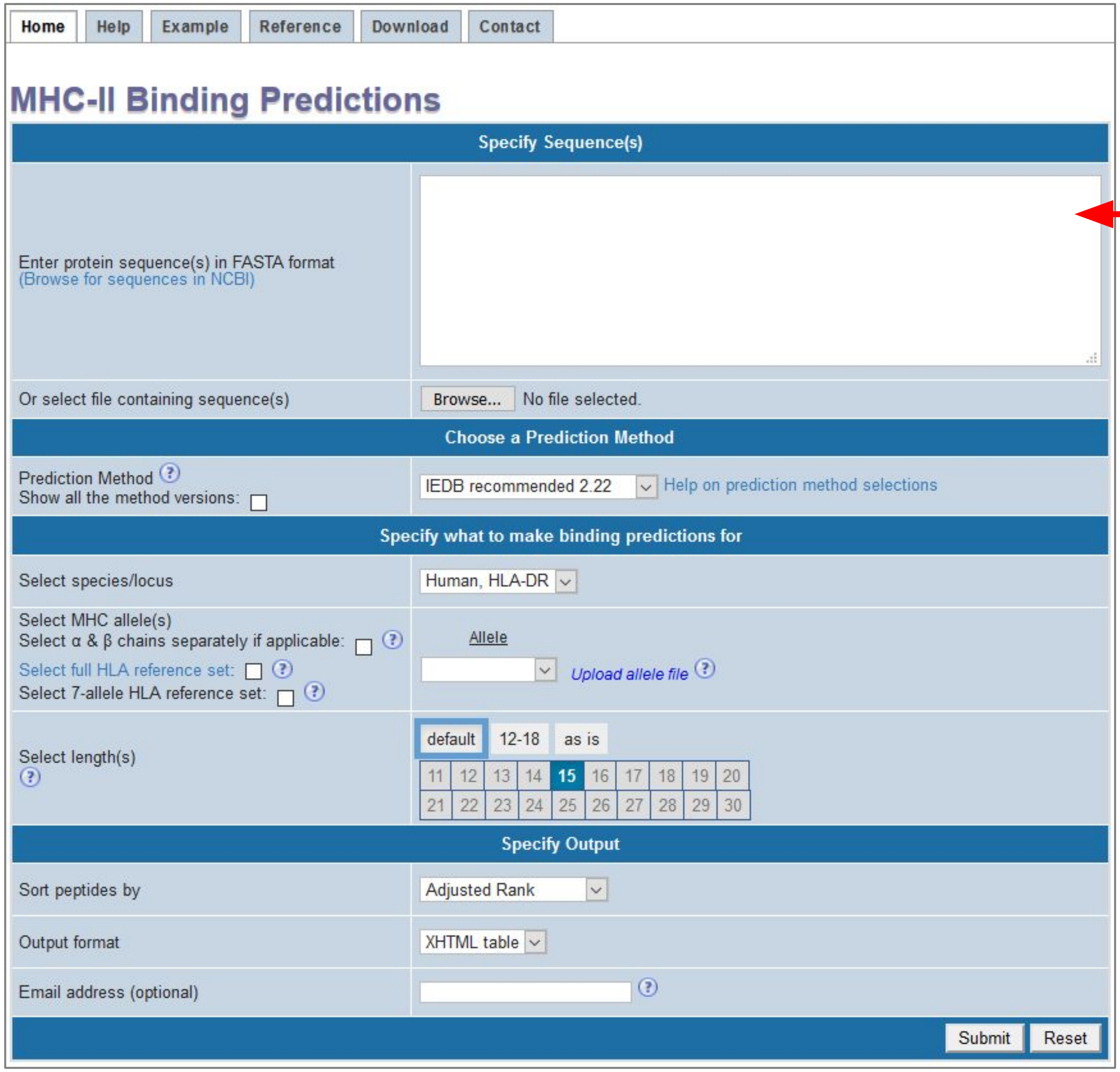
Sort peptides by	Adjusted Rank
Output format	XHTML table
Email address (optional)	?

Submit Reset

tools.iedb.org/mhcii/

MHC-II binding prediction interface

- Tool entry point layout similar to class I



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Or select file containing sequence(s)	Browse... No file selected.

Choose a Prediction Method

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Specify what to make binding predictions for

Select species/locus	Human, HLA-DR ⌄
Select MHC allele(s) Select α & β chains separately if applicable: ☐ ? Select full HLA reference set: ☐ ? Select 7-allele HLA reference set: ☐ ?	Allele ⌄ *Upload allele file* ?
Select length(s) ?	default 12-18 as is 11 12 13 14 **15** 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30

Specify Output

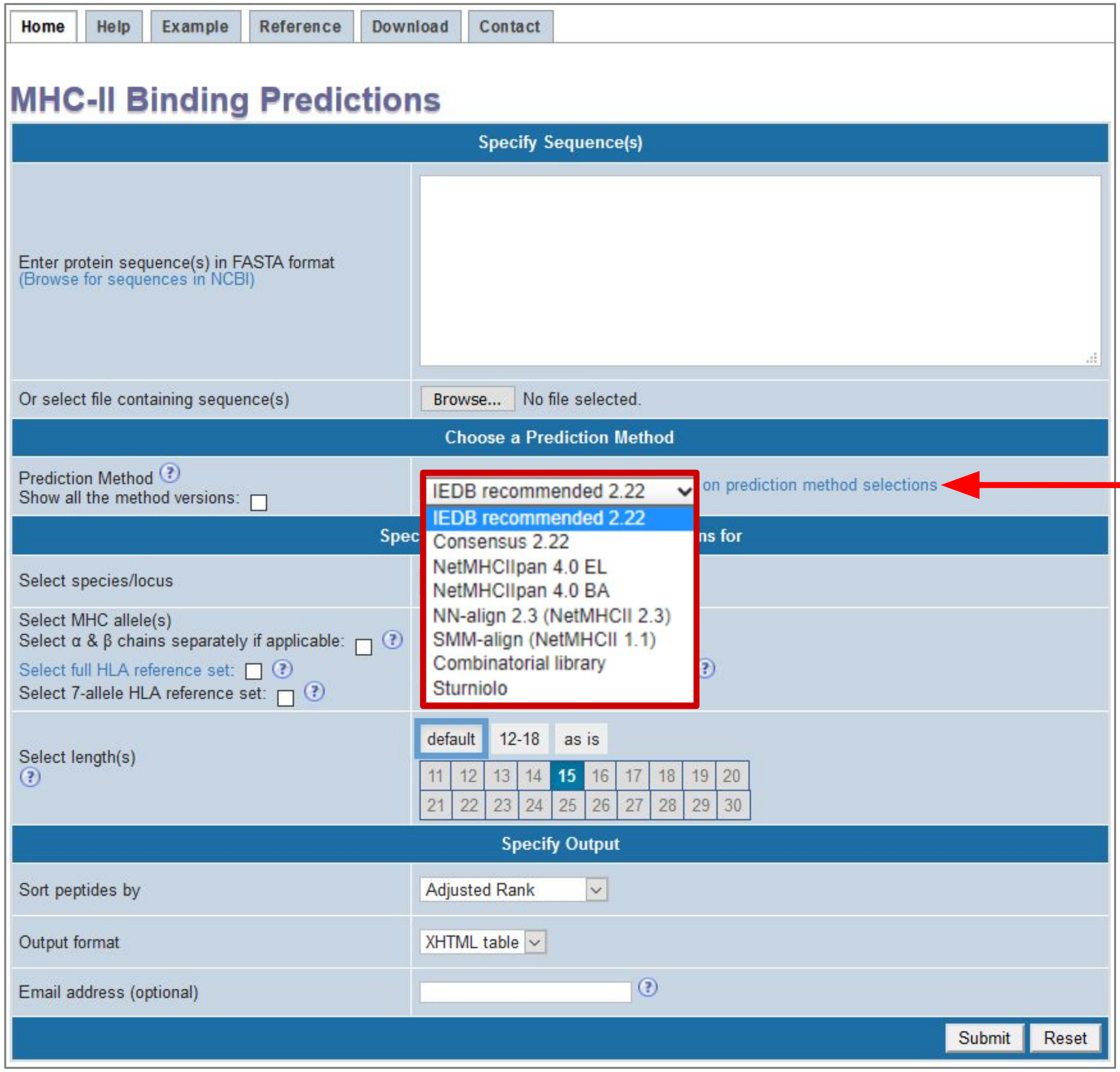
Sort peptides by	Adjusted Rank ⌄
Output format	XHTML table ⌄
Email address (optional)	?

tools.iedb.org/mhcii/

Insert protein sequence(s)

MHC-II binding prediction interface

- Tool entry point layout similar to class I



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format
(Browse for sequences in NCBI)

Or select file containing sequence(s) Browse... No file selected.

Choose a Prediction Method

Prediction Method ?
Show all the method versions: ☐

IEDB recommended 2.22
on prediction method selections

Spec … ns for

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐ ?
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Select length(s) ?

Specify Output

Sort peptides by: Adjusted Rank

Output format: XHTML table

Email address (optional) ?

tools.iedb.org/mhcii/

Select prediction method

MHC-II binding prediction interface

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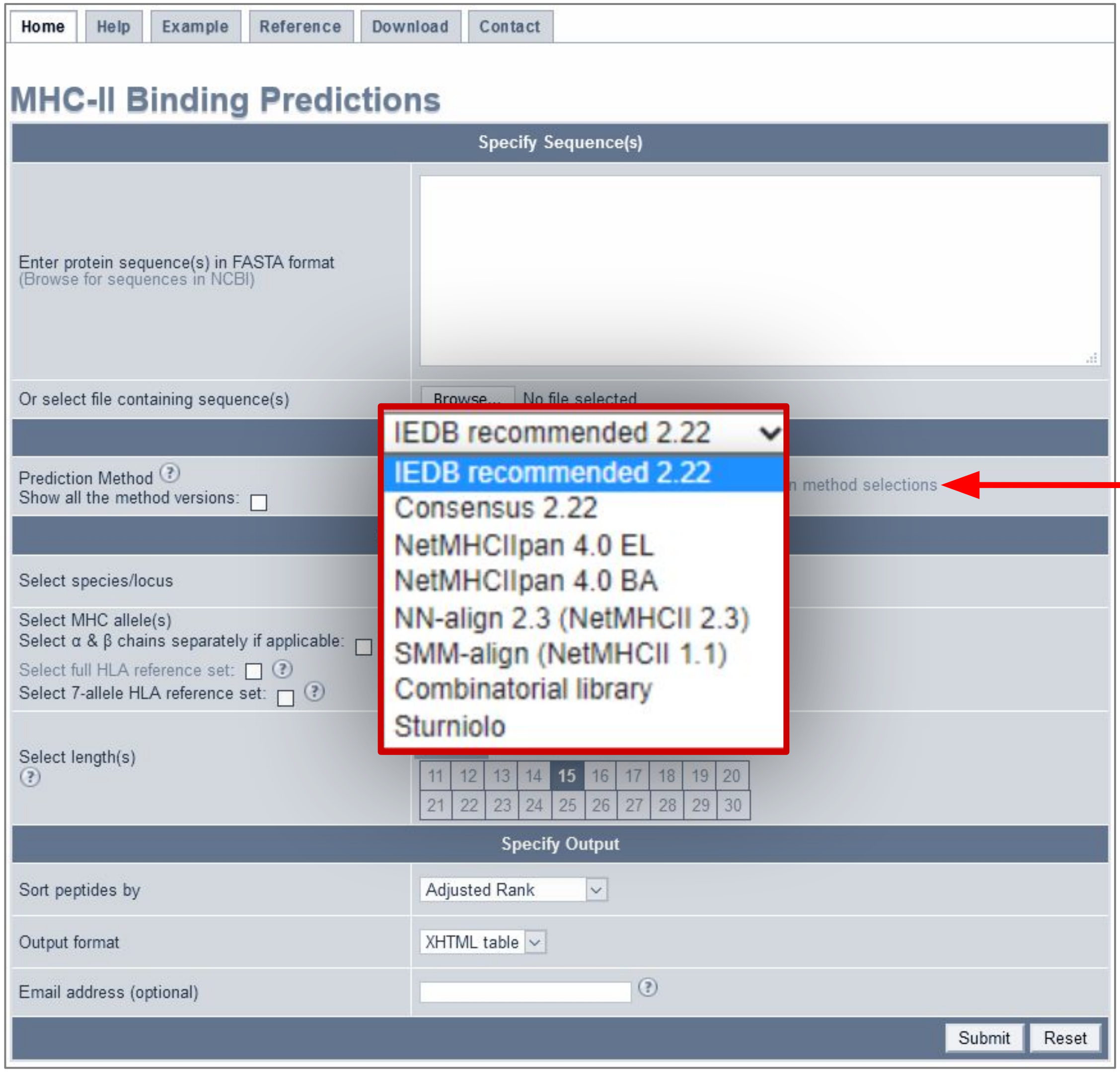


MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format
(Browse for sequences in NCBI)

Or select file containing sequence(s)

Prediction Method ?
Show all the method versions: ☐

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Select length(s)
?

Specify Output

Sort peptides by: Adjusted Rank

Output format: XHTML table

Email address (optional) ?

tools.iedb.org/mhcii/

Select prediction method

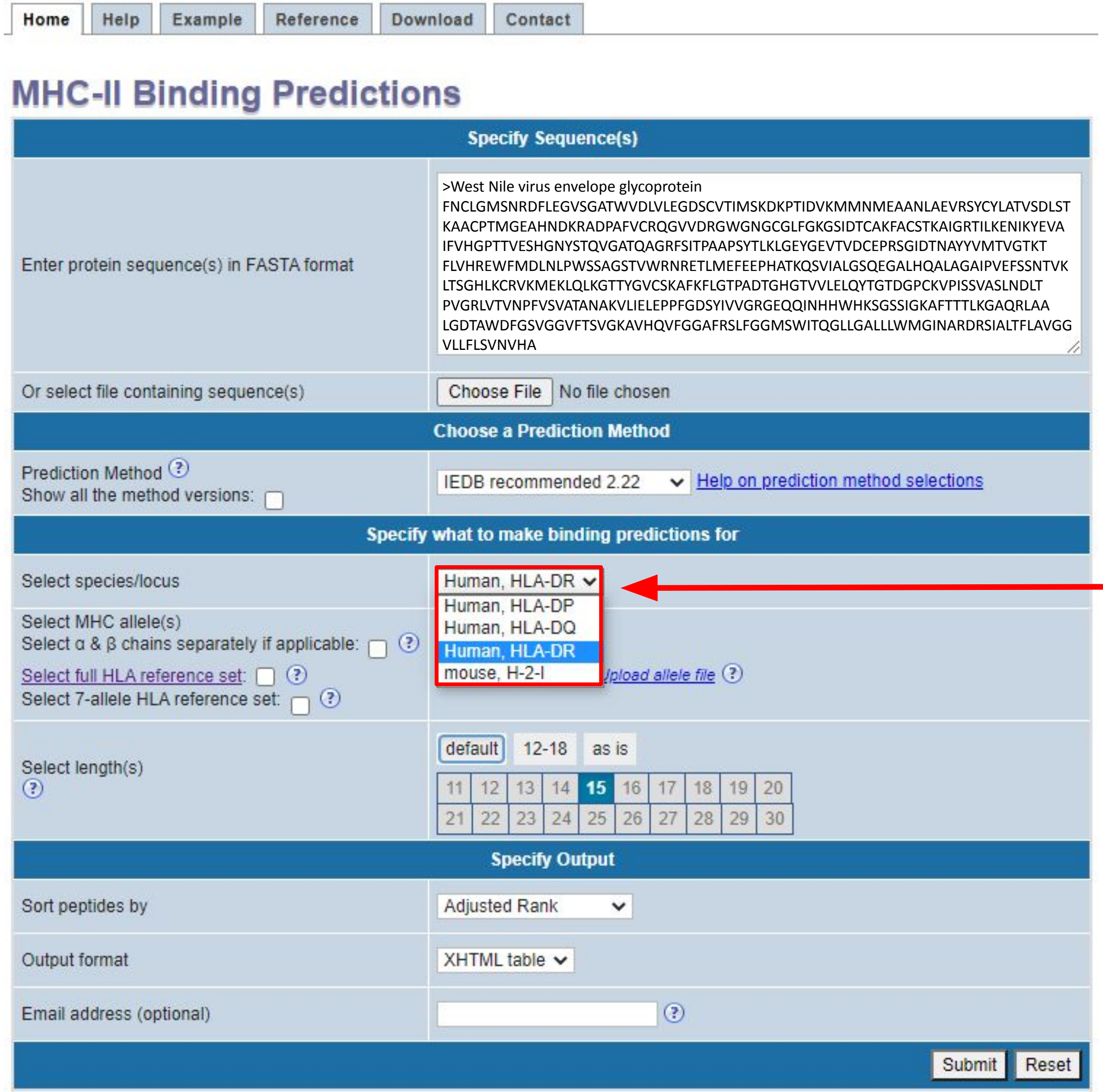
Guidelines: Choosing the prediction method

- Suggested method = “IEDB recommended”
  - Employs Consensus (Combination of NN-align, SMM-align & CombLib/Sturniolo) or NetMHCIIpan depending on the allele
  - Provides binding affinity & percentile rank for each method separately as well

- Recommendation will change with the new benchmark studies

MHC-II binding prediction – example

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format	>West Nile virus envelope glycoprotein FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYCYLATVSDLST KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTILKENIKYEVA IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYYVMTVGTKT FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAIPVEFSSNTVK LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPISSVASLNDLT PVGRLVTVNPFVSVATANAKVLIELEPPFGDSYIVVGRGEQQINHHWHKSGSSIGKAFTTTLKGAQRLAA LGDTAWDFGSVGGVFTSVGKAVHQVFGGAFRSLFGGMSWITQGLLGALLLWMGINARDRSIALTFLAVGG VLLFLSVNVHA
Or select file containing sequence(s)	Choose File No file chosen

Choose a Prediction Method

Prediction Method ? Show all the method versions: ☐	IEDB recommended 2.22 Help on prediction method selections

Specify what to make binding predictions for

Select species/locus	Human, HLA-DR Human, HLA-DP Human, HLA-DQ Human, HLA-DR mouse, H-2-I
Select MHC allele(s) Select α & β chains separately if applicable: ☐ ? Select full HLA reference set: ☐ ? Select 7-allele HLA reference set: ☐ ?	Upload allele file ?
Select length(s) ?	default 12-18 as is 11 12 13 14 **15** 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30

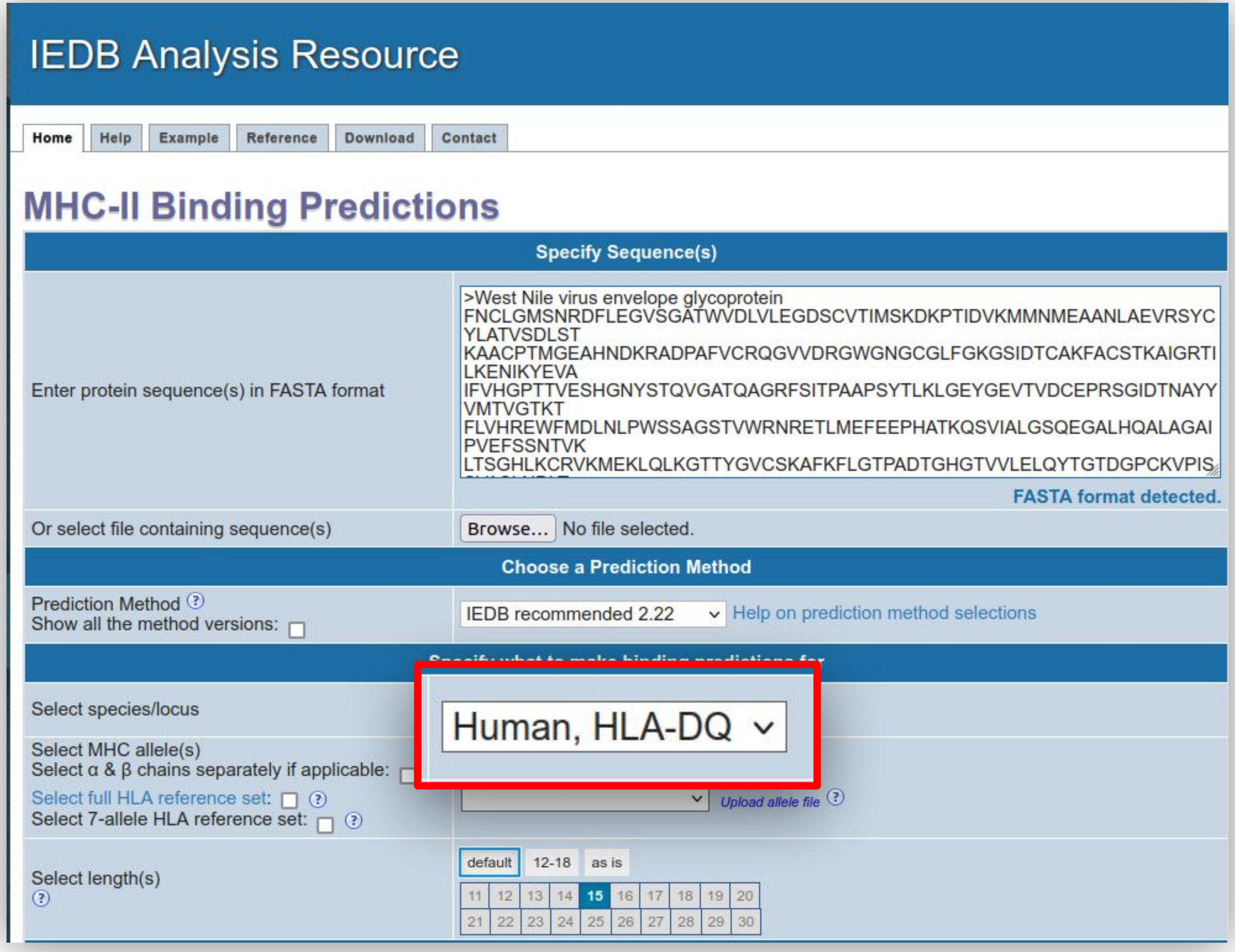
Specify Output

Sort peptides by	Adjusted Rank
Output format	XHTML table
Email address (optional)	?

Choose species & locus

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s) Browse... No file selected.

Choose a Prediction Method

Prediction Method ⓘ: IEDB recommended 2.22

Show all the method versions: ☐

Help on prediction method selections

Specify what to make binding predictions for

Select species/locus: Human, HLA-DQ

Select MHC allele(s)

Select α & β chains separately if applicable: ☐

Select full HLA reference set: ☐ ⓘ

Select 7-allele HLA reference set: ☐ ⓘ

Upload allele file ⓘ

Select length(s) ⓘ

default	12-18	as is							
11	12	13	14	**15**	16	17	18	19	20
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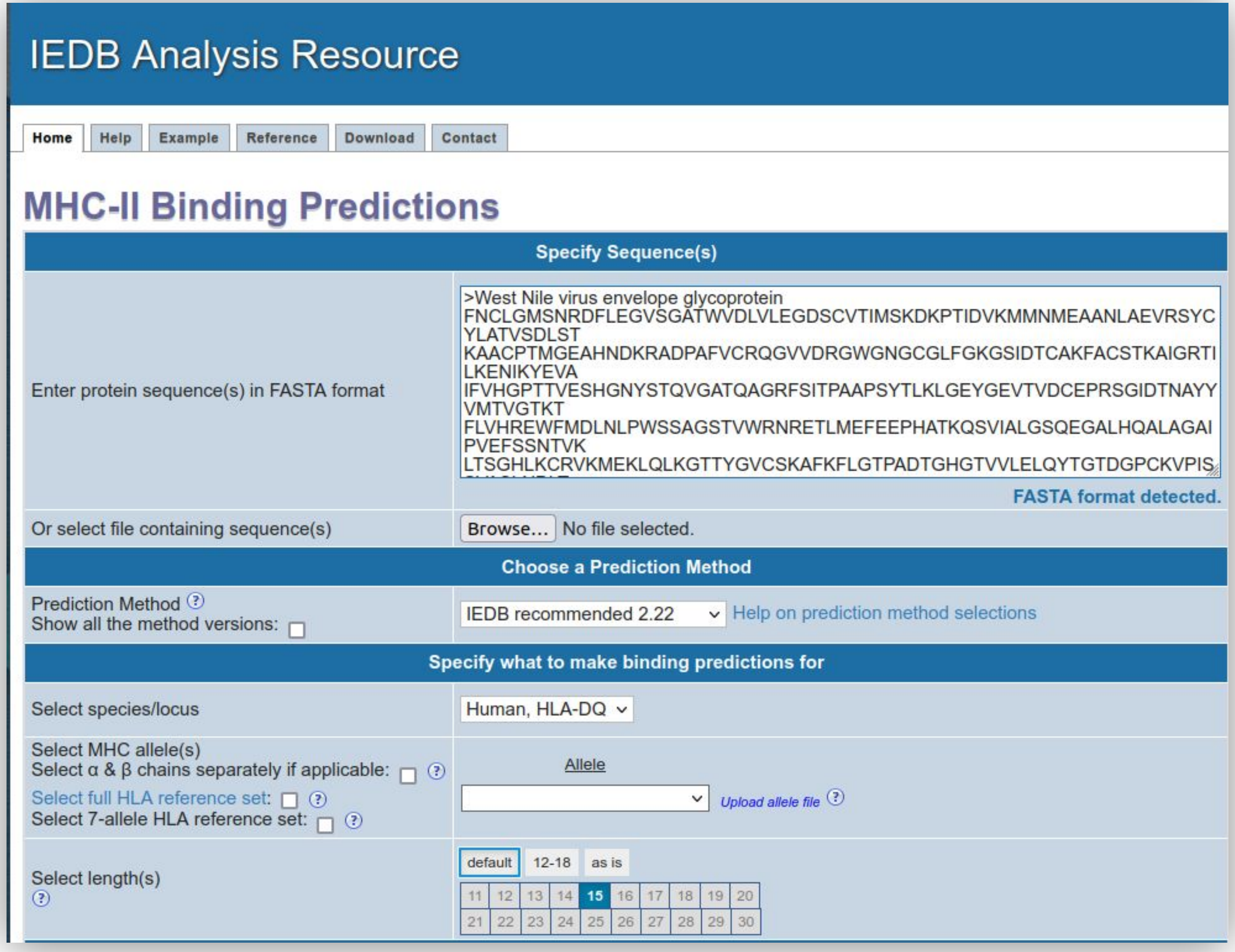
Allele selection - α and β chains

tools.iedb.org/mhcii/



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YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s): No file selected.

Choose a Prediction Method

Prediction Method ?
Show all the method versions: ☐

IEDB recommended 2.22 — Help on prediction method selections

Specify what to make binding predictions for

Select species/locus: Human, HLA-DQ

Select MHC allele(s)
Select α & β chains separately if applicable: ☐ ?
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Allele: (empty) — *Upload allele file* ?

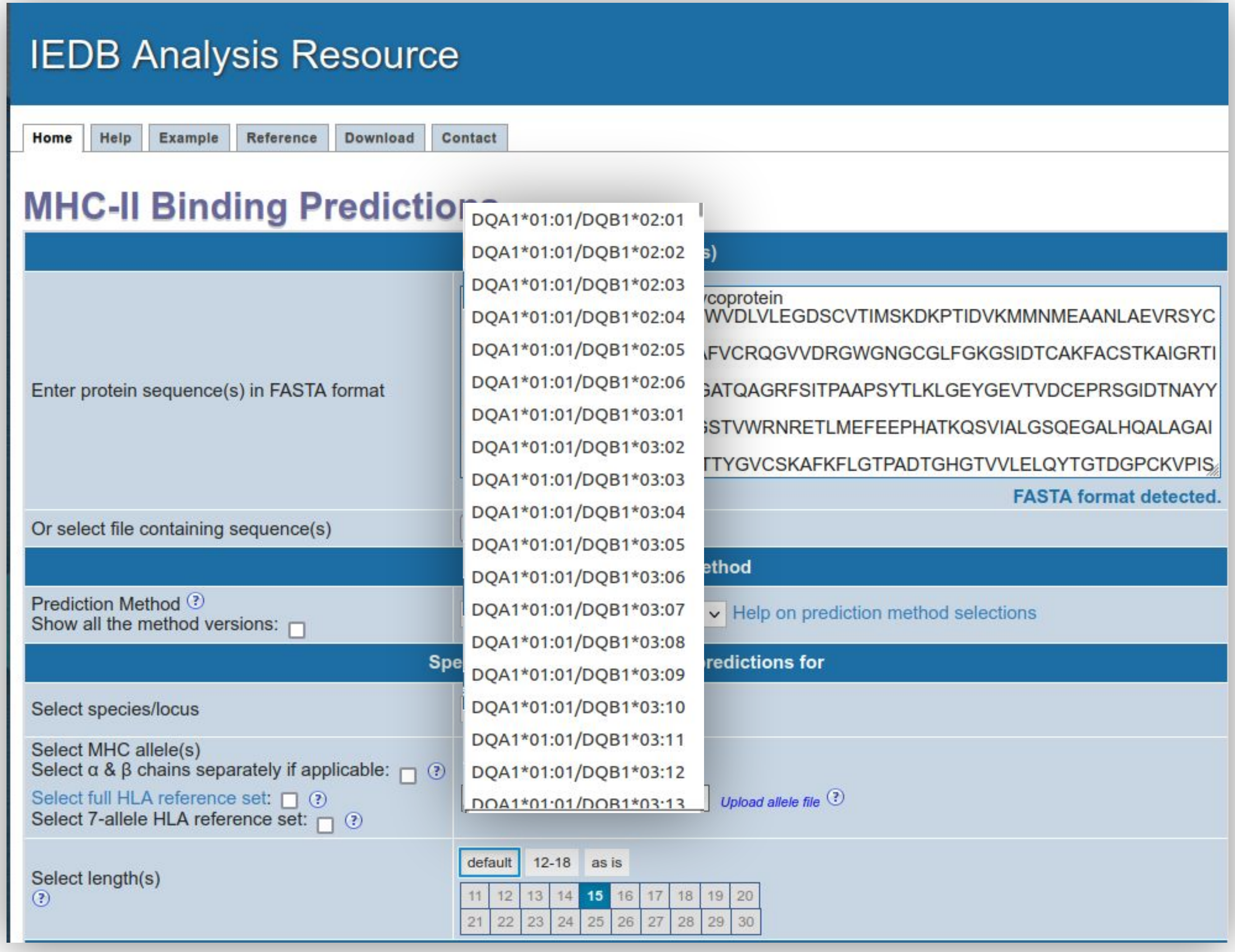
Select length(s) ?

default | 12-18 | as is

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictio

DQA1*01:01/DQB1*02:01
DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
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DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

s)

