IEDB
Immune Epitope Database & Tools

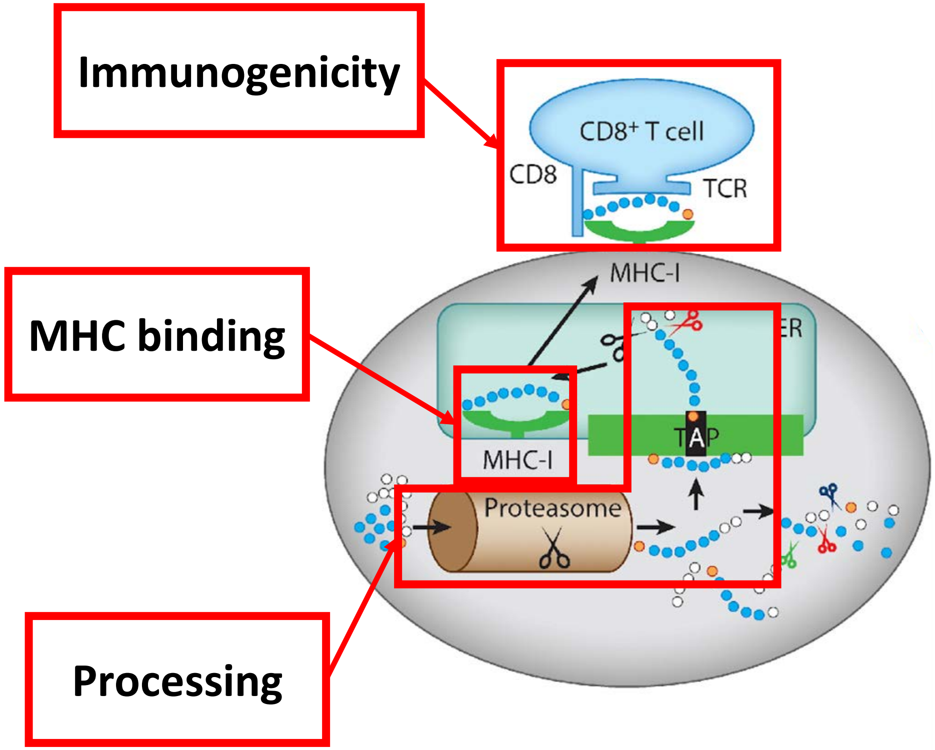
T Cell Class I Tools
Binding, Processing, Immunogenicity

Introduction

Presented by: J. Greenbaum, Bioinformatics Core Director

Endogonous Antigen Processing Pathway

(Class I)



Immunogenicity

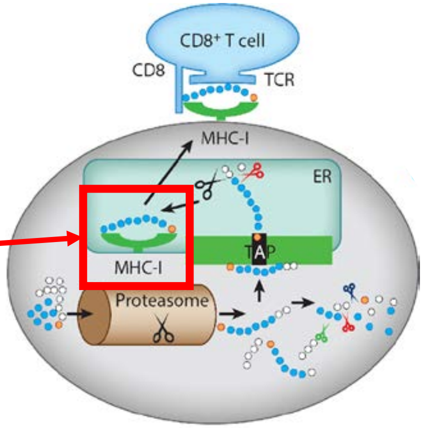
MHC binding

Processing

- Antigens generated within the cell
  - Viral particles
  - Self proteins
  - DRiPs (Defective Ribosomal Particles
- Different factors influence peptide being "epitope"

Peters et al, Annual Review of Immunology, 2020

MHC I Binding Prediction



MHC binding

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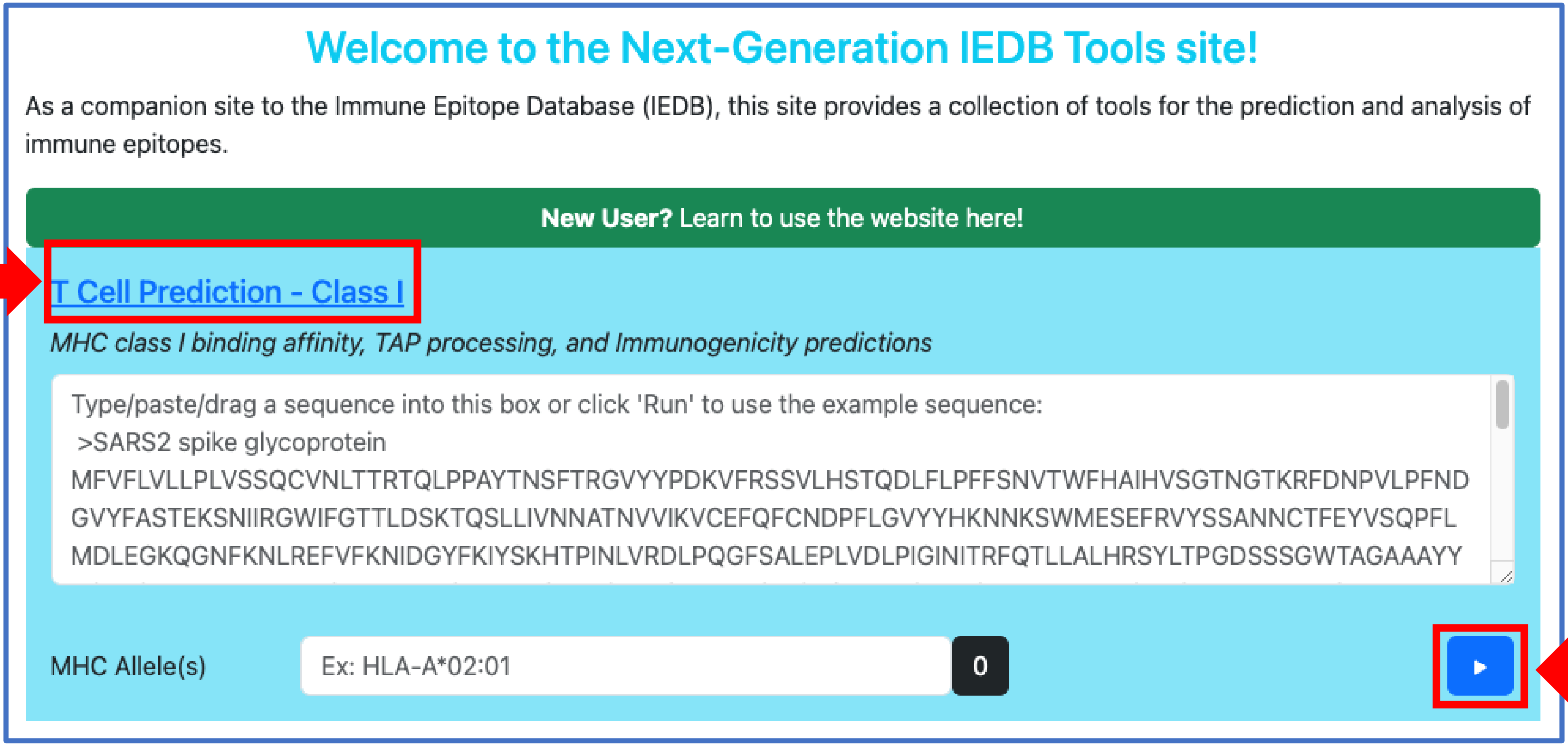

Welcome to the Next-Generation IEDB Tools site!