Enter protein sequence(s) in FASTA format

```
coprotein
WVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
FVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
ATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
STVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
TYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s)

ethod

Prediction Method ?
Show all the method versions: ☐

Help on prediction method selections

Spe ... redictions for

Select species/locus

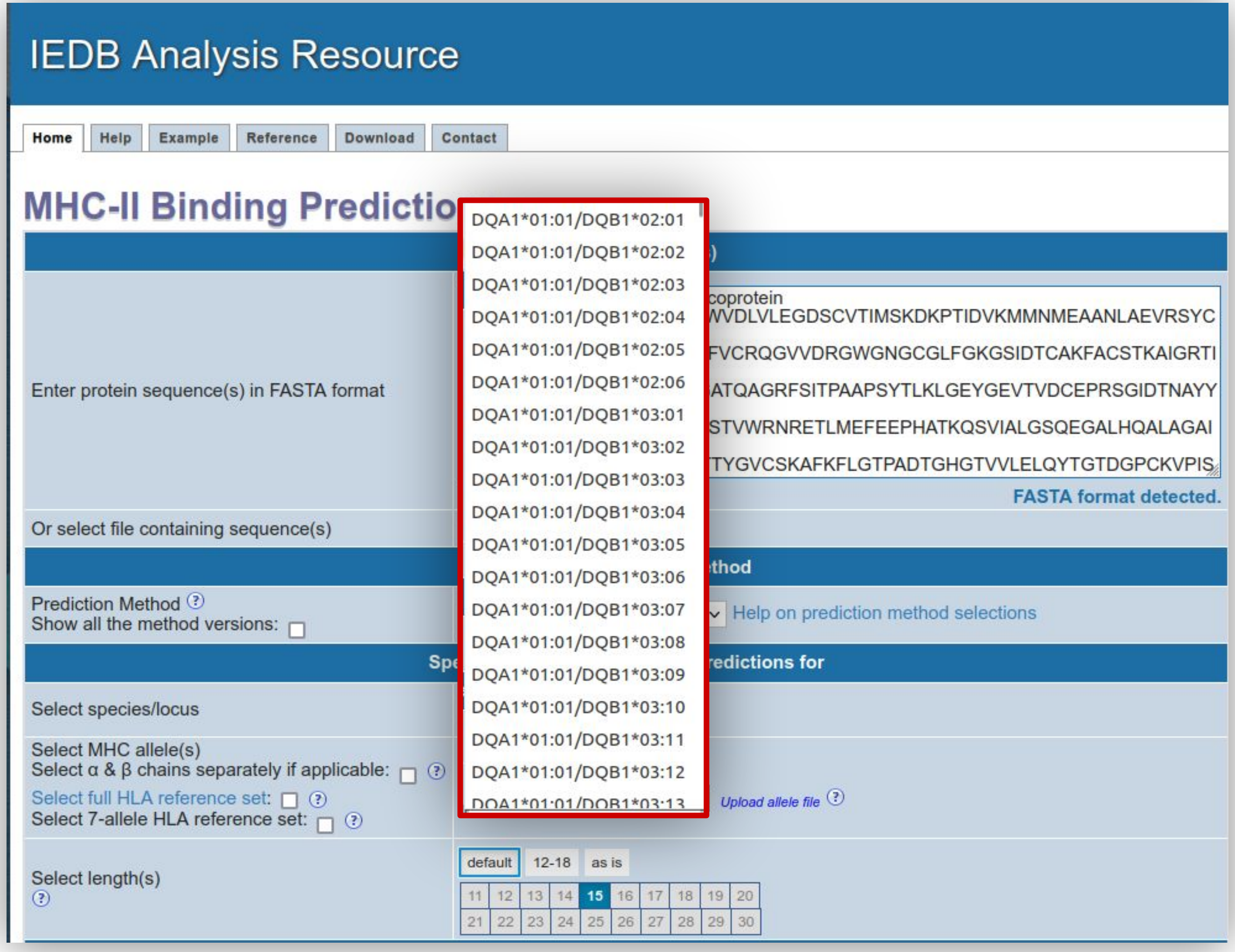
Select MHC allele(s)
Select α & β chains separately if applicable: ☐ ?
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Upload allele file ?

Select length(s) ?

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictio

DQA1*01:01/DQB1*02:01
DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
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DQA1*01:01/DQB1*03:01
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DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
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DQA1*01:01/DQB1*03:06
DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Enter protein sequence(s) in FASTA format

coprotein
WVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
FVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
ATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
STVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
TYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

thod

Prediction Method ?
Show all the method versions: ☐

Help on prediction method selections

Spe redictions for

Select species/locus

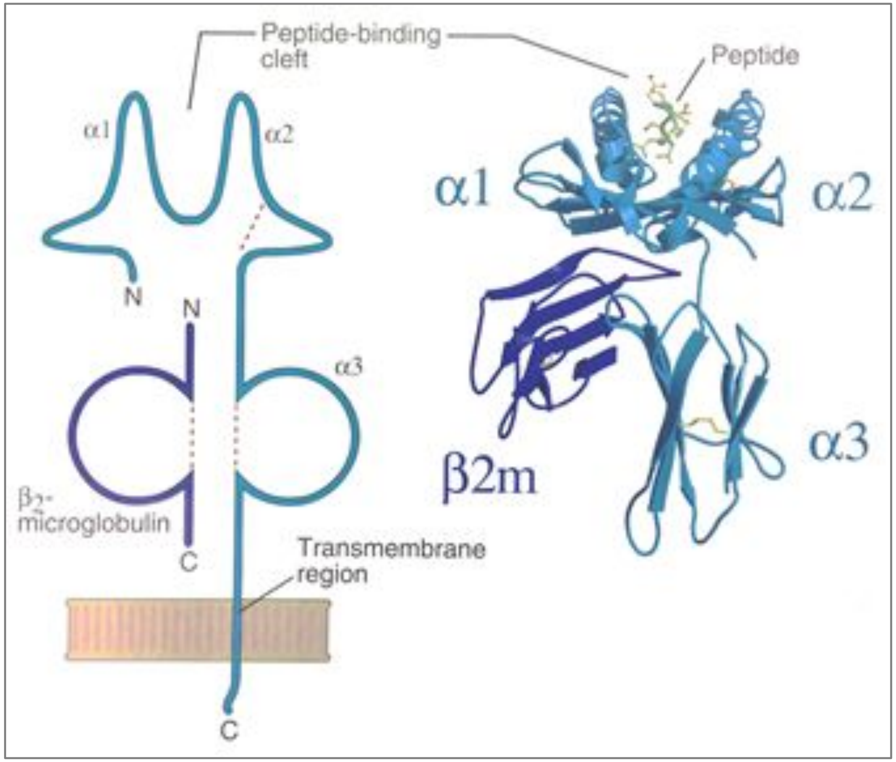
Select MHC allele(s)
Select α & β chains separately if applicable: ☐ ?
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Upload allele file ?

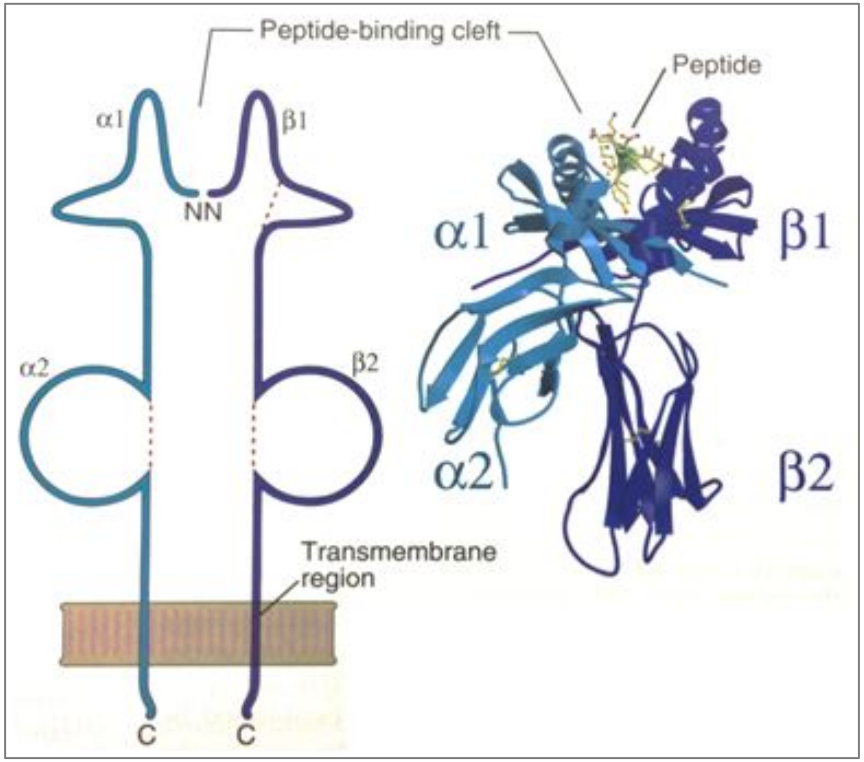
Select length(s)
?

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Differences between MHC-I and MHC-II

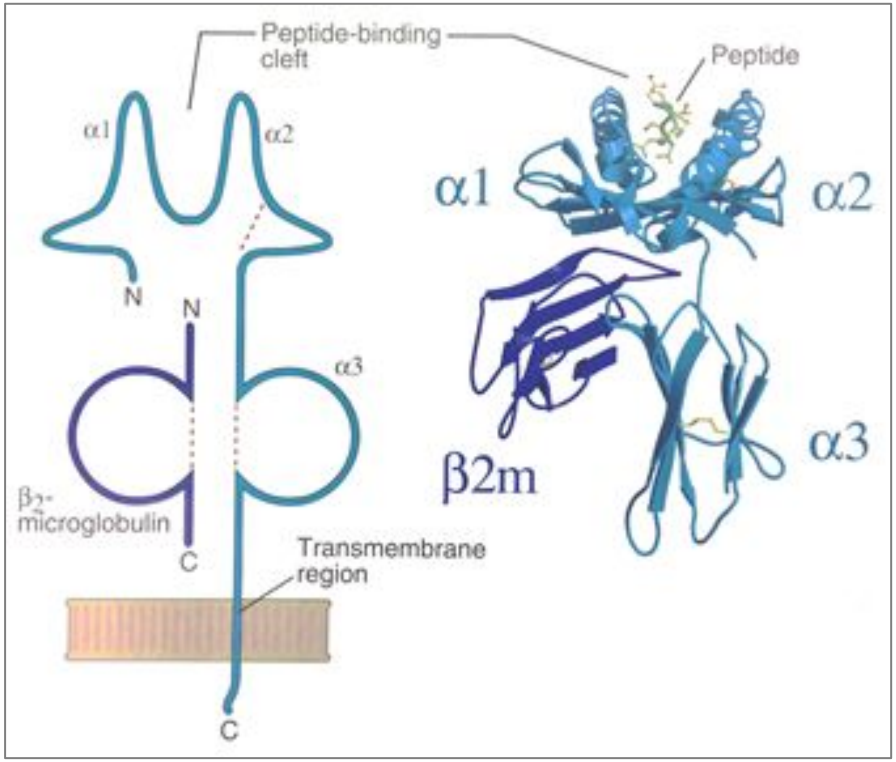


MHC-I

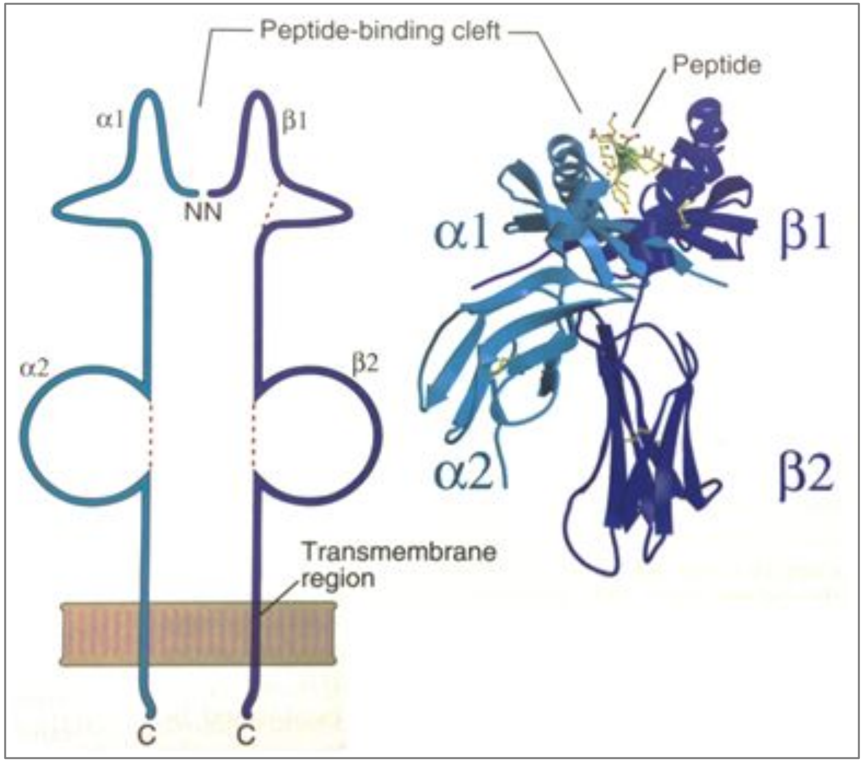


MHC-II

Differences between MHC-I and MHC-II

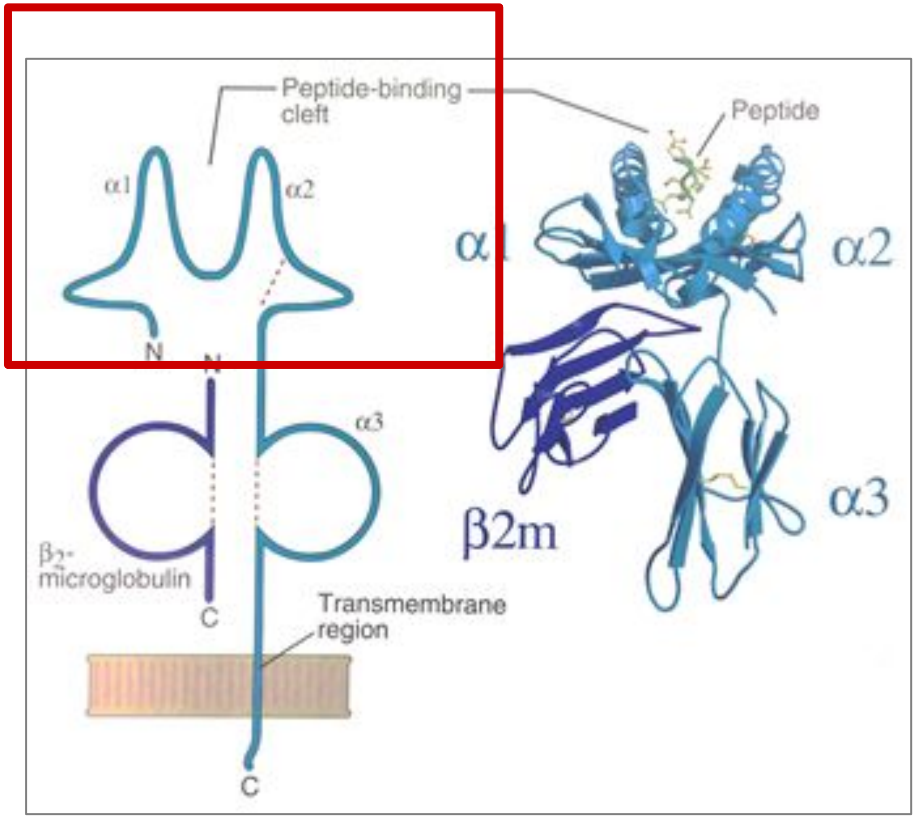


MHC-I

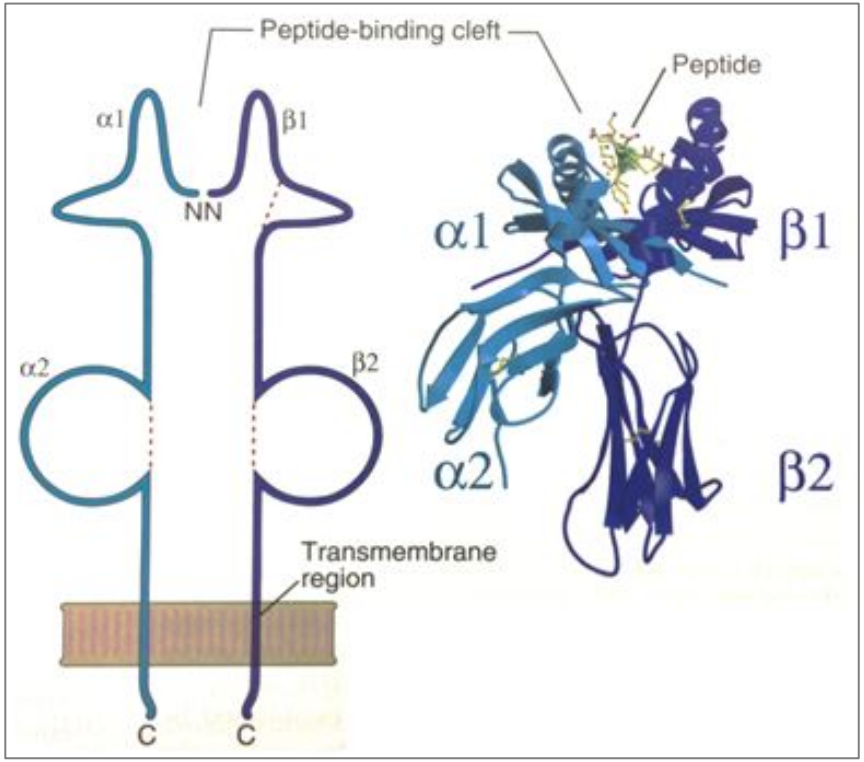


MHC-II

Differences between MHC-I and MHC-II

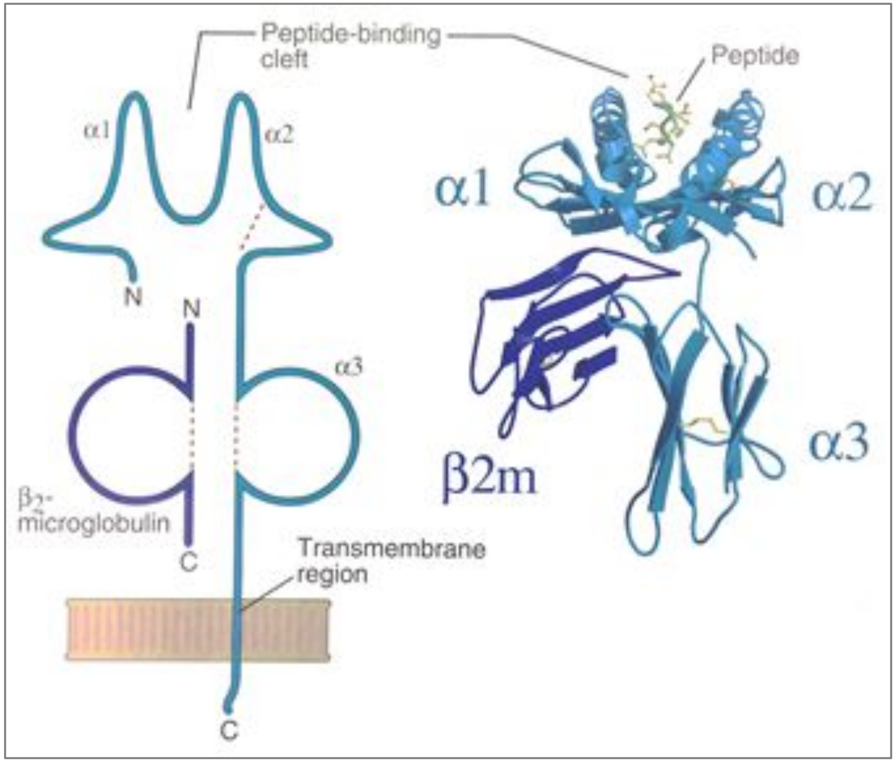


MHC-I

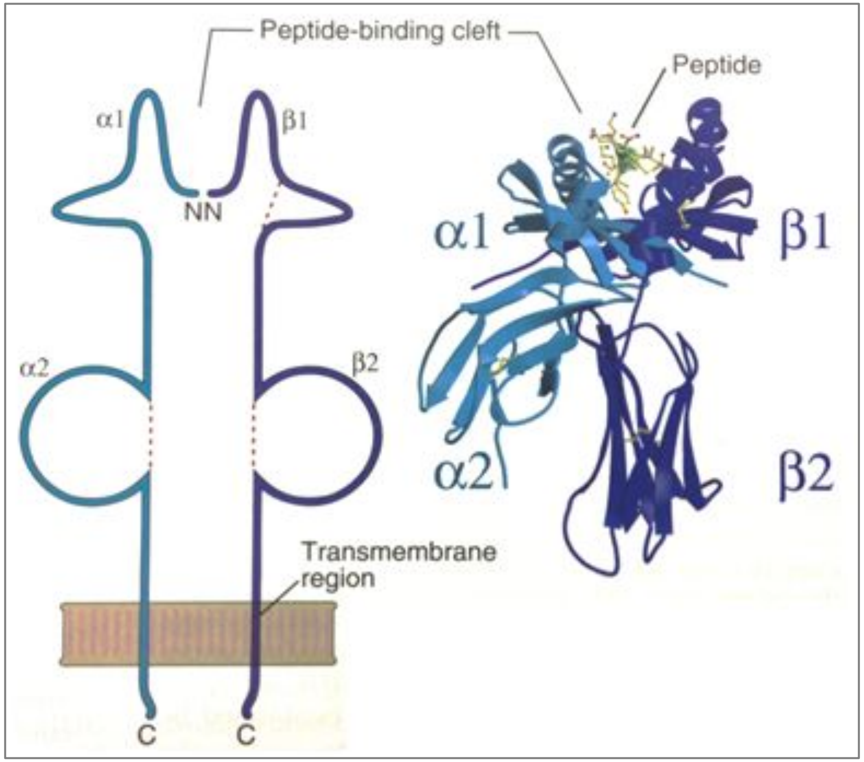


MHC-II

Differences between MHC-I and MHC-II

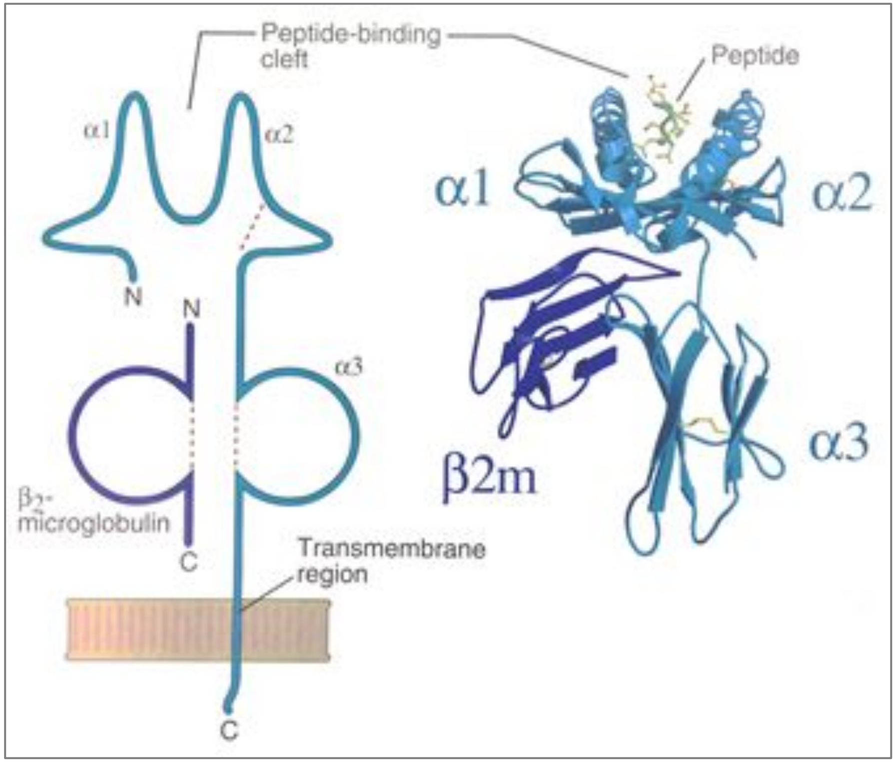


MHC-I

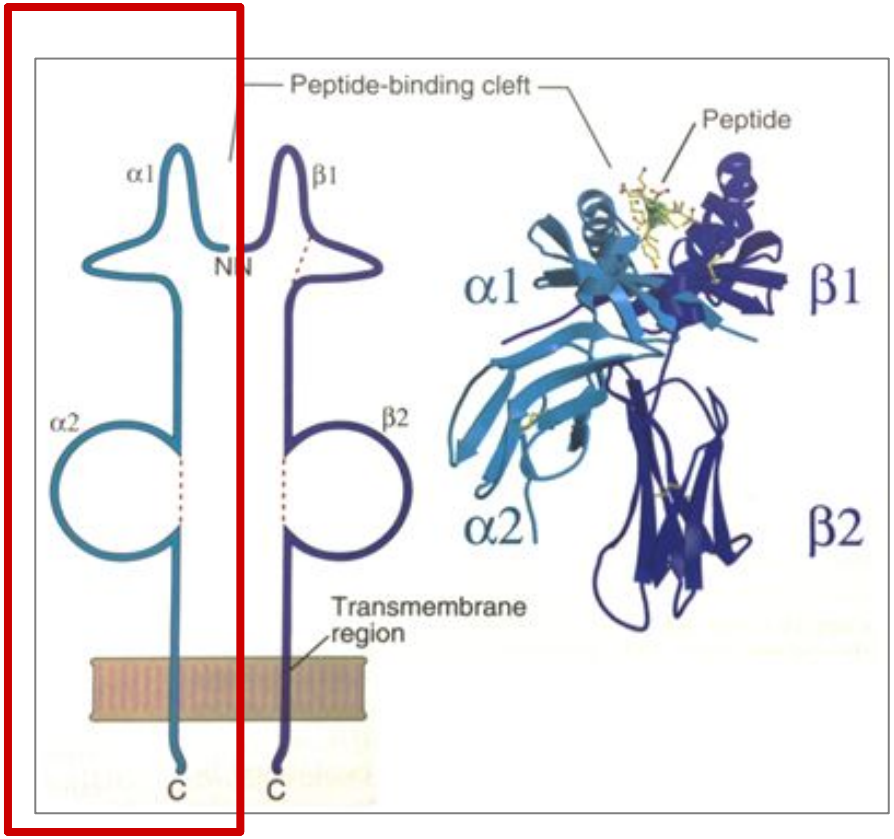


MHC-II

Differences between MHC-I and MHC-II

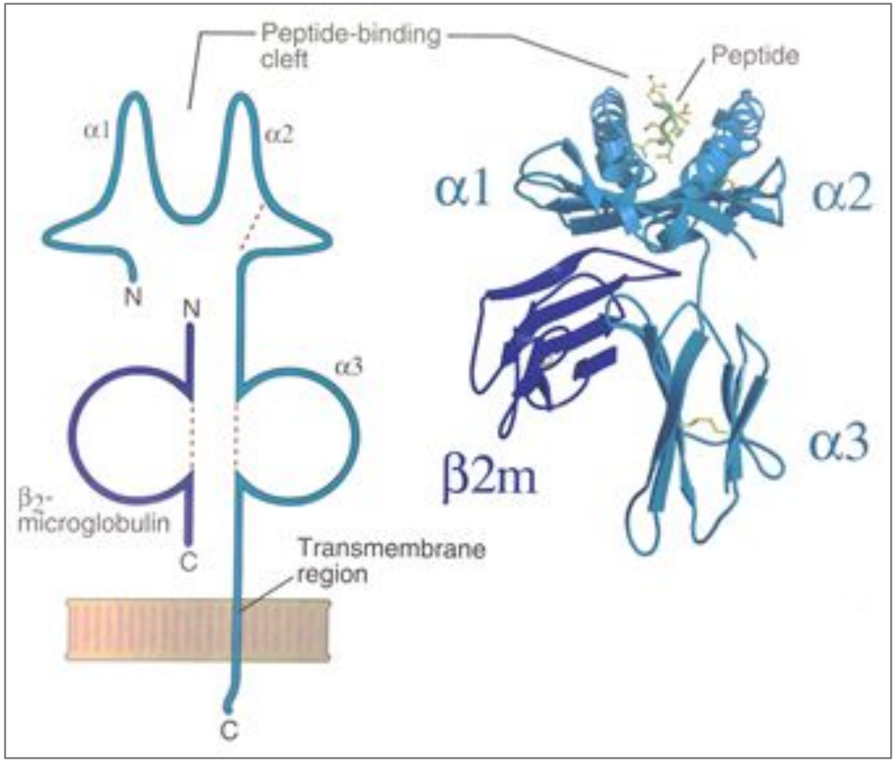


MHC-I

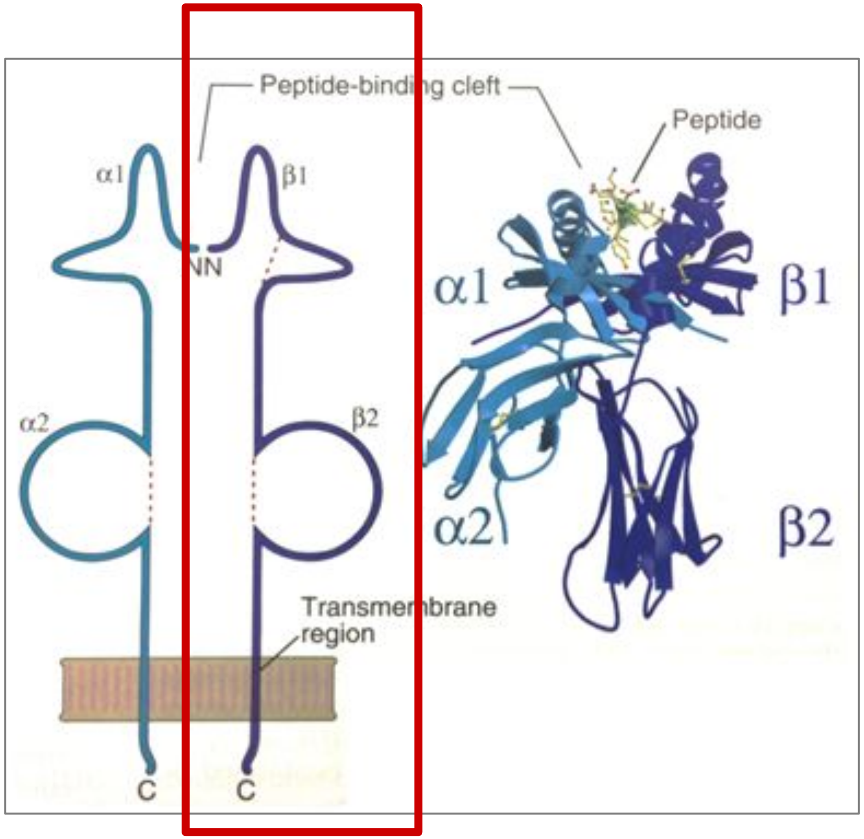


MHC-II

Differences between MHC-I and MHC-II

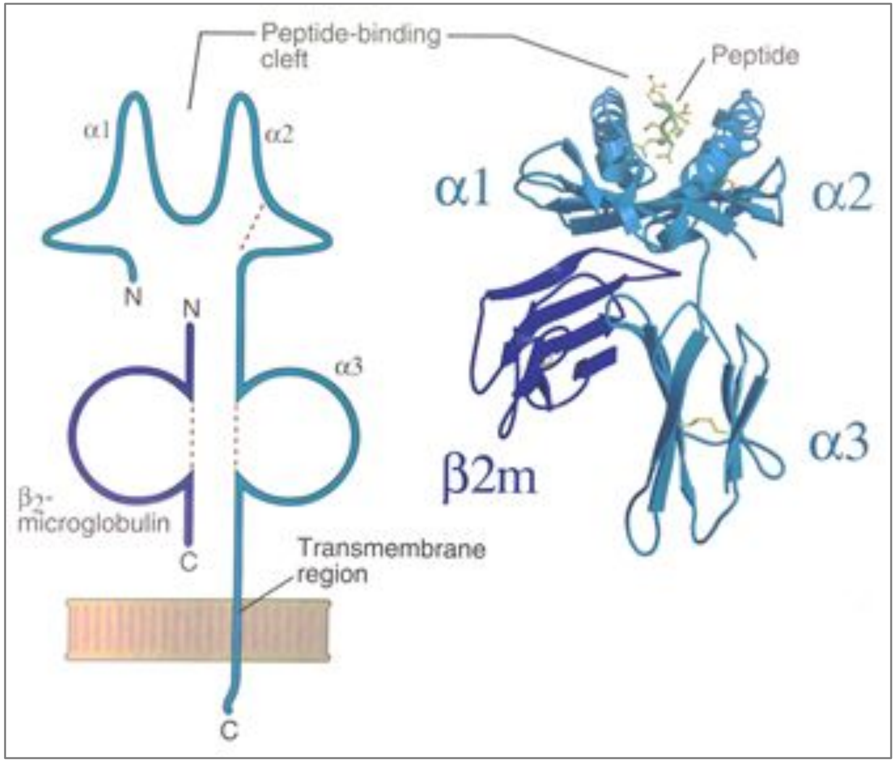


MHC-I

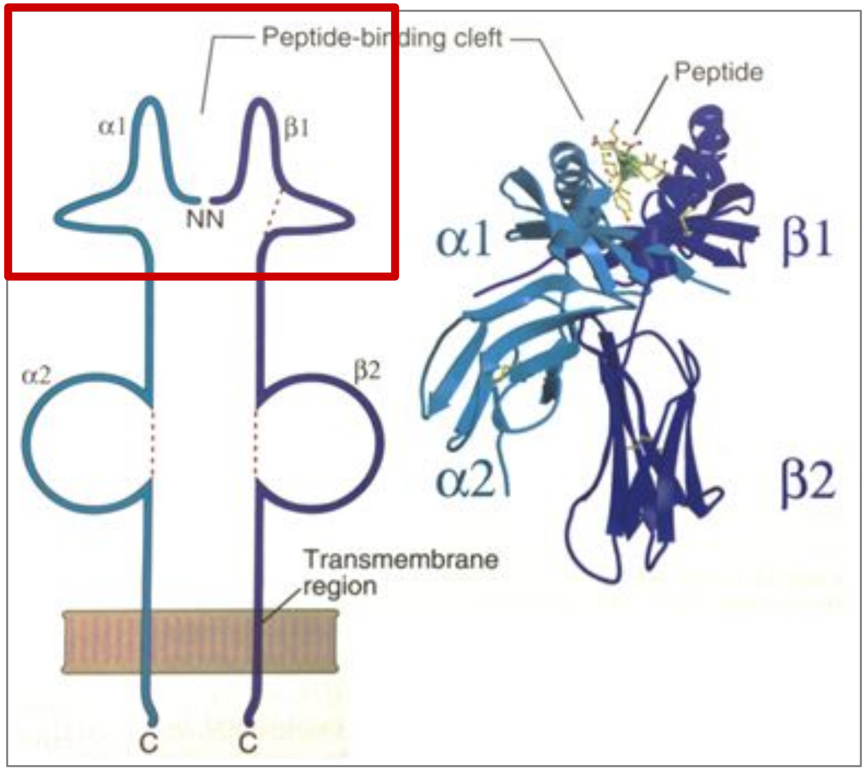


MHC-II

Differences between MHC-I and MHC-II



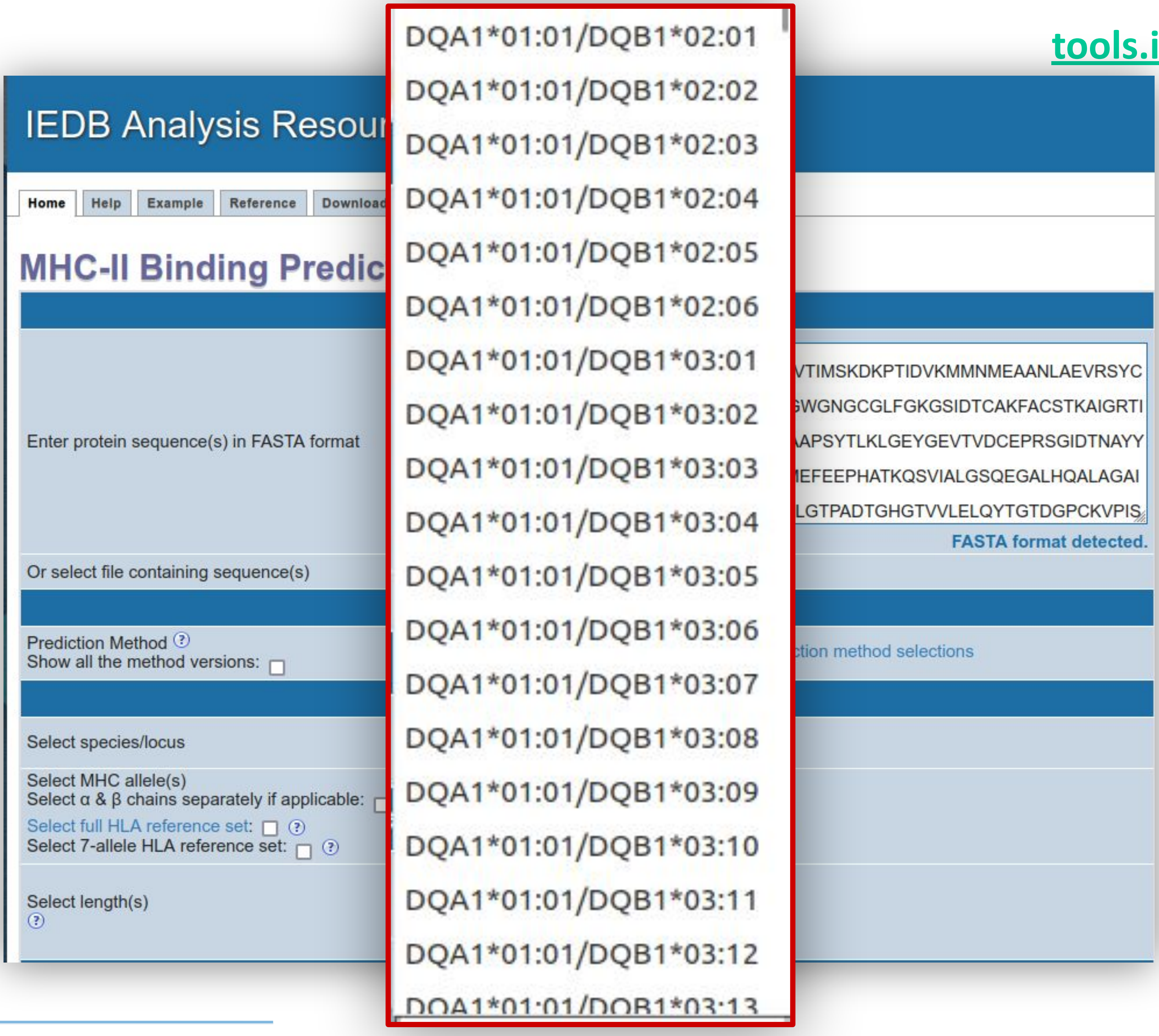
MHC-I



MHC-II

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method ?
Show all the method versions: ☐

ction method selections

Select species/locus

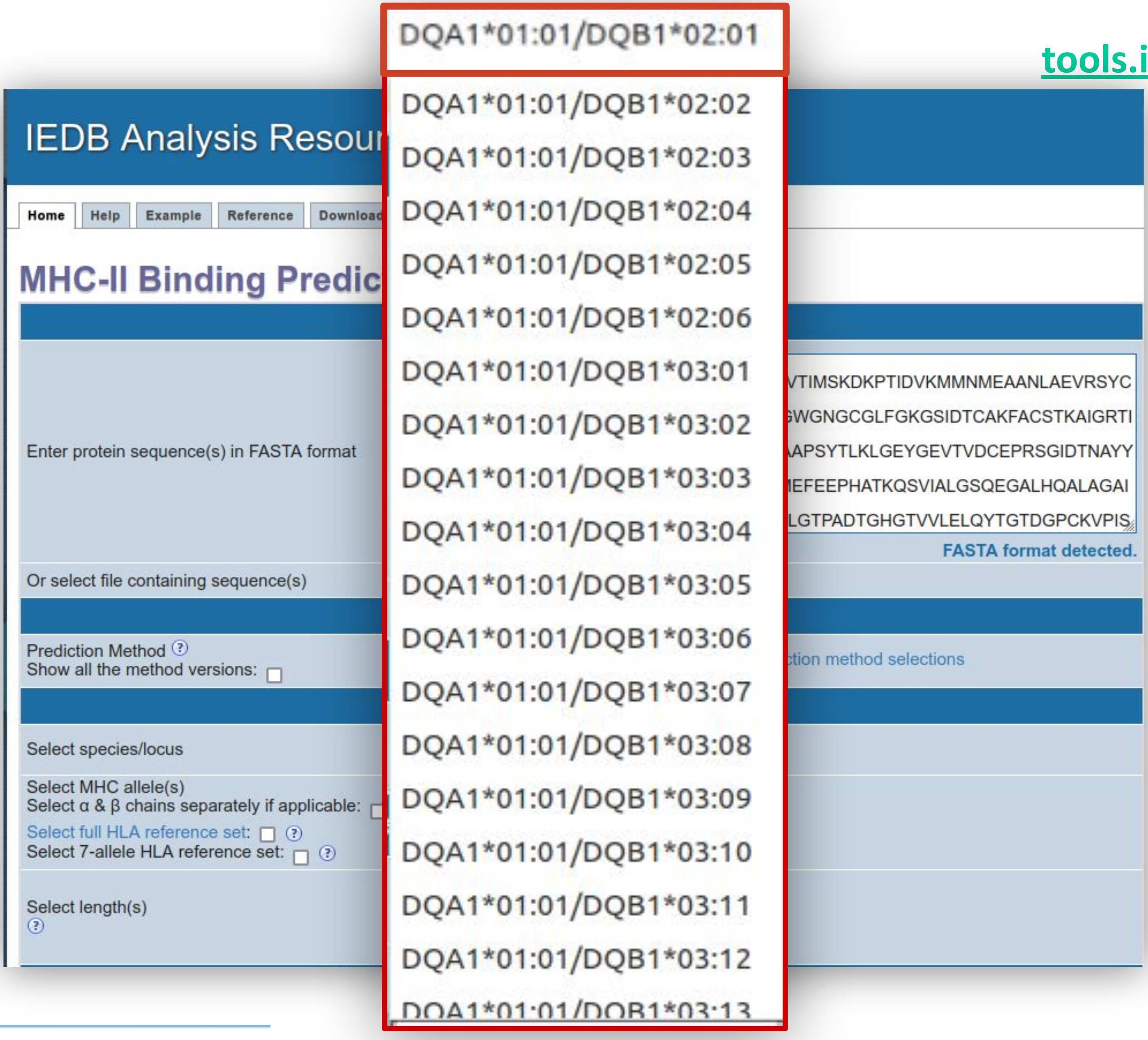
Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Select length(s)
?

DQA1*01:01/DQB1*02:01
DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
DQA1*01:01/DQB1*03:06
DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

ction method selections

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

DQA1*01:01/DQB1*02:01
DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
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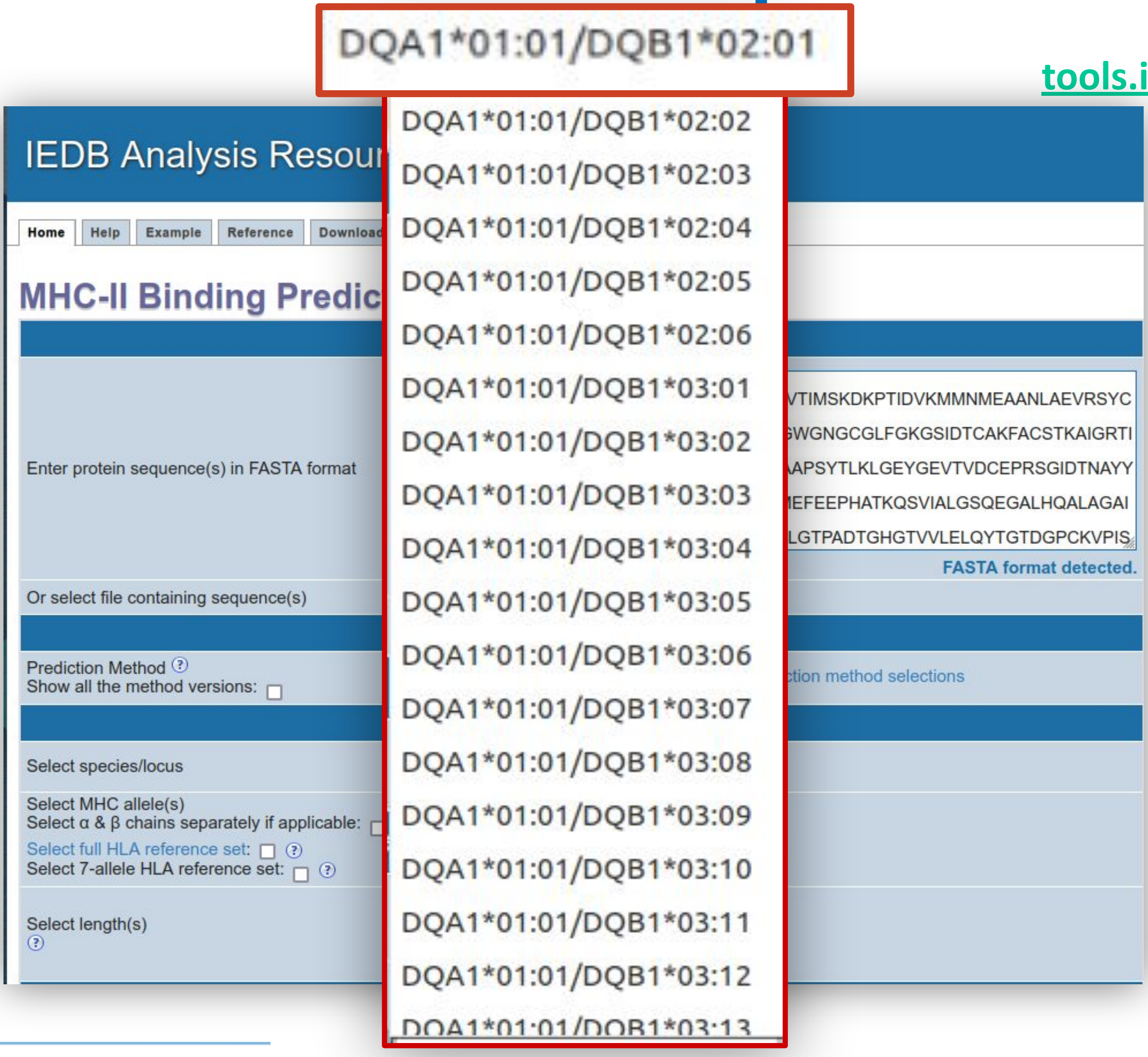
Allele selection - α and β chains

tools.iedb.org/mhcii/



DQA1*01:01/DQB1*02:01

MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

```
VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

ction method selections

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
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DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
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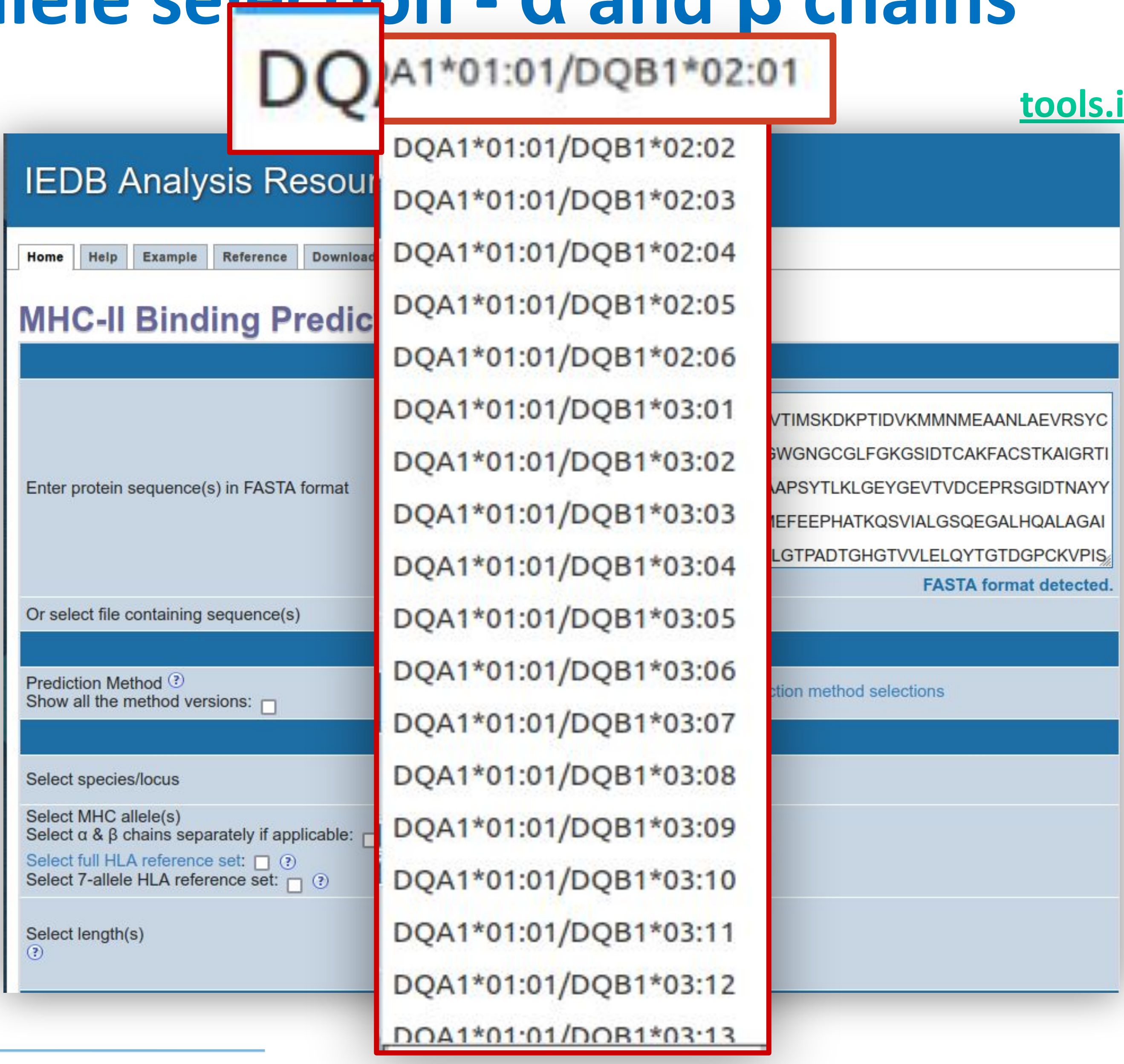
Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method ?
Show all the method versions: ☐

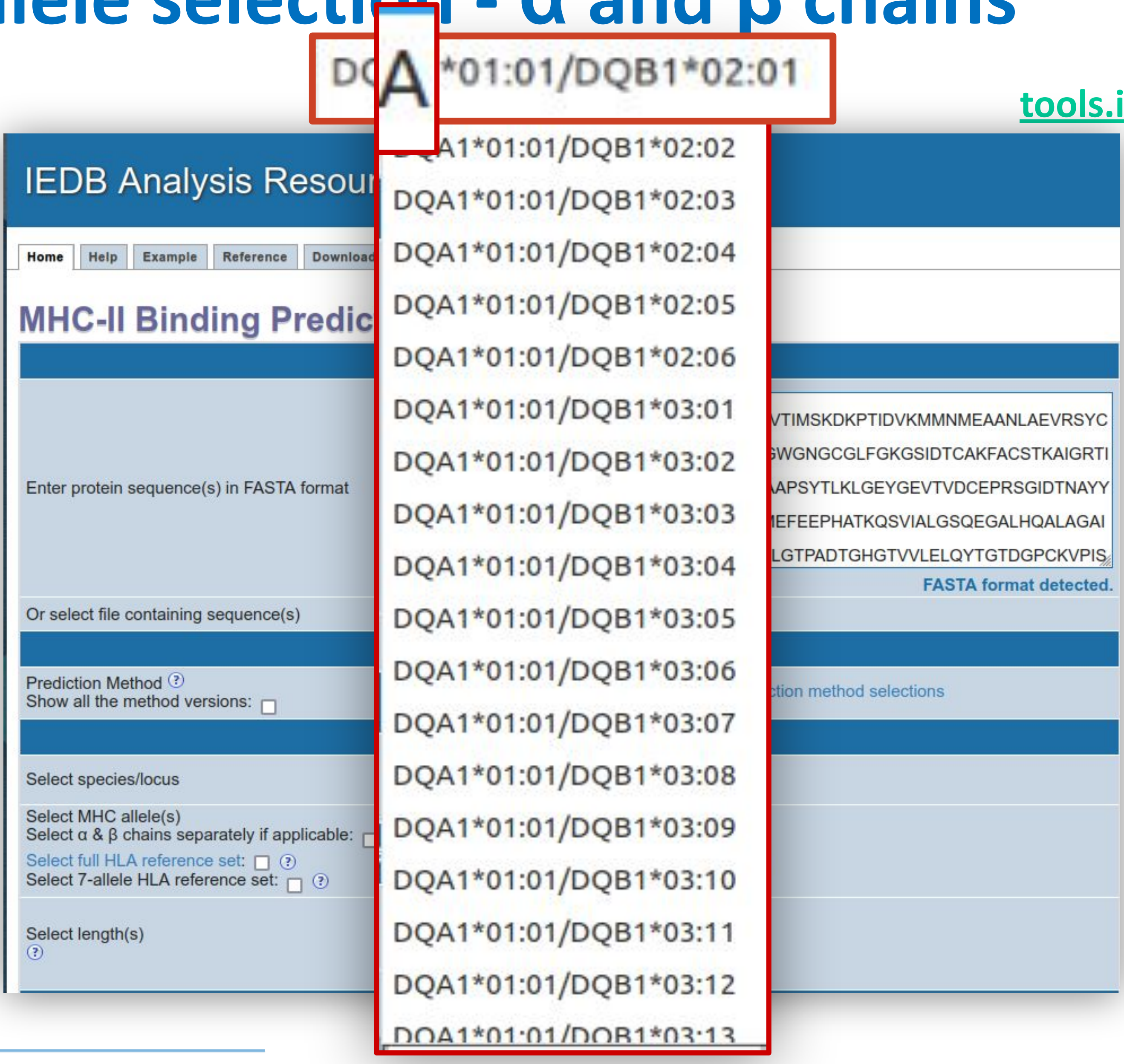
Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Select length(s)
?