As a companion site to the Immune Epitope Database (IEDB), this site provides a collection of tools for the prediction and analysis of immune epitopes.

New User? Learn to use the website here!

T Cell Prediction - Class I

MHC class I binding affinity, TAP processing, and Immunogenicity predictions

Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFND
GVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL
MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYY

MHC Allele(s): Ex: HLA-A*02:01

Class I MHC Molecule

- Expressed by almost all nucleated cells
- Presents antigen to **CD8+ T cells** (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin, aka B2M)
- The binding groove is **closed** at both ends and can accommodate peptides of **8-11 AA**
- Only **α chain** impacts binding

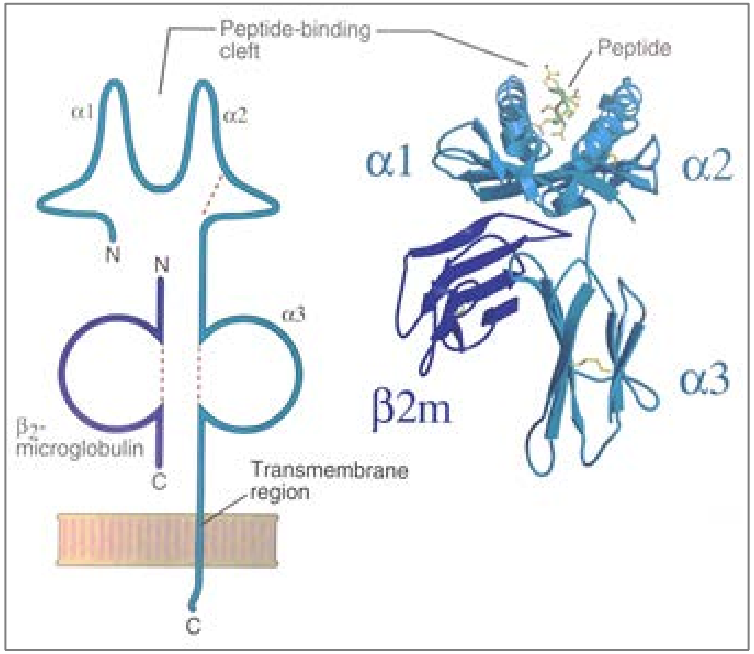

Figure Source
Cellular & Molecular Immunology, 5th Ed by Abbas and Lichtman

MHC Binding Predictions

- MHC molecules are **highly polymorphic** – thousands of different variants exist
- MHC-peptide binding is **promiscuous** in nature
- Experimental characterization of peptide–MHC interactions is highly **cost-intensive**
- Prediction methods facilitate selection of potential epitopes from a pool of peptides

Peptide binding data
HLA-A*01:01

Peptide	IC_{50}(nM)
ASFCGSPY	51.4
LTDFGLSK	739.3
FTSFFYRY	1285.0
KSVFNSLY	1466.0
RDWAHNSL	1804.6
FSSCPVAY	1939.4
RNWAHSSL	2201.7
LSCAASGF	2830.1
LASIDLKY	3464.0

+

Machine learning algorithms

MHC-I Binding Prediction – Example

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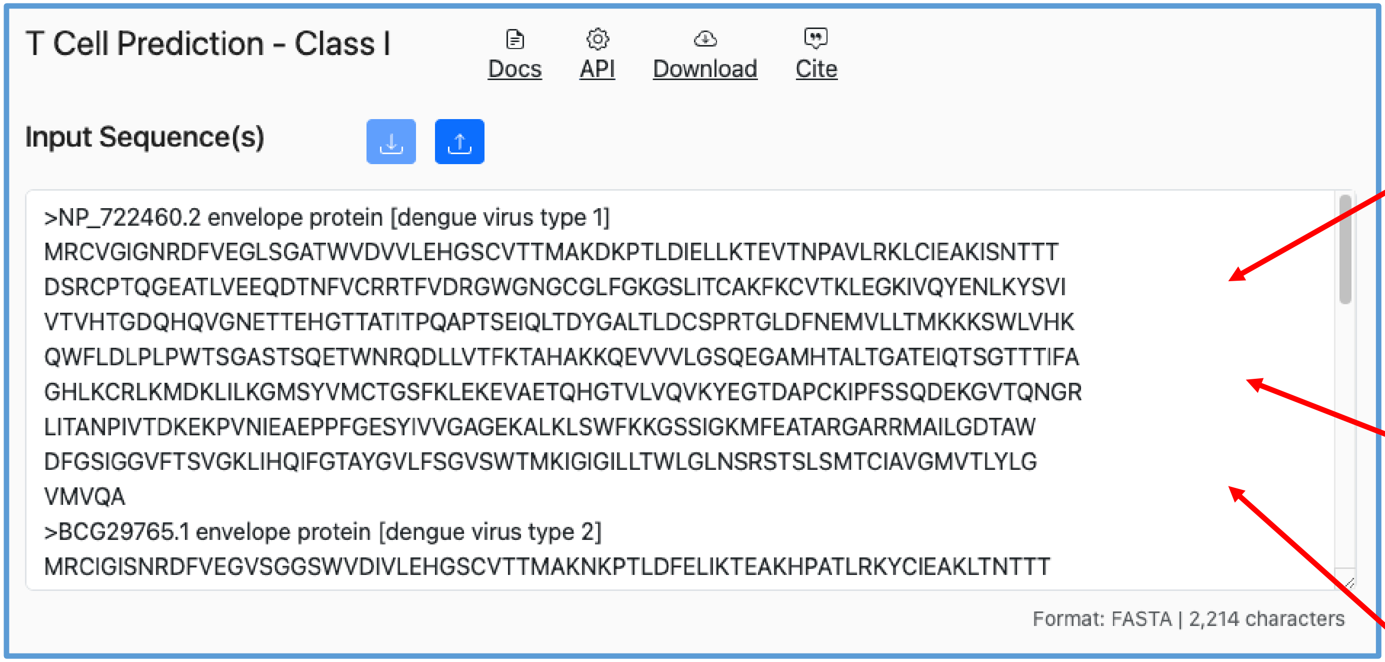
Antigen sequence
(type, copy/paste, or drag & drop)