Allele selection - α and β chains

tools.iedb.org/mhcii/



DQA1*01:01/DQB1*02:01

DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
DQA1*01:01/DQB1*03:06
DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

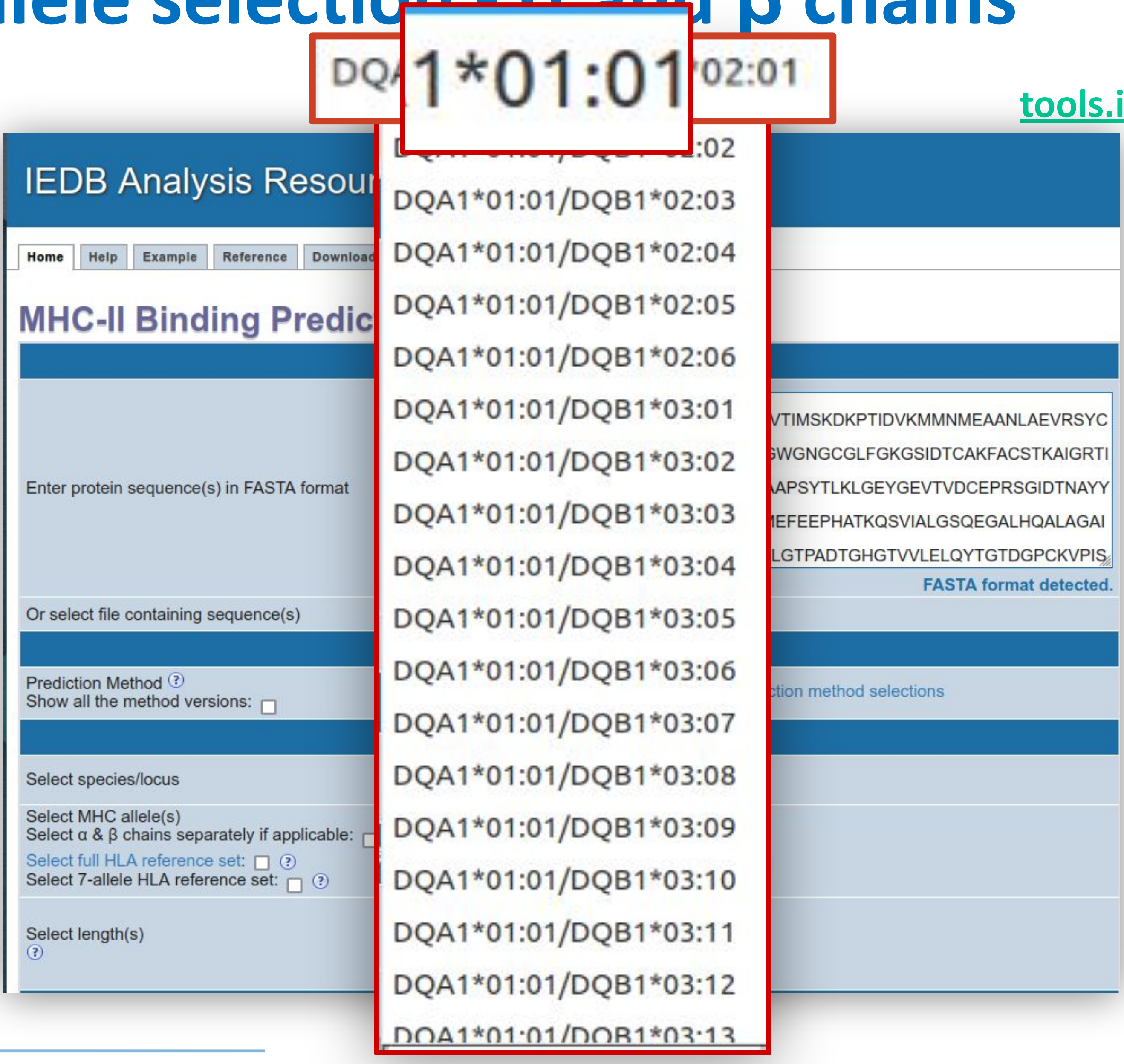
Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
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APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

tion method selections

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
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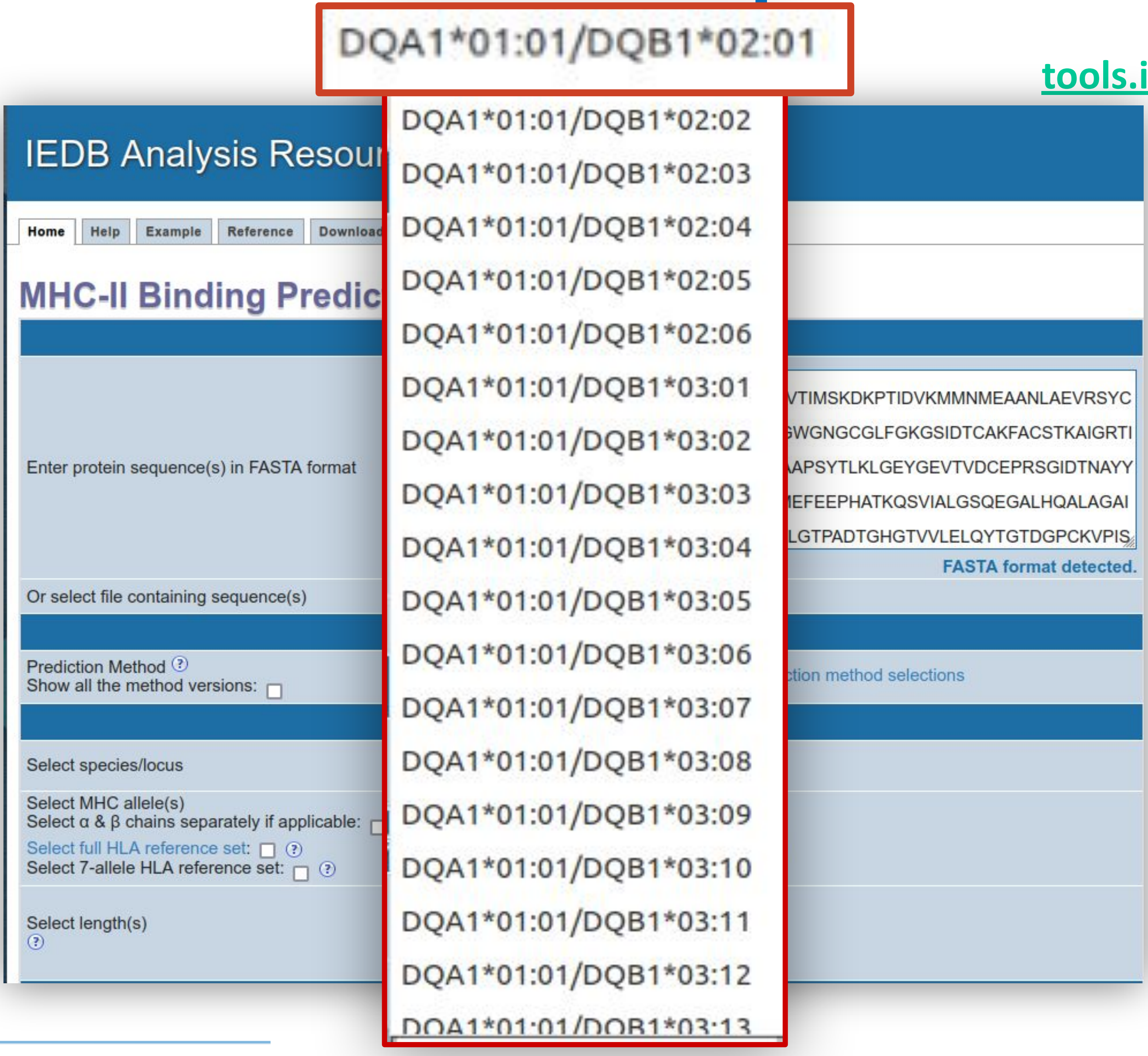
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Allele selection - α and β chains

tools.iedb.org/mhcii/



DQA1*01:01/DQB1*02:01

IEDB Analysis Resour

MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

ction method selections

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
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DQA1*01:01/DQB1*03:10
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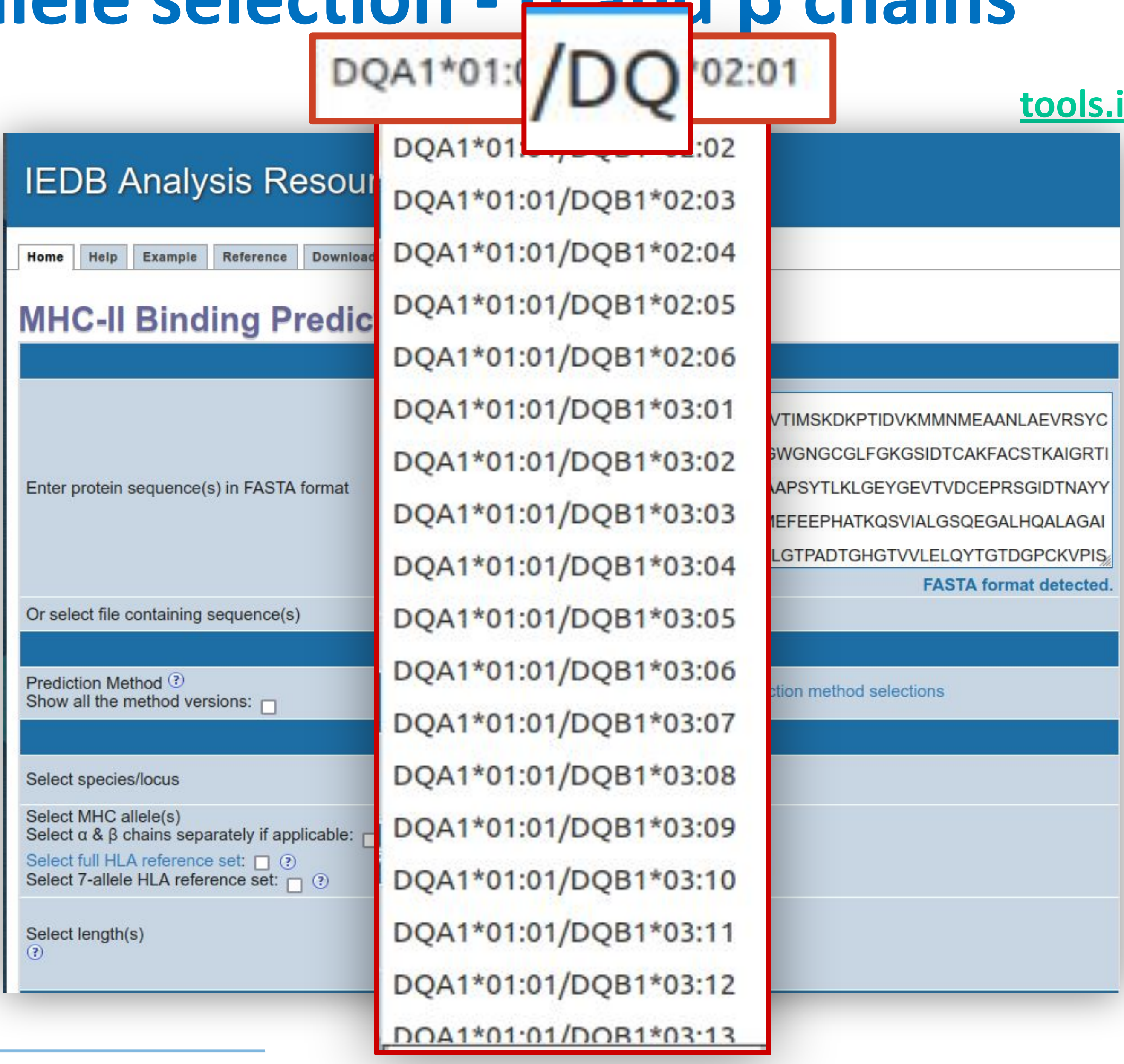
DQA1*01:01/DQB1*03:13

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

ction method selections

Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

DQA1*01 :02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
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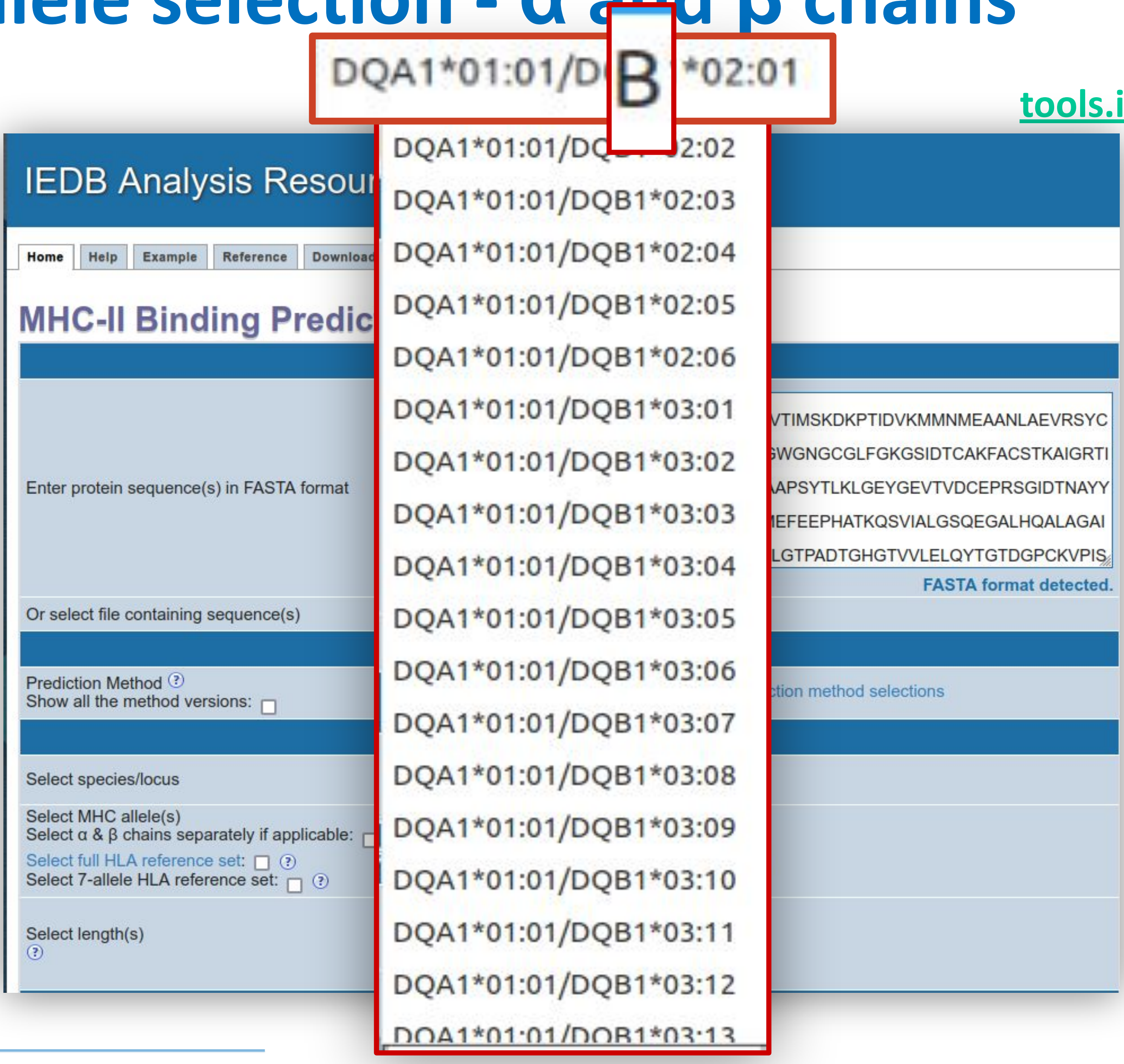
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Allele selection - α and β chains

tools.iedb.org/mhcii/



DQA1*01:01/D B *02:01

DQA1*01:01/DQ 2:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
DQA1*01:01/DQB1*03:06
DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method ?
Show all the method versions: ☐

ction method selections

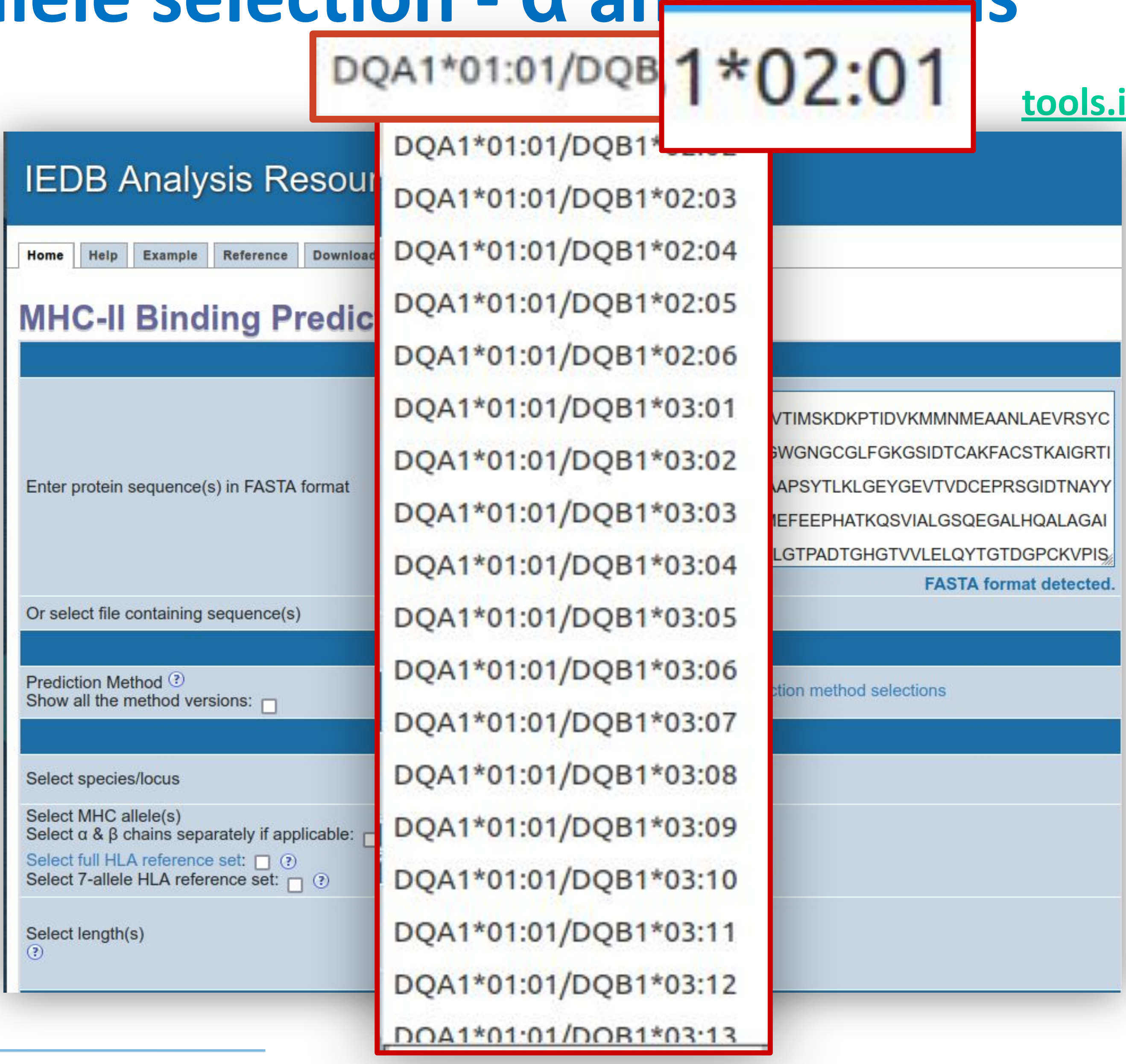
Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Select length(s)
?

Allele selection - α and ß chains

tools.iedb.org/mhcii/



DQA1*01:01/DQB1*02:01

IEDB Analysis Resour

MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method ?
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Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐ ?
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Select length(s)
?

DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
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DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
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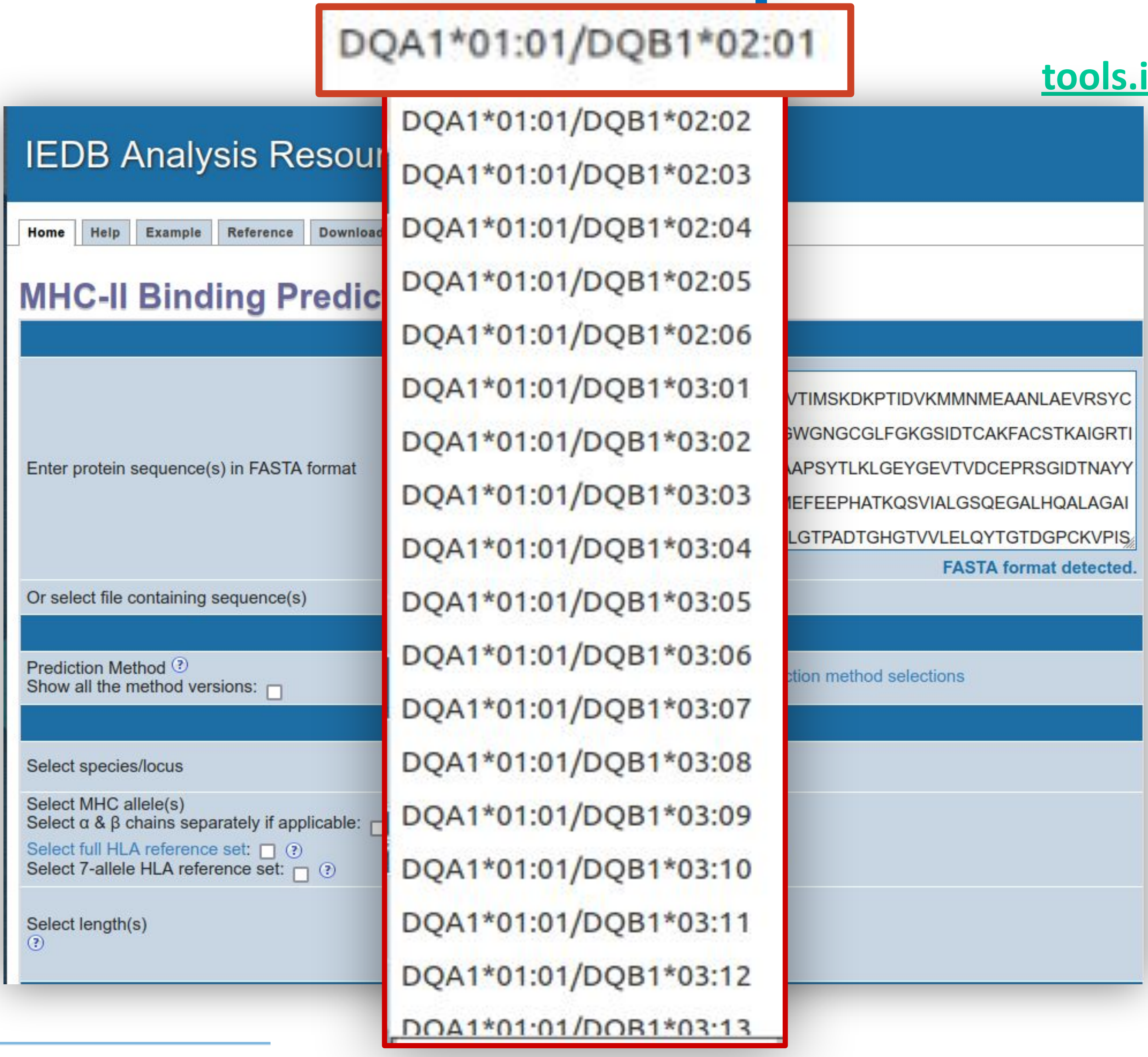
Allele selection - α and β chains

tools.iedb.org/mhcii/



DQA1*01:01/DQB1*02:01

DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
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DQA1*01:01/DQB1*03:05
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DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

IEDB Analysis Resour

MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

```
VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
IEFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s)

Prediction Method
Show all the method versions: ☐

ction method selections

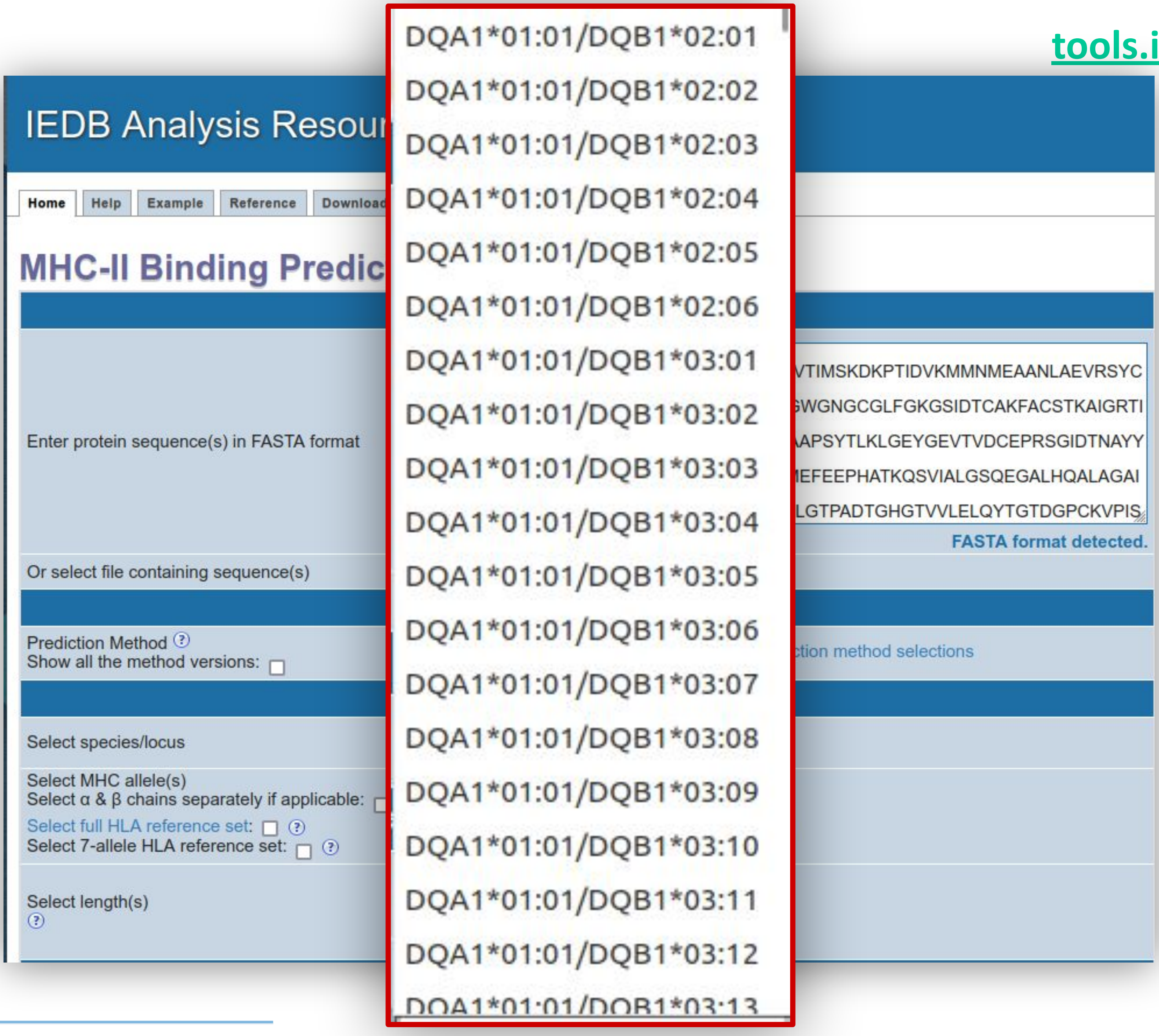
Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Select length(s)

Allele selection - α and β chains

tools.iedb.org/mhcii/



IEDB Analysis Resour

MHC-II Binding Predic

Enter protein sequence(s) in FASTA format

VTIMSKDKPTIDVKMMNMEAANLAEVRSYC
WGNGCGLFGKGSIDTCAKFACSTKAIGRTI
APSYTLKLGEYGEVTVDCEPRSGIDTNAYY
EFEEPHATKQSVIALGSQEGALHQALAGAI
LGTPADTGHGTVVLELQYTGTDGPCKVPIS

FASTA format detected.

Or select file containing sequence(s)

Prediction Method ?
Show all the method versions: ☐

ction method selections

Select species/locus

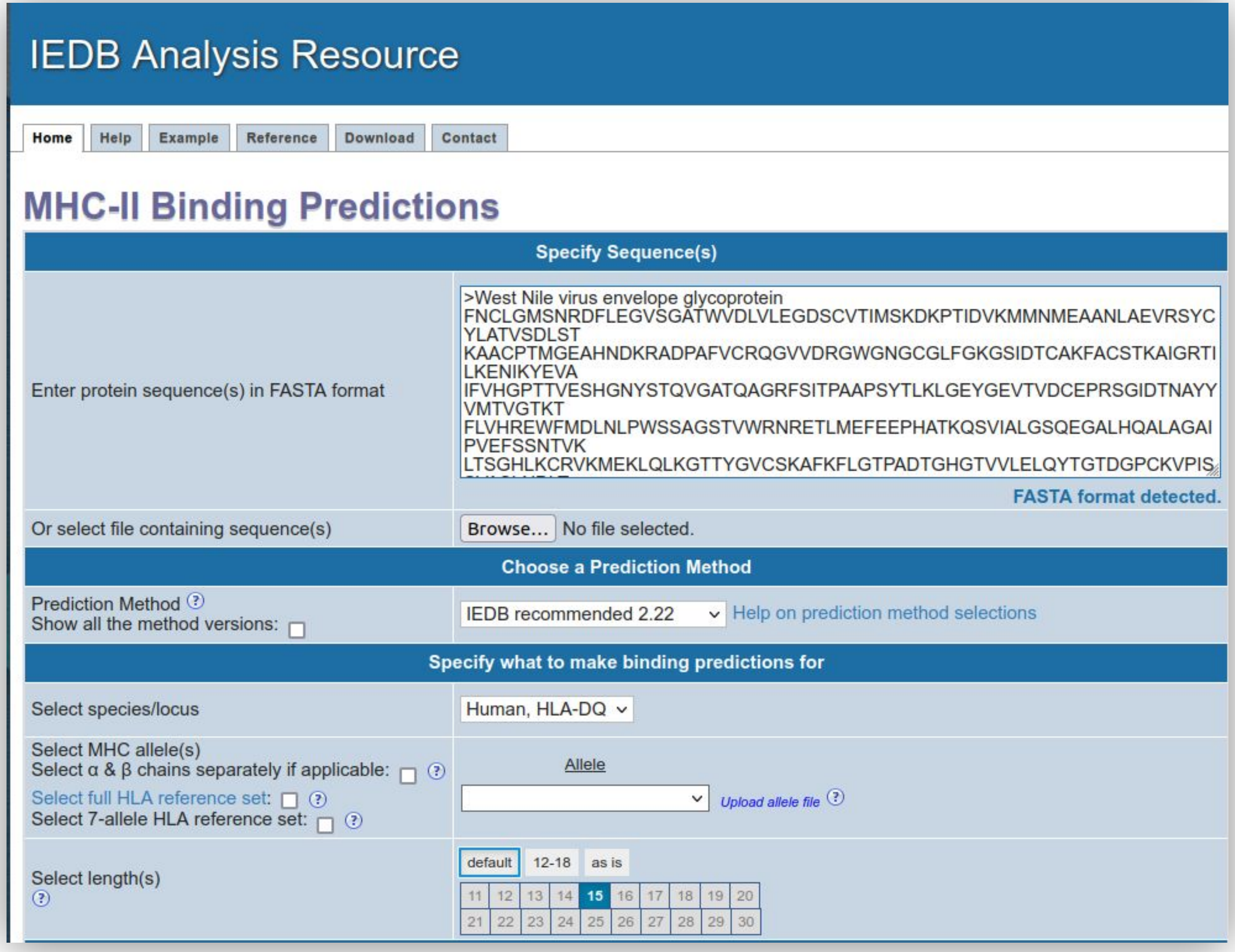
Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

Select length(s)
?

DQA1*01:01/DQB1*02:01
DQA1*01:01/DQB1*02:02
DQA1*01:01/DQB1*02:03
DQA1*01:01/DQB1*02:04
DQA1*01:01/DQB1*02:05
DQA1*01:01/DQB1*02:06
DQA1*01:01/DQB1*03:01
DQA1*01:01/DQB1*03:02
DQA1*01:01/DQB1*03:03
DQA1*01:01/DQB1*03:04
DQA1*01:01/DQB1*03:05
DQA1*01:01/DQB1*03:06
DQA1*01:01/DQB1*03:07
DQA1*01:01/DQB1*03:08
DQA1*01:01/DQB1*03:09
DQA1*01:01/DQB1*03:10
DQA1*01:01/DQB1*03:11
DQA1*01:01/DQB1*03:12
DQA1*01:01/DQB1*03:13

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s): No file selected.

Choose a Prediction Method

Prediction Method ⓘ
Show all the method versions: ☐

IEDB recommended 2.22 — Help on prediction method selections

Specify what to make binding predictions for

Select species/locus: Human, HLA-DQ

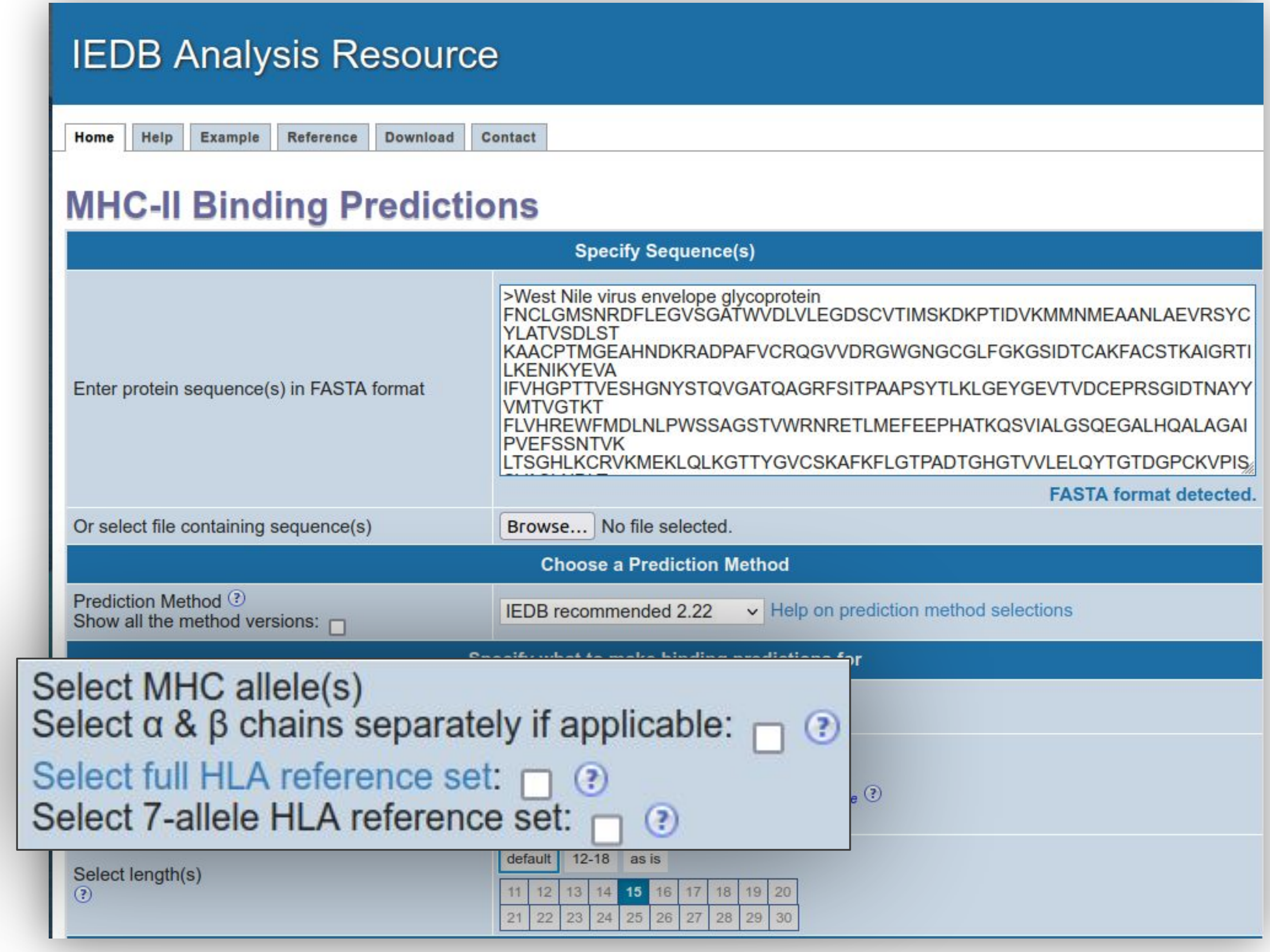
Select MHC allele(s)
Select α & β chains separately if applicable: ☐ ⓘ
Select full HLA reference set: ☐ ⓘ
Select 7-allele HLA reference set: ☐ ⓘ

Allele: — *Upload allele file* ⓘ

Select length(s) ⓘ: 15

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s): Browse... No file selected.

Choose a Prediction Method

Prediction Method ?: IEDB recommended 2.22 — Help on prediction method selections

Show all the method versions: ☐

Specify what to make binding predictions for

Select MHC allele(s)

Select α & β chains separately if applicable: ☐ ?

Select full HLA reference set: ☐ ?

Select 7-allele HLA reference set: ☐ ?

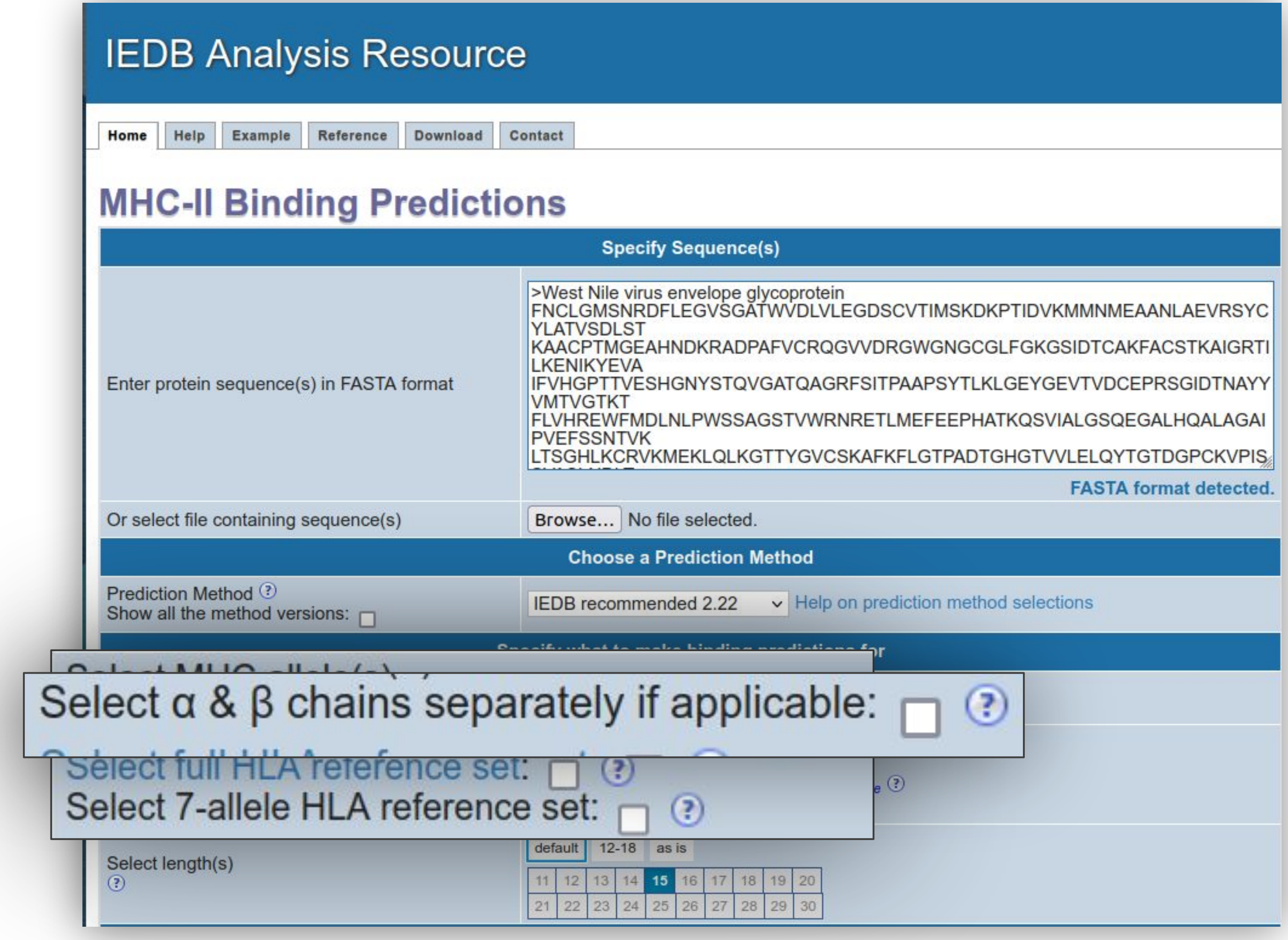
Select length(s) ?

default | 12-18 | as is

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s): Browse... No file selected.

Choose a Prediction Method

Prediction Method ⓘ: IEDB recommended 2.22 — Help on prediction method selections

Show all the method versions: ☐

Select α & β chains separately if applicable: ☐ ⓘ

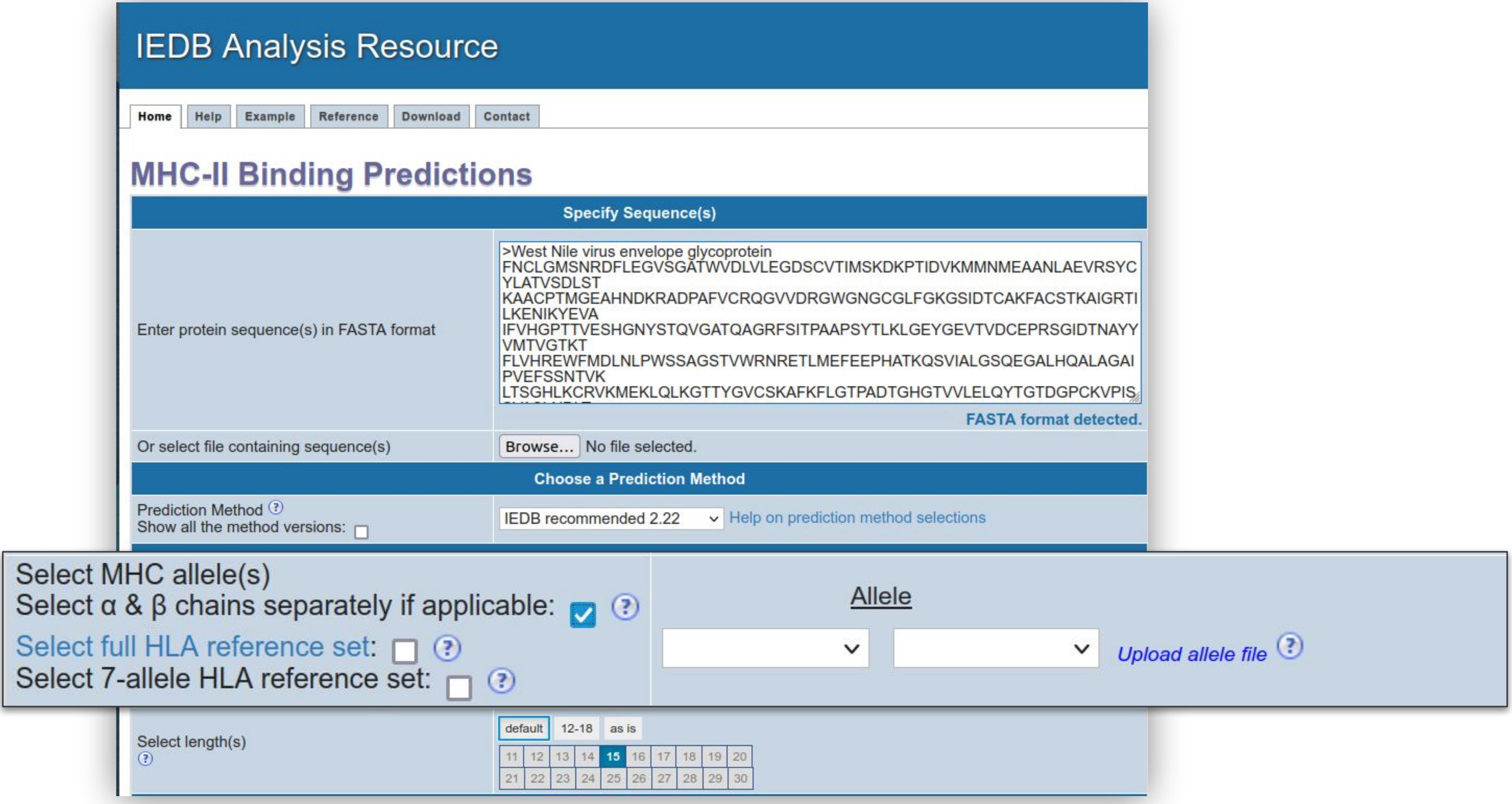
Select full HLA reference set: ☐ ⓘ

Select 7-allele HLA reference set: ☐ ⓘ

Select length(s) ⓘ

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYC
YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s): Browse... No file selected.

Choose a Prediction Method

Prediction Method ?
Show all the method versions: ☐

IEDB recommended 2.22 — Help on prediction method selections

Select MHC allele(s)
Select α & β chains separately if applicable: ☑ ?
Select full HLA reference set: ☐ ?
Select 7-allele HLA reference set: ☐ ?

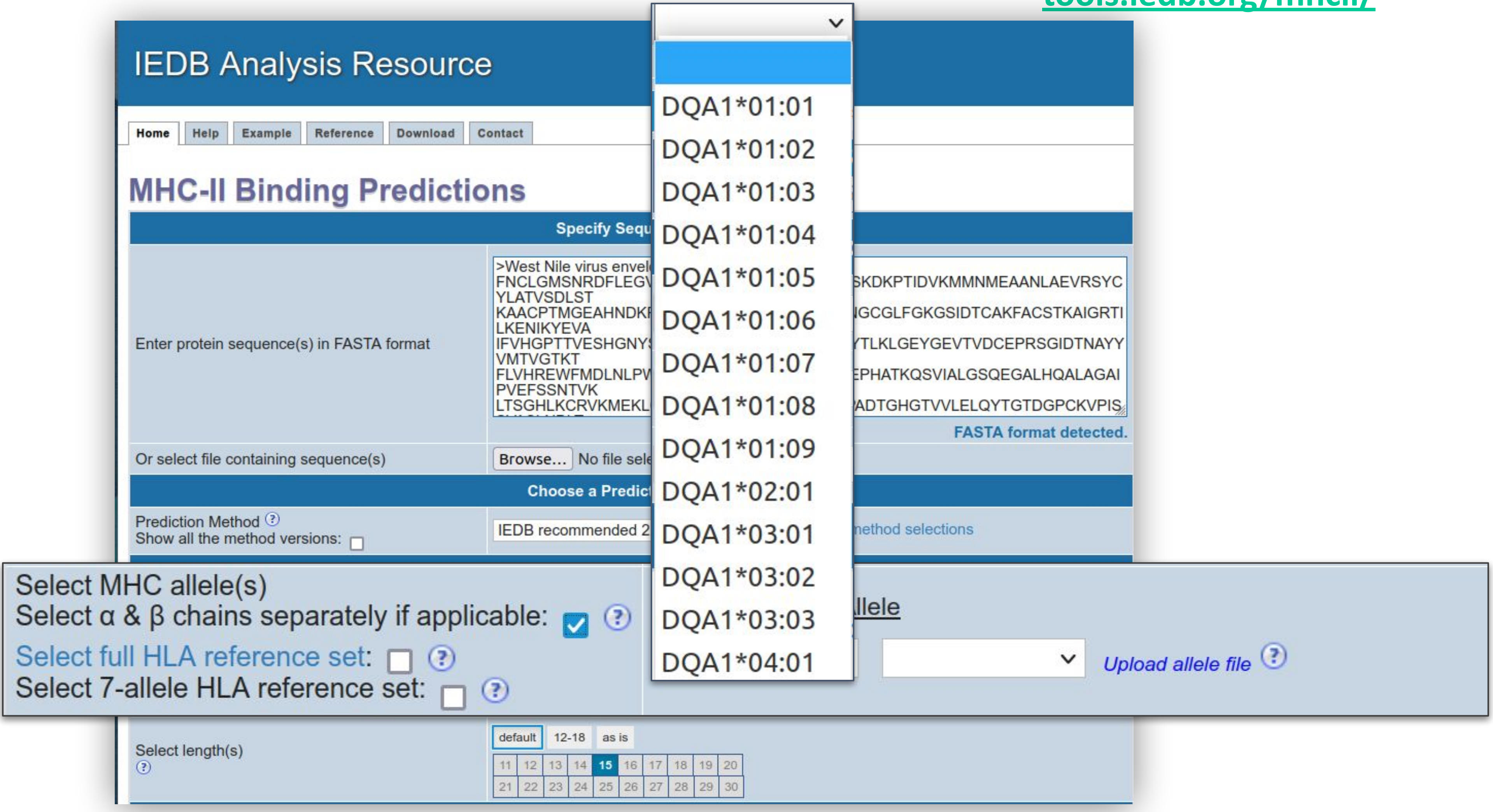
Allele

Upload allele file ?

Select length(s) ?

Allele selection - α and β chains

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequ

Enter protein sequence(s) in FASTA format

```
>West Nile virus envel
FNCLGMSNRDFLEGV                    SKDKPTIDVKMMNMEAANLAEVRSYC
YLATVSDLST
KAACPTMGEAHNDKI                    IGCGLFGKGSIDTCAKFACSTKAIGRTI
LKENIKYEVA
IFVHGPTTVESHGNY                    YTLKLGEYGEVTVDCEPRSGIDTNAYY
VMTVGTKT
FLVHREWFMDLNLPV                    EPHATKQSVIALGSQEGALHQALAGAI
PVEFSSNTVK
LTSGHLKCRVKMEKL                    ADTGHGTVVLELQYTGTDGPCKVPIS
```

FASTA format detected.

Or select file containing sequence(s) No file sele

Choose a Predict

Prediction Method: IEDB recommended 2

Show all the method versions: ☐

method selections

Select MHC allele(s)

Select α & β chains separately if applicable: ☑

Select full HLA reference set: ☐

Select 7-allele HLA reference set: ☐

llele

Select length(s)

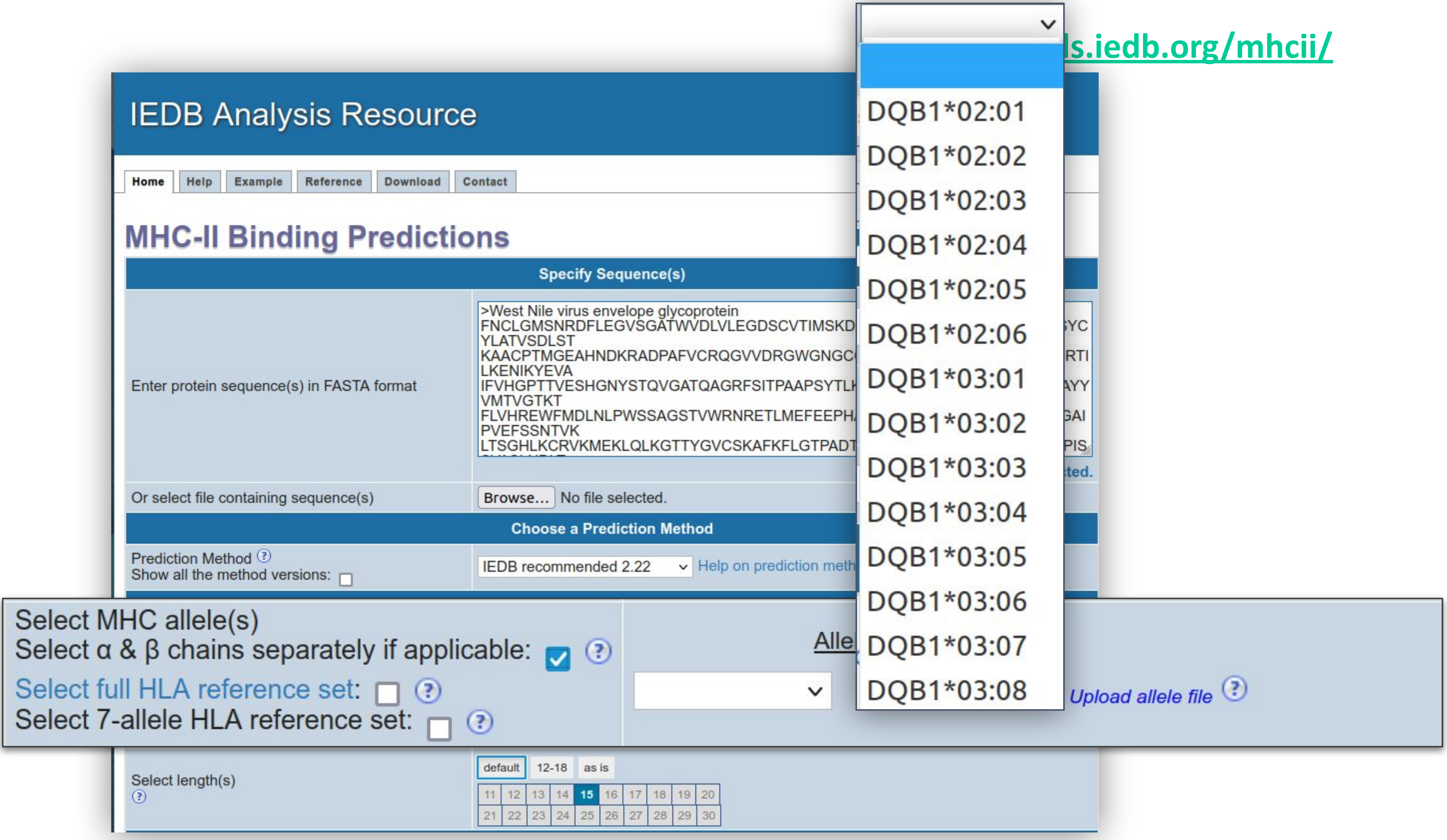
default | 12-18 | as is

11 12 13 14 **15** 16 17 18 19 20

21 22 23 24 25 26 27 28 29 30

Allele selection - α and β chains

ls.iedb.org/mhcii/



IEDB Analysis Resource

MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKD
YLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGC
LKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLK
VMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPH
PVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADT
```

Or select file containing sequence(s): Browse… No file selected.