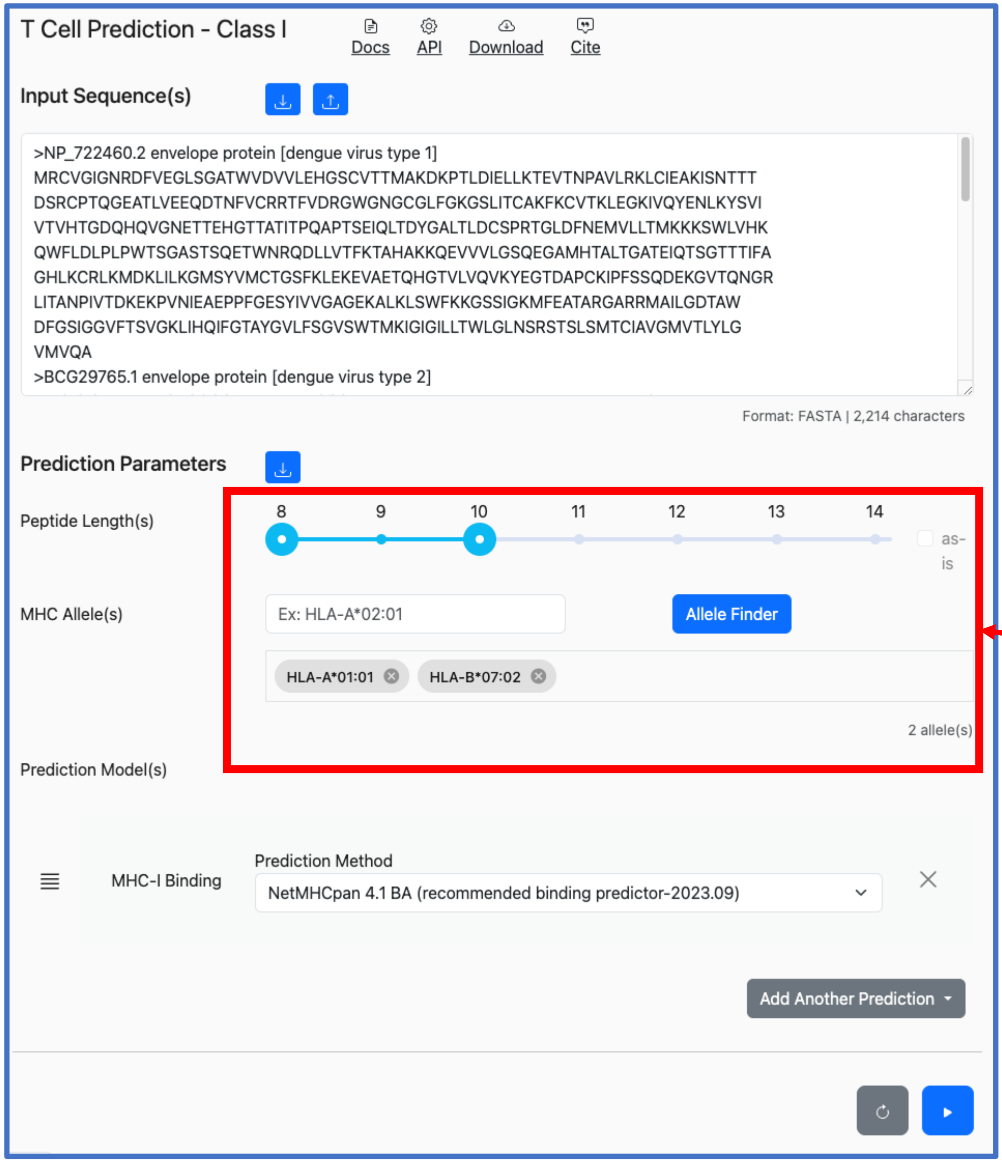


Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
MRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKHPATLRKYCIEAKLTNTTT
```

Format: FASTA | 2,214 characters

MHC-I Binding Prediction – Example



Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 – 10 (scale 8, 9, 10, 11, 12, 13, 14) ☐ as-is

MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01 ⊗ HLA-B*07:02 ⊗

2 allele(s)

Prediction Model(s)

MHC-I Binding — Prediction Method: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

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Specify allele(s) & peptide length

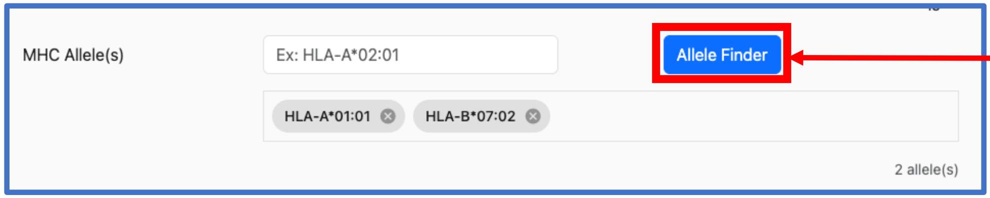
Allele Selection – Reference Set for Global Coverage

- Reference set of 27 alleles
- Covers > 97% of population

https://iedb.zendesk.com/entries/25054538-HLA-allele-frequencies

HLA-A	Frequency	HLA-B	Frequency
A*01:01	16.2	B*07:02	13.3
A*02:01	25.2	B*08:01	11.5
A*02:03	3.3	B*15:01	5.2
A*02:06	4.9	B*35:01	6.5
A*03:01	15.4	B*40:01	10.3
A*11:01	12.9	B*44:02	9.2
A*23:01	6.4	B*44:03	7.6
A*24:02	16.8	B*51:01	5.5
A*26:01	4.7	B*53:01	5.4
A*30:01	5.1	B*57:01	3.2
A*30:02	5.0	B*58:01	3.6
A*31:01	4.7		
A*32:01	5.7		
A*33:01	3.2		
A*68:01	4.6		
A*68:02	3.3		

Using the Reference Allele Panel


MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01, HLA-B*07:02

2 allele(s)

Open the 'Allele Finder'


Number of Selected Alleles: 2

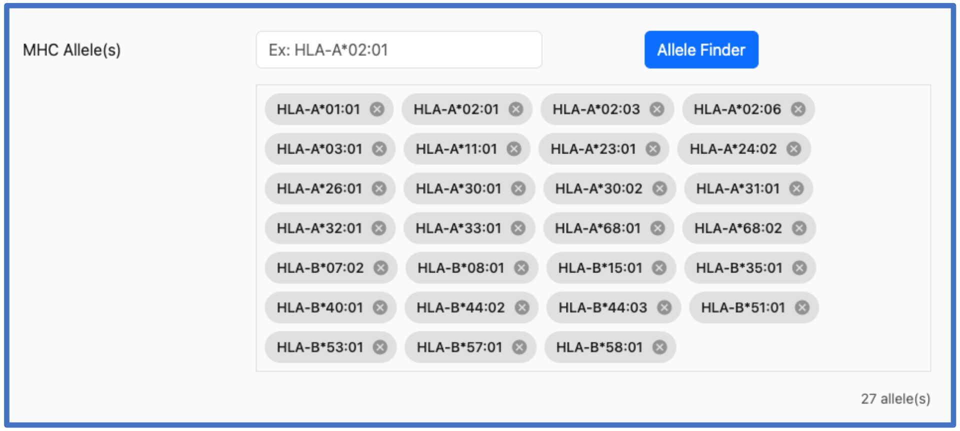
MHC Allele(s): HLA-A*01:01, HLA-B*07:02

- HLA-A*01:01
- HLA-B*07:02

Covers ~97% of the human population

Click on '27 Allele Panel'

Click Submit


MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01, HLA-A*02:01, HLA-A*02:03, HLA-A*02:06, HLA-A*03:01, HLA-A*11:01, HLA-A*23:01, HLA-A*24:02, HLA-A*26:01, HLA-A*30:01, HLA-A*30:02, HLA-A*31:01, HLA-A*32:01, HLA-A*33:01, HLA-A*68:01, HLA-A*68:02, HLA-B*07:02, HLA-B*08:01, HLA-B*15:01, HLA-B*35:01, HLA-B*40:01, HLA-B*44:02, HLA-B*44:03, HLA-B*51:01, HLA-B*53:01, HLA-B*57:01, HLA-B*58:01

27 allele(s)

Natural Length Distribution in Epitope Prediction

- Alleles differ in their preference for lengths on binding and presentation of peptides

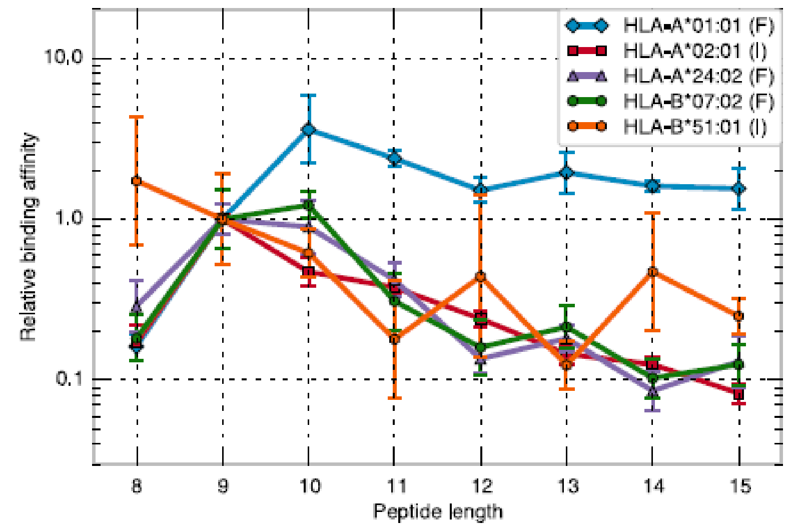


FIGURE 1. Peptide binding-length preference for five common HLA alleles. The length preference for each HLA was determined by measuring

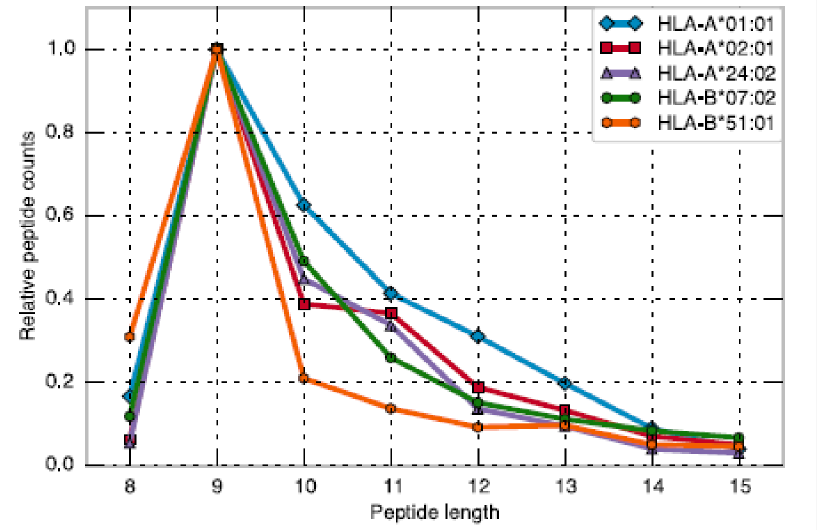
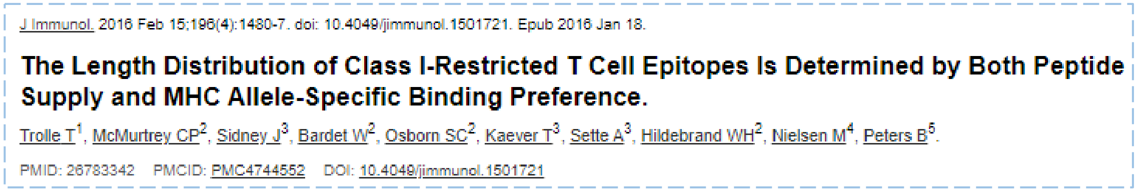


FIGURE 2. Length profiles of naturally presented peptides for five HLA molecules. Large datasets of HLA-I ligands were determined by the elu-