Choose a Prediction Method

Prediction Method: IEDB recommended 2.22 — Help on prediction meth

Show all the method versions: ☐

Select MHC allele(s)

Select α & β chains separately if applicable: ☑

Select full HLA reference set: ☐

Select 7-allele HLA reference set: ☐

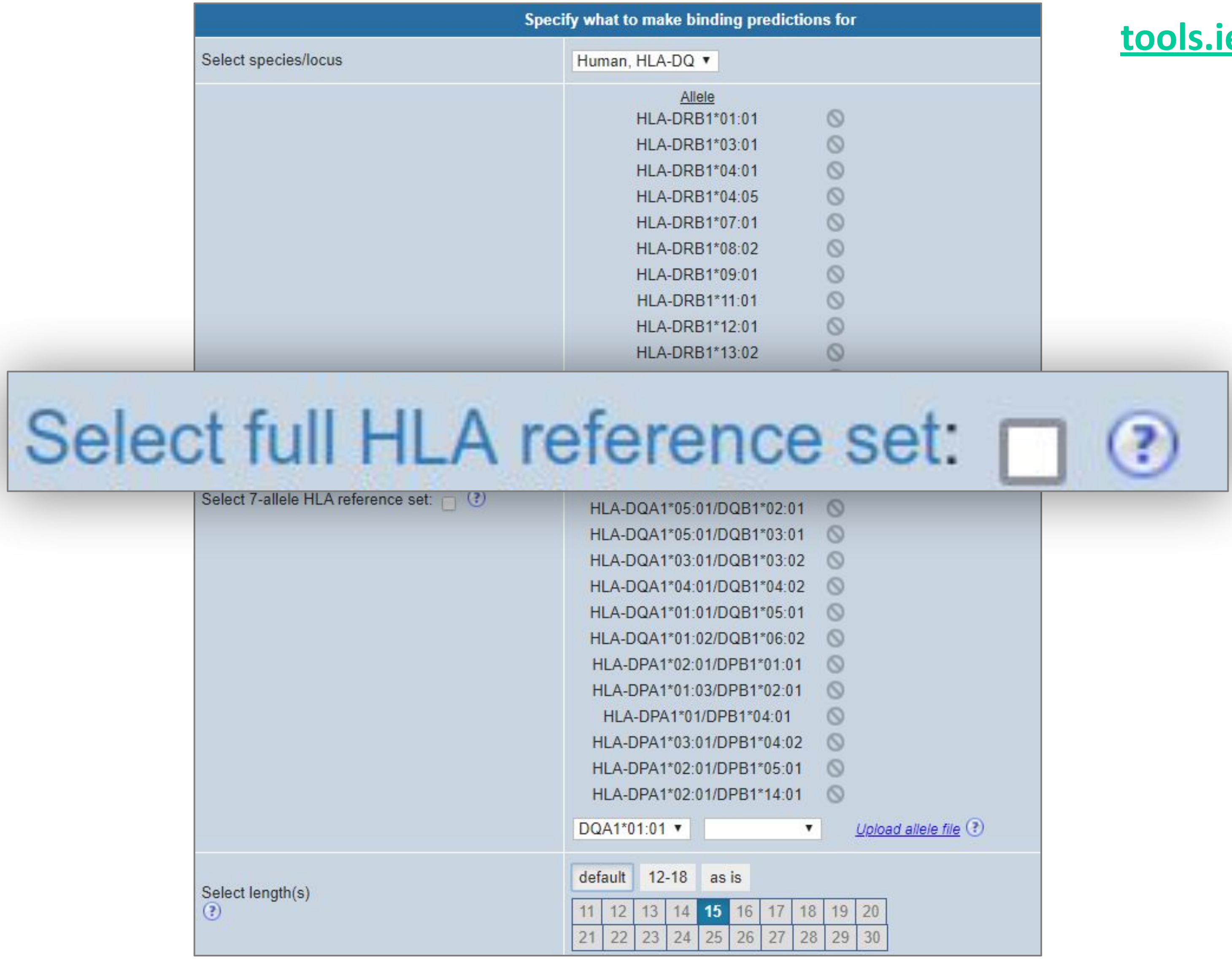
Alle

Upload allele file

Select length(s)

Allele selection – 27 allele reference set

tools.iedb.org/mhcii/



Specify what to make binding predictions for

Select species/locus: Human, HLA-DQ ▾

Select full HLA reference set: ☐ (?)

Select 7-allele HLA reference set: ☐ (?)

Allele

- HLA-DRB1*01:01 ⊘
- HLA-DRB1*03:01 ⊘
- HLA-DRB1*04:01 ⊘
- HLA-DRB1*04:05 ⊘
- HLA-DRB1*07:01 ⊘
- HLA-DRB1*08:02 ⊘
- HLA-DRB1*09:01 ⊘
- HLA-DRB1*11:01 ⊘
- HLA-DRB1*12:01 ⊘
- HLA-DRB1*13:02 ⊘
- HLA-DQA1*05:01/DQB1*02:01 ⊘
- HLA-DQA1*05:01/DQB1*03:01 ⊘
- HLA-DQA1*03:01/DQB1*03:02 ⊘
- HLA-DQA1*04:01/DQB1*04:02 ⊘
- HLA-DQA1*01:01/DQB1*05:01 ⊘
- HLA-DQA1*01:02/DQB1*06:02 ⊘
- HLA-DPA1*02:01/DPB1*01:01 ⊘
- HLA-DPA1*01:03/DPB1*02:01 ⊘
- HLA-DPA1*01/DPB1*04:01 ⊘
- HLA-DPA1*03:01/DPB1*04:02 ⊘
- HLA-DPA1*02:01/DPB1*05:01 ⊘
- HLA-DPA1*02:01/DPB1*14:01 ⊘

DQA1*01:01 ▾ | ▾ | Upload allele file (?)

Select length(s) (?)

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Allele selection – 27 allele reference set

tools.iedb.org/mhcii/

Specify what to make binding predictions for

Select species/locus: Human, HLA-DQ

Select MHC allele(s)
Select α & β chains separately if applicable: ☑
Select full HLA reference set: ☑
Select 7-allele HLA reference set: ☐

Allele
HLA-DRB1*01:01
HLA-DRB1*03:01
HLA-DRB1*04:01
HLA-DRB1*04:05
HLA-DRB1*07:01
HLA-DRB1*08:02
HLA-DRB1*09:01
HLA-DRB1*11:01
HLA-DRB1*12:01
HLA-DRB1*13:02
HLA-DRB1*15:01
HLA-DRB3*01:01
HLA-DRB3*02:02
HLA-DRB4*01:01
HLA-DRB5*01:01
HLA-DQA1*05:01/DQB1*02:01
HLA-DQA1*05:01/DQB1*03:01
HLA-DQA1*03:01/DQB1*03:02
HLA-DQA1*04:01/DQB1*04:02
HLA-DQA1*01:01/DQB1*05:01
HLA-DQA1*01:02/DQB1*06:02
HLA-DPA1*02:01/DPB1*01:01
HLA-DPA1*01:03/DPB1*02:01
HLA-DPA1*01/DPB1*04:01
HLA-DPA1*03:01/DPB1*04:02
HLA-DPA1*02:01/DPB1*05:01
HLA-DPA1*02:01/DPB1*14:01

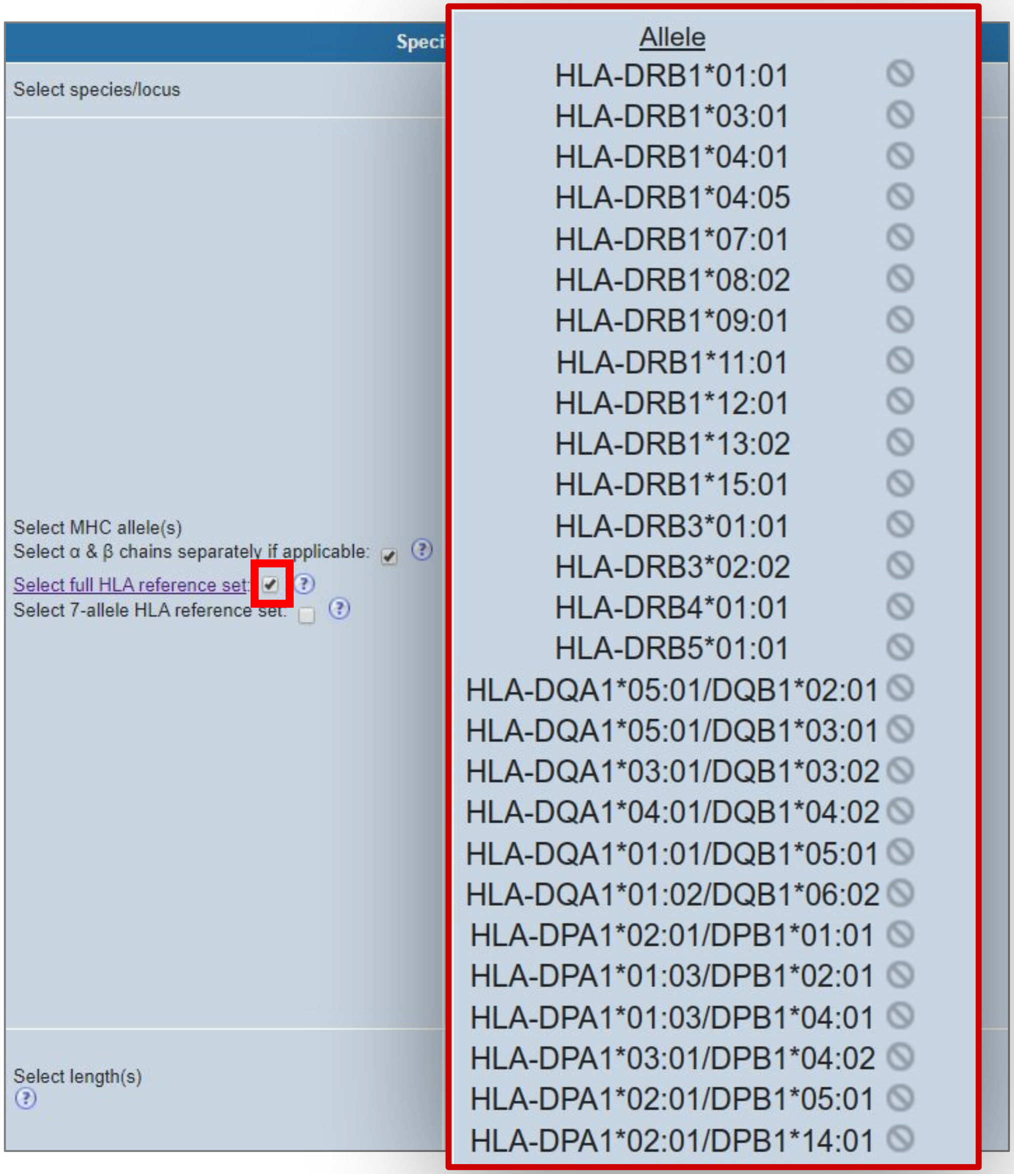
DQA1*01:01

Upload allele file

Select length(s): 15

Allele selection – 27 allele reference set

tools.iedb.org/mhcii/



Speci

Select species/locus

Select MHC allele(s)

Select α & β chains separately if applicable: ☑

Select full HLA reference set: ☑

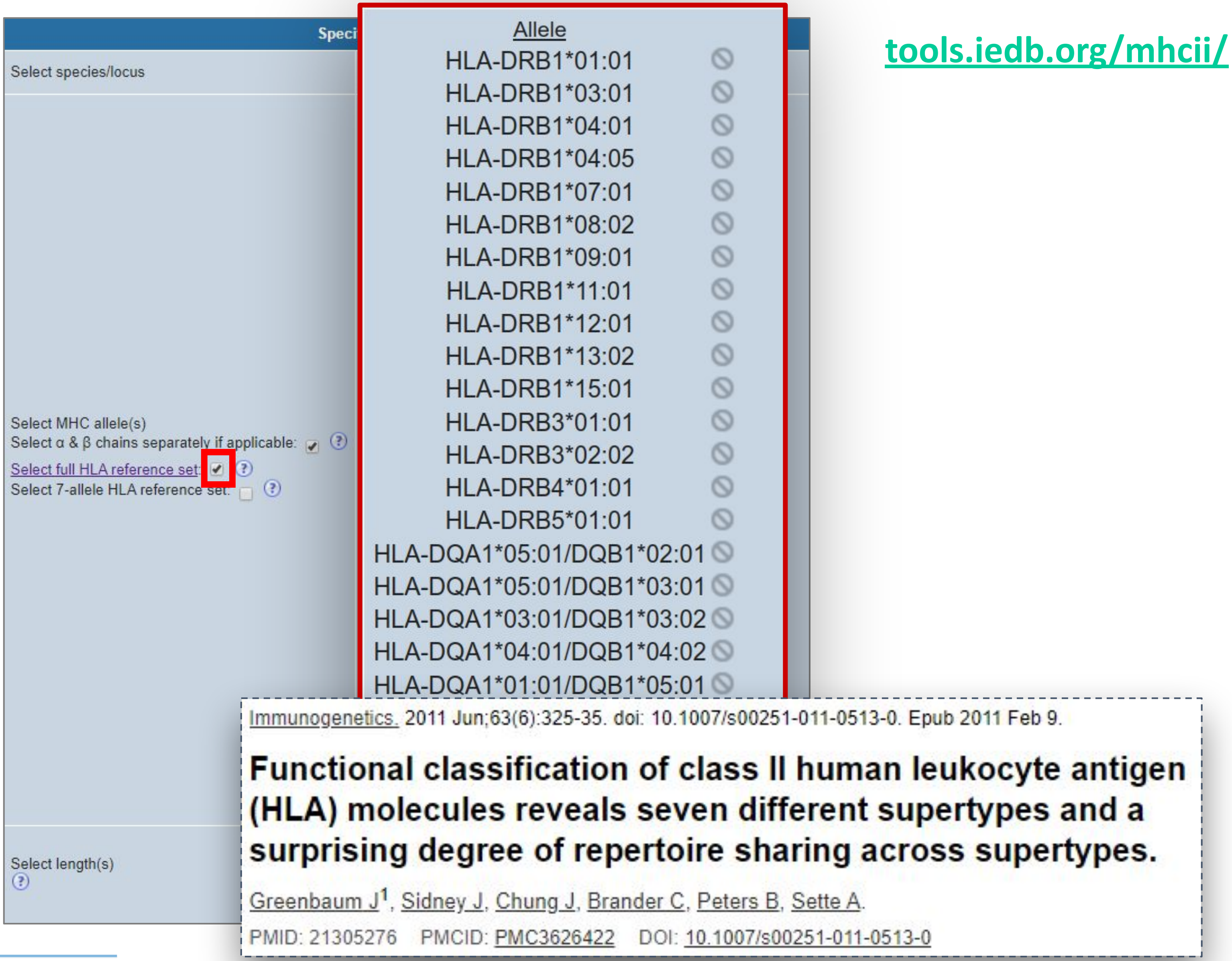
Select 7-allele HLA reference set: ☐

Select length(s)

Allele
HLA-DRB1*01:01
HLA-DRB1*03:01
HLA-DRB1*04:01
HLA-DRB1*04:05
HLA-DRB1*07:01
HLA-DRB1*08:02
HLA-DRB1*09:01
HLA-DRB1*11:01
HLA-DRB1*12:01
HLA-DRB1*13:02
HLA-DRB1*15:01
HLA-DRB3*01:01
HLA-DRB3*02:02
HLA-DRB4*01:01
HLA-DRB5*01:01
HLA-DQA1*05:01/DQB1*02:01
HLA-DQA1*05:01/DQB1*03:01
HLA-DQA1*03:01/DQB1*03:02
HLA-DQA1*04:01/DQB1*04:02
HLA-DQA1*01:01/DQB1*05:01
HLA-DQA1*01:02/DQB1*06:02
HLA-DPA1*02:01/DPB1*01:01
HLA-DPA1*01:03/DPB1*02:01
HLA-DPA1*01:03/DPB1*04:01
HLA-DPA1*03:01/DPB1*04:02
HLA-DPA1*02:01/DPB1*05:01
HLA-DPA1*02:01/DPB1*14:01

Allele selection – 27 allele reference set

tools.iedb.org/mhcii/



Select species/locus

Select MHC allele(s)

Select α & β chains separately if applicable: ☑

Select full HLA reference set: ☑

Select 7-allele HLA reference set: ☐

Select length(s)

Allele
HLA-DRB1*01:01
HLA-DRB1*03:01
HLA-DRB1*04:01
HLA-DRB1*04:05
HLA-DRB1*07:01
HLA-DRB1*08:02
HLA-DRB1*09:01
HLA-DRB1*11:01
HLA-DRB1*12:01
HLA-DRB1*13:02
HLA-DRB1*15:01
HLA-DRB3*01:01
HLA-DRB3*02:02
HLA-DRB4*01:01
HLA-DRB5*01:01
HLA-DQA1*05:01/DQB1*02:01
HLA-DQA1*05:01/DQB1*03:01
HLA-DQA1*03:01/DQB1*03:02
HLA-DQA1*04:01/DQB1*04:02
HLA-DQA1*01:01/DQB1*05:01

Immunogenetics. 2011 Jun;63(6):325-35. doi: 10.1007/s00251-011-0513-0. Epub 2011 Feb 9.

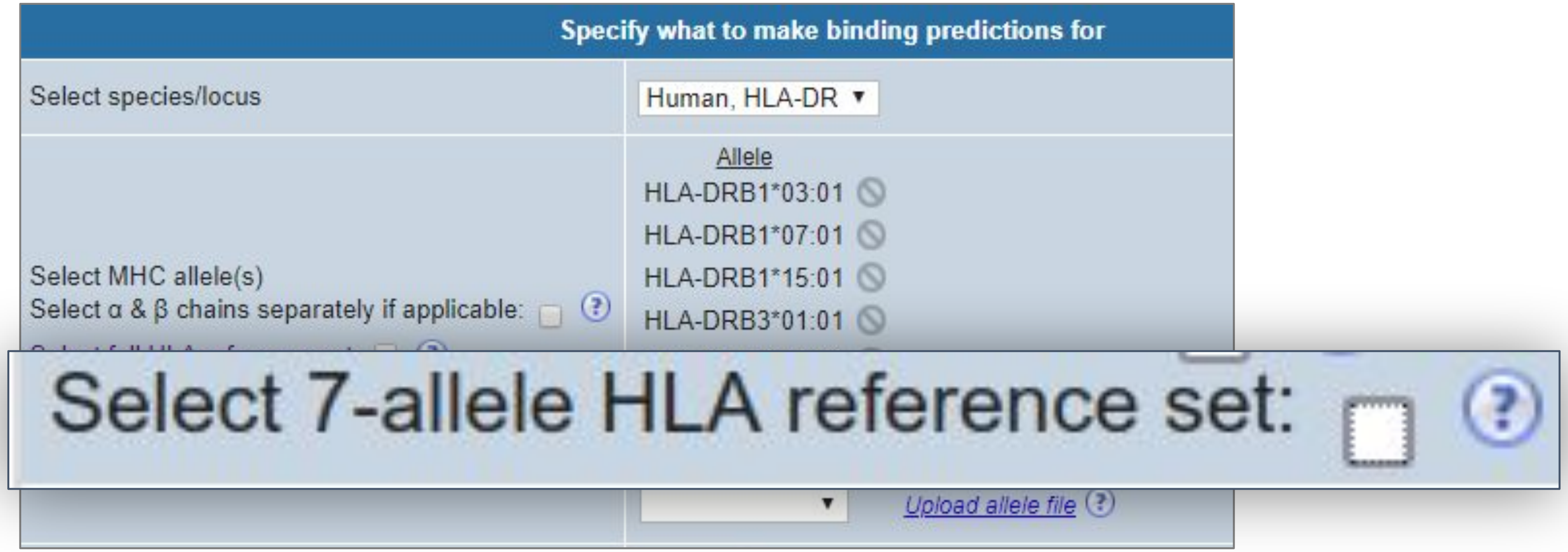
Functional classification of class II human leukocyte antigen (HLA) molecules reveals seven different supertypes and a surprising degree of repertoire sharing across supertypes.

Greenbaum J[1], Sidney J, Chung J, Brander C, Peters B, Sette A.

PMID: 21305276 PMCID: PMC3626422 DOI: 10.1007/s00251-011-0513-0

Allele selection – 7 allele set

tools.iedb.org/mhcii/



Specify what to make binding predictions for

Select species/locus: Human, HLA-DR

Select MHC allele(s)

Select α & β chains separately if applicable: ☐

Allele
HLA-DRB1*03:01
HLA-DRB1*07:01
HLA-DRB1*15:01
HLA-DRB3*01:01

Select 7-allele HLA reference set: ☐

J Immunol Methods. 2015 Jul;422:28-34. doi: 10.1016/j.jim.2015.03.022. Epub 2015 Apr 7.

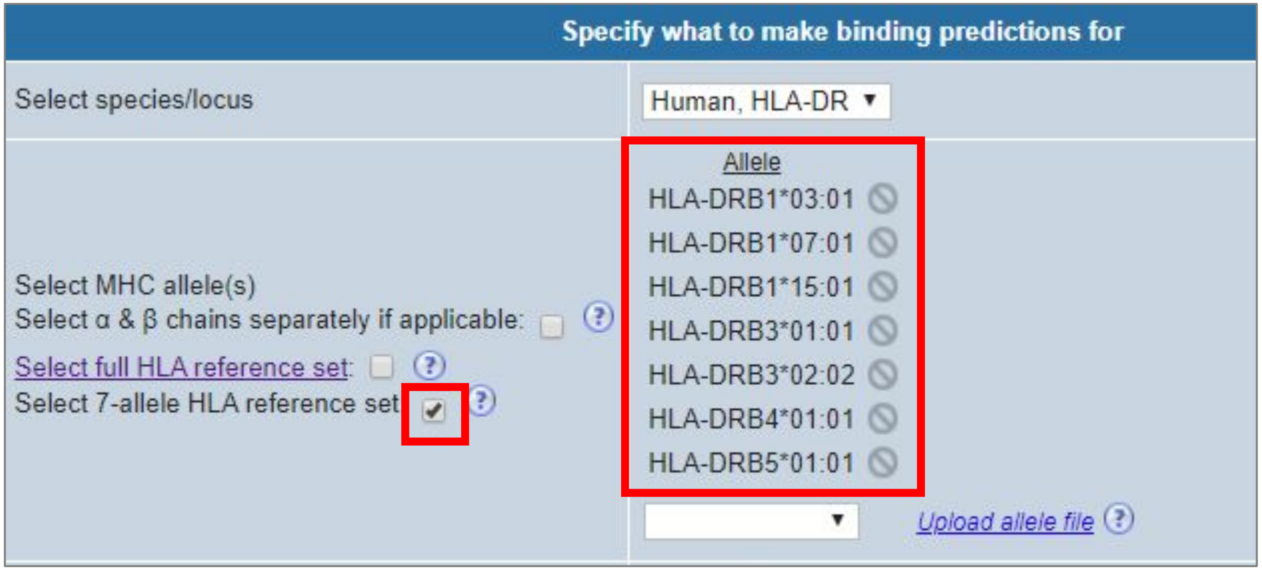
Development and validation of a broad scheme for prediction of HLA class II restricted T cell epitopes.

Paul S[1], Lindestam Arlehamn CS[2], Scriba TJ[3], Dillon MB[2], Oseroff C[2], Hinz D[2], McKinney DM[2], Carrasco Pro S[4], Sidney J[2], Peters B[2], Sette A[2].

PMID: 25862607 PMCID: PMC4458426 DOI: 10.1016/j.jim.2015.03.022

Allele selection – 7 allele set

tools.iedb.org/mhcii/



Specify what to make binding predictions for

Select species/locus: Human, HLA-DR

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set ☑

Allele
HLA-DRB1*03:01
HLA-DRB1*07:01
HLA-DRB1*15:01
HLA-DRB3*01:01
HLA-DRB3*02:02
HLA-DRB4*01:01
HLA-DRB5*01:01

J Immunol Methods. 2015 Jul;422:28-34. doi: 10.1016/j.jim.2015.03.022. Epub 2015 Apr 7.

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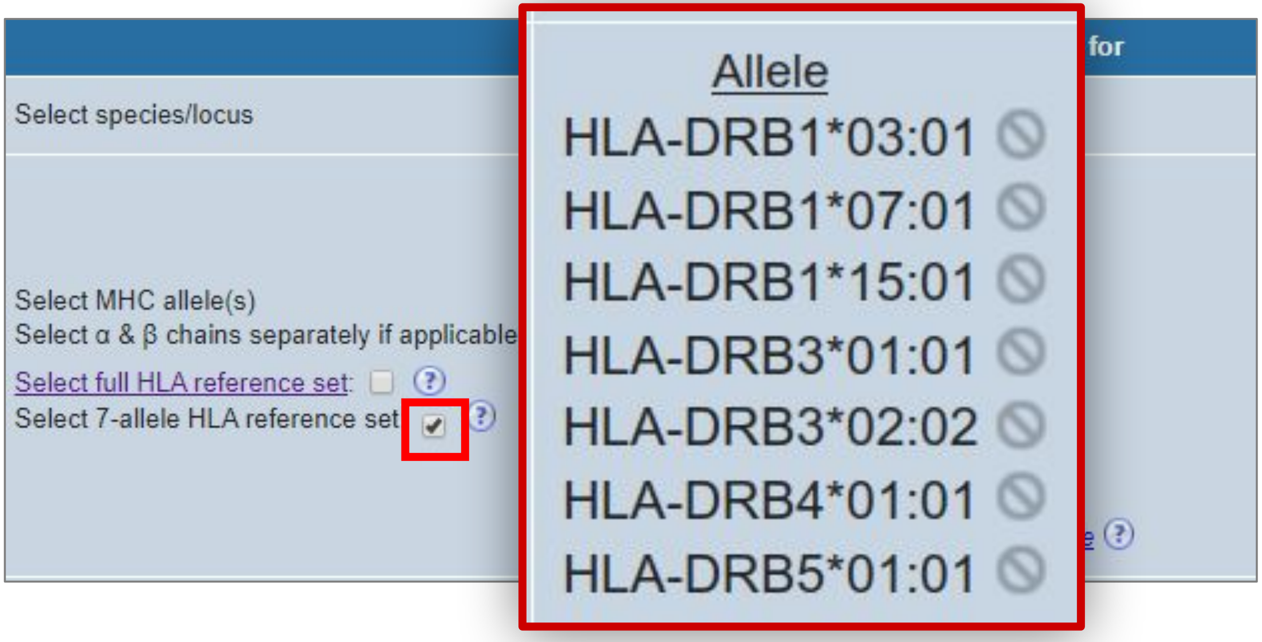
PMID: 25862607 PMCID: PMC4458426 DOI: 10.1016/j.jim.2015.03.022

Allele selection – 7 allele set

tools.iedb.org/mhcii/



Select species/locus

Select MHC allele(s)
Select α & β chains separately if applicable

Select full HLA reference set: ☐

Select 7-allele HLA reference set ☑

Allele
- HLA-DRB1*03:01
- HLA-DRB1*07:01
- HLA-DRB1*15:01
- HLA-DRB3*01:01
- HLA-DRB3*02:02
- HLA-DRB4*01:01
- HLA-DRB5*01:01

J Immunol Methods. 2015 Jul;422:28-34. doi: 10.1016/j.jim.2015.03.022. Epub 2015 Apr 7.

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PMID: 25862607 PMCID: PMC4458426 DOI: 10.1016/j.jim.2015.03.022

“7-allele” method

- Aim was to capture maximum immune response with minimum no. of peptides
- 6 peptide datasets with measured immune responses (SFCs/106 PBMCs)
- 15 or 16-mer peptide sets with 10 AA residues overlapping

Dataset	Purpose	No. of Antigens	Total peptides	No. of donors	Reference
Der p/f (House dust mite)	Training data	4	156	20	Hinz et al., 2015, CEA
Phl p (Timothy grass)	Training data	10	425	25	Oseroff et al., 2010, JI
TB-1	Training data	4	71	18	Arlehamn et al., 2012, JI
TB-2	Training data	11	499	32	Arlehamn et al., 2016, PLoS Path
Cockroach	Validation data	6	463	19	Dillon et al., 2015, CEA
Pertussis	Validation data	9	785	23	Bancroft et al., 2016, CEA
TOTAL		44	2399	137	

“7-allele” method

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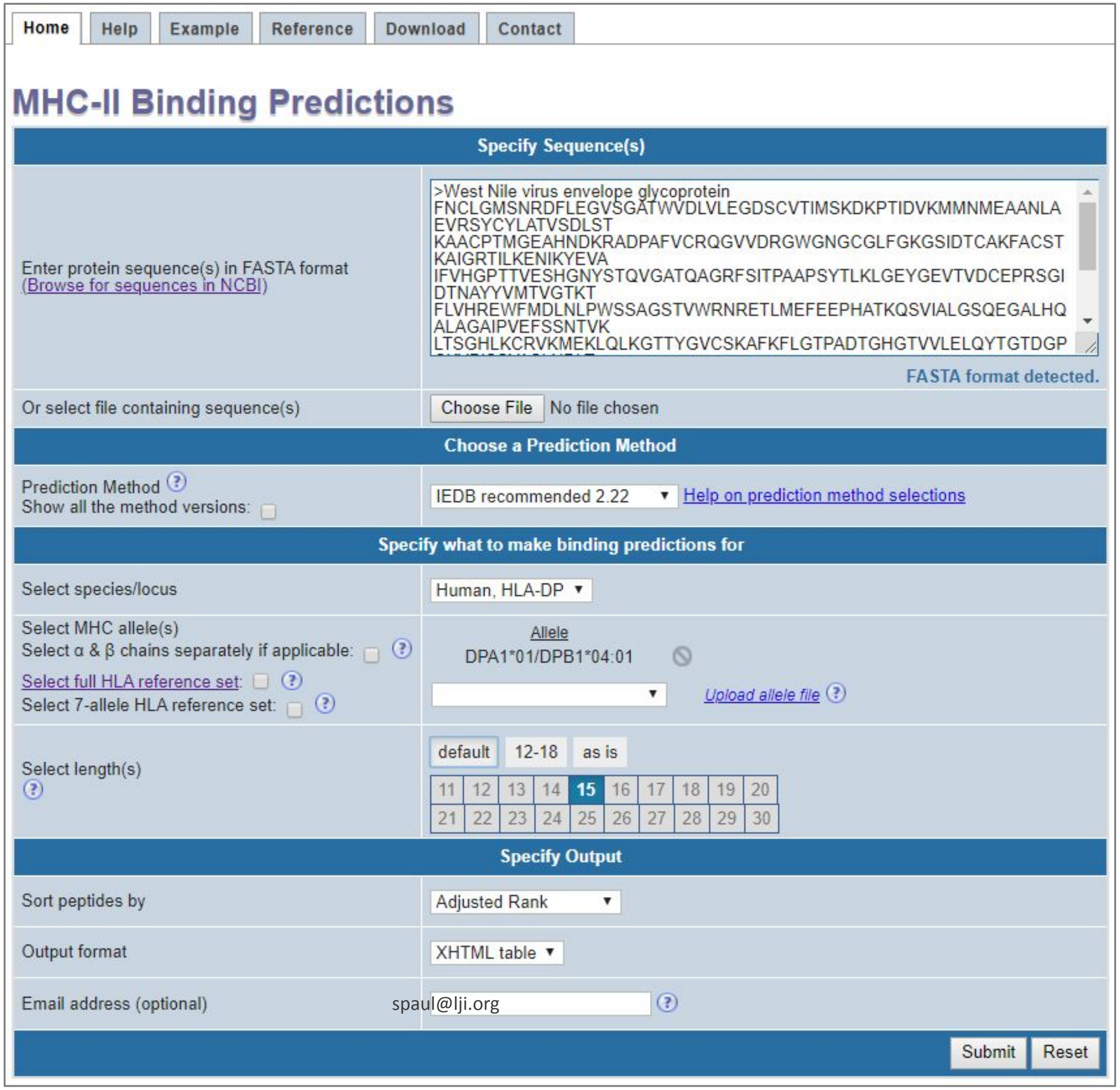
PMID: 25862607 PMCID: PMC4458426 DOI: 10.1016/j.jim.2015.03.022

Cockroach	Validation data	6	463	19	Dillon et al., 2015, CEA
Pertussis	Validation data	9	785	23	Bancroft et al., 2016, CEA
TOTAL		44	2399	137	

MHC-II binding prediction – example

tools.iedb.org/mhcii/



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format (Browse for sequences in NCBI)

```
>West Nile virus envelope glycoprotein
FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLA
EVRSYCYLATVSDLST
KAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACST
KAIGRTILKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGI
DTNAYYVMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQ
ALAGAIPVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGP
```

FASTA format detected.

Or select file containing sequence(s): Choose File No file chosen

Choose a Prediction Method

Prediction Method: IEDB recommended 2.22 ▾ Help on prediction method selections

Show all the method versions: ☐

Specify what to make binding predictions for

Select species/locus: Human, HLA-DP ▾

Select MHC allele(s): Allele DPA1*01/DPB1*04:01

Select α & β chains separately if applicable: ☐

Select full HLA reference set: ☐

Select 7-allele HLA reference set: ☐

Upload allele file

Select length(s): default 12-18 as is

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Specify Output

Sort peptides by: Adjusted Rank ▾

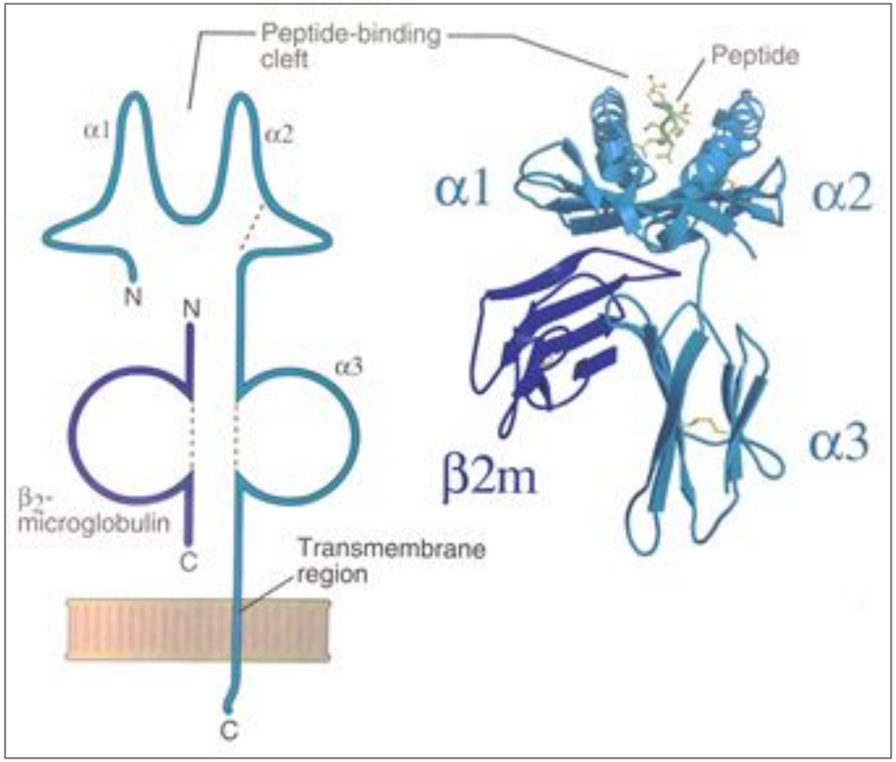
Output format: XHTML table ▾

Email address (optional): spaul@lji.org

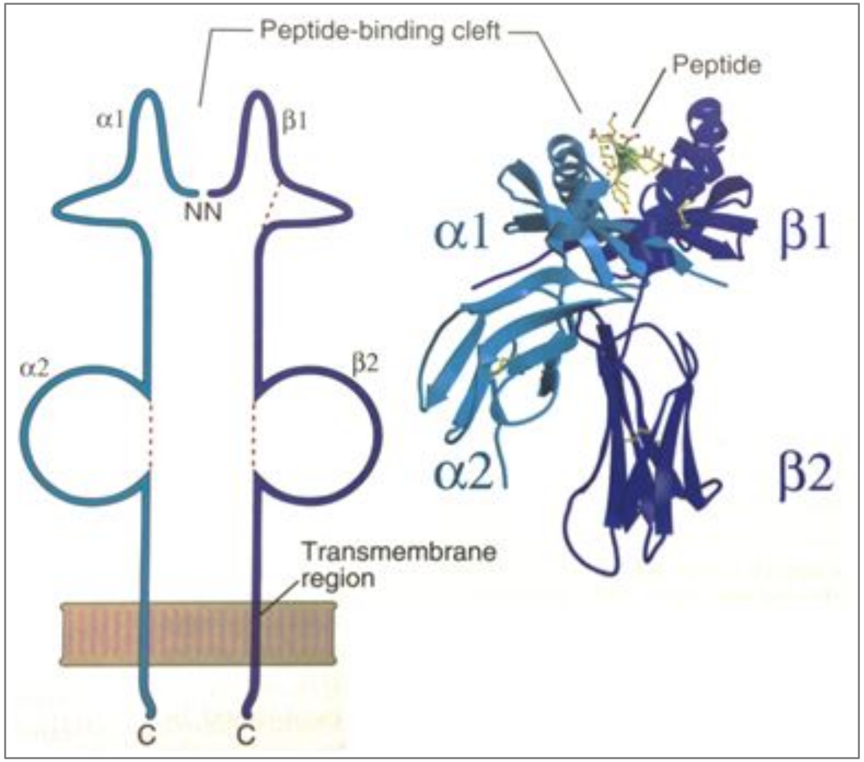
Submit Reset

Length selection

Differences between MHC-I and MHC-II

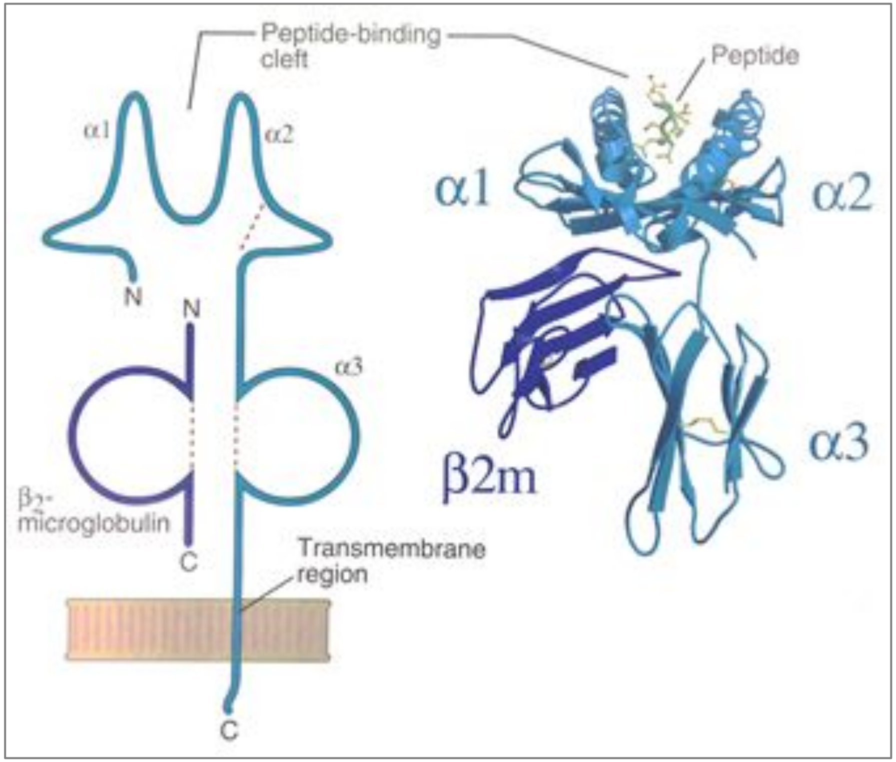


MHC-I

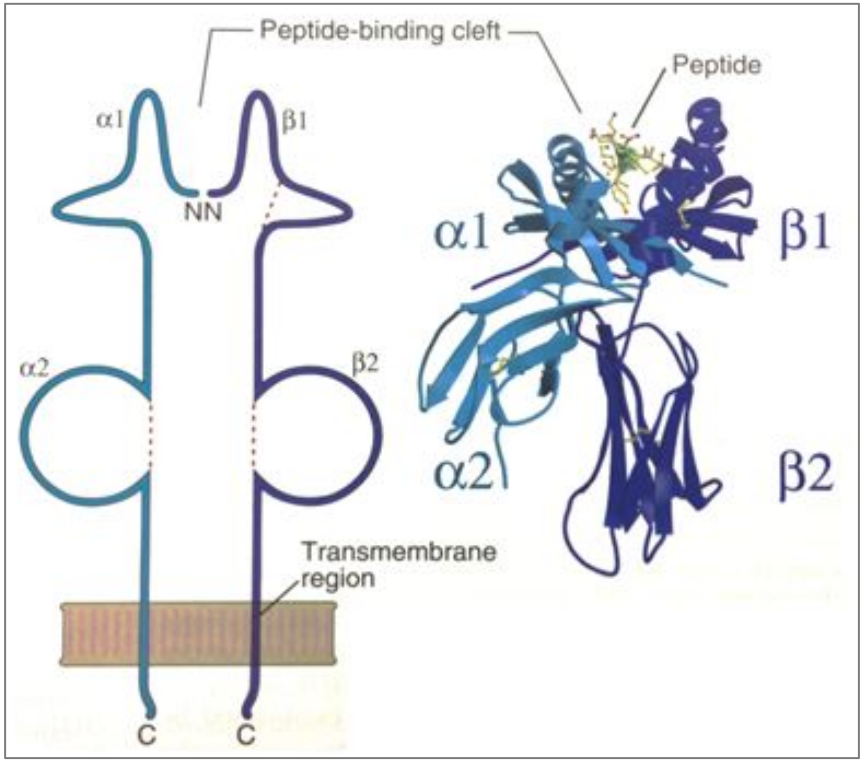


MHC-II

Differences between MHC-I and MHC-II

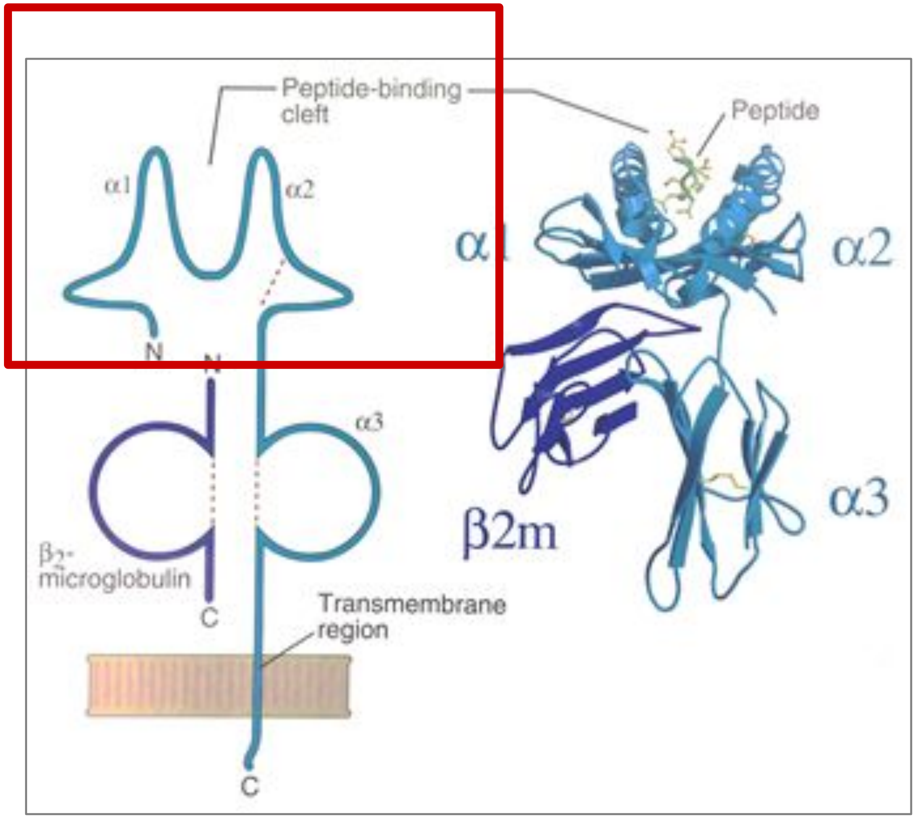


MHC-I

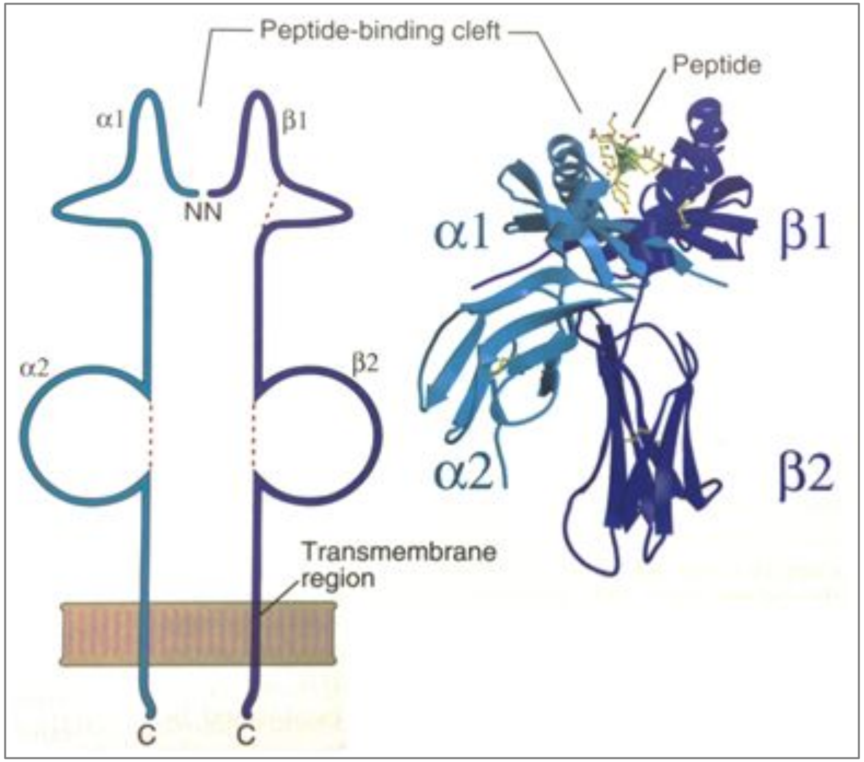


MHC-II

Differences between MHC-I and MHC-II

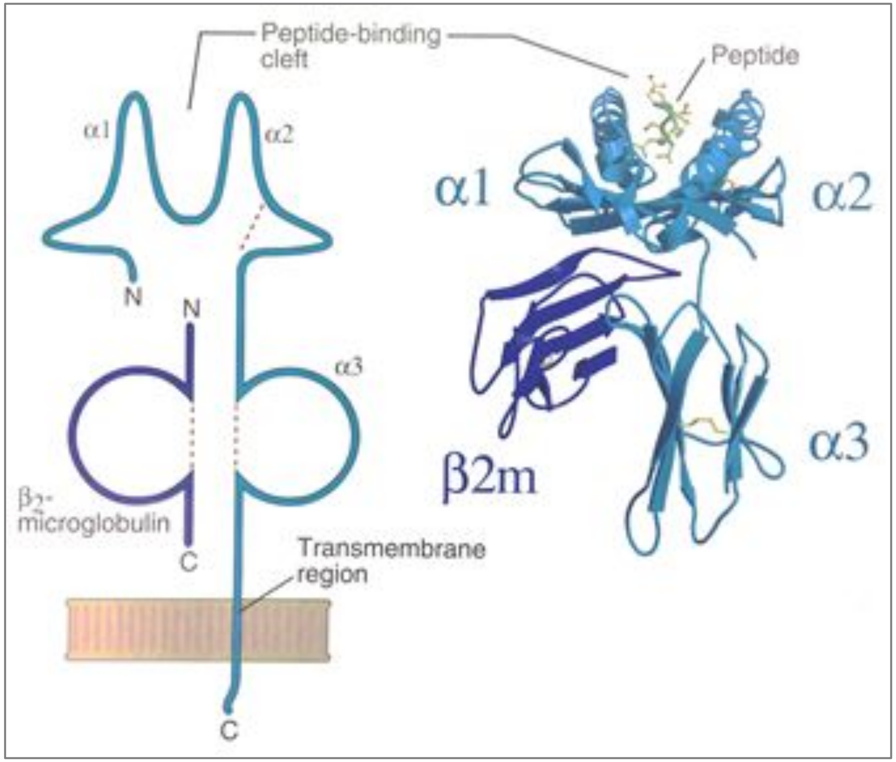


MHC-I

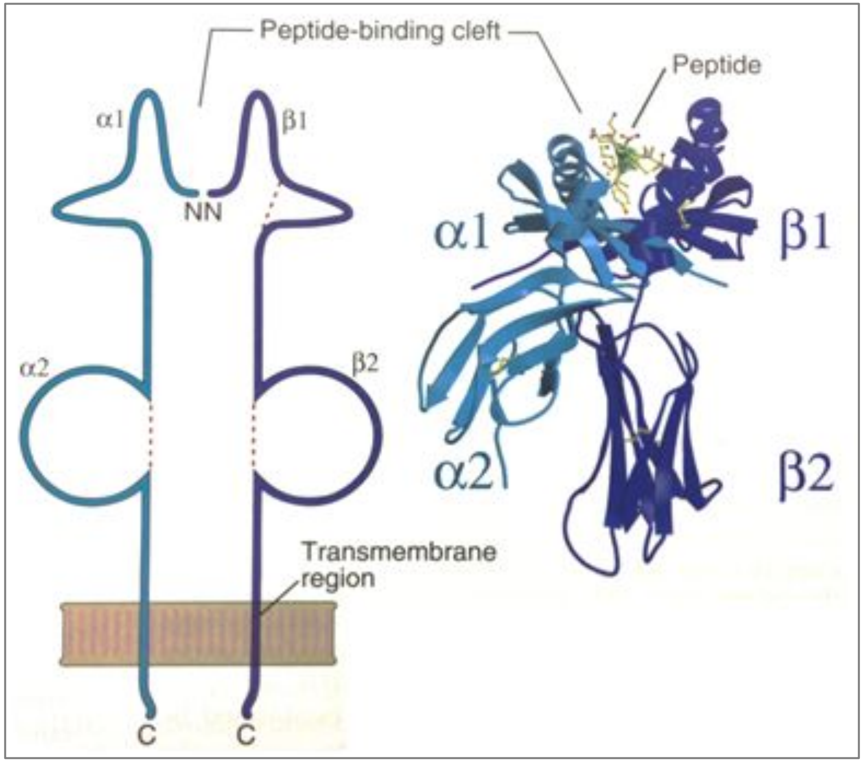


MHC-II

Differences between MHC-I and MHC-II

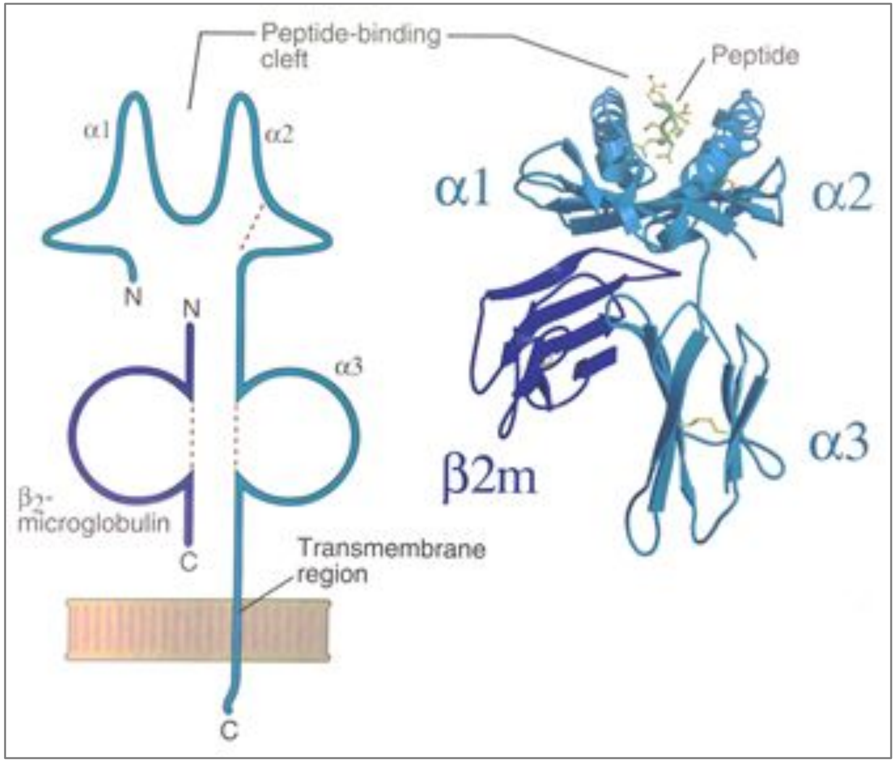


MHC-I



MHC-II

Differences between MHC-I and MHC-II



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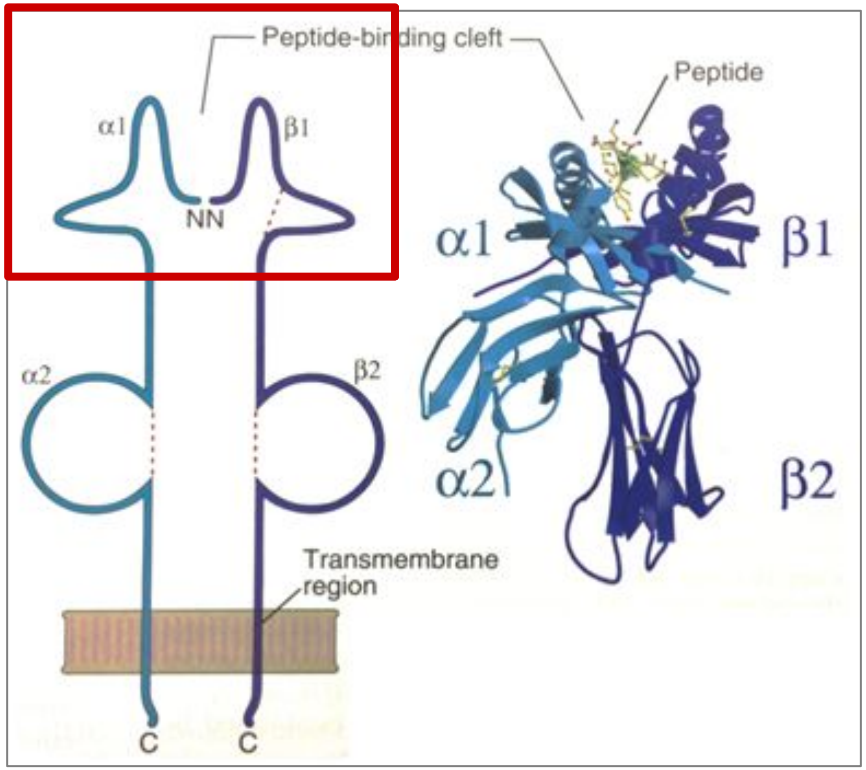
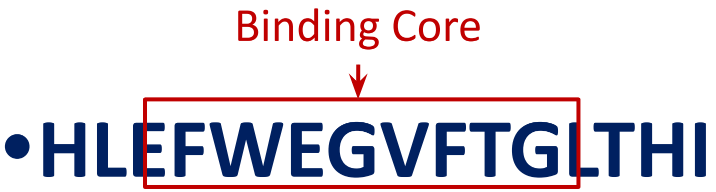


MHC-II

Class II binding peptide “Binding core”

- 9 AA core within the peptide that interacts with the binding groove of MHC molecule



- **HLEFWEGVFTGLTHI**

- Challenge: Correct identification of the binding core
- Needs proper alignment of the binding core with the binding groove

“Peptide flanking residues” (PFR)

- Residues flanking the binding core - interacts with MHC molecule outside the groove.

Binding Core

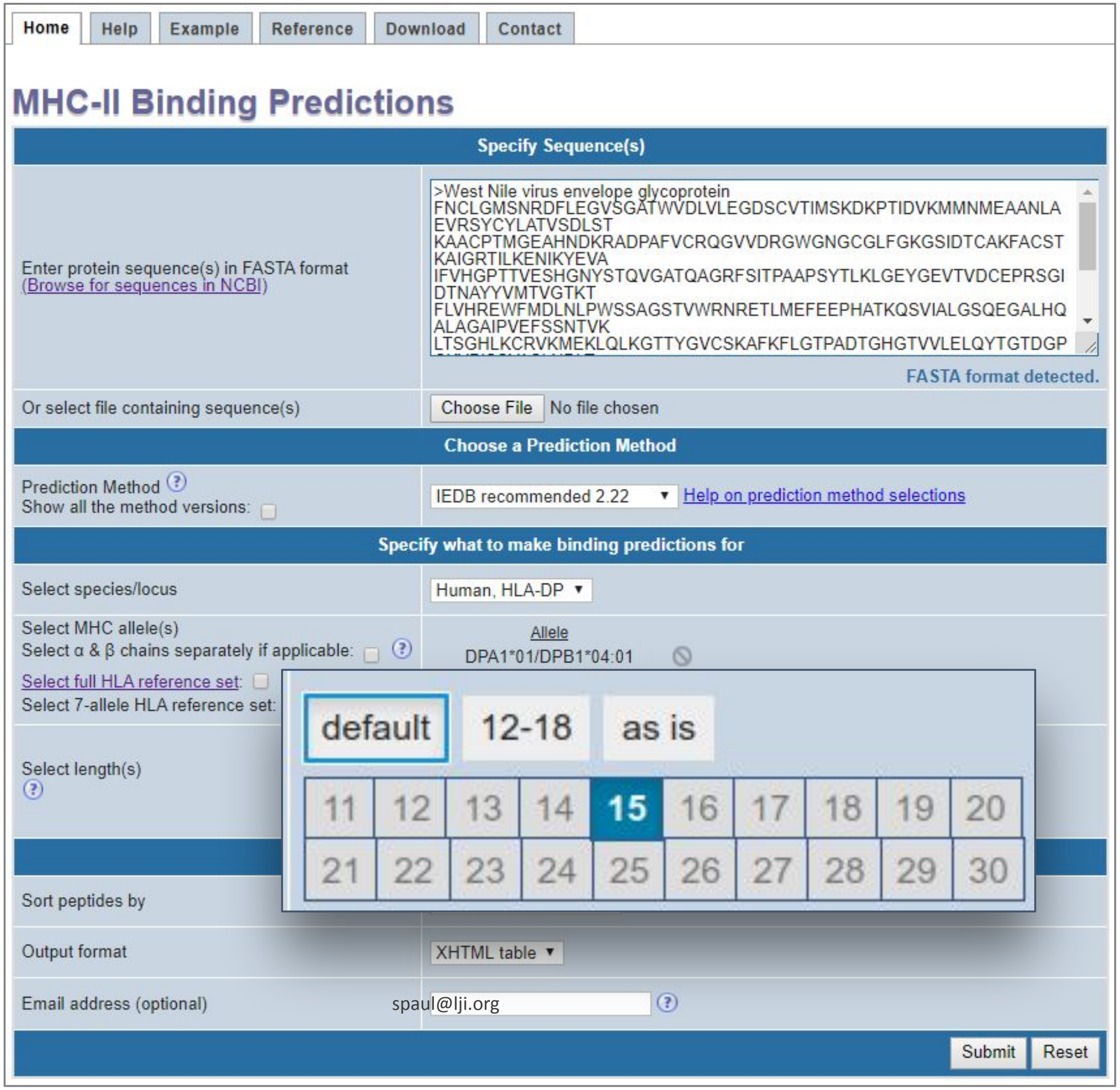
- HLEFWEGVFTGLTHI

Peptide flanking residues

- Challenge: PFR length & composition influence binding.