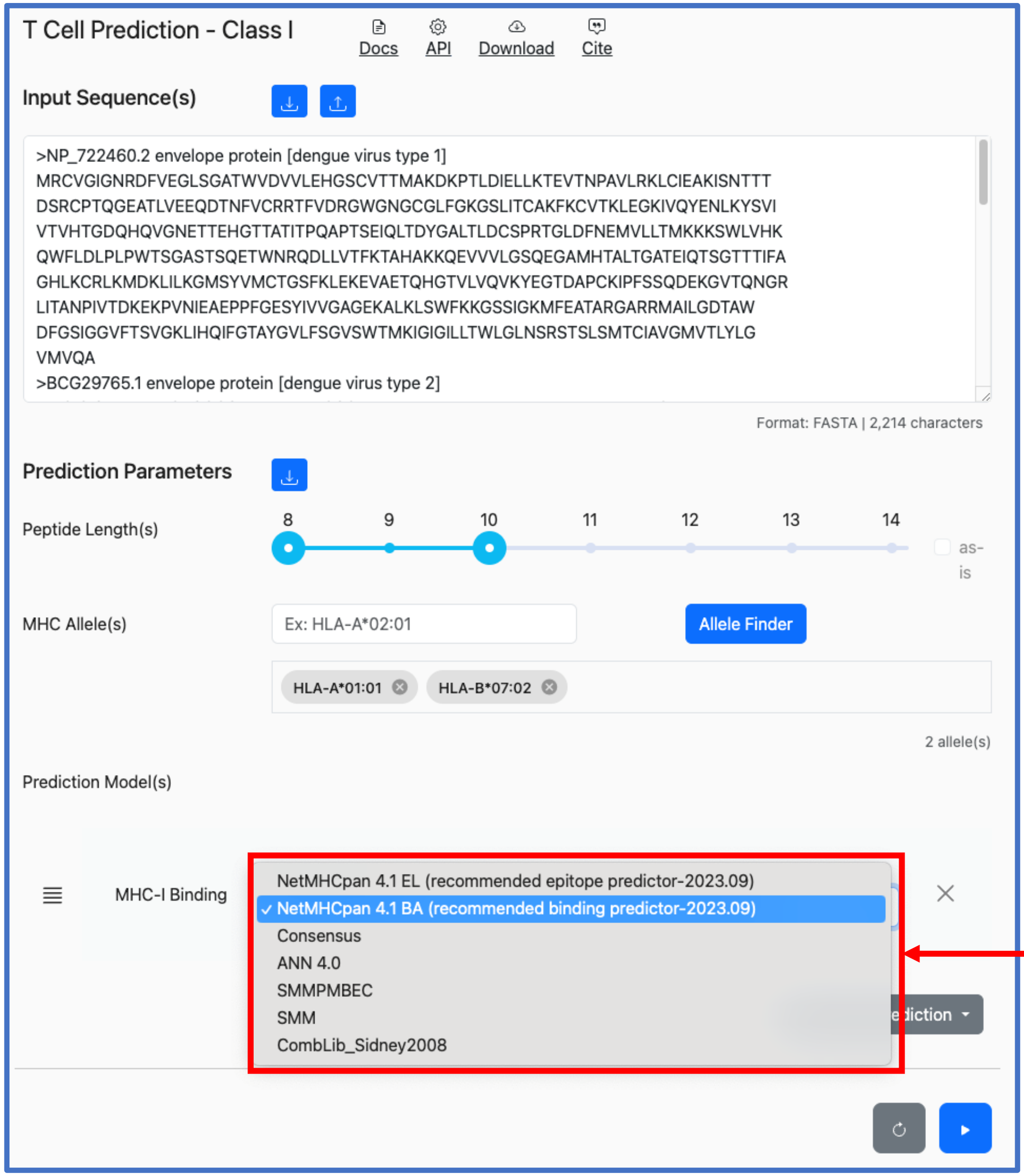

J Immunol. 2016 Feb 15;196(4):1480-7. doi: 10.4049/jimmunol.1501721. Epub 2016 Jan 18.

The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference.

Trolle T[1], McMurtrey CP[2], Sidney J[3], Bardet W[2], Osborn SC[2], Kaever T[3], Sette A[3], Hildebrand WH[2], Nielsen M[4], Peters B[5].

PMID: 26783342 PMCID: PMC4744552 DOI: 10.4049/jimmunol.1501721

MHC-I Binding Prediction – Example



T Cell Prediction - Class I

Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 9 10 11 12 13 14 ☐ as-is

MHC Allele(s): Ex: HLA-A*02:01 Allele Finder

HLA-A*01:01 ⊗ HLA-B*07:02 ⊗

2 allele(s)

Prediction Model(s)

≡ MHC-I Binding

- NetMHCpan 4.1 EL (recommended epitope predictor-2023.09)
- ✓ NetMHCpan 4.1 BA (recommended binding predictor-2023.09)
- Consensus
- ANN 4.0
- SMMPMBEC
- SMM
- CombLib_Sidney2008

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Prediction method

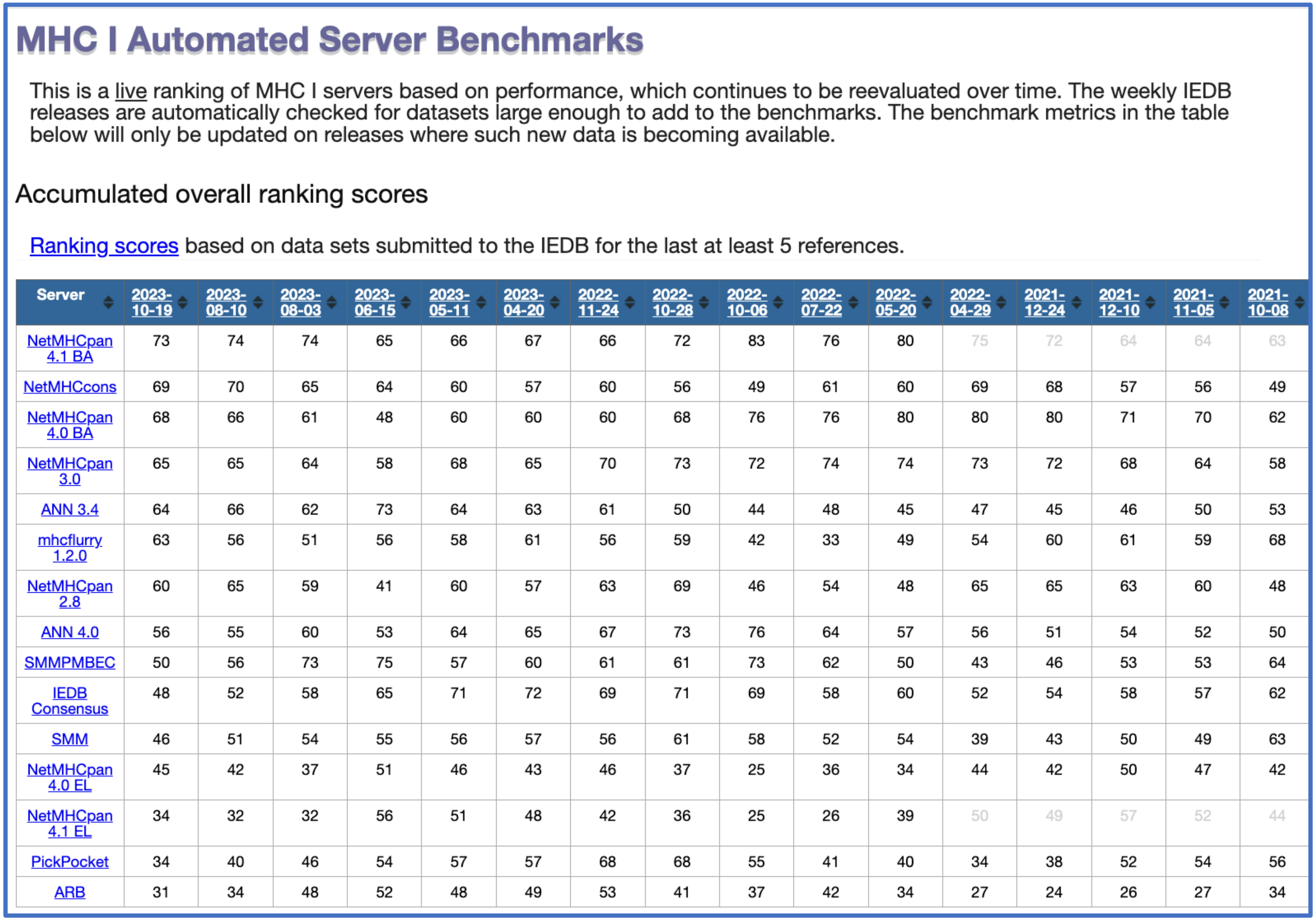
Guidelines: Choosing the Prediction Method

IEDB Tools Version	Recommended Method
2023.09 (current)	NetMHCPan 4.1 EL (epitope) NetMHCPan 4.1 BA (binding)
2023.05	NetMHCPan 4.1 EL
2020.04	NetMHCPan 4.0 EL
2.22 and earlier	Consensus, if available; otherwise, NetMHCpan

- IEDB-recommended **epitope** predictor
  - Employs NetMHCpan **EL** 4.1 across all alleles
- IEDB-recommended **binding** predictor
  - Employs NetMHCpan **BA** 4.1 across all alleles
- Recommendation will change with the new benchmark studies

MHC Class I binding prediction benchmarks

tools.iedb.org/auto_bench/mhci/weekly/



MHC I Automated Server Benchmarks

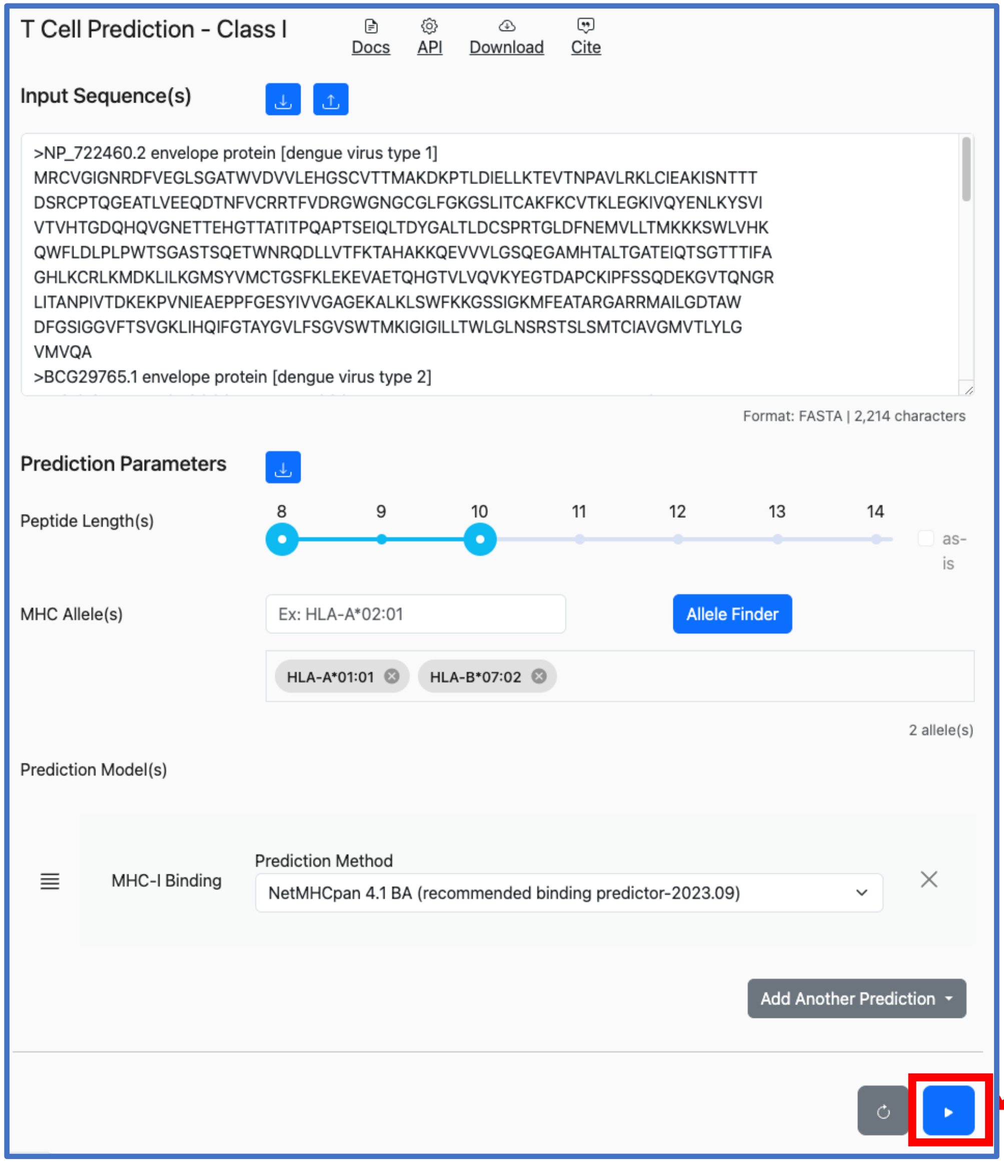
This is a live ranking of MHC I servers based on performance, which continues to be reevaluated over time. The weekly IEDB releases are automatically checked for datasets large enough to add to the benchmarks. The benchmark metrics in the table below will only be updated on releases where such new data is becoming available.

Accumulated overall ranking scores

Ranking scores based on data sets submitted to the IEDB for the last at least 5 references.

Server	2023-10-19	2023-08-10	2023-08-03	2023-06-15	2023-05-11	2023-04-20	2022-11-24	2022-10-28	2022-10-06	2022-07-22	2022-05-20	2022-04-29	2021-12-24	2021-12-10	2021-11-05	2021-10-08
NetMHCpan 4.1 BA	73	74	74	65	66	67	66	72	83	76	80	75	72	64	64	63
NetMHCcons	69	70	65	64	60	57	60	56	49	61	60	69	68	57	56	49
NetMHCpan 4.0 BA	68	66	61	48	60	60	60	68	76	76	80	80	80	71	70	62
NetMHCpan 3.0	65	65	64	58	68	65	70	73	72	74	74	73	72	68	64	58