MHC-II binding prediction – example

tools.iedb.org/mhcii/



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KAIGRTILKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGI
DTNAYYVMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQ
ALAGAIPVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGP
```

FASTA format detected.

Or select file containing sequence(s): Choose File No file chosen

Choose a Prediction Method

Prediction Method ⓘ: IEDB recommended 2.22 ▾ Help on prediction method selections
Show all the method versions: ☐

Specify what to make binding predictions for

Select species/locus: Human, HLA-DP ▾

Select MHC allele(s)
Select α & β chains separately if applicable: ☐ ⓘ
Allele: DPA1*01/DPB1*04:01

Select full HLA reference set: ☐
Select 7-allele HLA reference set:

Select length(s) ⓘ

Sort peptides by

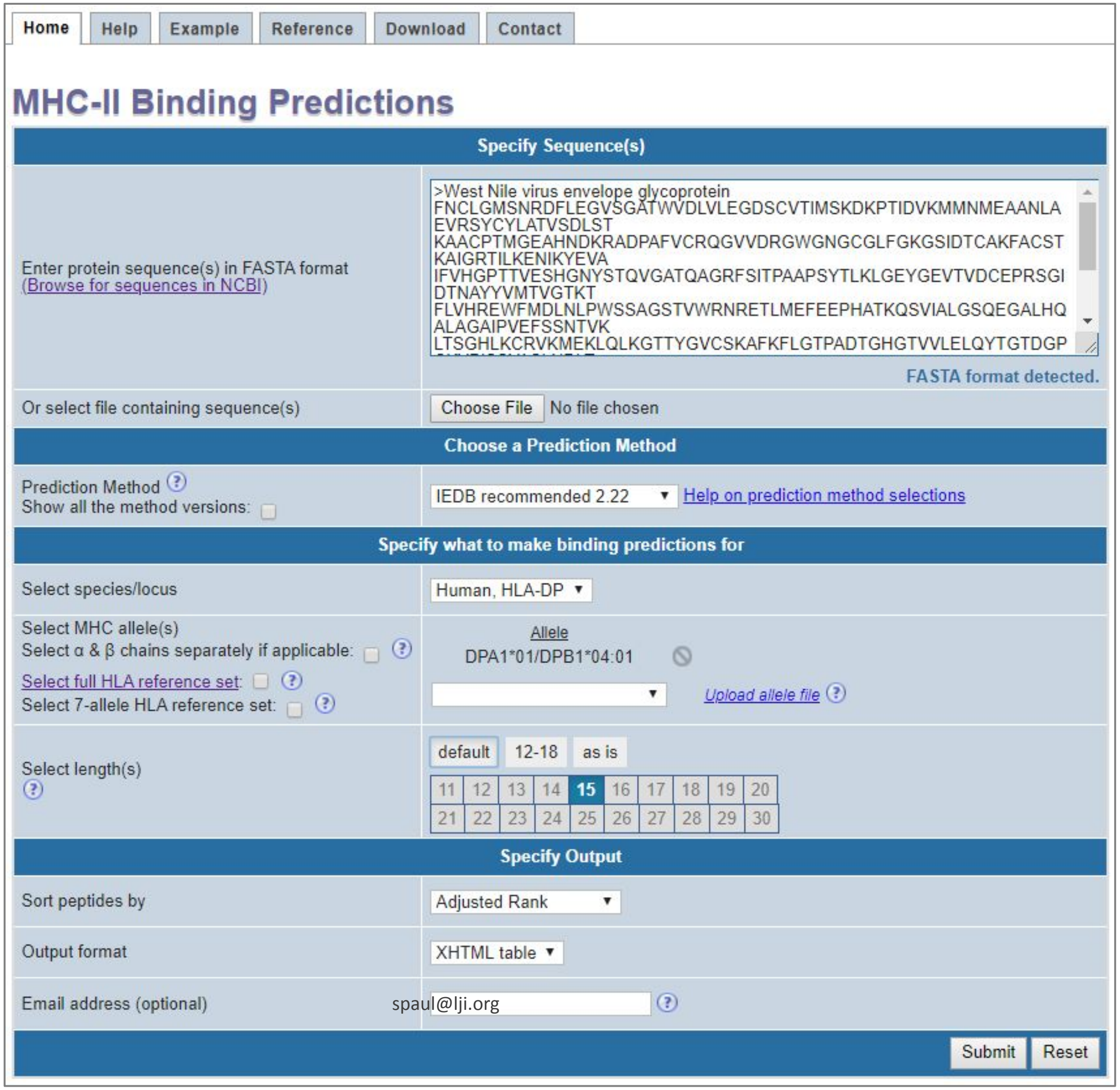
Output format: XHTML table ▾

Email address (optional): spaul@lji.org ⓘ

Length selection

MHC-II binding prediction – example

tools.iedb.org/mhcii/



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DTNAYYVMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQ
ALAGAIPVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGP
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Select α & β chains separately if applicable: ☐

Select full HLA reference set: ☐

Select 7-allele HLA reference set: ☐

Select length(s): default | 12-18 | as is

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Specify Output

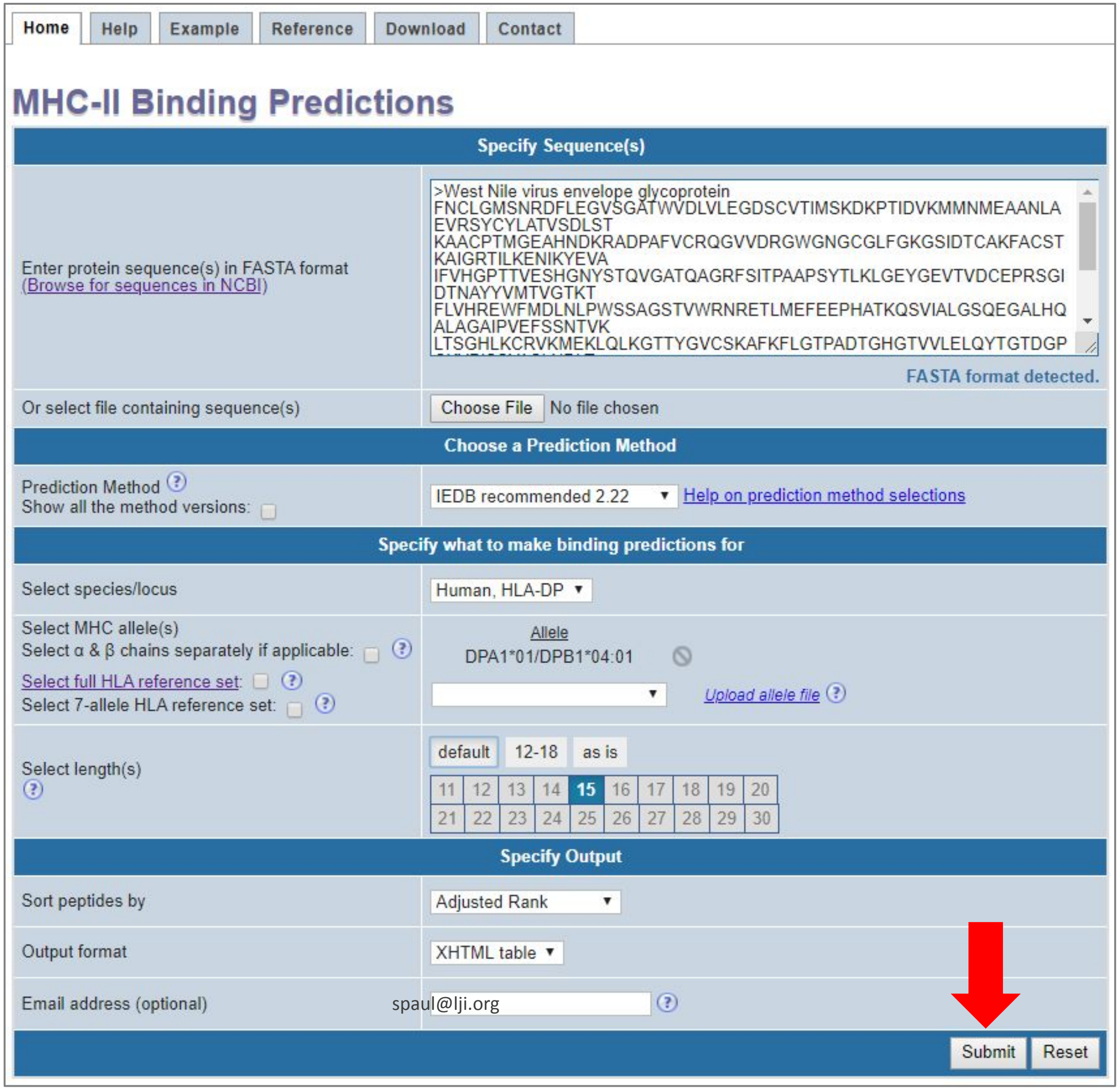
Sort peptides by: Adjusted Rank

Output format: XHTML table

Email address (optional): spaul@lji.org

MHC-II binding prediction – example

tools.iedb.org/mhcii/



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KAIGRTILKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGI
DTNAYYVMTVGTKT
FLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQ
ALAGAIPVEFSSNTVK
LTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGP
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Prediction Method: IEDB recommended 2.22 (Help on prediction method selections)
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Select species/locus: Human, HLA-DP

Select MHC allele(s)
Select α & β chains separately if applicable: ☐
Select full HLA reference set: ☐
Select 7-allele HLA reference set: ☐

Allele
DPA1*01/DPB1*04:01

Upload allele file

Select length(s): default | 12-18 | as is

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Specify Output

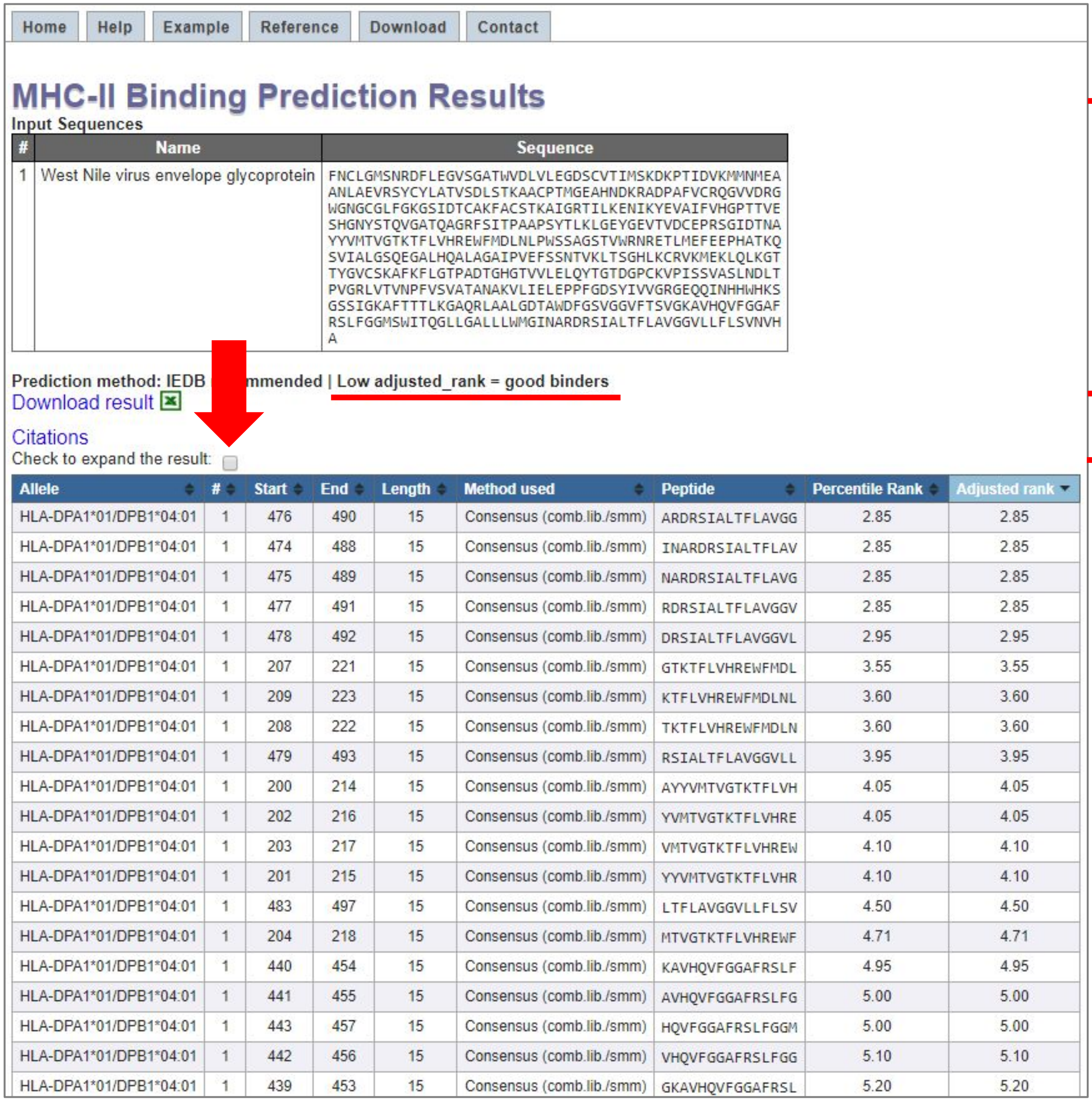
Sort peptides by: Adjusted Rank

Output format: XHTML table

Email address (optional): spaul@lji.org

MHC-II binding prediction – example

tools.iedb.org/mhcii/



MHC-II Binding Prediction Results

Input Sequences

#	Name	Sequence
1	West Nile virus envelope glycoprotein	FNCLGMSNRDFLEGVSGATWVDLVLEGDSCVTIMSKDKPTIDVKMMNMEAANLAEVRSYCYLATVSDLSTKAACPTMGEAHNDKRADPAFVCRQGVVDRGWGNGCGLFGKGSIDTCAKFACSTKAIGRTILKENIKYEVAIFVHGPTTVESHGNYSTQVGATQAGRFSITPAAPSYTLKLGEYGEVTVDCEPRSGIDTNAYYVMTVGTKTFLVHREWFMDLNLPWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQALAGAIPVEFSSNTVKLTSGHLKCRVKMEKLQLKGTTYGVCSKAFKFLGTPADTGHGTVVLELQYTGTDGPCKVPISSVASLNDLTPVGRLVTVNPFVSVATANAKVLIELEPPFGDSYIVVGRGEQQINHHWHKSGSSIGKAFTTTLKGAQRLAALGDTAWDFGSVGGVFTSVGKAVHQVFGGAFRSLFGGMSWITQGLLGALLLWMGINARDRSIALTFLAVGGVLLFLSVNVHA

Prediction method: IEDB mmended | Low adjusted_rank = good binders

Download result

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Check to expand the result: ☐

Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted rank
HLA-DPA1*01/DPB1*04:01	1	476	490	15	Consensus (comb.lib./smm)	ARDRSIALTFLAVGG	2.85	2.85
HLA-DPA1*01/DPB1*04:01	1	474	488	15	Consensus (comb.lib./smm)	INARDRSIALTFLAV	2.85	2.85
HLA-DPA1*01/DPB1*04:01	1	475	489	15	Consensus (comb.lib./smm)	NARDRSIALTFLAVG	2.85	2.85
HLA-DPA1*01/DPB1*04:01	1	477	491	15	Consensus (comb.lib./smm)	RDRSIALTFLAVGGV	2.85	2.85
HLA-DPA1*01/DPB1*04:01	1	478	492	15	Consensus (comb.lib./smm)	DRSIALTFLAVGGVL	2.95	2.95
HLA-DPA1*01/DPB1*04:01	1	207	221	15	Consensus (comb.lib./smm)	GTKTFLVHREWFMDL	3.55	3.55
HLA-DPA1*01/DPB1*04:01	1	209	223	15	Consensus (comb.lib./smm)	KTFLVHREWFMDLNL	3.60	3.60
HLA-DPA1*01/DPB1*04:01	1	208	222	15	Consensus (comb.lib./smm)	TKTFLVHREWFMDLN	3.60	3.60
HLA-DPA1*01/DPB1*04:01	1	479	493	15	Consensus (comb.lib./smm)	RSIALTFLAVGGVLL	3.95	3.95
HLA-DPA1*01/DPB1*04:01	1	200	214	15	Consensus (comb.lib./smm)	AYYVMTVGTKTFLVH	4.05	4.05
HLA-DPA1*01/DPB1*04:01	1	202	216	15	Consensus (comb.lib./smm)	YVMTVGTKTFLVHRE	4.05	4.05
HLA-DPA1*01/DPB1*04:01	1	203	217	15	Consensus (comb.lib./smm)	VMTVGTKTFLVHREW	4.10	4.10
HLA-DPA1*01/DPB1*04:01	1	201	215	15	Consensus (comb.lib./smm)	YYVMTVGTKTFLVHR	4.10	4.10
HLA-DPA1*01/DPB1*04:01	1	483	497	15	Consensus (comb.lib./smm)	LTFLAVGGVLLFLSV	4.50	4.50
HLA-DPA1*01/DPB1*04:01	1	204	218	15	Consensus (comb.lib./smm)	MTVGTKTFLVHREWF	4.71	4.71
HLA-DPA1*01/DPB1*04:01	1	440	454	15	Consensus (comb.lib./smm)	KAVHQVFGGAFRSLF	4.95	4.95
HLA-DPA1*01/DPB1*04:01	1	441	455	15	Consensus (comb.lib./smm)	AVHQVFGGAFRSLFG	5.00	5.00
HLA-DPA1*01/DPB1*04:01	1	443	457	15	Consensus (comb.lib./smm)	HQVFGGAFRSLFGGM	5.00	5.00
HLA-DPA1*01/DPB1*04:01	1	442	456	15	Consensus (comb.lib./smm)	VHQVFGGAFRSLFGG	5.10	5.10
HLA-DPA1*01/DPB1*04:01	1	439	453	15	Consensus (comb.lib./smm)	GKAVHQVFGGAFRSL	5.20	5.20

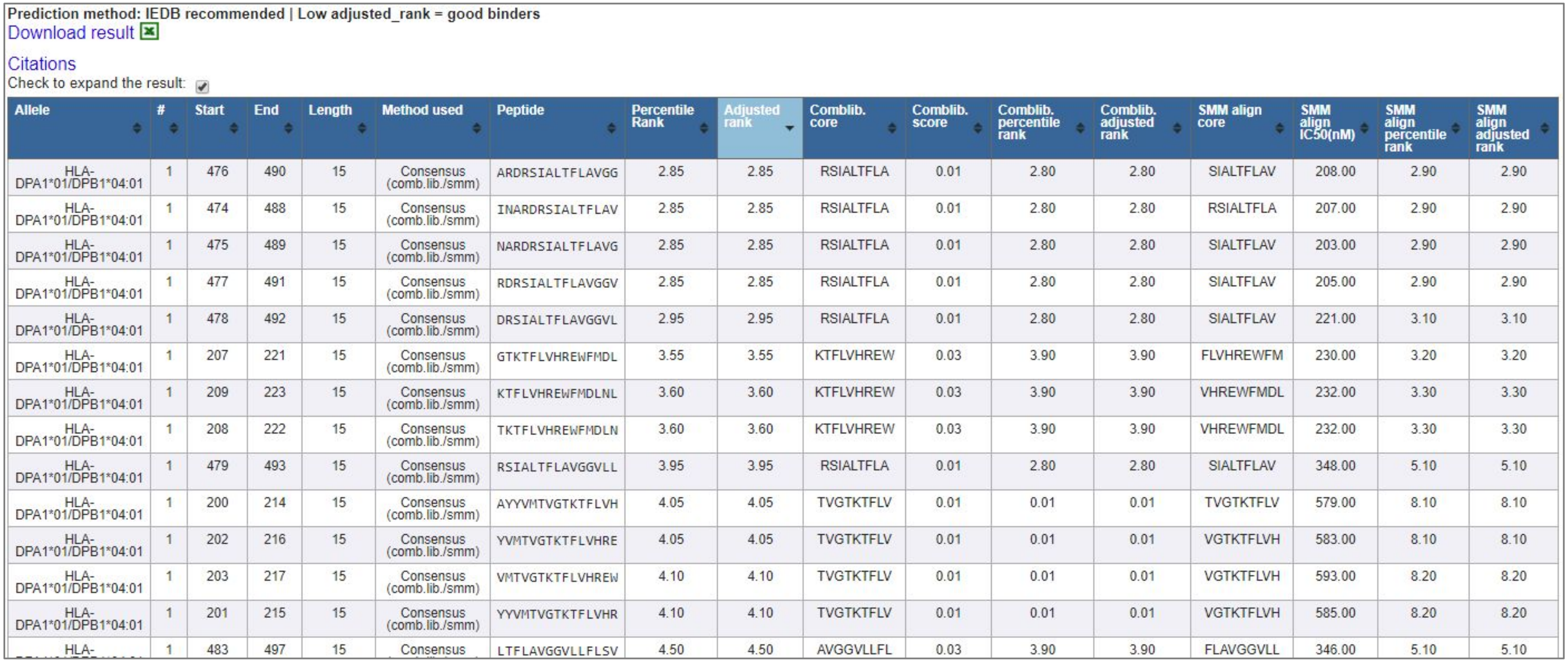
Input sequence

Output
(sorted low-to-high by adjusted rank)

The **adjusted rank** is the percentile rank adjusted based on the frequency of peptide lengths.

MHC-II binding prediction – example

tools.iedb.org/mhcii/



Prediction method: IEDB recommended | Low adjusted_rank = good binders

Download result

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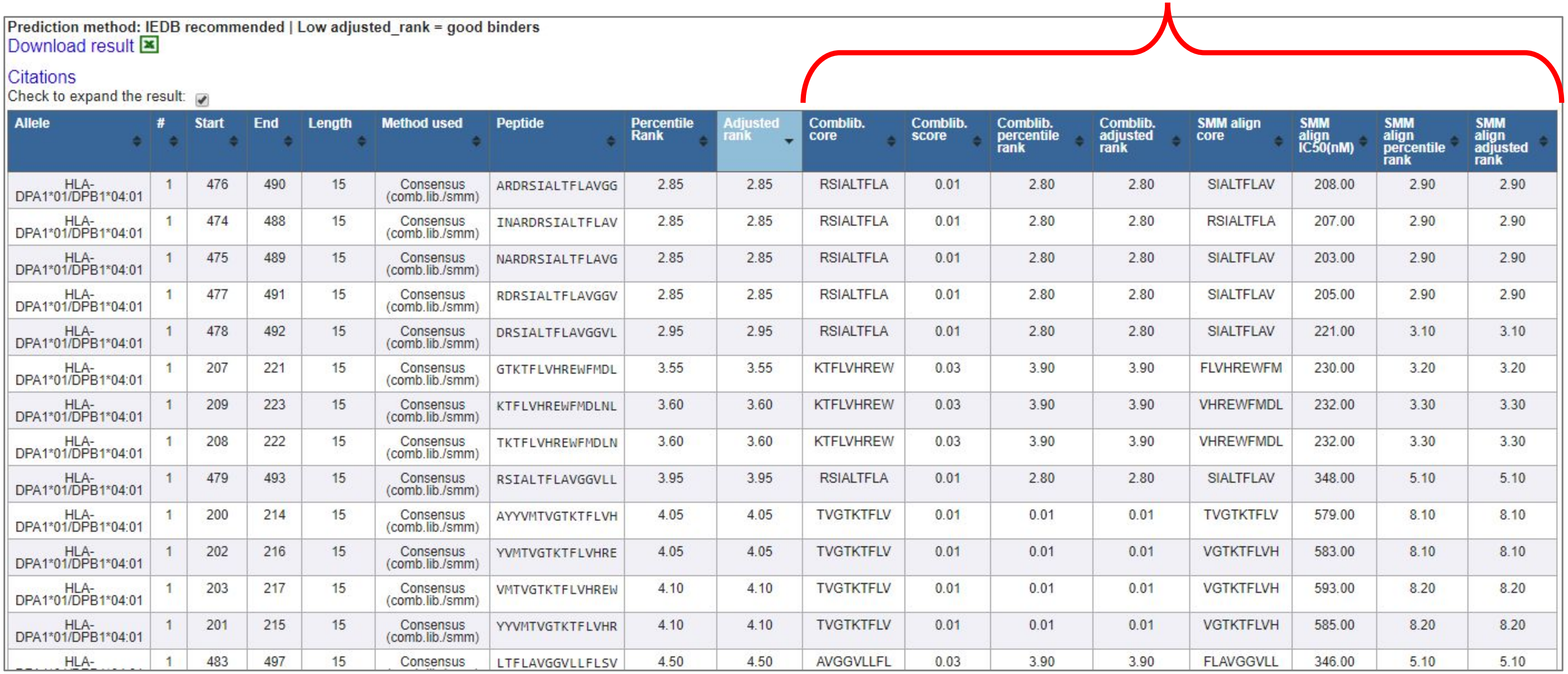
Check to expand the result: ☑

Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Comblib. core	Comblib. score	Comblib. percentile rank	Comblib. adjusted rank	SMM align core	SMM align IC50(nM)	SMM align percentile rank	SMM align adjusted rank
HLA-DPA1*01/DPB1*04:01	1	476	490	15	Consensus (comb.lib./smm)	ARDRSIALTFLAVGG	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	208.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	474	488	15	Consensus (comb.lib./smm)	INARDRSIALTFLAV	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	RSIALTFLA	207.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	475	489	15	Consensus (comb.lib./smm)	NARDRSIALTFLAVG	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	203.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	477	491	15	Consensus (comb.lib./smm)	RDRSIALTFLAVGGV	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	205.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	478	492	15	Consensus (comb.lib./smm)	DRSIALTFLAVGGVL	2.95	2.95	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	221.00	3.10	3.10
HLA-DPA1*01/DPB1*04:01	1	207	221	15	Consensus (comb.lib./smm)	GTKTFLVHREWFMDL	3.55	3.55	KTFLVHREW	0.03	3.90	3.90	FLVHREWFM	230.00	3.20	3.20
HLA-DPA1*01/DPB1*04:01	1	209	223	15	Consensus (comb.lib./smm)	KTFLVHREWFMDLNL	3.60	3.60	KTFLVHREW	0.03	3.90	3.90	VHREWFMDL	232.00	3.30	3.30
HLA-DPA1*01/DPB1*04:01	1	208	222	15	Consensus (comb.lib./smm)	TKTFLVHREWFMDLN	3.60	3.60	KTFLVHREW	0.03	3.90	3.90	VHREWFMDL	232.00	3.30	3.30
HLA-DPA1*01/DPB1*04:01	1	479	493	15	Consensus (comb.lib./smm)	RSIALTFLAVGGVLL	3.95	3.95	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	348.00	5.10	5.10
HLA-DPA1*01/DPB1*04:01	1	200	214	15	Consensus (comb.lib./smm)	AYYVMTVGTKTFLVH	4.05	4.05	TVGTKTFLV	0.01	0.01	0.01	TVGTKTFLV	579.00	8.10	8.10
HLA-DPA1*01/DPB1*04:01	1	202	216	15	Consensus (comb.lib./smm)	YVMTVGTKTFLVHRE	4.05	4.05	TVGTKTFLV	0.01	0.01	0.01	VGTKTFLVH	583.00	8.10	8.10
HLA-DPA1*01/DPB1*04:01	1	203	217	15	Consensus (comb.lib./smm)	VMTVGTKTFLVHREW	4.10	4.10	TVGTKTFLV	0.01	0.01	0.01	VGTKTFLVH	593.00	8.20	8.20
HLA-DPA1*01/DPB1*04:01	1	201	215	15	Consensus (comb.lib./smm)	YYVMTVGTKTFLVHR	4.10	4.10	TVGTKTFLV	0.01	0.01	0.01	VGTKTFLVH	585.00	8.20	8.20
HLA-	1	483	497	15	Consensus	LTFLAVGGVLLFLSV	4.50	4.50	AVGGVLLFL	0.03	3.90	3.90	FLAVGGVLL	346.00	5.10	5.10

MHC-II binding prediction – example

tools.iedb.org/mhcii/

Individual scores for different methods



Prediction method: IEDB recommended | Low adjusted_rank = good binders

Download result

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Check to expand the result: ☑

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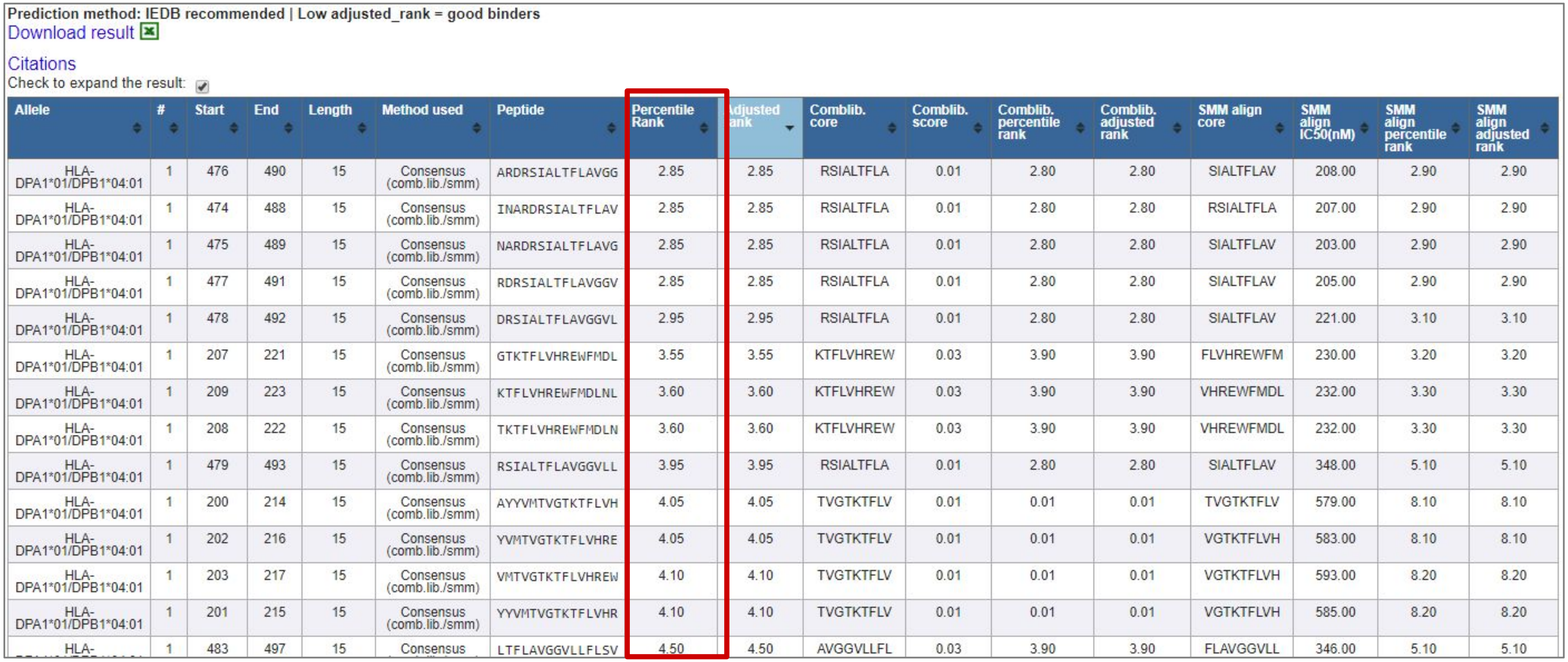
HLA-DPA1*01/DPB1*04:01	1	208	222	15	Consensus (comb.lib./smm)	TKTFLVHREWFMDLN	3.60	3.60	KTFLVHREW	0.03	3.90	3.90	VHREWFMDL	232.00	3.30	3.30
HLA-DPA1*01/DPB1*04:01	1	479	493	15	Consensus (comb.lib./smm)	RSIALTFLAVGGVLL	3.95	3.95	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	348.00	5.10	5.10
HLA-DPA1*01/DPB1*04:01	1	200	214	15	Consensus (comb.lib./smm)	AYYVMTVGTKTFLVH	4.05	4.05	TVGTKTFLV	0.01	0.01	0.01	TVGTKTFLV	579.00	8.10	8.10
HLA-DPA1*01/DPB1*04:01	1	202	216	15	Consensus (comb.lib./smm)	YVMTVGTKTFLVHRE	4.05	4.05	TVGTKTFLV	0.01	0.01	0.01	VGTKTFLVH	583.00	8.10	8.10
HLA-DPA1*01/DPB1*04:01	1	203	217	15	Consensus (comb.lib./smm)	VMTVGTKTFLVHREW	4.10	4.10	TVGTKTFLV	0.01	0.01	0.01	VGTKTFLVH	593.00	8.20	8.20
HLA-DPA1*01/DPB1*04:01	1	201	215	15	Consensus (comb.lib./smm)	YYVMTVGTKTFLVHR	4.10	4.10	TVGTKTFLV	0.01	0.01	0.01	VGTKTFLVH	585.00	8.20	8.20
HLA-	1	483	497	15	Consensus	LTFLAVGGVLLFLSV	4.50	4.50	AVGGVLLFL	0.03	3.90	3.90	FLAVGGVLL	346.00	5.10	5.10

MHC-II binding prediction – example

tools.iedb.org/mhcii/



Prediction method: IEDB recommended | Low adjusted_rank = good binders

Download result

Citations

Check to expand the result: ☑

Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted ank	Comblib. core	Comblib. score	Comblib. percentile rank	Comblib. adjusted rank	SMM align core	SMM align IC50(nM)	SMM align percentile rank	SMM align adjusted rank
HLA-DPA1*01/DPB1*04:01	1	476	490	15	Consensus (comb.lib./smm)	ARDRSIALTFLAVGG	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	208.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	474	488	15	Consensus (comb.lib./smm)	INARDRSIALTFLAV	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	RSIALTFLA	207.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	475	489	15	Consensus (comb.lib./smm)	NARDRSIALTFLAVG	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	203.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	477	491	15	Consensus (comb.lib./smm)	RDRSIALTFLAVGGV	2.85	2.85	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	205.00	2.90	2.90
HLA-DPA1*01/DPB1*04:01	1	478	492	15	Consensus (comb.lib./smm)	DRSIALTFLAVGGVL	2.95	2.95	RSIALTFLA	0.01	2.80	2.80	SIALTFLAV	221.00	3.10	3.10
HLA-DPA1*01/DPB1*04:01	1	207	221	15	Consensus (comb.lib./smm)	GTKTFLVHREWFMDL	3.55	3.55	KTFLVHREW	0.03	3.90	3.90	FLVHREWFM	230.00	3.20	3.20
HLA-DPA1*01/DPB1*04:01	1	209	223	15	Consensus (comb.lib./smm)	KTFLVHREWFMDLNL	3.60	3.60	KTFLVHREW	0.03	3.90	3.90	VHREWFMDL	232.00	3.30	3.30
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Other differences between class I & II tools

- Lesser accuracy compared to class-I tool

Class I		Class II	
Method	**AUC***	**Method**	**AUC***
NetMHCpan-4.0	0.960[1]	NetMHCIIpan-3.2	0.781[2]
SMM	0.894[3]	SMM-align	0.763[4]

** The AUCs reported here are from different studies and obtained from different data sets*

- Less stringent threshold for selecting binders than class-I

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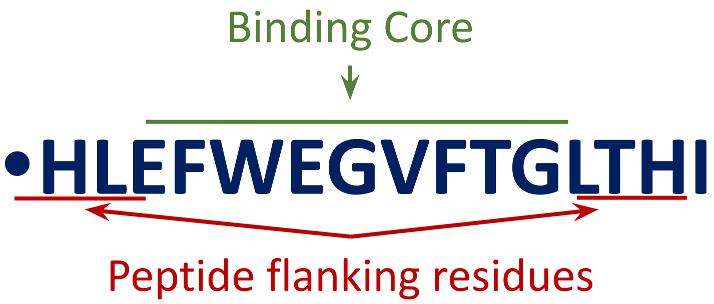
Issue of overlapping peptides

- Residues flanking the binding core - interacts with MHC molecule outside the groove.



Binding Core

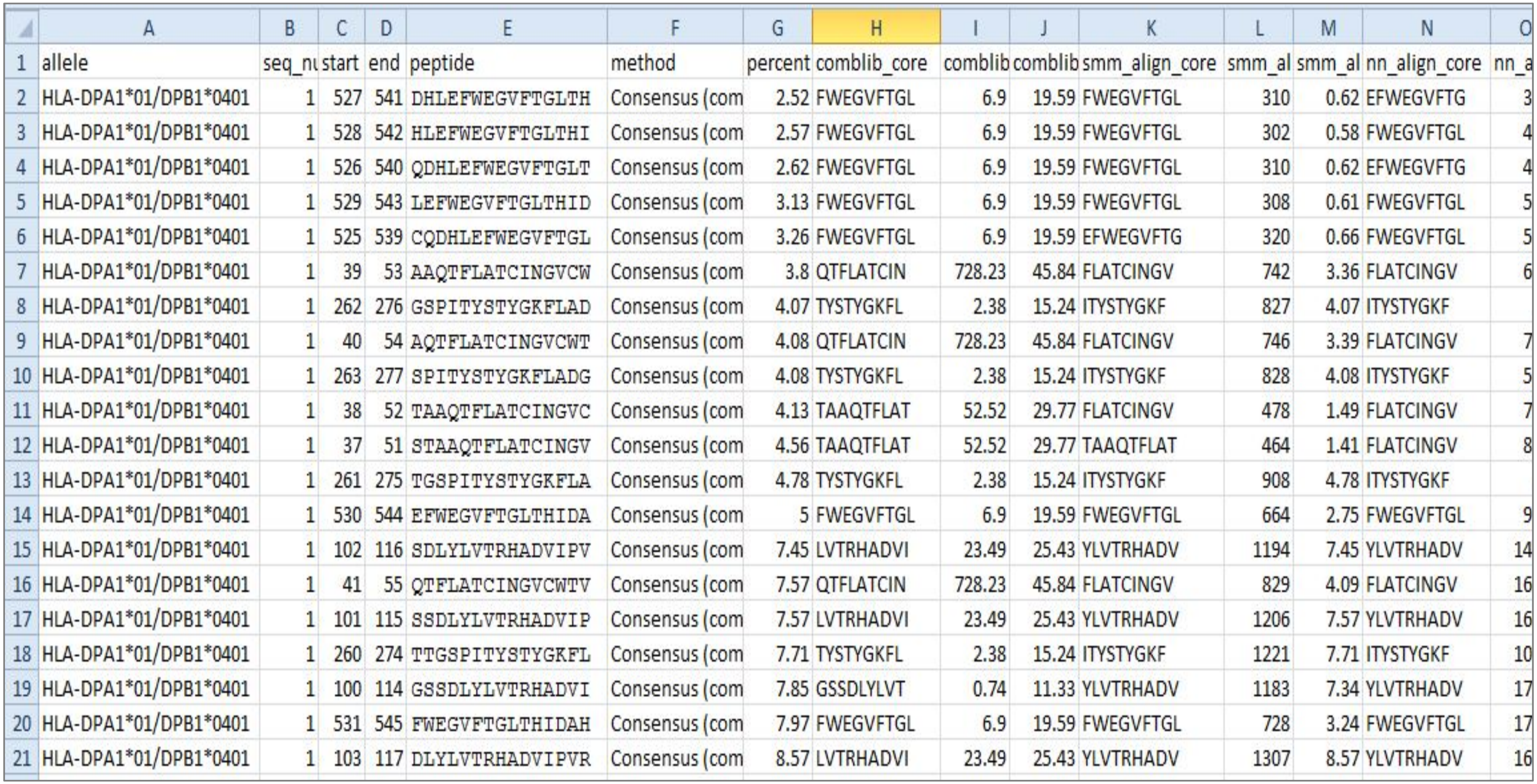
- **HLEFWEGVFTGLTHI**

Peptide flanking residues

- Challenge: PFR length & composition influence binding.

Issue of overlapping peptides

- The tool breaks the sequence into all possible 15-mers - Peptides overlapping by 14 amino acid residues



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1	allele	seq_nu	start	end	peptide	method	percent	comblib_core	comblib	comblib	smm_align_core	smm_al	smm_al	nn_align_core	nn_a
2	HLA-DPA1*01/DPB1*0401	1	527	541	DHLEFWEGVFTGLTH	Consensus (com	2.52	FWEGVFTGL	6.9	19.59	FWEGVFTGL	310	0.62	EFWEGVFTG	3
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7	HLA-DPA1*01/DPB1*0401	1	39	53	AAQTFLATCINGVCW	Consensus (com	3.8	QTFLATCIN	728.23	45.84	FLATCINGV	742	3.36	FLATCINGV	6
8	HLA-DPA1*01/DPB1*0401	1	262	276	GSPITYSTYGKFLAD	Consensus (com	4.07	TYSTYGKFL	2.38	15.24	ITYSTYGKF	827	4.07	ITYSTYGKF	
9	HLA-DPA1*01/DPB1*0401	1	40	54	AQTFLATCINGVCWT	Consensus (com	4.08	QTFLATCIN	728.23	45.84	FLATCINGV	746	3.39	FLATCINGV	7
10	HLA-DPA1*01/DPB1*0401	1	263	277	SPITYSTYGKFLADG	Consensus (com	4.08	TYSTYGKFL	2.38	15.24	ITYSTYGKF	828	4.08	ITYSTYGKF	5
11	HLA-DPA1*01/DPB1*0401	1	38	52	TAAQTFLATCINGVC	Consensus (com	4.13	TAAQTFLAT	52.52	29.77	FLATCINGV	478	1.49	FLATCINGV	7
12	HLA-DPA1*01/DPB1*0401	1	37	51	STAAQTFLATCINGV	Consensus (com	4.56	TAAQTFLAT	52.52	29.77	TAAQTFLAT	464	1.41	FLATCINGV	8
13	HLA-DPA1*01/DPB1*0401	1	261	275	TGSPITYSTYGKFLA	Consensus (com	4.78	TYSTYGKFL	2.38	15.24	ITYSTYGKF	908	4.78	ITYSTYGKF	
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16	HLA-DPA1*01/DPB1*0401	1	41	55	QTFLATCINGVCWTV	Consensus (com	7.57	QTFLATCIN	728.23	45.84	FLATCINGV	829	4.09	FLATCINGV	16
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18	HLA-DPA1*01/DPB1*0401	1	260	274	TTGSPITYSTYGKFL	Consensus (com	7.71	TYSTYGKFL	2.38	15.24	ITYSTYGKF	1221	7.71	ITYSTYGKF	10
19	HLA-DPA1*01/DPB1*0401	1	100	114	GSSDLYLVTRHADVI	Consensus (com	7.85	GSSDLYLVT	0.74	11.33	YLVTRHADV	1183	7.34	YLVTRHADV	17
20	HLA-DPA1*01/DPB1*0401	1	531	545	FWEGVFTGLTHIDAH	Consensus (com	7.97	FWEGVFTGL	6.9	19.59	FWEGVFTGL	728	3.24	FWEGVFTGL	17
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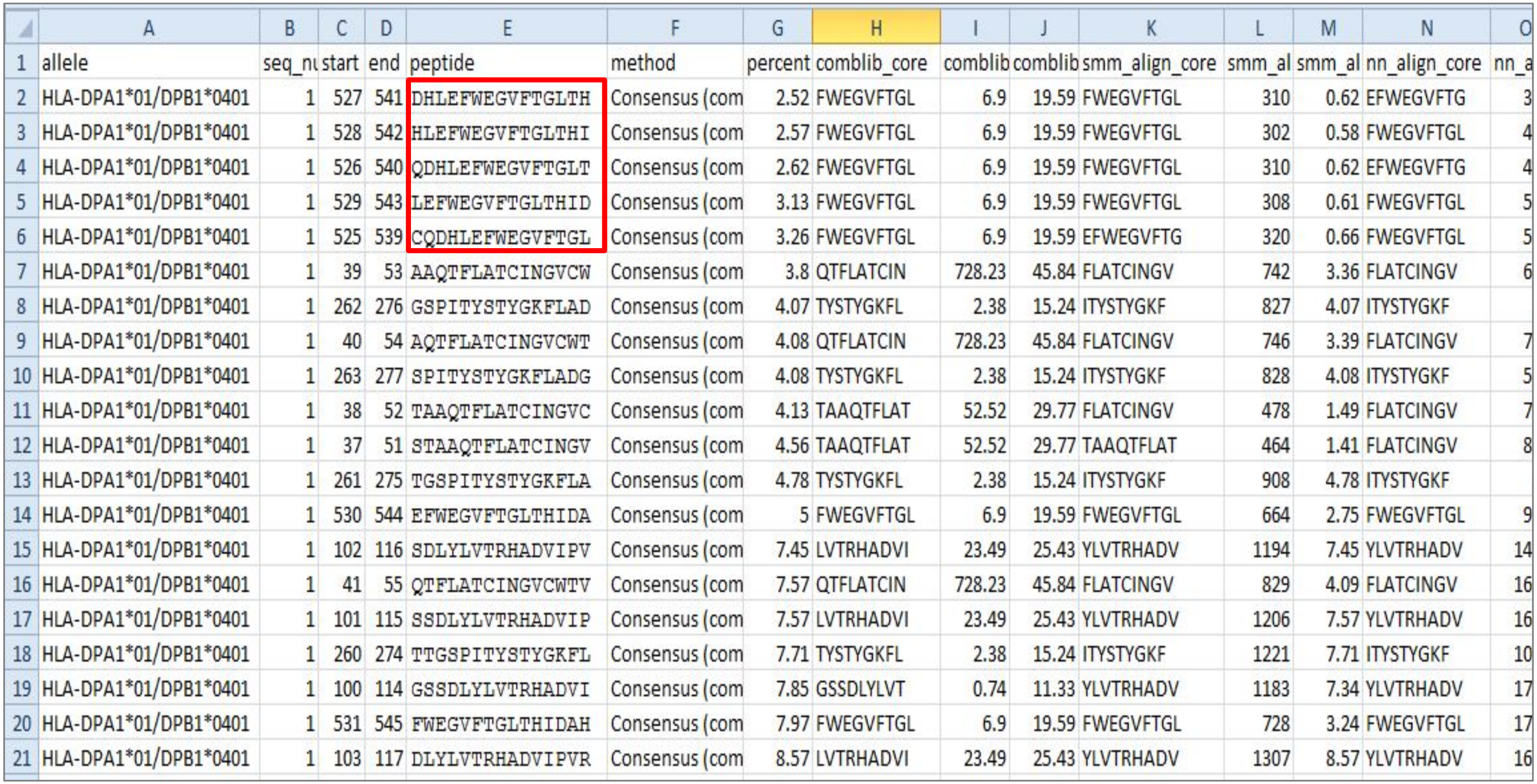
- The tool breaks the sequence into all possible 15-mers - Peptides overlapping by 14 amino acid residues



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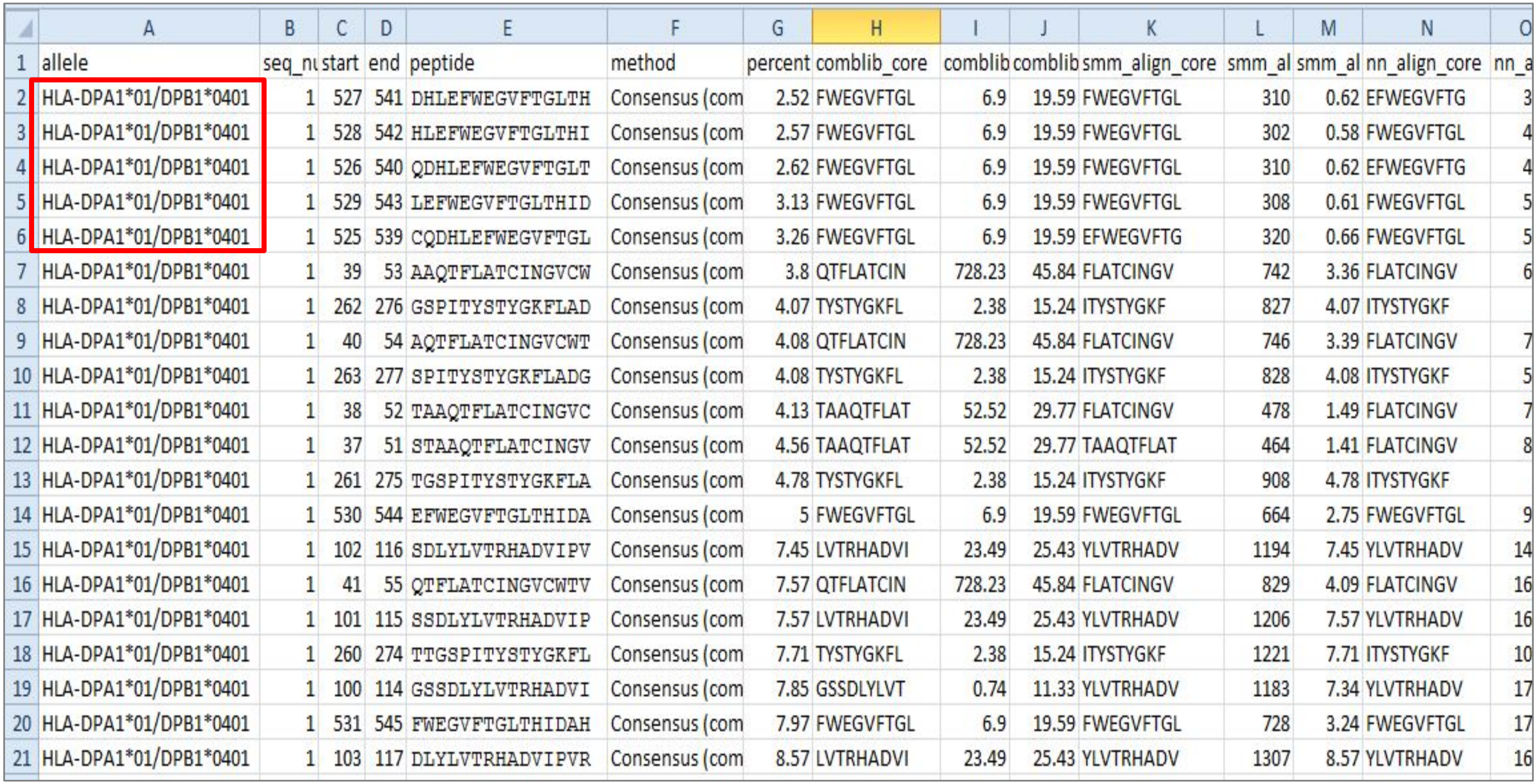

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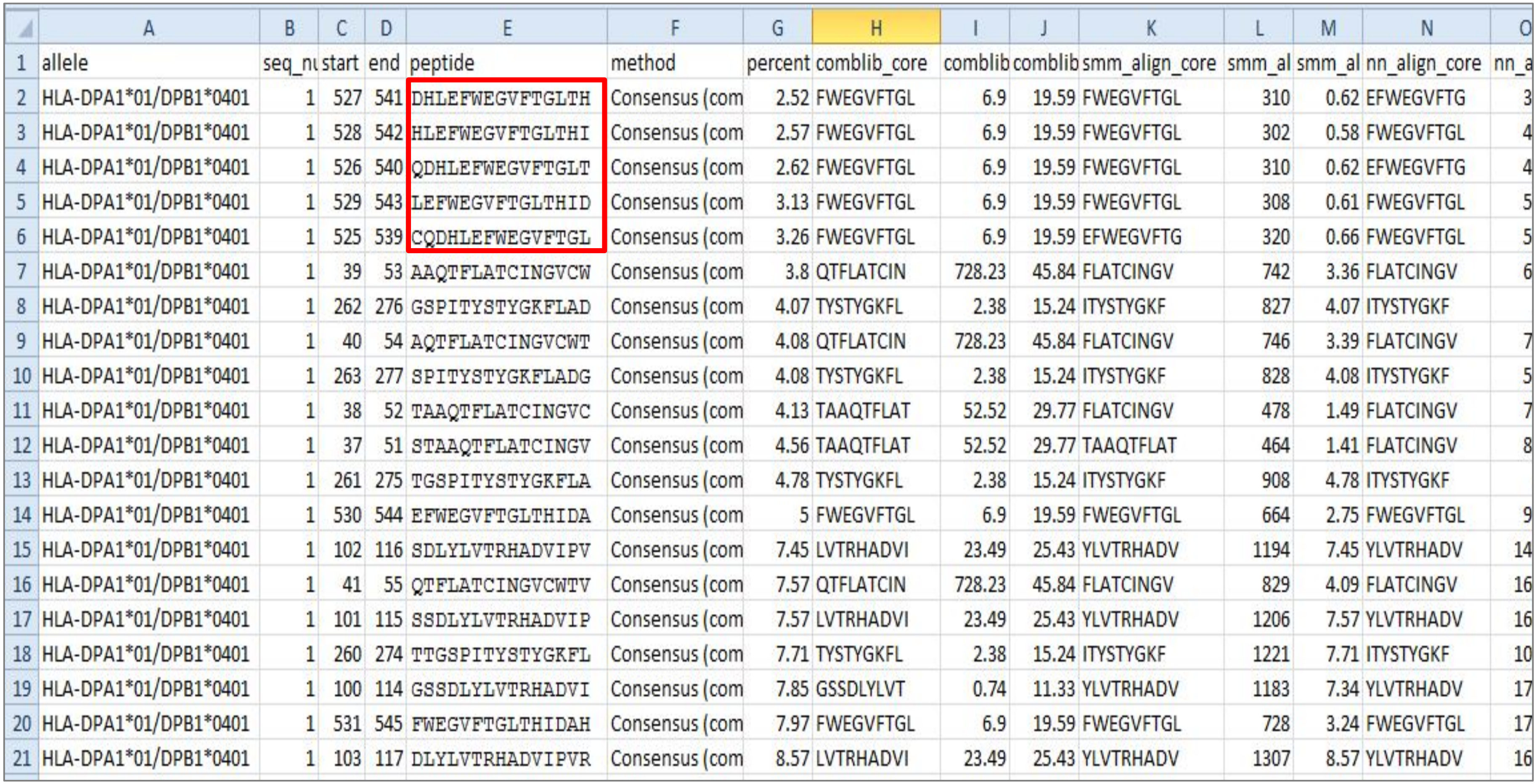
15	HLA-DPA1*01/DPB1*0401	1	102	116	SDLYLVTRHADVIPV	Consensus (com	7.45	LVTRHADVI	23.49	25.43	YLVTRHADV	1194	7.45	YLVTRHADV	14
16	HLA-DPA1*01/DPB1*0401	1	41	55	QTFLATCINGVCWTV	Consensus (com	7.57	QTFLATCIN	728.23	45.84	FLATCINGV	829	4.09	FLATCINGV	16
17	HLA-DPA1*01/DPB1*0401	1	101	115	SSDLYLVTRHADVIP	Consensus (com	7.57	LVTRHADVI	23.49	25.43	YLVTRHADV	1206	7.57	YLVTRHADV	16
18	HLA-DPA1*01/DPB1*0401	1	260	274	TTGSPITYSTYGKFL	Consensus (com	7.71	TYSTYGKFL	2.38	15.24	ITYSTYGKF	1221	7.71	ITYSTYGKF	10
19	HLA-DPA1*01/DPB1*0401	1	100	114	GSSDLYLVTRHADVI	Consensus (com	7.85	GSSDLYLVT	0.74	11.33	YLVTRHADV	1183	7.34	YLVTRHADV	17
20	HLA-DPA1*01/DPB1*0401	1	531	545	FWEGVFTGLTHIDAH	Consensus (com	7.97	FWEGVFTGL	6.9	19.59	FWEGVFTGL	728	3.24	FWEGVFTGL	17
21	HLA-DPA1*01/DPB1*0401	1	103	117	DLYLVTRHADVIPVR	Consensus (com	8.57	LVTRHADVI	23.49	25.43	YLVTRHADV	1307	8.57	YLVTRHADV	16

Issue of overlapping peptides

- The tool breaks the sequence into all possible 15-mers - Peptides overlapping by 14 amino acid residues



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	allele	seq_nı	start	end	peptide	method	percent	comblib_core	comblib	comblib	smm_align_core	smm_al	smm_al	nn_align_core	nn_a
2	HLA-DPA1*01/DPB1*0401	1	527	541	DHLEFWEGVFTGLTH	Consensus (com	2.52	FWEGVFTGL	6.9	19.59	FWEGVFTGL	310	0.62	EFWEGVFTG	3
3	HLA-DPA1*01/DPB1*0401	1	528	542	HLEFWEGVFTGLTHI	Consensus (com	2.57	FWEGVFTGL	6.9	19.59	FWEGVFTGL	302	0.58	FWEGVFTGL	4
4	HLA-DPA1*01/DPB1*0401	1	526	540	QDHLEFWEGVFTGLT	Consensus (com	2.62	FWEGVFTGL	6.9	19.59	FWEGVFTGL	310	0.62	EFWEGVFTG	4
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6	HLA-DPA1*01/DPB1*0401	1	525	539	CQDHLEFWEGVFTGL	Consensus (com	3.26	FWEGVFTGL	6.9	19.59	EFWEGVFTG	320	0.66	FWEGVFTGL	5
7	HLA-DPA1*01/DPB1*0401	1	39	53	AAQTFLATCINGVCW	Consensus (com	3.8	QTFLATCIN	728.23	45.84	FLATCINGV	742	3.36	FLATCINGV	6
8	HLA-DPA1*01/DPB1*0401	1	262	276	GSPITYSTYGKFLAD	Consensus (com	4.07	TYSTYGKFL	2.38	15.24	ITYSTYGKF	827	4.07	ITYSTYGKF	
9	HLA-DPA1*01/DPB1*0401	1	40	54	AQTFLATCINGVCWT	Consensus (com	4.08	QTFLATCIN	728.23	45.84	FLATCINGV	746	3.39	FLATCINGV	7
10	HLA-DPA1*01/DPB1*0401	1	263	277	SPITYSTYGKFLADG	Consensus (com	4.08	TYSTYGKFL	2.38	15.24	ITYSTYGKF	828	4.08	ITYSTYGKF	5
11	HLA-DPA1*01/DPB1*0401	1	38	52	TAAQTFLATCINGVC	Consensus (com	4.13	TAAQTFLAT	52.52	29.77	FLATCINGV	478	1.49	FLATCINGV	7
12	HLA-DPA1*01/DPB1*0401	1	37	51	STAAQTFLATCINGV	Consensus (com	4.56	TAAQTFLAT	52.52	29.77	TAAQTFLAT	464	1.41	FLATCINGV	8
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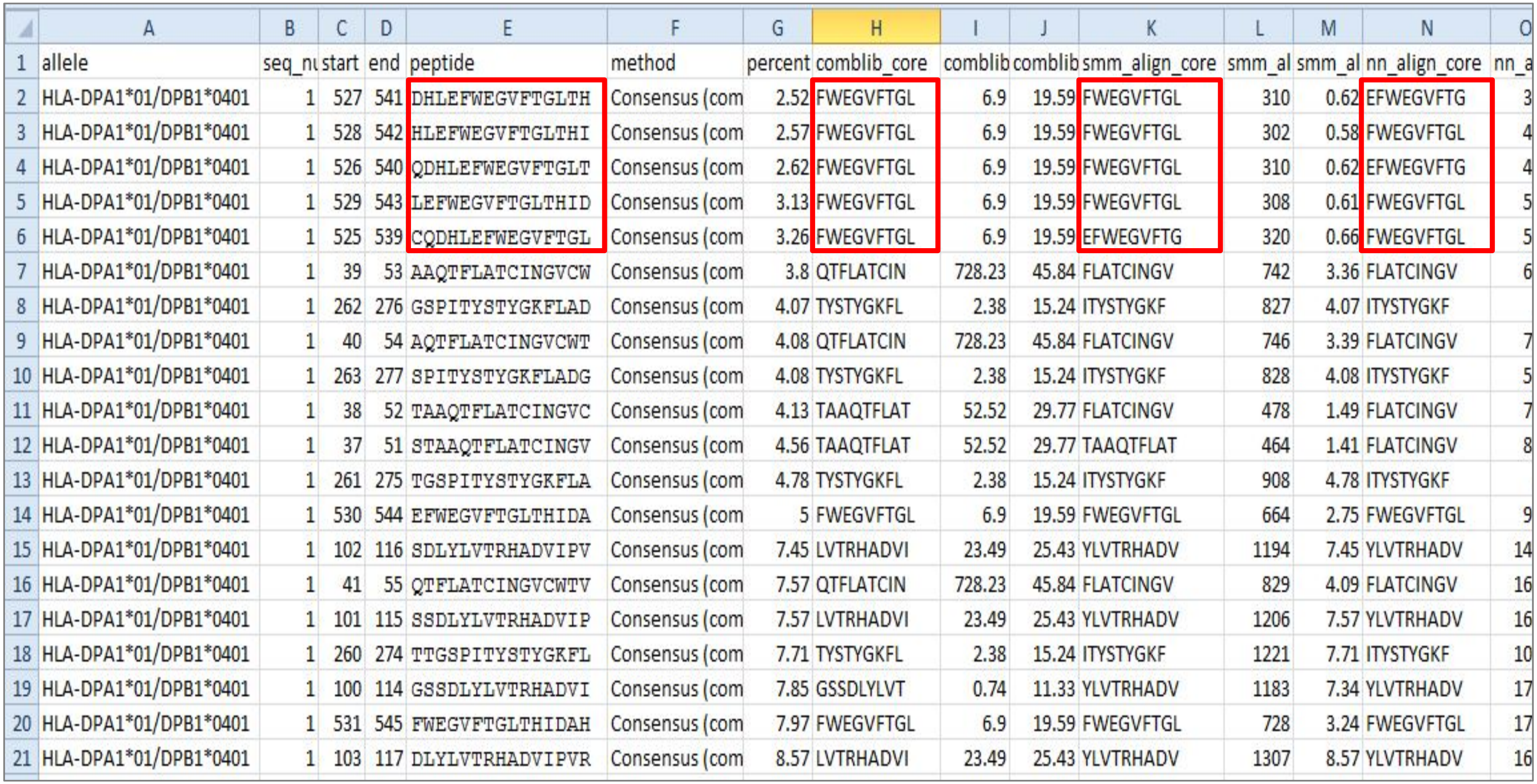

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1	allele	seq_nu	start	end	peptide	method	percent	comblib_core	comblib	comblib	smm_align_core	smm_al	smm_al	nn_align_core	nn_a
2	HLA-DPA1*01/DPB1*0401	1	527	541	DHLEFWEGVFTGLTH	Consensus (com	2.52	FWEGVFTGL	6.9	19.59	FWEGVFTGL	310	0.62	EFWEGVFTG	3
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5	HLA-DPA1*01/DPB1*0401	1	529	543	LEFWEGVFTGLTHID	Consensus (com	3.13	FWEGVFTGL	6.9	19.59	FWEGVFTGL	308	0.61	FWEGVFTGL	5
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7	HLA-DPA1*01/DPB1*0401	1	39	53	AAQTFLATCINGVCW	Consensus (com	3.8	QTFLATCIN	728.23	45.84	FLATCINGV	742	3.36	FLATCINGV	6
8	HLA-DPA1*01/DPB1*0401	1	262	276	GSPITYSTYGKFLAD	Consensus (com	4.07	TYSTYGKFL	2.38	15.24	ITYSTYGKF	827	4.07	ITYSTYGKF	
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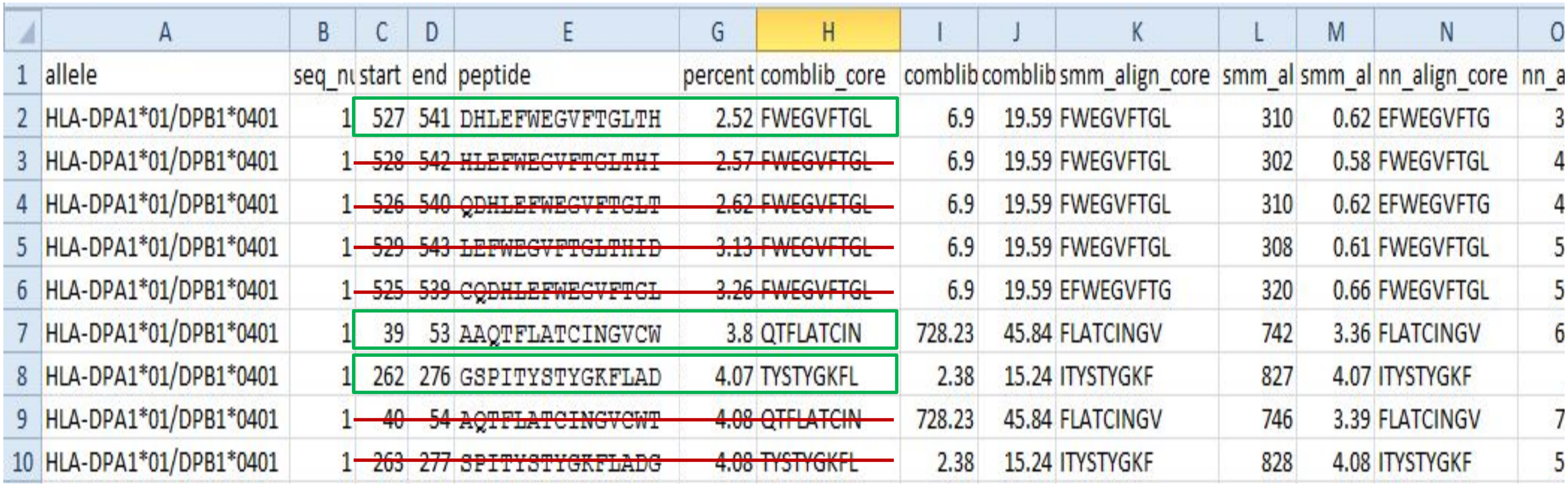
Issue of overlapping peptides: Solution

- Post-processing:
  - Remove largely overlapping peptides after prediction (based on same binding core or position)



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1	allele	seq_nu	start	end	peptide	percent	comblib_core	comblib	comblib	smm_align_core	smm_al	smm_al	nn_align_core	nn_a
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3	HLA-DPA1*01/DPB1*0401	1	~~528~~	~~542~~	~~HLEFWEGVFTGLTHI~~	~~2.57~~	~~FWEGVFTGL~~	6.9	19.59	FWEGVFTGL	302	0.58	FWEGVFTGL	4
4	HLA-DPA1*01/DPB1*0401	1	~~526~~	~~540~~	~~QDHLEFWEGVFTGLT~~	~~2.62~~	~~FWEGVFTGL~~	6.9	19.59	FWEGVFTGL	310	0.62	EFWEGVFTG	4
5	HLA-DPA1*01/DPB1*0401	1	~~529~~	~~543~~	~~LEFWEGVFTGLTHID~~	~~3.13~~	~~FWEGVFTGL~~	6.9	19.59	FWEGVFTGL	308	0.61	FWEGVFTGL	5
6	HLA-DPA1*01/DPB1*0401	1	~~525~~	~~539~~	~~CQDHLEFWEGVFTGL~~	~~3.26~~	~~FWEGVFTGL~~	6.9	19.59	EFWEGVFTG	320	0.66	FWEGVFTGL	5
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9	HLA-DPA1*01/DPB1*0401	1	~~40~~	~~54~~	~~AQTFLATCINGVCWT~~	~~4.08~~	~~QTFLATCIN~~	728.23	45.84	FLATCINGV	746	3.39	FLATCINGV	7
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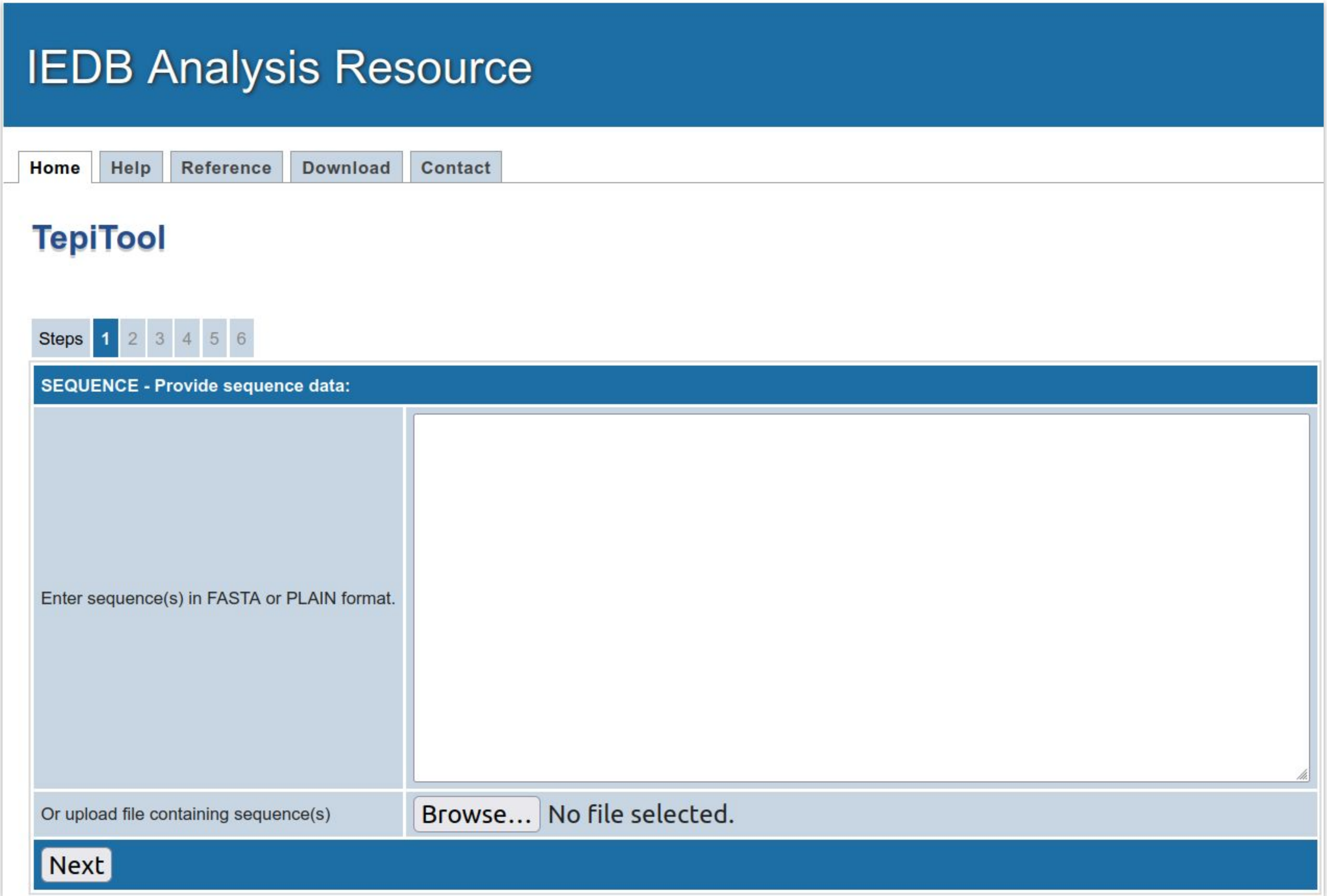
TepiTool

tools.iedb.org/tepitool



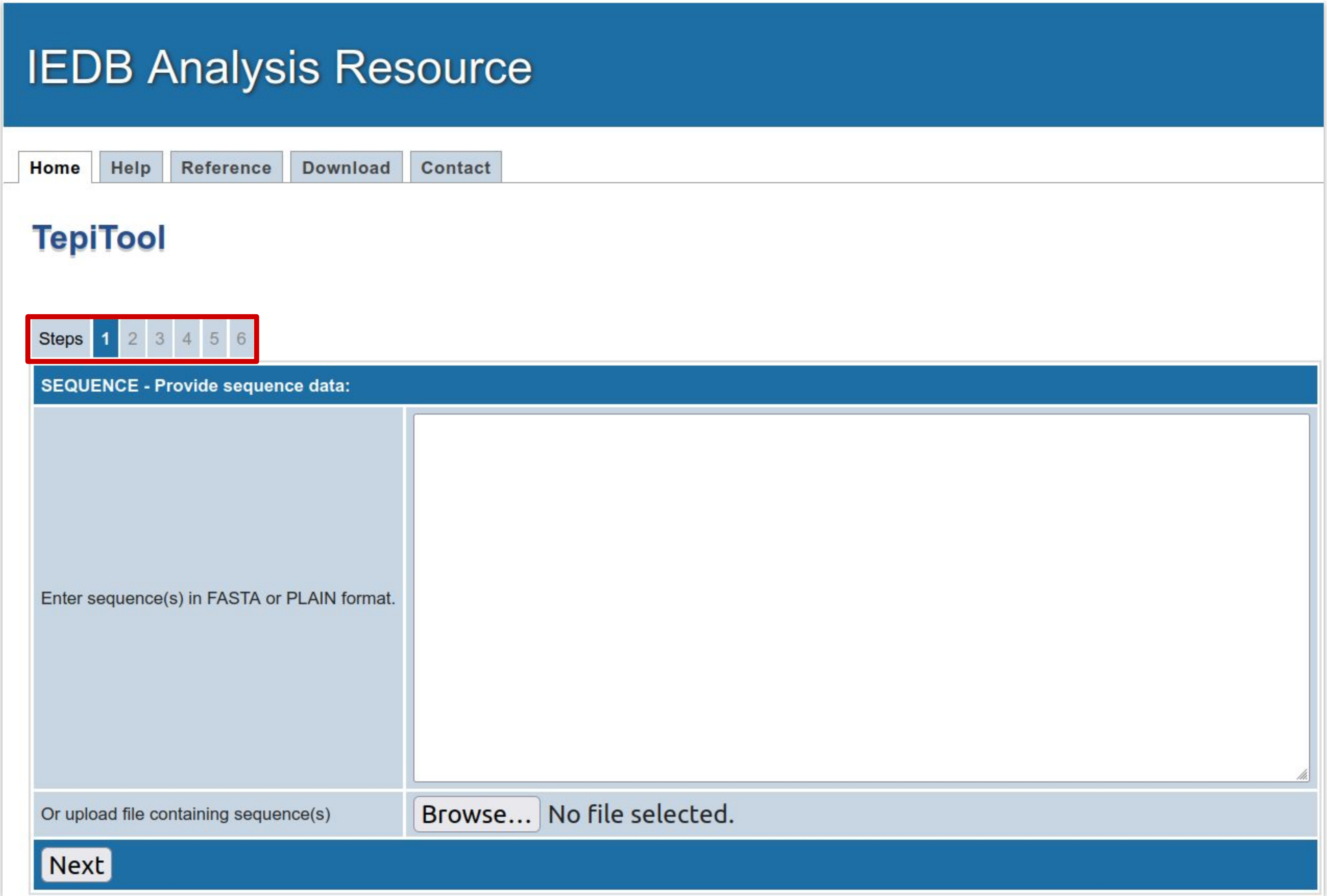
SEQUENCE - Provide sequence data:

Enter sequence(s) in FASTA or PLAIN format.

Or upload file containing sequence(s)

TepiTool

tools.iedb.org/tepitool



TepiTool

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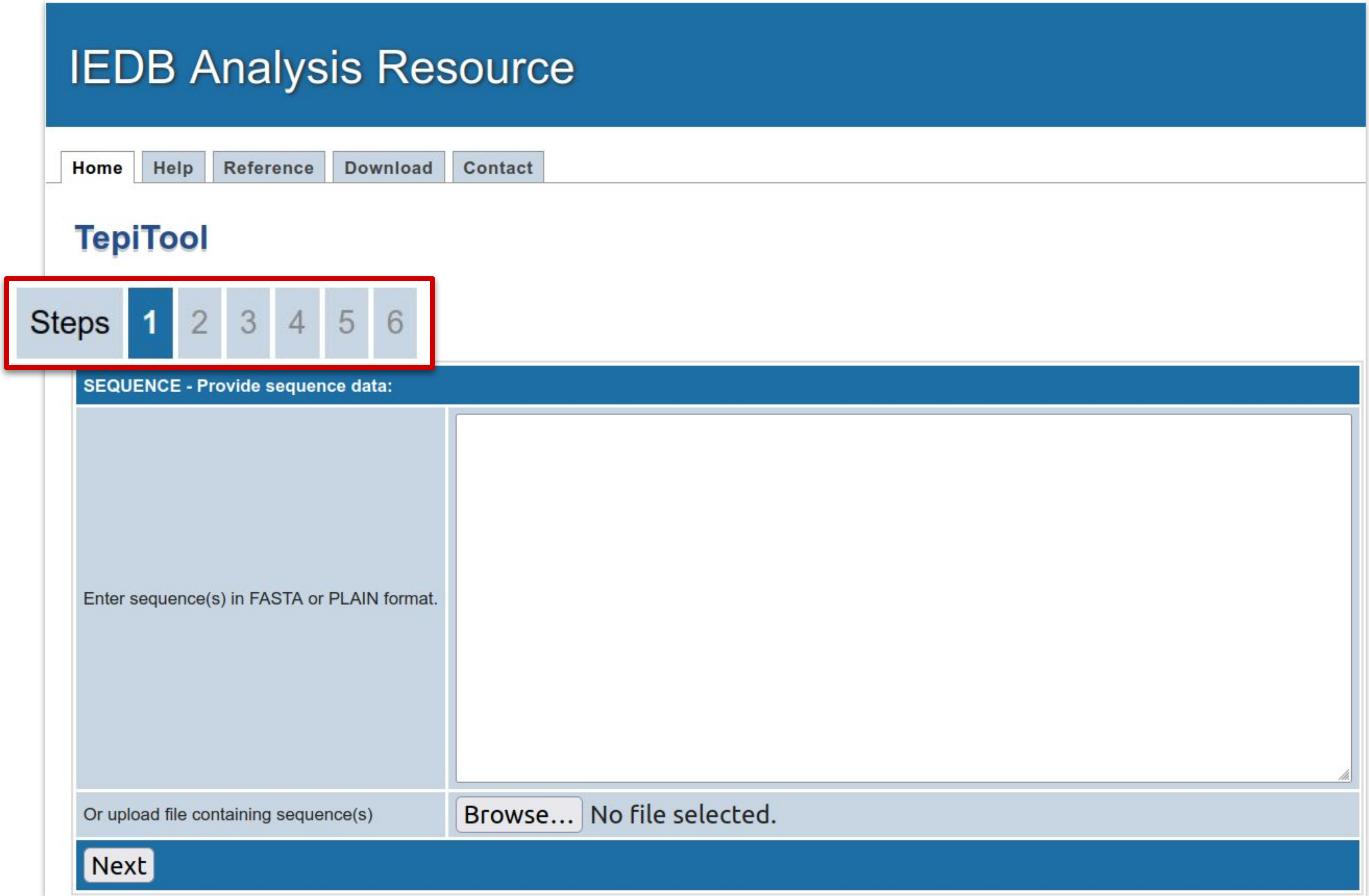
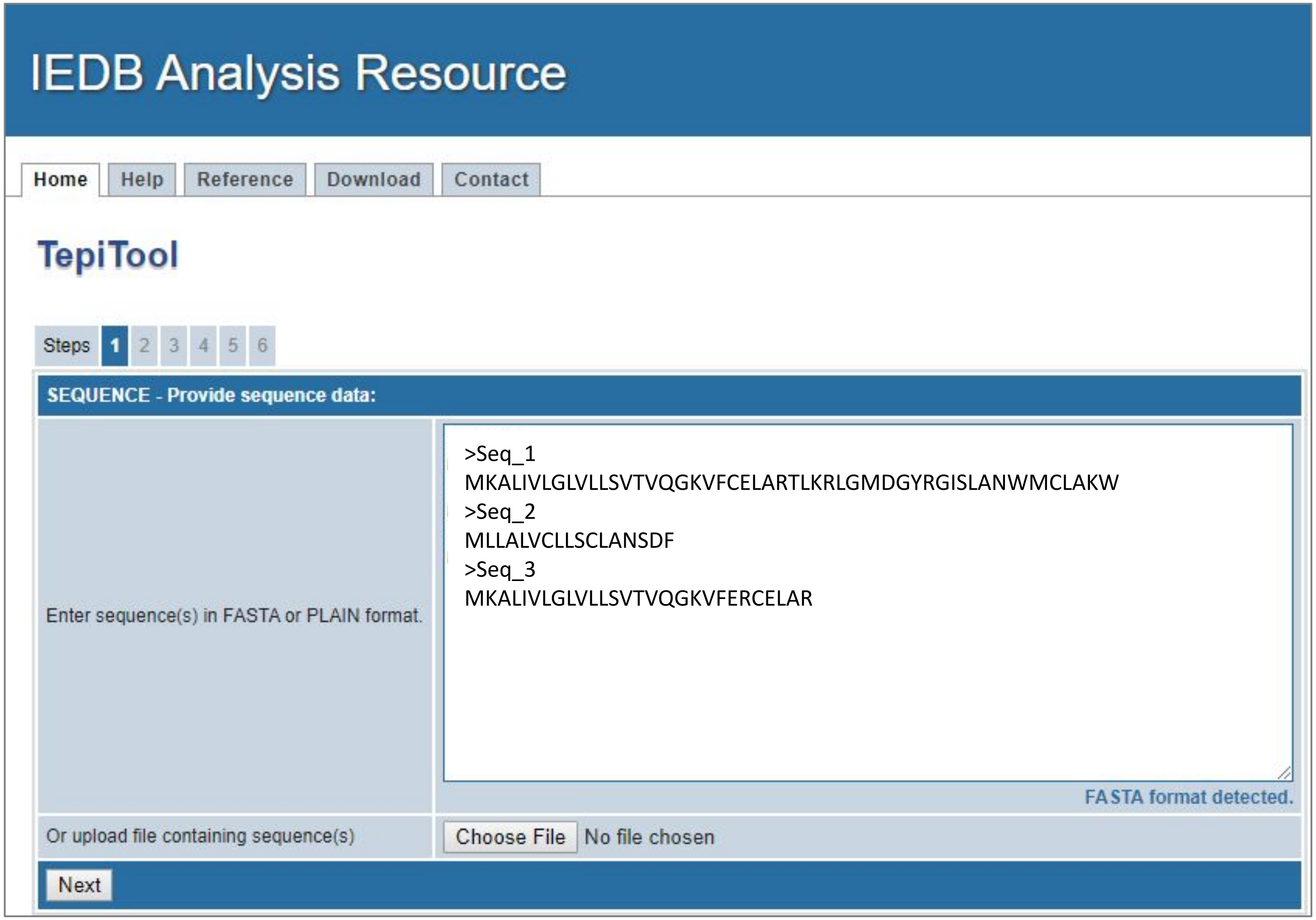


Enter sequence(s) in FASTA or PLAIN format.

Or upload file containing sequence(s) No file selected.

Step 1: Sequence data

tools.iedb.org/tepitool/



TepiTool

SEQUENCE - Provide sequence data:

Enter sequence(s) in FASTA or PLAIN format.

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>Seq_1
MKALIVLGLVLLSVTVQGKVFCELARTLKRLGMDGYRGISLANWMCLAKW
>Seq_2
MLLALVCLLSCLANSDF
>Seq_3
MKALIVLGLVLLSVTVQGKVFERCELAR
```