ANN 3.4	64	66	62	73	64	63	61	50	44	48	45	47	45	46	50	53
mhcflurry 1.2.0	63	56	51	56	58	61	56	59	42	33	49	54	60	61	59	68
NetMHCpan 2.8	60	65	59	41	60	57	63	69	46	54	48	65	65	63	60	48
ANN 4.0	56	55	60	53	64	65	67	73	76	64	57	56	51	54	52	50
SMMPMBEC	50	56	73	75	57	60	61	61	73	62	50	43	46	53	53	64
IEDB Consensus	48	52	58	65	71	72	69	71	69	58	60	52	54	58	57	62
SMM	46	51	54	55	56	57	56	61	58	52	54	39	43	50	49	63
NetMHCpan 4.0 EL	45	42	37	51	46	43	46	37	25	36	34	44	42	50	47	42
NetMHCpan 4.1 EL	34	32	32	56	51	48	42	36	25	26	39	50	49	57	52	44
PickPocket	34	40	46	54	57	57	68	68	55	41	40	34	38	52	54	56
ARB	31	34	48	52	48	49	53	41	37	42	34	27	24	26	27	34

MHC-I Binding Prediction – Example



T Cell Prediction - Class I

Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 9 10 11 12 13 14 ☐ as-is

MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01 ⊗ HLA-B*07:02 ⊗

2 allele(s)

Prediction Model(s)

MHC-I Binding

Prediction Method: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

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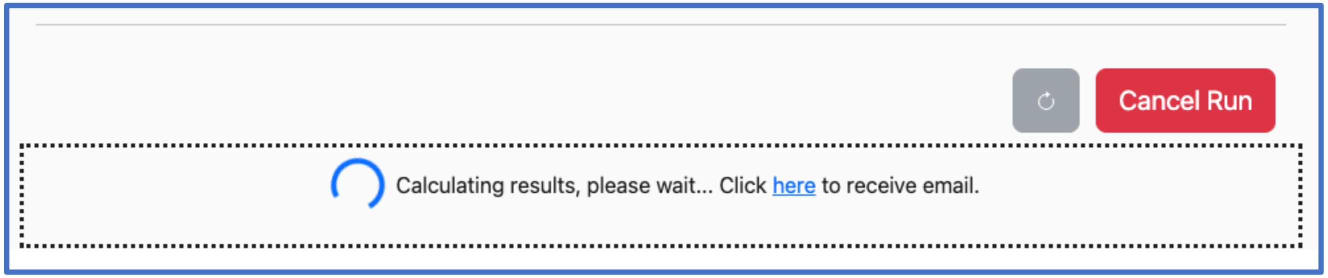
Run!

How the Tool Works

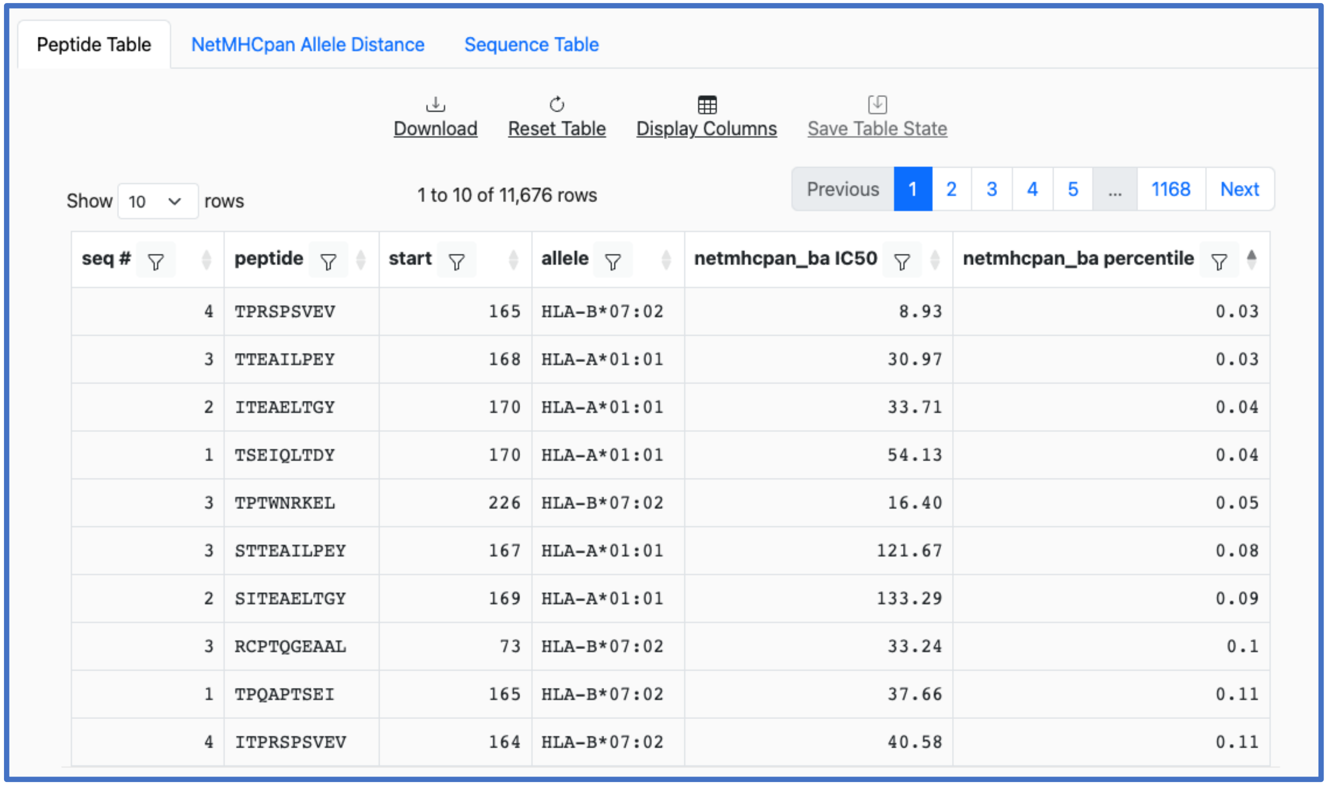
- Breaks the sequence into all possible peptides of chosen length(s), unless ‘as-is’ option is selected