FASTA format detected.

Or upload file containing sequence(s)

Step 2: Species & allele class

tools.iedb.org/tepitool/

SPECIES & ALLELE CLASS - Select the host species and MHC allele class:

Host species

- Chimpanzee
- Cow
- Gorilla
- Human
- Macaque
- Mouse
- Pig

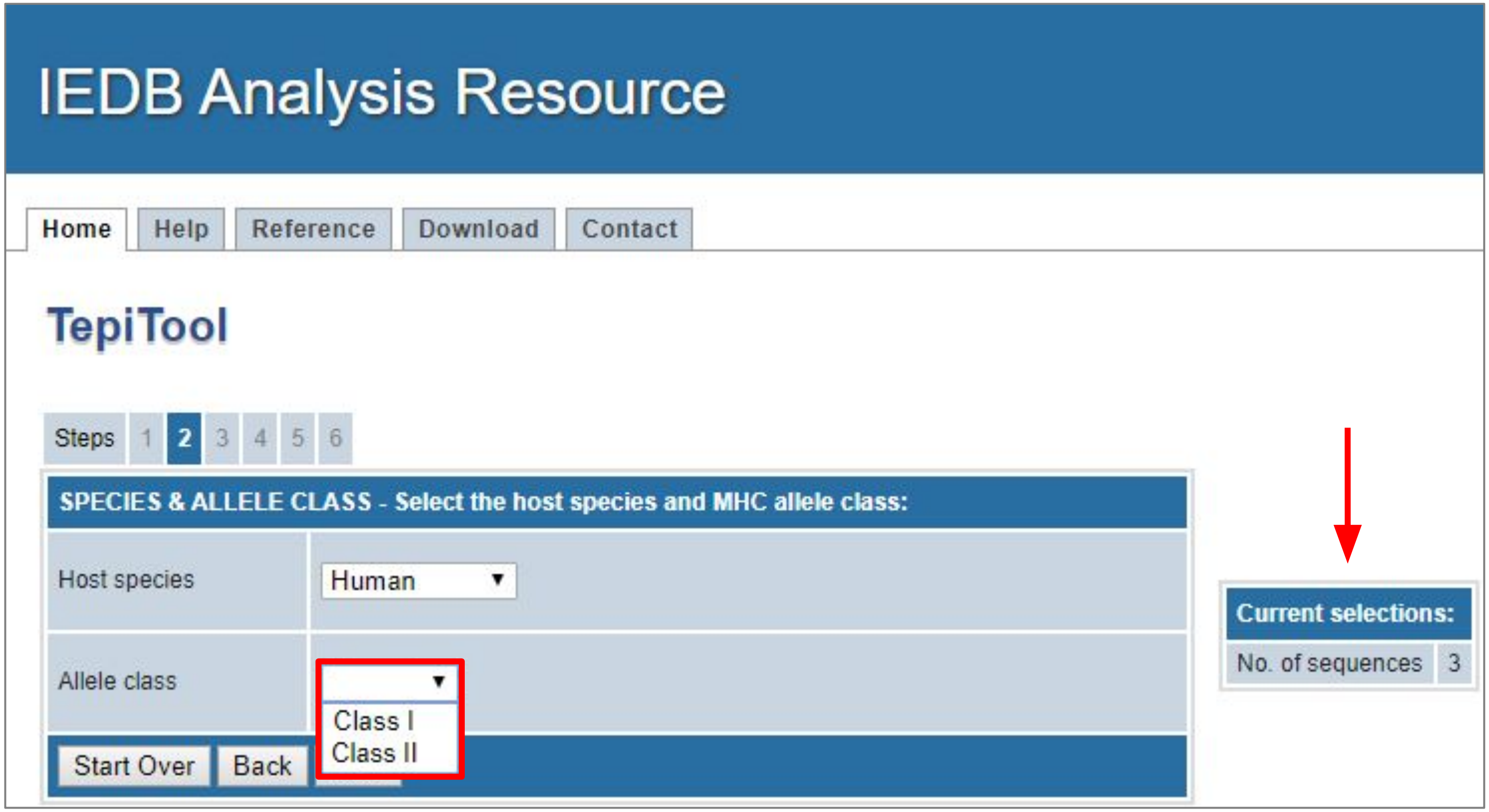
Allele class

Current selections:

No. of sequences	3

Step 2: Species & allele class

tools.iedb.org/tepitool/



SPECIES & ALLELE CLASS - Select the host species and MHC allele class:

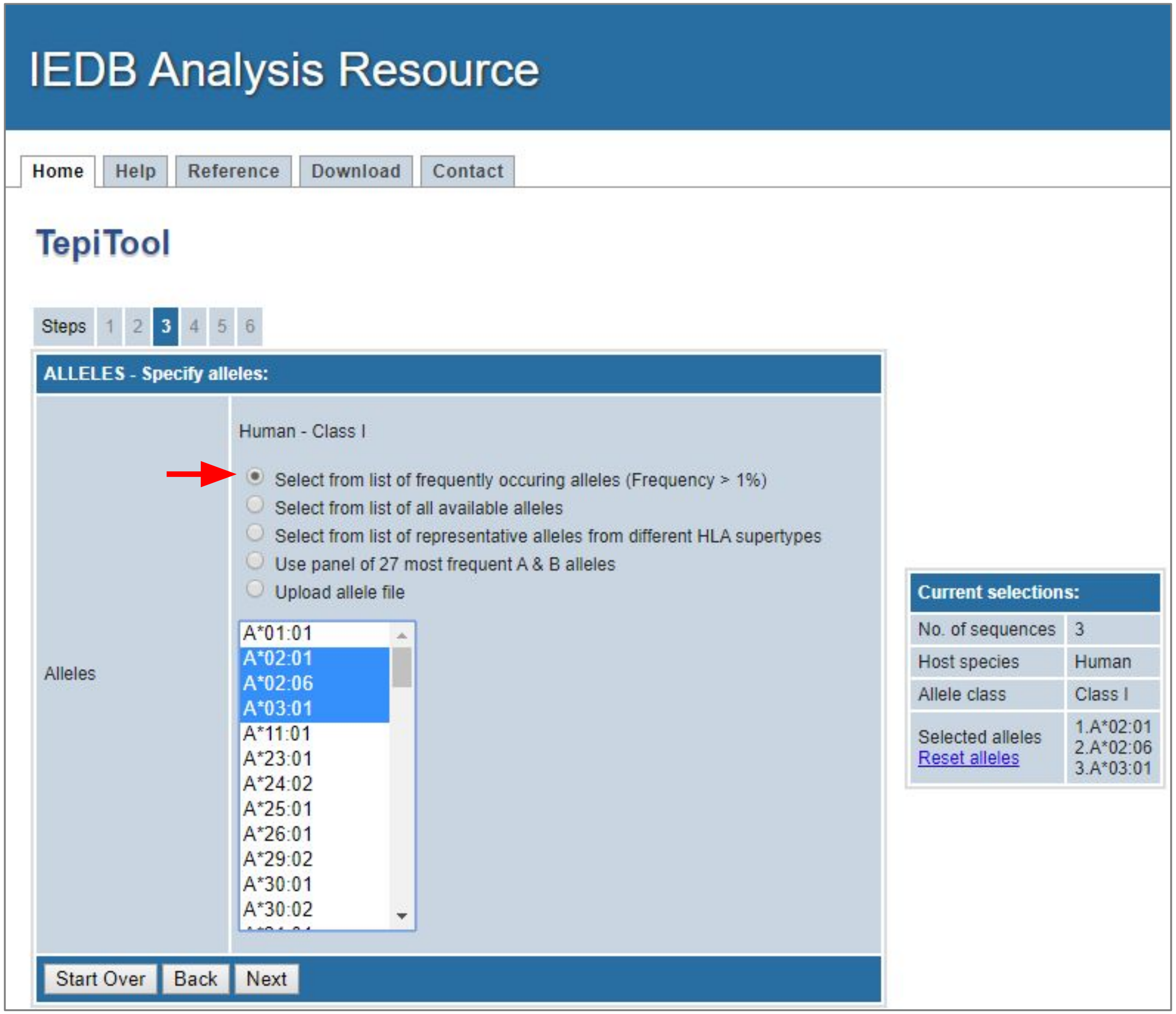
Host species	Human
Allele class	

Current selections:

No. of sequences	3

Step 3: Alleles - Class I

tools.iedb.org/tepitool/



TepiTool

ALLELES - Specify alleles:

Alleles

Human - Class I

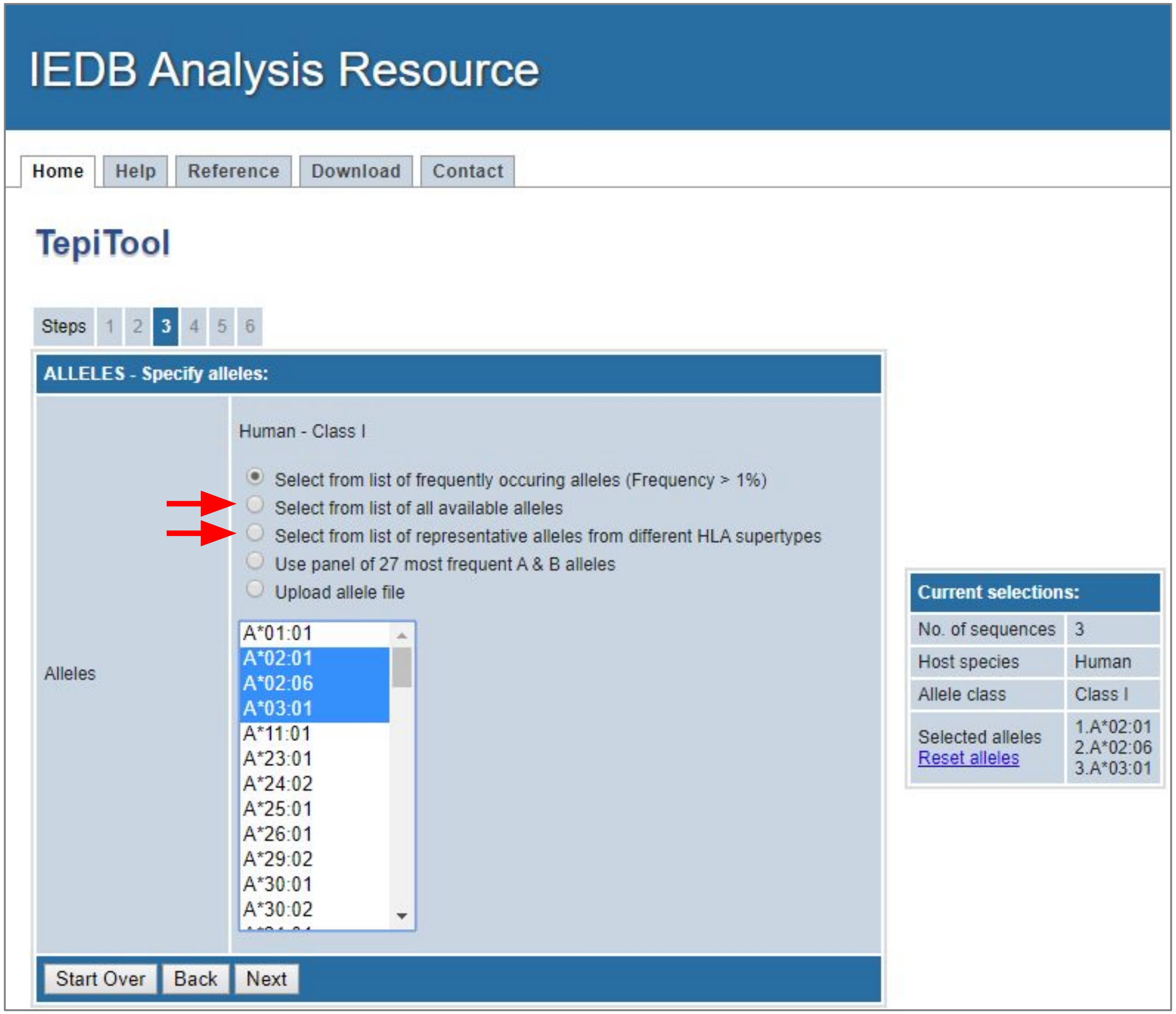
- ● Select from list of frequently occuring alleles (Frequency > 1%)
- ○ Select from list of all available alleles
- ○ Select from list of representative alleles from different HLA supertypes
- ○ Use panel of 27 most frequent A & B alleles
- ○ Upload allele file

A*01:01
A*02:01
A*02:06
A*03:01
A*11:01
A*23:01
A*24:02
A*25:01
A*26:01
A*29:02
A*30:01
A*30:02

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles Reset alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 3: Alleles - Class I

tools.iedb.org/tepitool/



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A*02:06
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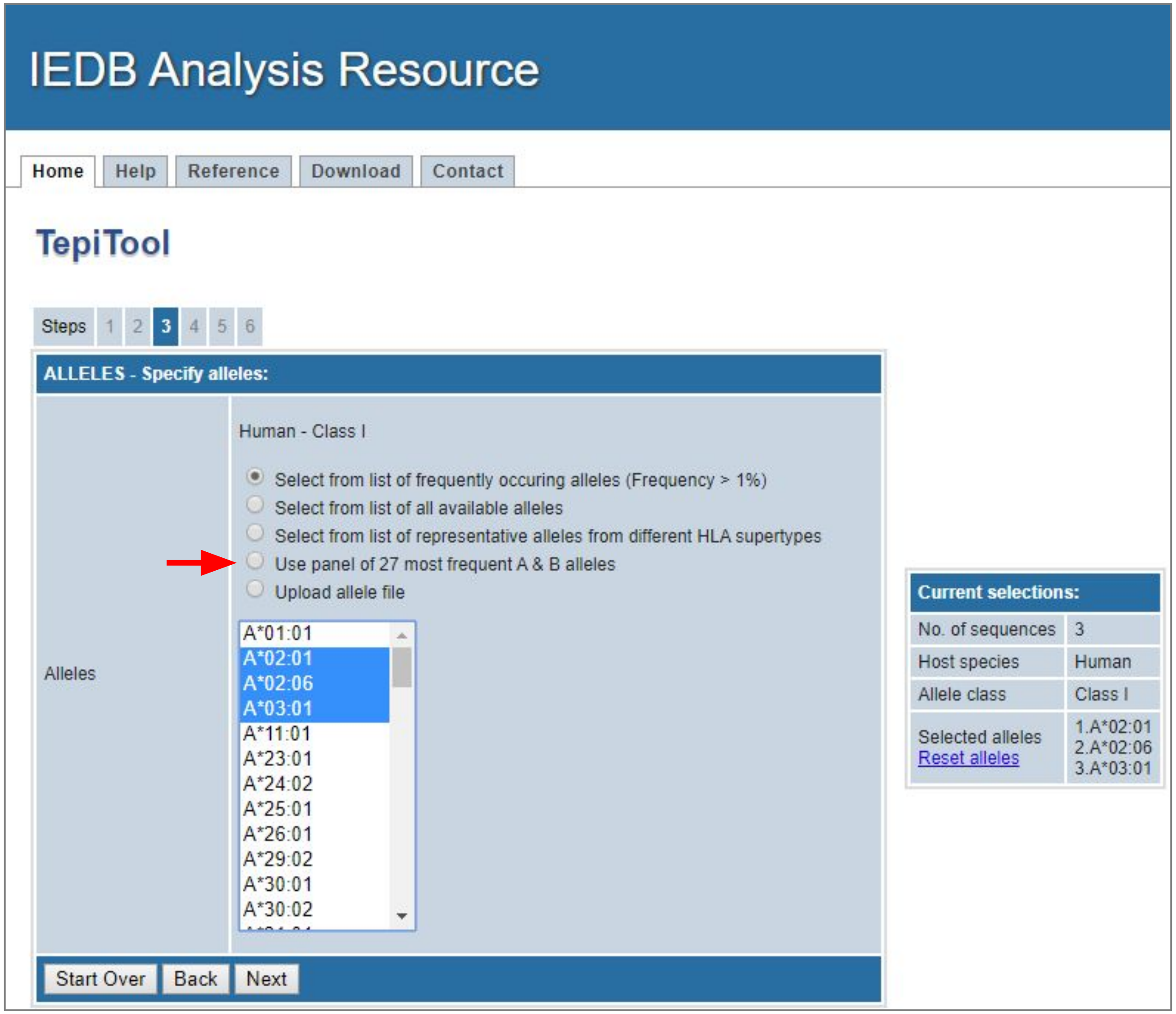
A*11:01
A*23:01
A*24:02
A*25:01
A*26:01
A*29:02
A*30:01
A*30:02

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles Reset alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 3: Alleles - Class I

tools.iedb.org/tepitool/



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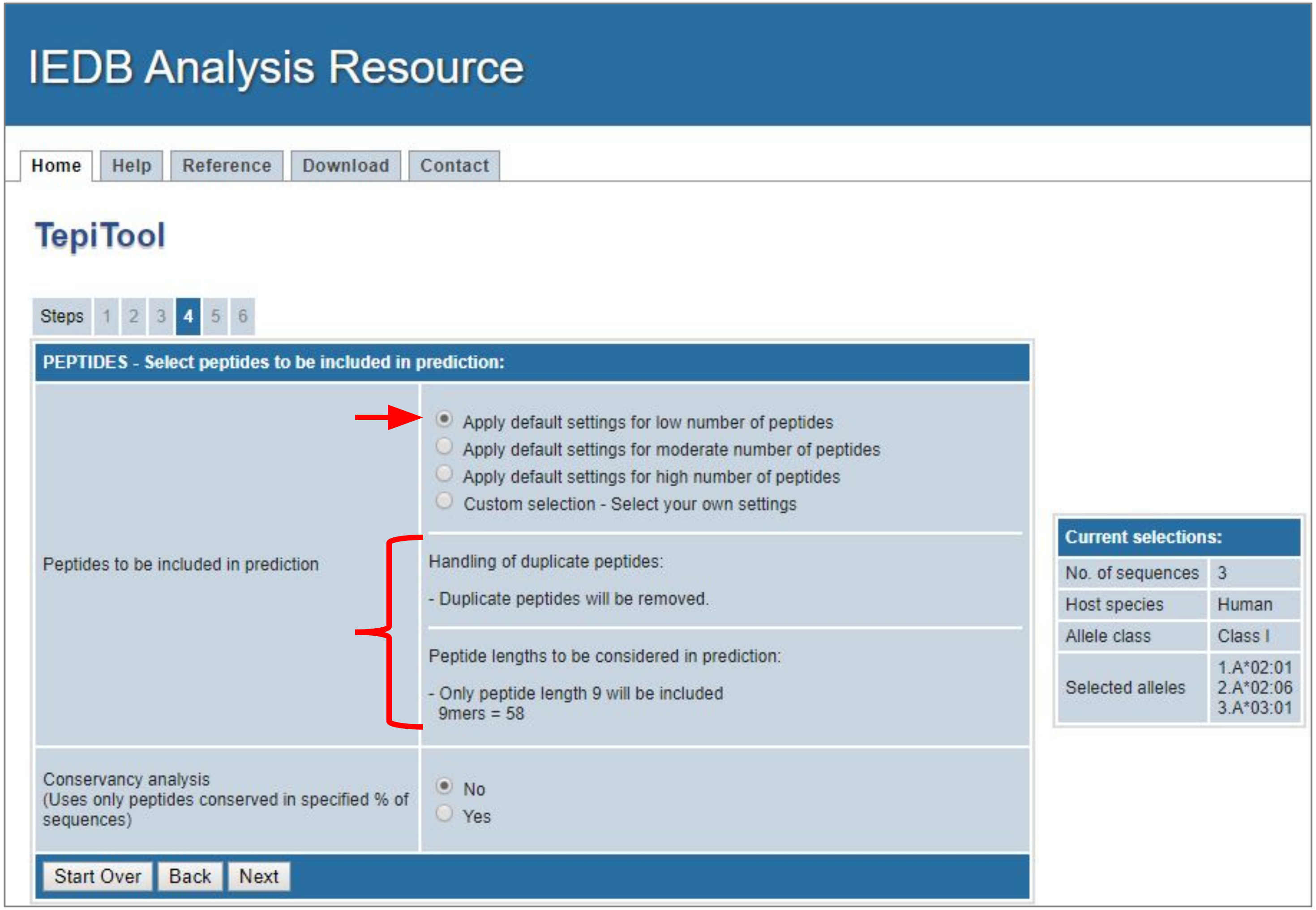
A*01:01
A*02:01
A*02:06
A*03:01
A*11:01
A*23:01
A*24:02
A*25:01
A*26:01
A*29:02
A*30:01
A*30:02

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles Reset alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 4: Peptides - Class I

tools.iedb.org/tepitool/



TepiTool

Steps 1 2 3 **4** 5 6

PEPTIDES - Select peptides to be included in prediction:

Peptides to be included in prediction

● Apply default settings for low number of peptides
○ Apply default settings for moderate number of peptides
○ Apply default settings for high number of peptides
○ Custom selection - Select your own settings

Handling of duplicate peptides:

- Duplicate peptides will be removed.

Peptide lengths to be considered in prediction:

- Only peptide length 9 will be included
9mers = 58

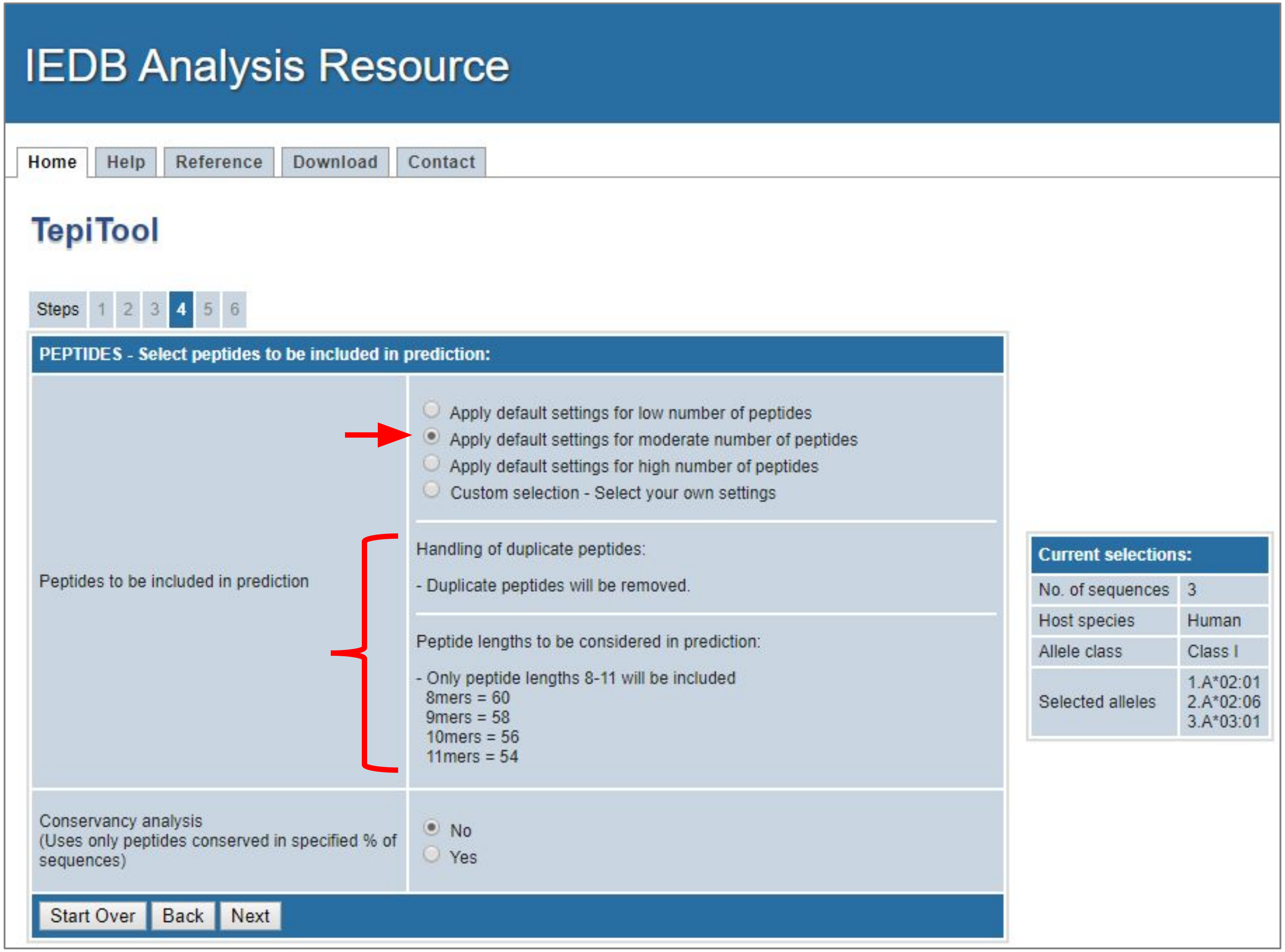
Conservancy analysis
(Uses only peptides conserved in specified % of sequences)

● No
○ Yes

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 4: Peptides - Class I

tools.iedb.org/tepitool/



TepiTool

PEPTIDES - Select peptides to be included in prediction:

Peptides to be included in prediction

○ Apply default settings for low number of peptides
● Apply default settings for moderate number of peptides
○ Apply default settings for high number of peptides
○ Custom selection - Select your own settings

Handling of duplicate peptides:

- Duplicate peptides will be removed.

Peptide lengths to be considered in prediction:

- Only peptide lengths 8-11 will be included

8mers = 60
9mers = 58
10mers = 56
11mers = 54

Conservancy analysis (Uses only peptides conserved in specified % of sequences)

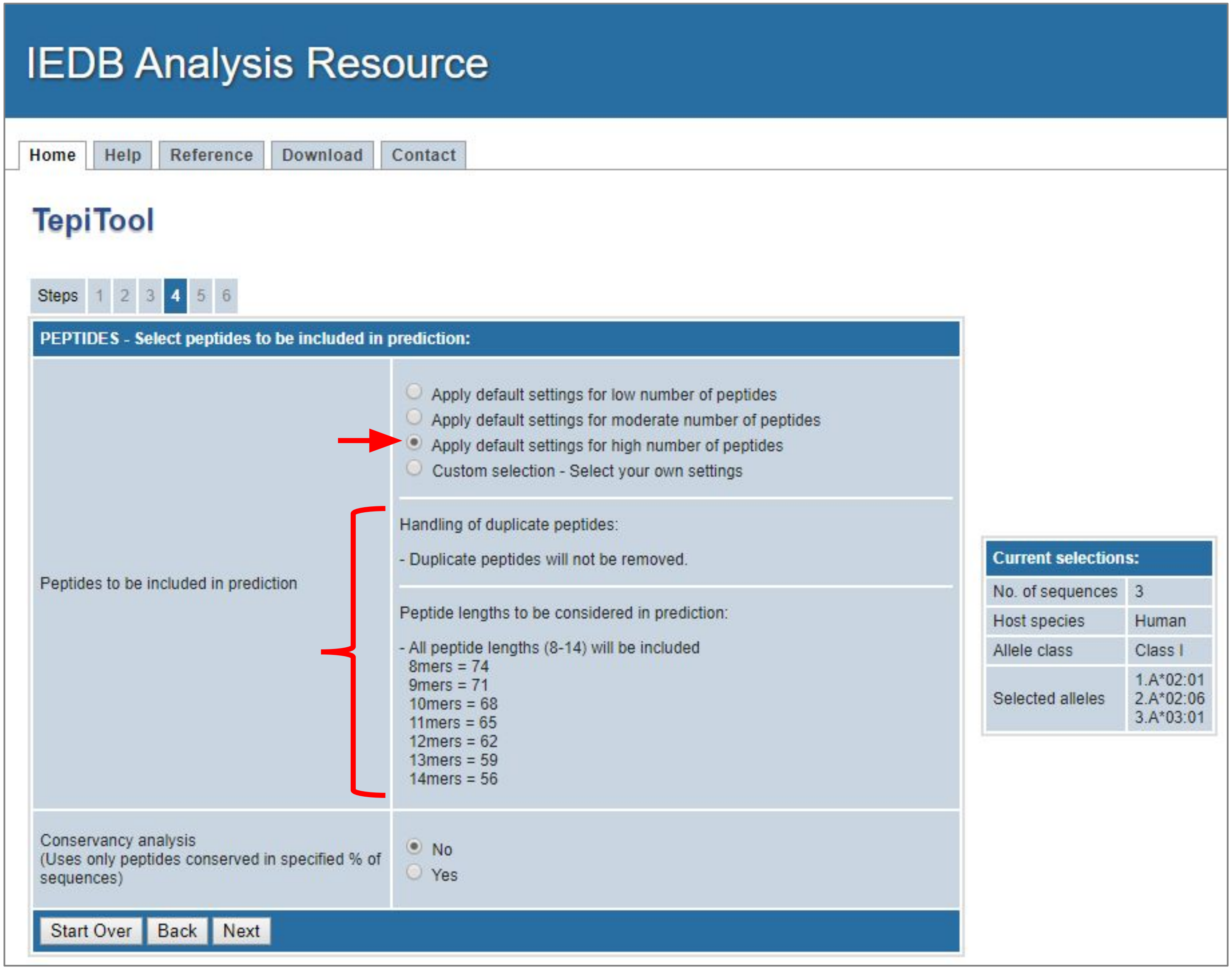
● No
○ Yes

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 4: Peptides - Class I

tools.iedb.org/tepitool/



PEPTIDES - Select peptides to be included in prediction:

Peptides to be included in prediction

- ○ Apply default settings for low number of peptides
- ○ Apply default settings for moderate number of peptides
- ● Apply default settings for high number of peptides
- ○ Custom selection - Select your own settings

Handling of duplicate peptides:

- Duplicate peptides will not be removed.

Peptide lengths to be considered in prediction:

- All peptide lengths (8-14) will be included

8mers = 74
9mers = 71
10mers = 68
11mers = 65
12mers = 62
13mers = 59
14mers = 56

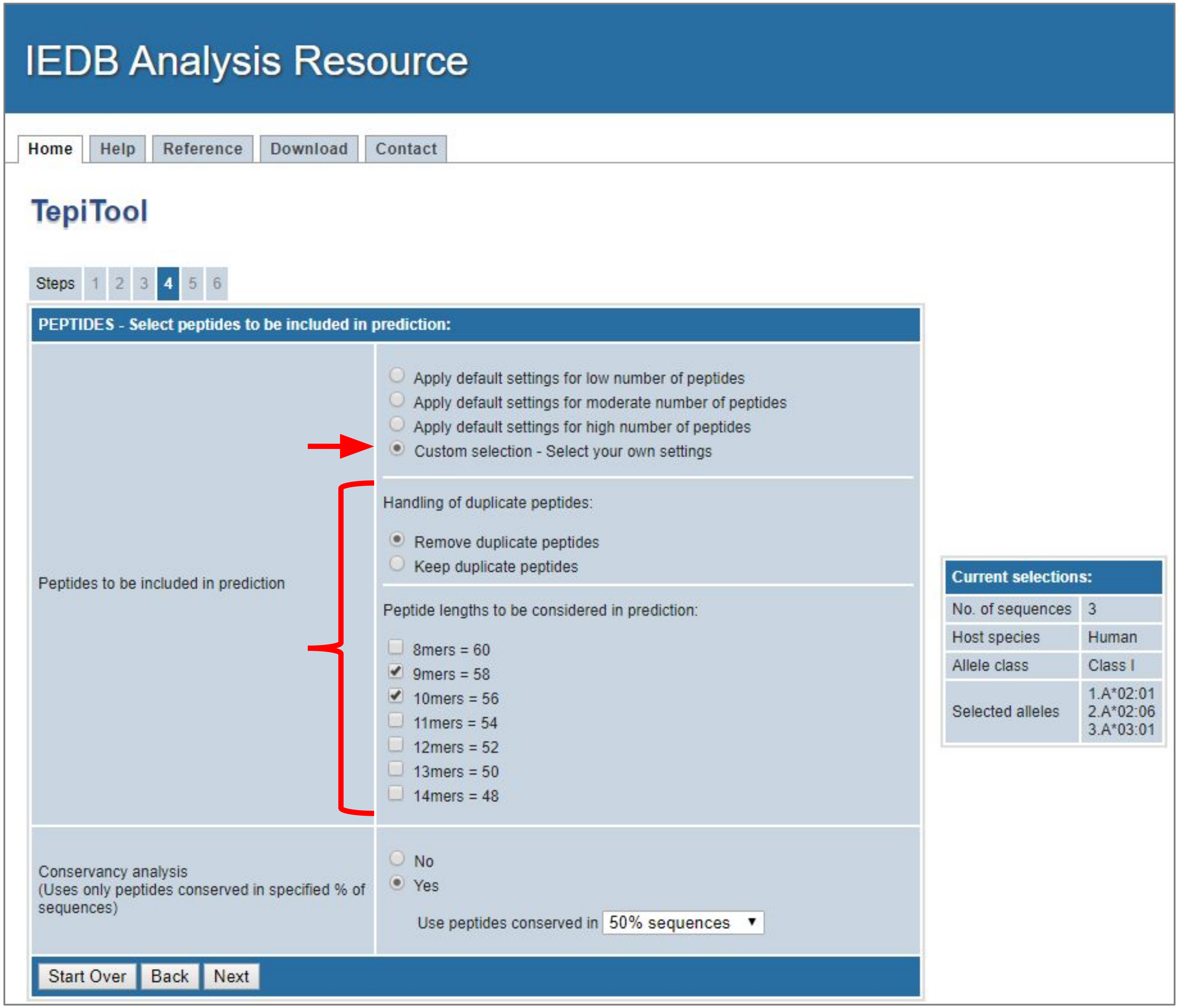
Conservancy analysis (Uses only peptides conserved in specified % of sequences)

- ● No
- ○ Yes

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 4: Peptides - Class I

tools.iedb.org/tepitool/



TepiTool

Steps 1 2 3 **4** 5 6

PEPTIDES - Select peptides to be included in prediction:

Peptides to be included in prediction

○ Apply default settings for low number of peptides
○ Apply default settings for moderate number of peptides
○ Apply default settings for high number of peptides
● Custom selection - Select your own settings

Handling of duplicate peptides:

● Remove duplicate peptides
○ Keep duplicate peptides

Peptide lengths to be considered in prediction:

☐ 8mers = 60
☑ 9mers = 58
☑ 10mers = 56
☐ 11mers = 54
☐ 12mers = 52
☐ 13mers = 50
☐ 14mers = 48

Conservancy analysis
(Uses only peptides conserved in specified % of sequences)

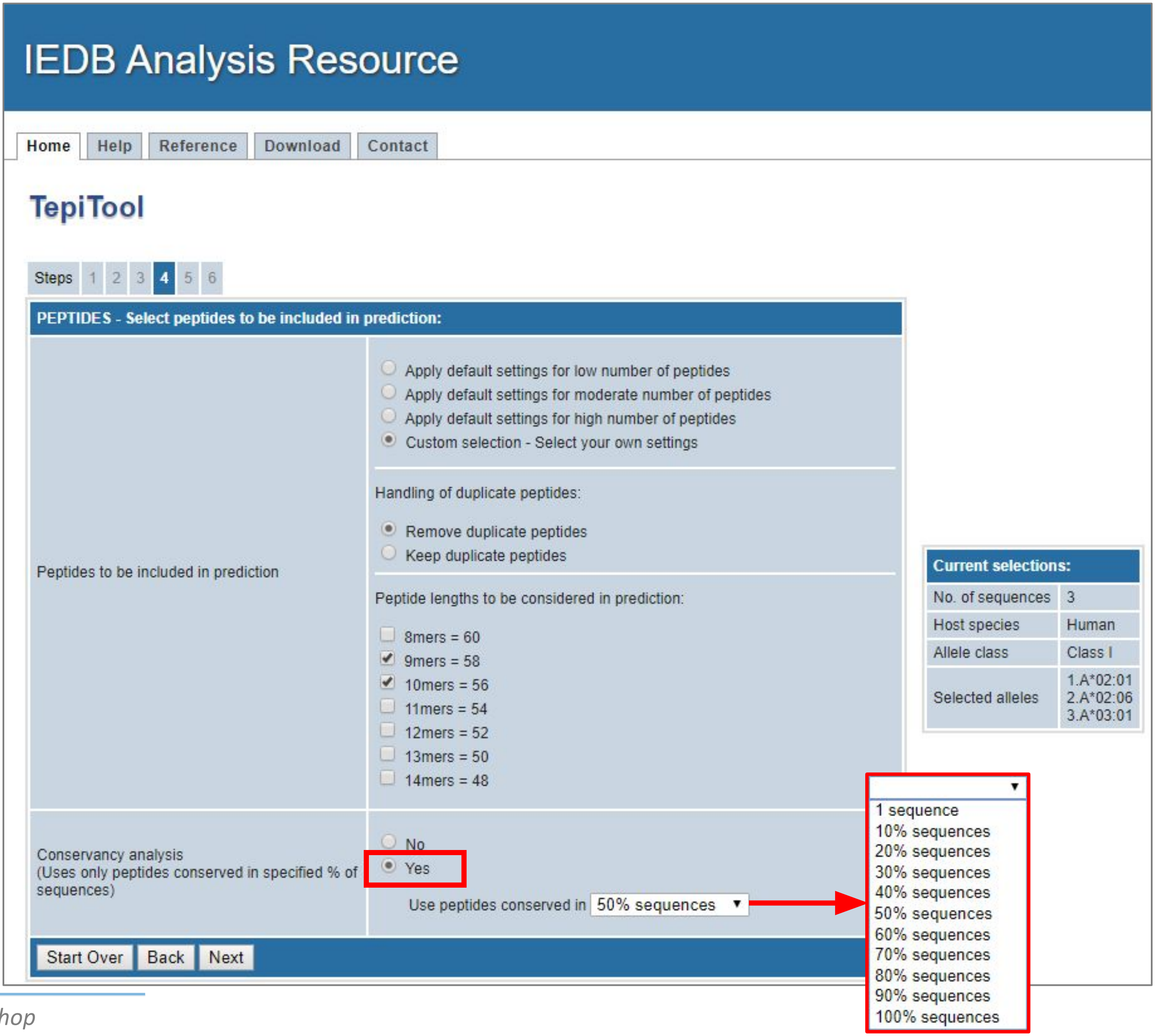
○ No
● Yes

Use peptides conserved in 50% sequences ▼

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 4: Peptides - Class I

tools.iedb.org/tepitool/



TepiTool

PEPTIDES - Select peptides to be included in prediction:

Peptides to be included in prediction

○ Apply default settings for low number of peptides
○ Apply default settings for moderate number of peptides
○ Apply default settings for high number of peptides
● Custom selection - Select your own settings

Handling of duplicate peptides:

● Remove duplicate peptides
○ Keep duplicate peptides

Peptide lengths to be considered in prediction:

☐ 8mers = 60
☑ 9mers = 58
☑ 10mers = 56
☐ 11mers = 54
☐ 12mers = 52
☐ 13mers = 50
☐ 14mers = 48

Conservancy analysis
(Uses only peptides conserved in specified % of sequences)

○ No
● Yes

Use peptides conserved in 50% sequences ▼

1 sequence
10% sequences
20% sequences
30% sequences
40% sequences
50% sequences
60% sequences
70% sequences
80% sequences
90% sequences
100% sequences

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01

Step 5: Method - Class I

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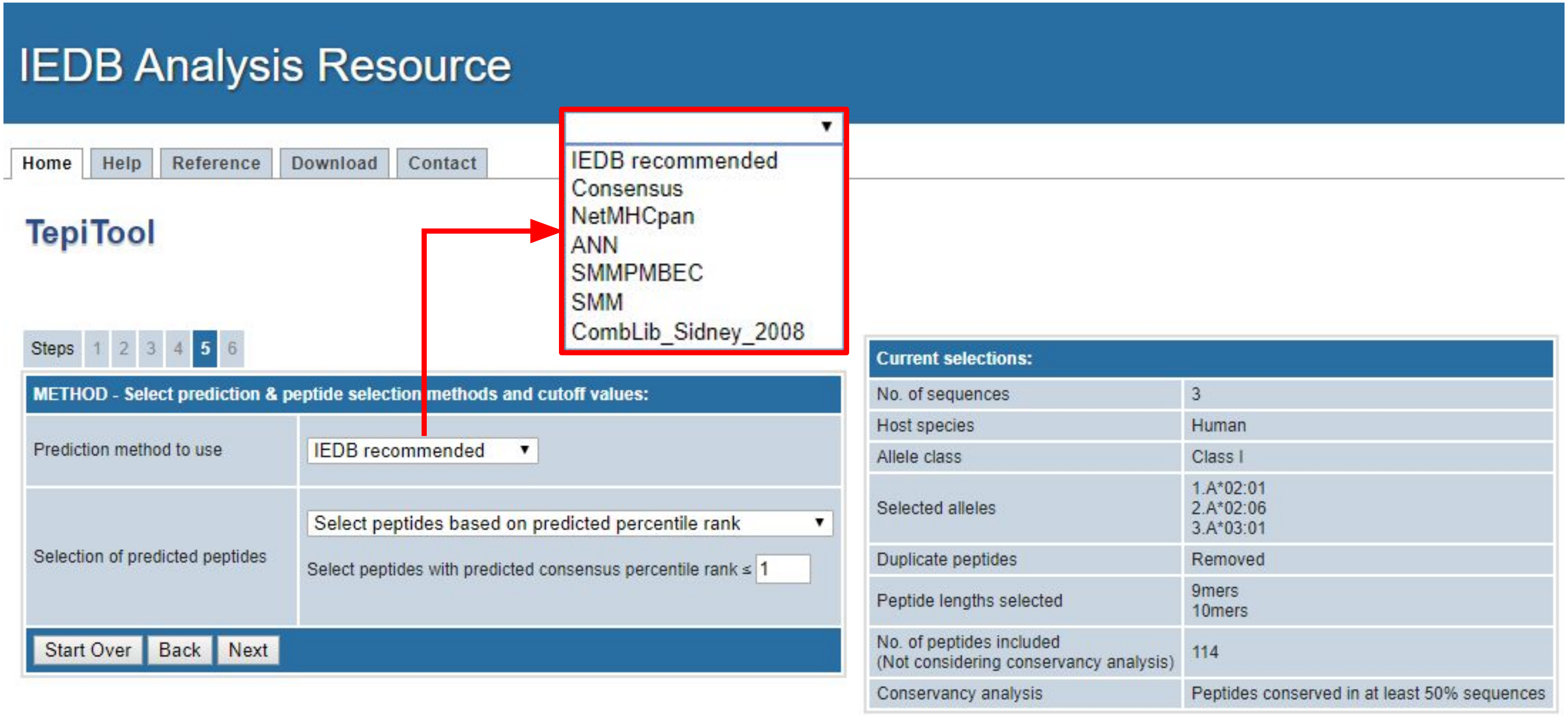


METHOD - Select prediction & peptide selection methods and cutoff values:

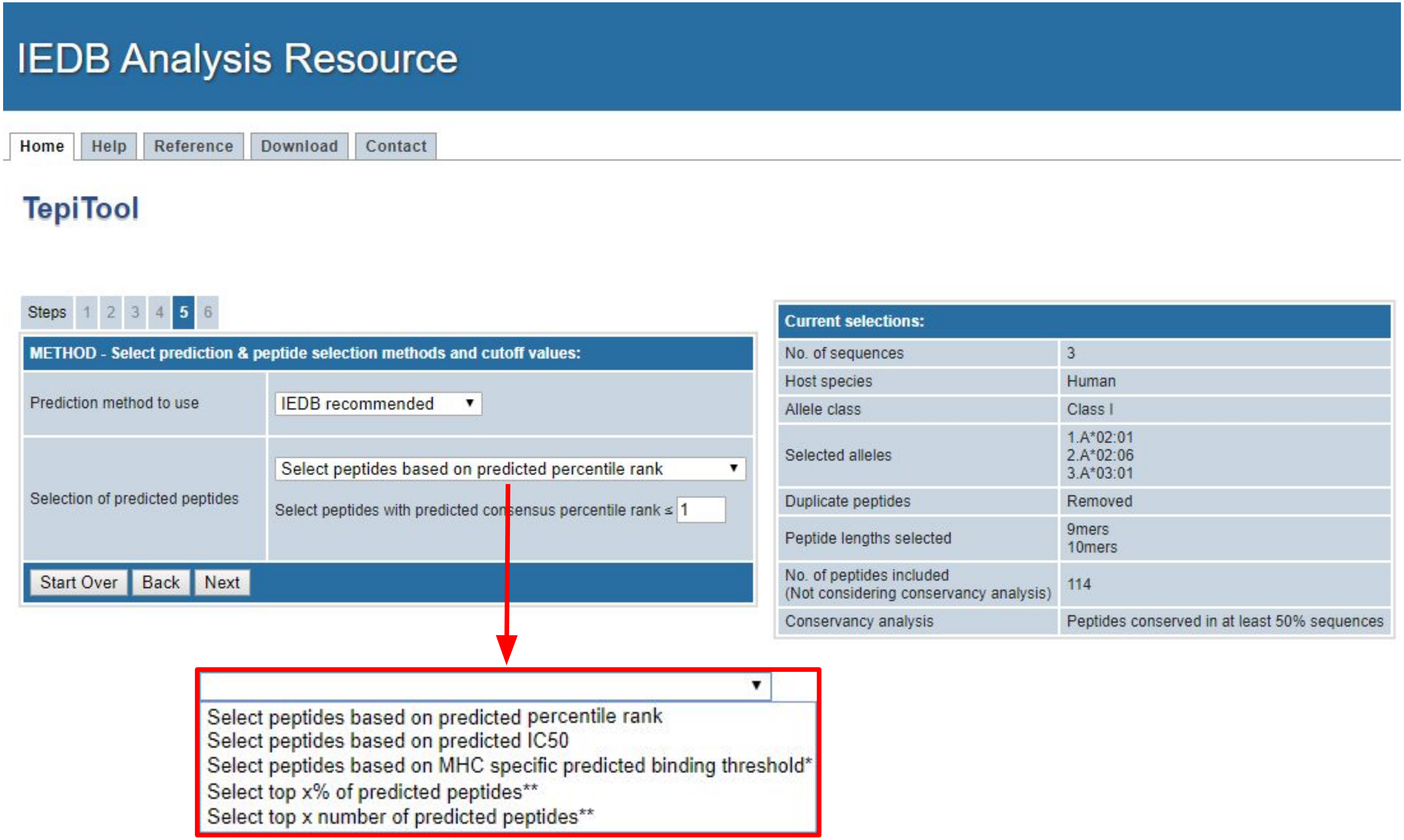
Prediction method to use	IEDB recommended
Selection of predicted peptides	Select peptides based on predicted percentile rank Select peptides with predicted consensus percentile rank ≤ 1

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01
Duplicate peptides	Removed
Peptide lengths selected	9mers 10mers
No. of peptides included (Not considering conservancy analysis)	114
Conservancy analysis	Peptides conserved in at least 50% sequences

Step 5: Method - Class I

tools.iedb.org/tepitool/



TepiTool

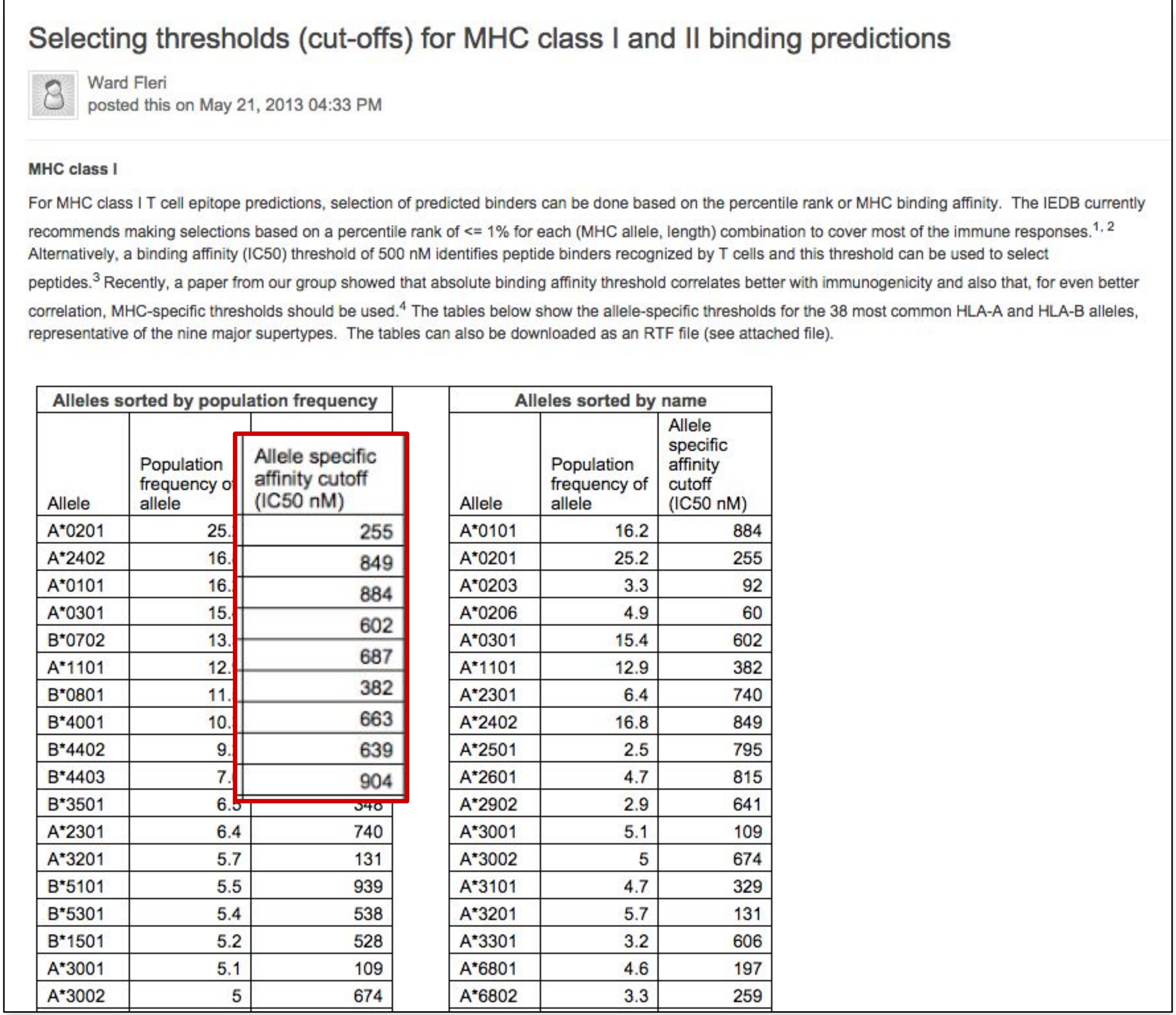
METHOD - Select prediction & peptide selection methods and cutoff values:

Prediction method to use	IEDB recommended ▾
Selection of predicted peptides	Select peptides based on predicted percentile rank ▾ Select peptides with predicted consensus percentile rank ≤ 1

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class I
Selected alleles	1.A*02:01 2.A*02:06 3.A*03:01
Duplicate peptides	Removed
Peptide lengths selected	9mers 10mers
No. of peptides included (Not considering conservancy analysis)	114
Conservancy analysis	Peptides conserved in at least 50% sequences

- Select peptides based on predicted percentile rank
- Select peptides based on predicted IC50
- Select peptides based on MHC specific predicted binding threshold*
- Select top x% of predicted peptides**
- Select top x number of predicted peptides**



Selecting thresholds (cut-offs) for MHC class I and II binding predictions

Ward Fleri
posted this on May 21, 2013 04:33 PM

MHC class I

For MHC class I T cell epitope predictions, selection of predicted binders can be done based on the percentile rank or MHC binding affinity. The IEDB currently recommends making selections based on a percentile rank of <= 1% for each (MHC allele, length) combination to cover most of the immune responses.[1, 2] Alternatively, a binding affinity (IC50) threshold of 500 nM identifies peptide binders recognized by T cells and this threshold can be used to select peptides.[3] Recently, a paper from our group showed that absolute binding affinity threshold correlates better with immunogenicity and also that, for even better correlation, MHC-specific thresholds should be used.[4] The tables below show the allele-specific thresholds for the 38 most common HLA-A and HLA-B alleles, representative of the nine major supertypes. The tables can also be downloaded as an RTF file (see attached file).

Alleles sorted by population frequency

Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
A*0201	25.	255
A*2402	16.	849
A*0101	16.	884
A*0301	15.	602
B*0702	13.	687
A*1101	12.	382
B*0801	11.	663
B*4001	10.	639
B*4402	9.	904
B*4403	7.	
B*3501	6.5	348
A*2301	6.4	740
A*3201	5.7	131
B*5101	5.5	939
B*5301	5.4	538
B*1501	5.2	528
A*3001	5.1	109
A*3002	5	674

Alleles sorted by name

Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
A*0101	16.2	884
A*0201	25.2	255
A*0203	3.3	92
A*0206	4.9	60
A*0301	15.4	602
A*1101	12.9	382
A*2301	6.4	740
A*2402	16.8	849
A*2501	2.5	795
A*2601	4.7	815
A*2902	2.9	641
A*3001	5.1	109
A*3002	5	674
A*3101	4.7	329
A*3201	5.7	131
A*3301	3.2	606
A*6801	4.6	197
A*6802	3.3	259

Step 5: Method - Class I

tools.iedb.org/tepitool/

METHOD - Select prediction & peptide selection methods and cutoff values:

Prediction method to use: IEDB recommended ▼

Selection of predicted peptides: Select peptides based on MHC specific predicted binding tl ▼

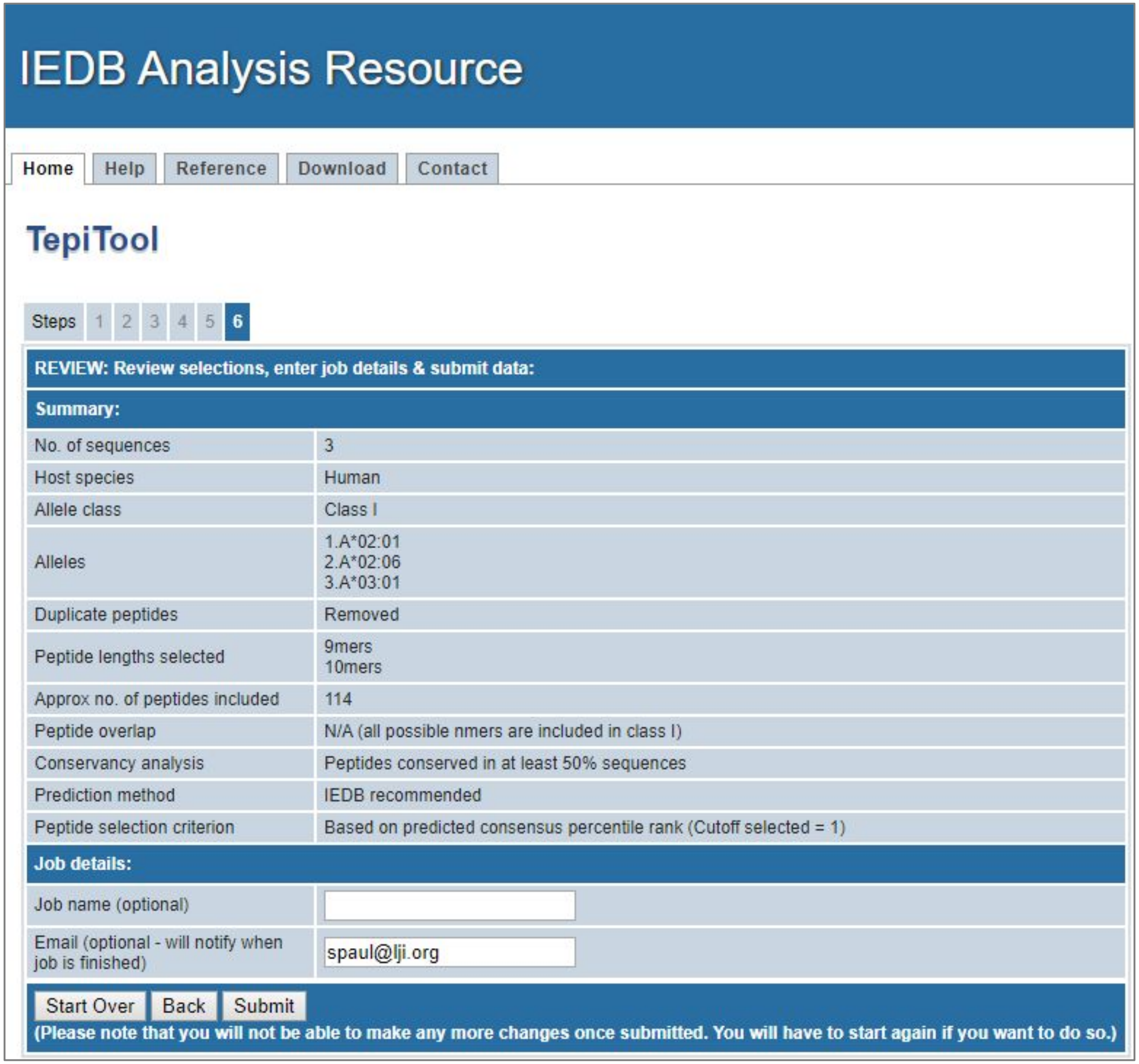
(*Each MHC allele has its own IC50 threshold.
Predicted peptides will correspond to 75% of immune response.
Prediction method is SMM)

As of now, only the following alleles are covered by this method:
A*01:01
A*02:01
A*02:03
A*02:06
A*03:01
A*11:01
A*23:01
A*24:02
A*25:01
A*26:01
A*29:02
A*30:01
A*30:02
A*31:01
A*32:01
A*33:01
A*68:01
A*68:02
B*07:02
B*08:01
B*14:02
B*15:01
B*18:01
B*27:05
B*35:01
B*35:03
B*38:01
B*39:01
B*40:01
B*40:02
B*44:02
B*44:03
B*46:01
B*48:01
B*51:01
B*53:01
B*57:01
B*58:01

Please refer this paper for more details: Paul et al. (2013) J of Immunol. 191(12): 5831-5839.

Step 5: Method - Class I

tools.iedb.org/tepitool/



REVIEW: Review selections, enter job details & submit data:

Summary:	
No. of sequences	3
Host species	Human
Allele class	Class I
Alleles	1.A*02:01 2.A*02:06 3.A*03:01
Duplicate peptides	Removed
Peptide lengths selected	9mers 10mers
Approx no. of peptides included	114
Peptide overlap	N/A (all possible nmers are included in class I)
Conservancy analysis	Peptides conserved in at least 50% sequences
Prediction method	IEDB recommended
Peptide selection criterion	Based on predicted consensus percentile rank (Cutoff selected = 1)

Job details:	
Job name (optional)	
Email (optional - will notify when job is finished)	spaul@lji.org

(Please note that you will not be able to make any more changes once submitted. You will have to start again if you want to do so.)

Step 4: Peptides - Class II

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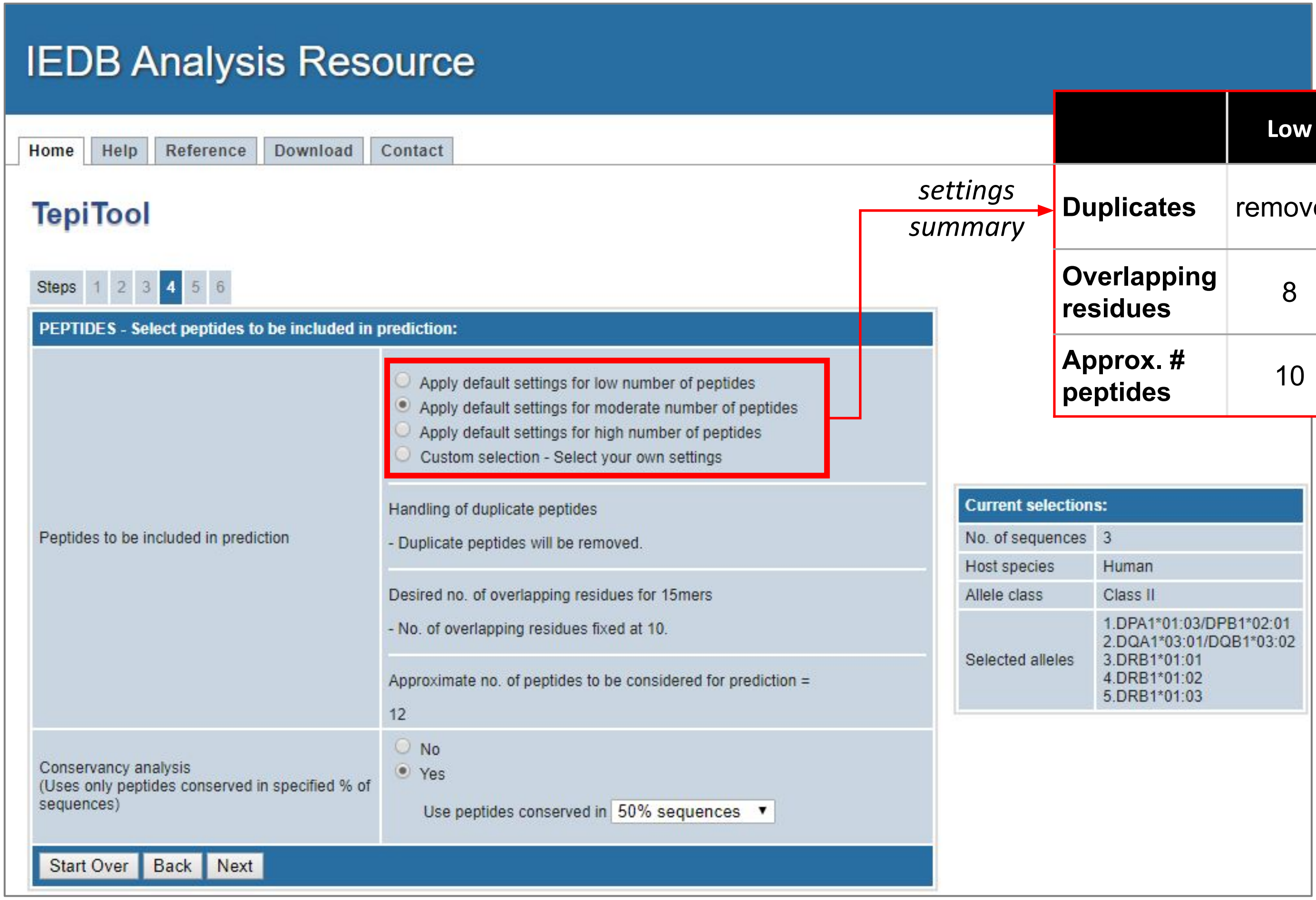


PEPTIDES - Select peptides to be included in prediction:

Peptides to be included in prediction

- ○ Apply default settings for low number of peptides
- ● Apply default settings for moderate number of peptides
- ○ Apply default settings for high number of peptides
- ○ Custom selection - Select your own settings

Handling of duplicate peptides

- Duplicate peptides will be removed.

Desired no. of overlapping residues for 15mers

- No. of overlapping residues fixed at 10.

Approximate no. of peptides to be considered for prediction =

12

Conservancy analysis (Uses only peptides conserved in specified % of sequences)

- ○ No
- ● Yes

Use peptides conserved in 50% sequences ▼

Current selections:

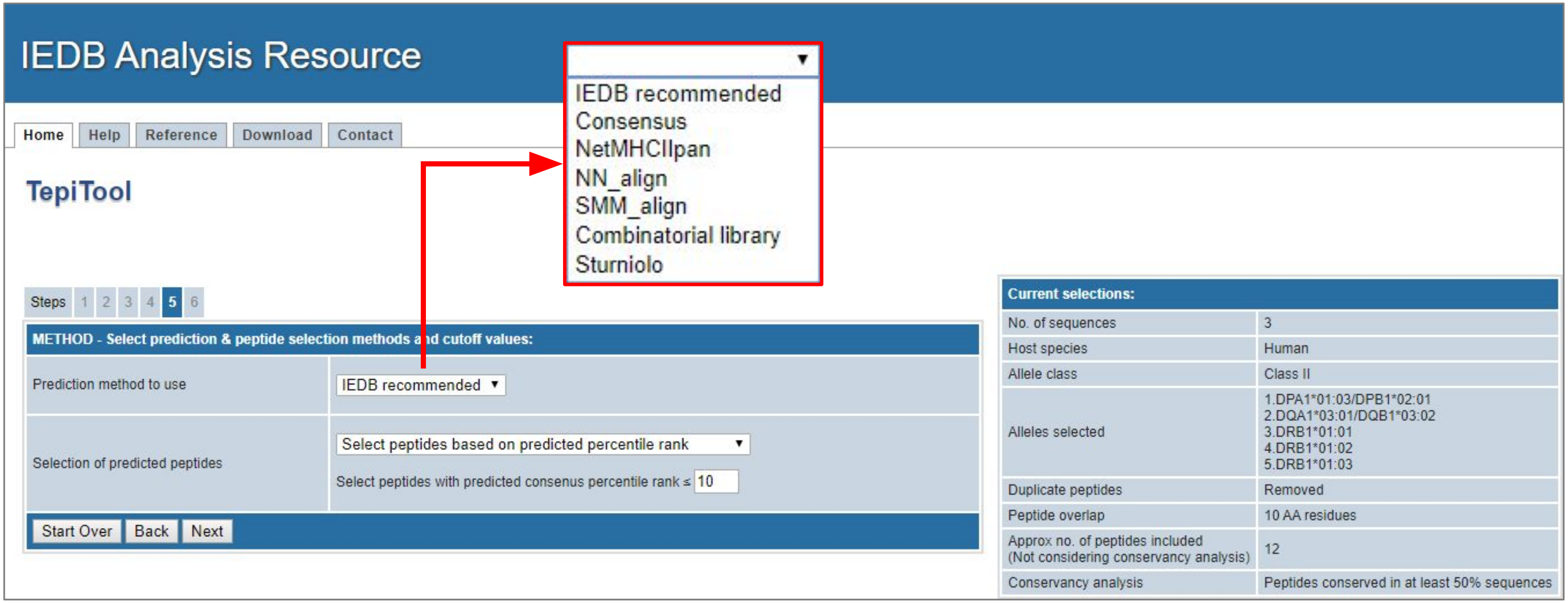
No. of sequences	3
Host species	Human
Allele class	Class II
Selected alleles	1.DPA1*01:03/DPB1*02:01 2.DQA1*03:01/DQB1*03:02 3.DRB1*01:01 4.DRB1*01:02 5.DRB1*01:03

settings summary

	Low	Moderate	High	Custom
Duplicates	removed	removed	not removed	user selects
Overlapping residues	8	10	10	user selects
Approx. # peptides	10	12	14	12

Step 5: Method - Class II

tools.iedb.org/tepitool/



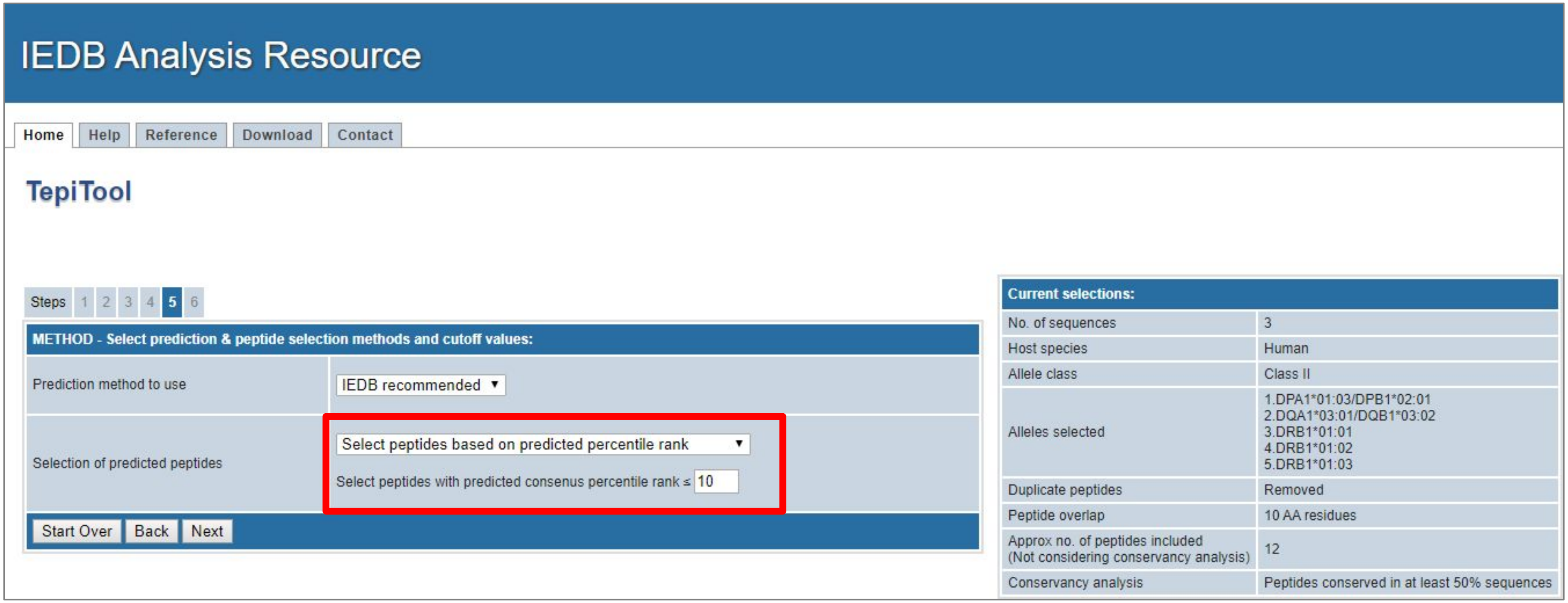
METHOD - Select prediction & peptide selection methods and cutoff values:

Prediction method to use	IEDB recommended ▼
Selection of predicted peptides	Select peptides based on predicted percentile rank ▼ Select peptides with predicted consenus percentile rank ≤ 10

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class II
Alleles selected	1.DPA1*01:03/DPB1*02:01 2.DQA1*03:01/DQB1*03:02 3.DRB1*01:01 4.DRB1*01:02 5.DRB1*01:03
Duplicate peptides	Removed
Peptide overlap	10 AA residues
Approx no. of peptides included (Not considering conservancy analysis)	12
Conservancy analysis	Peptides conserved in at least 50% sequences

Step 5: Method - Class II

tools.iedb.org/tepitool/



TepiTool

METHOD - Select prediction & peptide selection methods and cutoff values:

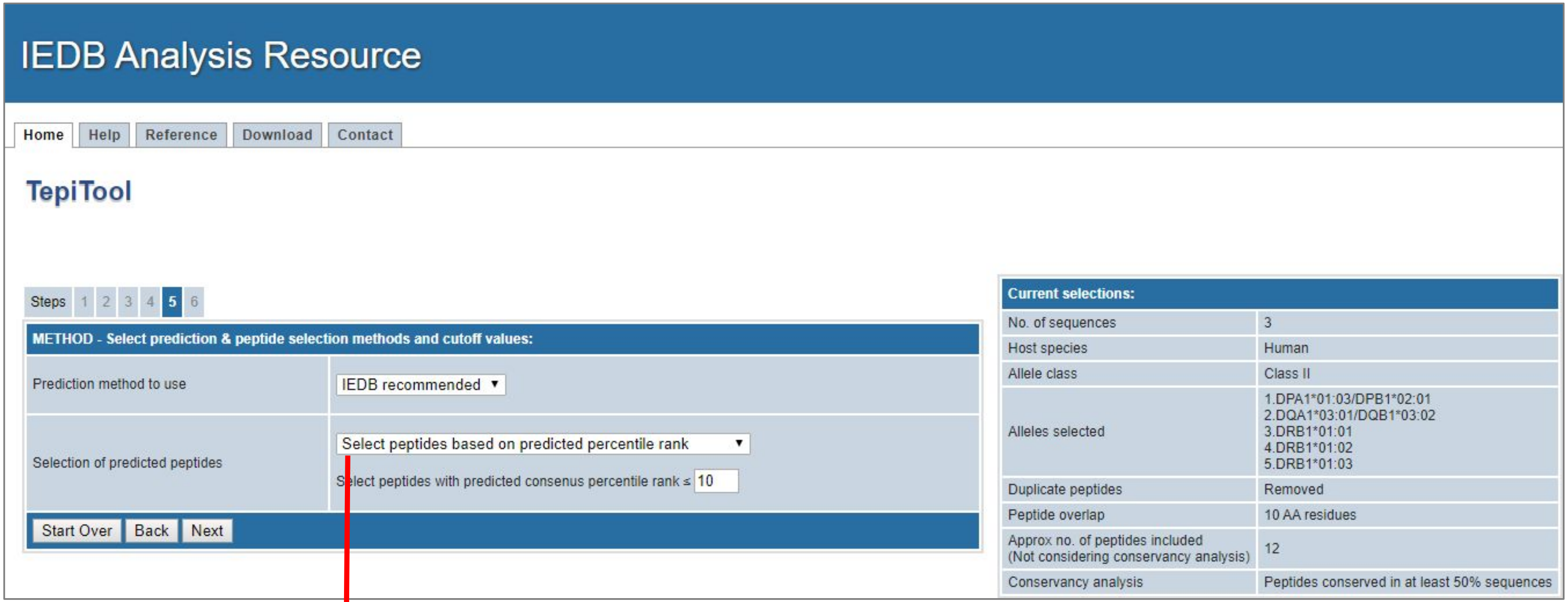
Prediction method to use	IEDB recommended ▾
Selection of predicted peptides	Select peptides based on predicted percentile rank ▾ Select peptides with predicted consenus percentile rank ≤ 10

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class II
Alleles selected	1.DPA1*01:03/DPB1*02:01 2.DQA1*03:01/DQB1*03:02 3.DRB1*01:01 4.DRB1*01:02 5.DRB1*01:03
Duplicate peptides	Removed
Peptide overlap	10 AA residues
Approx no. of peptides included (Not considering conservancy analysis)	12
Conservancy analysis	Peptides conserved in at least 50% sequences

Step 5: Method - Class II

tools.iedb.org/tepitool/



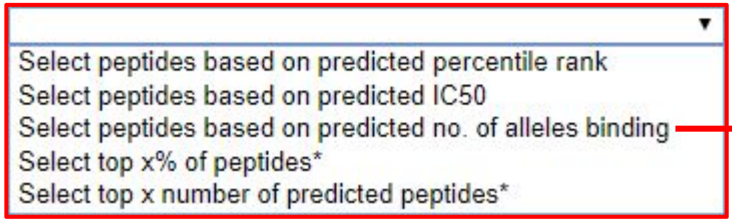
TepiTool

Steps 1 2 3 4 **5** 6

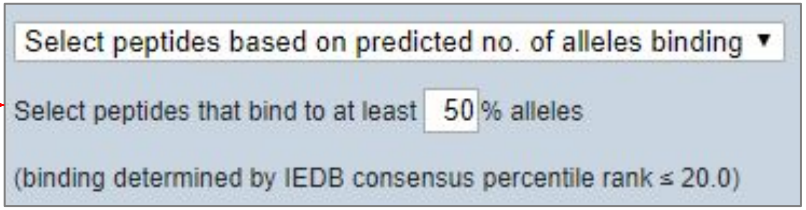
METHOD - Select prediction & peptide selection methods and cutoff values:

Prediction method to use	IEDB recommended ▾
Selection of predicted peptides	Select peptides based on predicted percentile rank ▾ Select peptides with predicted consensus percentile rank ≤ 10

Current selections:	
No. of sequences	3
Host species	Human
Allele class	Class II
Alleles selected	1.DPA1*01:03/DPB1*02:01 2.DQA1*03:01/DQB1*03:02 3.DRB1*01:01 4.DRB1*01:02 5.DRB1*01:03
Duplicate peptides	Removed
Peptide overlap	10 AA residues
Approx no. of peptides included (Not considering conservancy analysis)	12
Conservancy analysis	Peptides conserved in at least 50% sequences


- Select peptides based on predicted percentile rank
- Select peptides based on predicted IC50
- Select peptides based on predicted no. of alleles binding
- Select top x% of peptides*
- Select top x number of predicted peptides*

exclusive to class II


Select peptides based on predicted no. of alleles binding ▾

Select peptides that bind to at least 50 % alleles

(binding determined by IEDB consensus percentile rank ≤ 20.0)

Step 3-5: Class II -7 allele method

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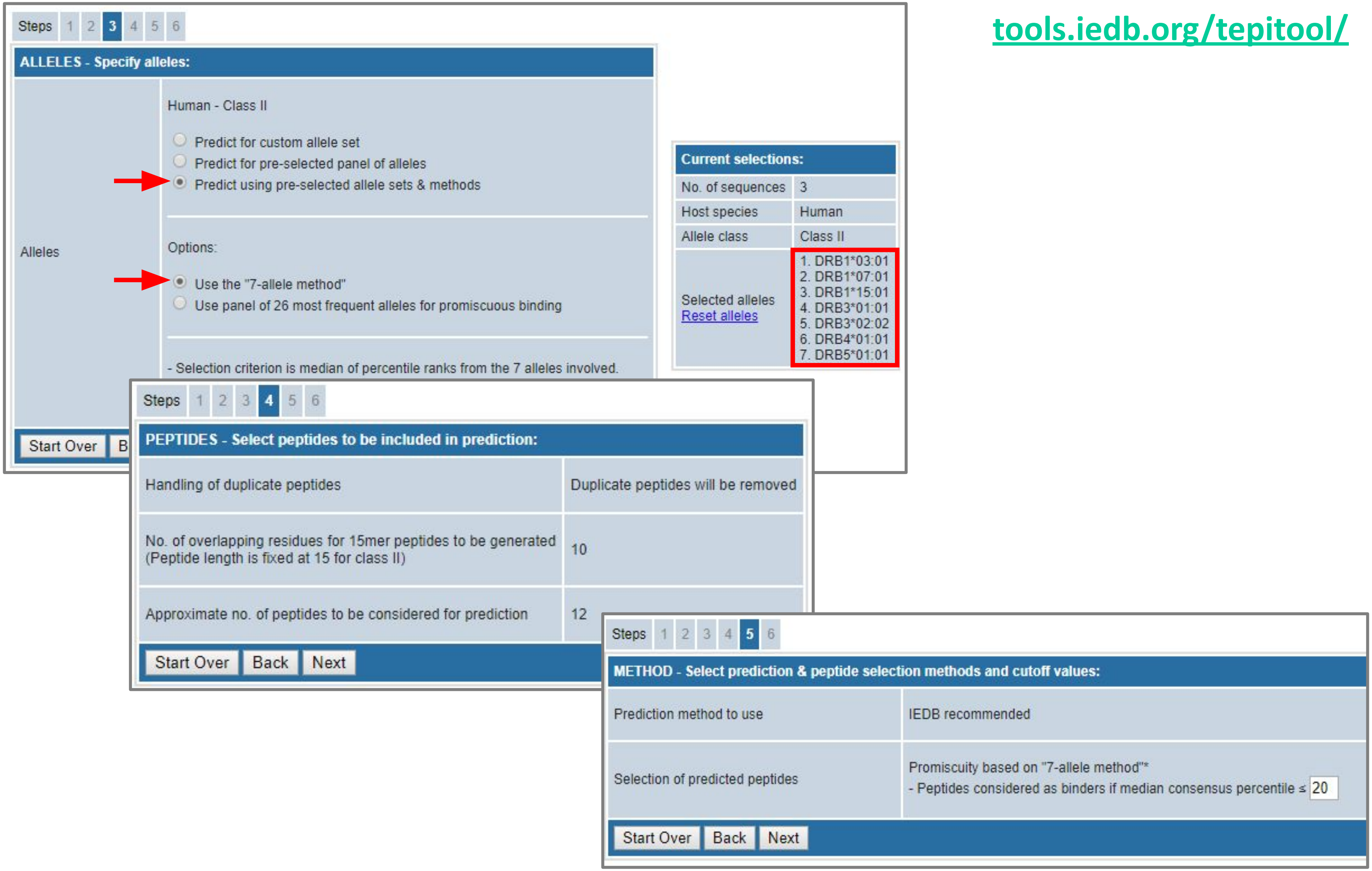

ALLELES - Specify alleles:

Alleles

Human - Class II

○ Predict for custom allele set
○ Predict for pre-selected panel of alleles
● Predict using pre-selected allele sets & methods

Options:

● Use the "7-allele method"
○ Use panel of 26 most frequent alleles for promiscuous binding

- Selection criterion is median of percentile ranks from the 7 alleles involved.

Current selections:

No. of sequences	3
Host species	Human
Allele class	Class II
Selected alleles Reset alleles	1. DRB1*03:01 2. DRB1*07:01 3. DRB1*15:01 4. DRB3*01:01 5. DRB3*02:02 6. DRB4*01:01 7. DRB5*01:01

PEPTIDES - Select peptides to be included in prediction:

Handling of duplicate peptides	Duplicate peptides will be removed
No. of overlapping residues for 15mer peptides to be generated (Peptide length is fixed at 15 for class II)	10
Approximate no. of peptides to be considered for prediction	12

METHOD - Select prediction & peptide selection methods and cutoff values:

Prediction method to use	IEDB recommended
Selection of predicted peptides	Promiscuity based on "7-allele method"* - Peptides considered as binders if median consensus percentile ≤ 20

TepiTool

`tools.iedb.org/tepitool`

`help@iedb.org`