- Predicts the binding affinity / elution score for each peptide based on the method
- Compares the predicted affinity / elution score to that of a large set of randomly selected peptides
- Assigns a percentile rank depending on individual predicted affinity / elution score
- Calculates the median percentile rank

MHC-I Binding Prediction – Example

nextgen-tools.iedb.org/tc1



Calculating results, please wait... Click here to receive email.



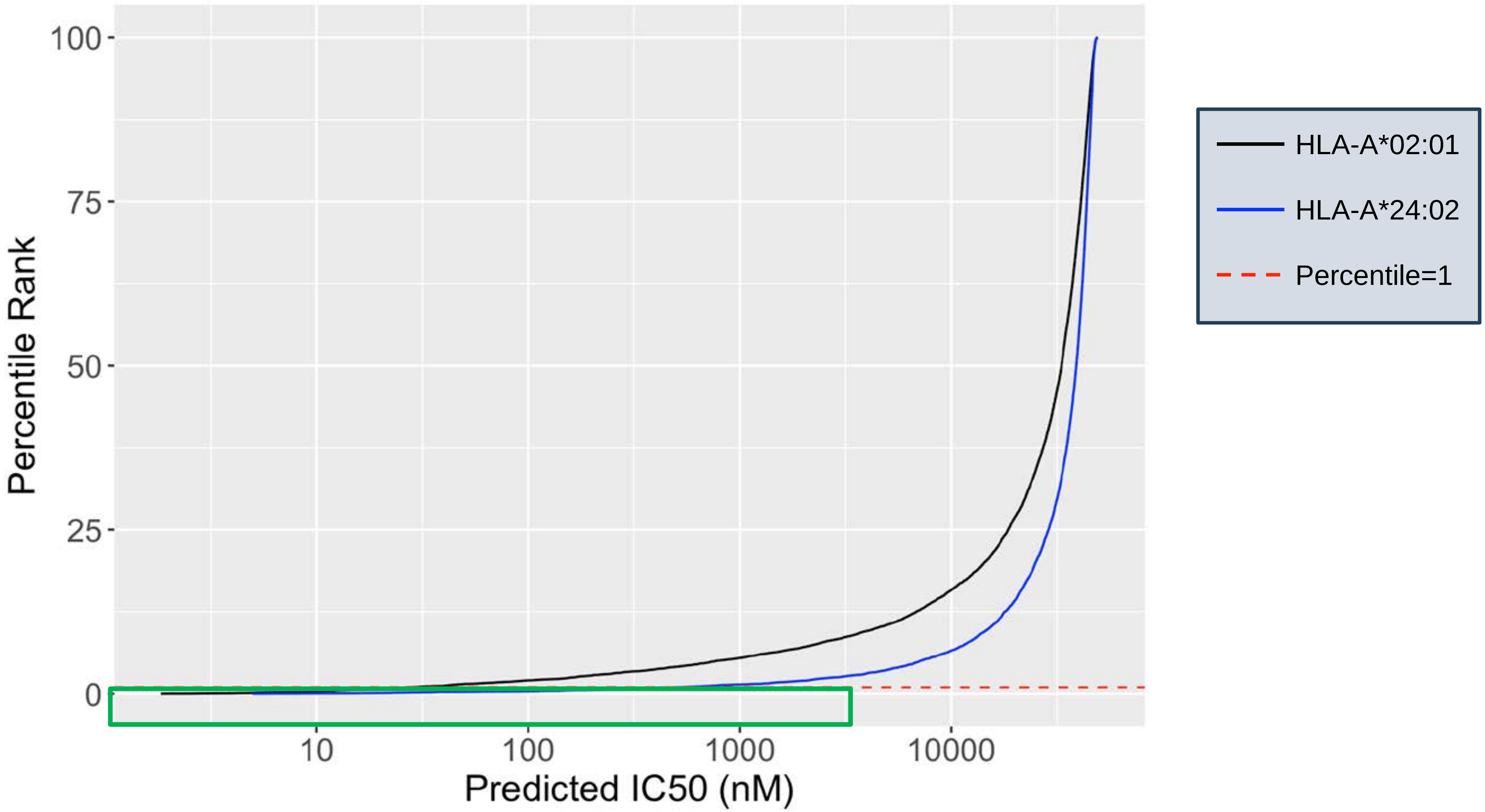
1 to 10 of 11,676 rows

seq #	peptide	start	allele	netmhcpan_ba IC50	netmhcpan_ba percentile
4	TPRSPSVEV	165	HLA-B*07:02	8.93	0.03
3	TTEAILPEY	168	HLA-A*01:01	30.97	0.03
2	ITEAELTGY	170	HLA-A*01:01	33.71	0.04
1	TSEIQLTDY	170	HLA-A*01:01	54.13	0.04
3	TPTWNRKEL	226	HLA-B*07:02	16.40	0.05
3	STTEAILPEY	167	HLA-A*01:01	121.67	0.08
2	SITEAELTGY	169	HLA-A*01:01	133.29	0.09
3	RCPTQGEAAL	73	HLA-B*07:02	33.24	0.1
1	TPQAPTSEI	165	HLA-B*07:02	37.66	0.11
4	ITPRSPSVEV	164	HLA-B*07:02	40.58	0.11

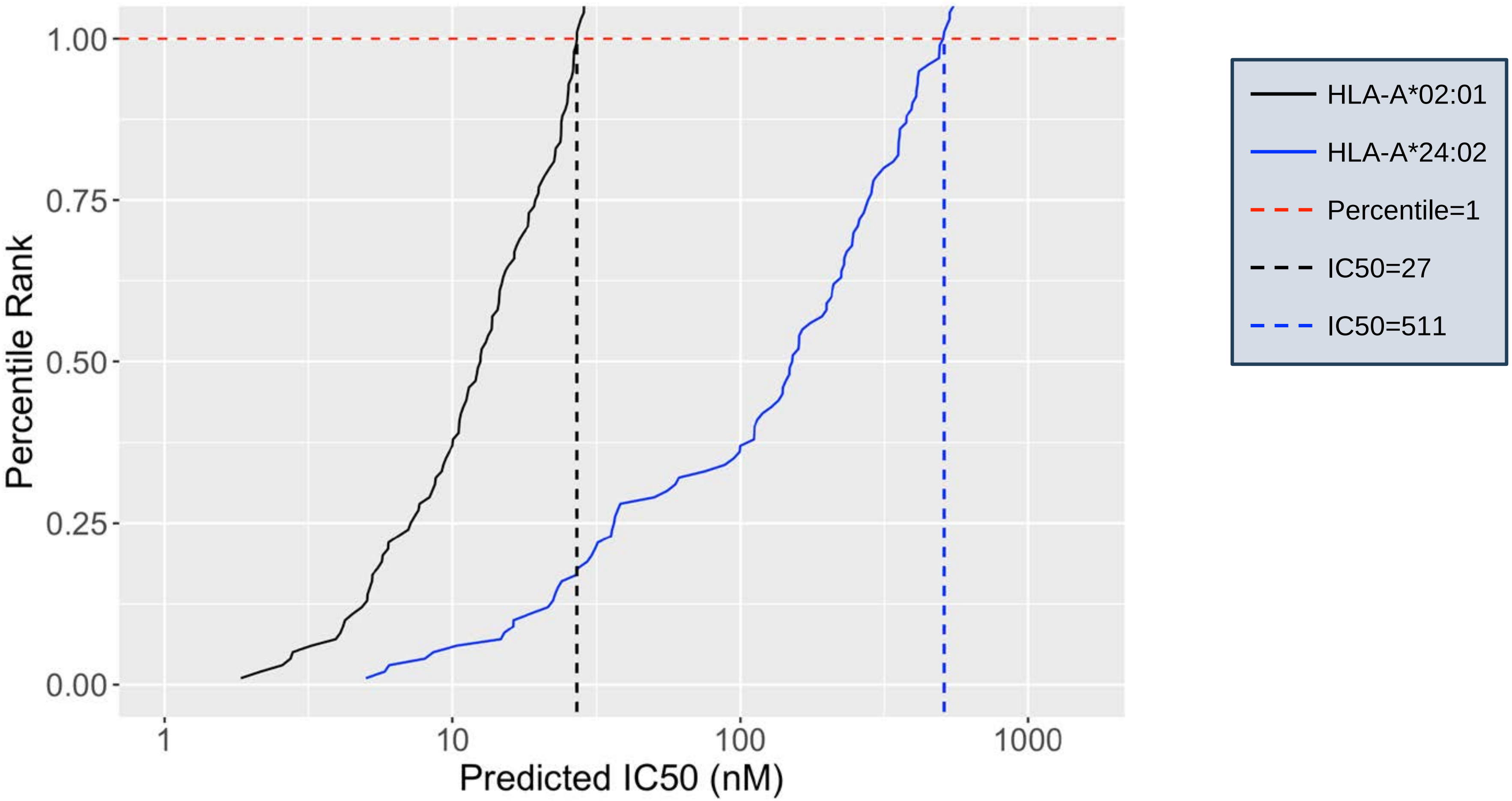
Output
(sorted low-to-high by percentile rank)

A **percentile rank** for a peptide is the percentage of randomly sampled peptides scoring better than the peptide.

IC50 value distributions vary by allele

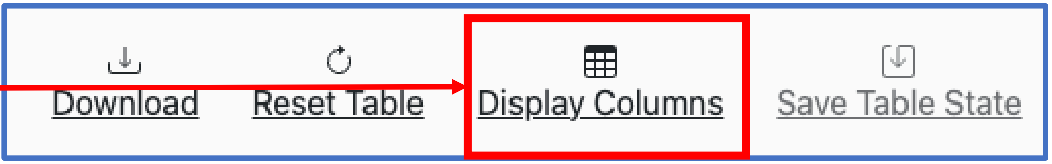


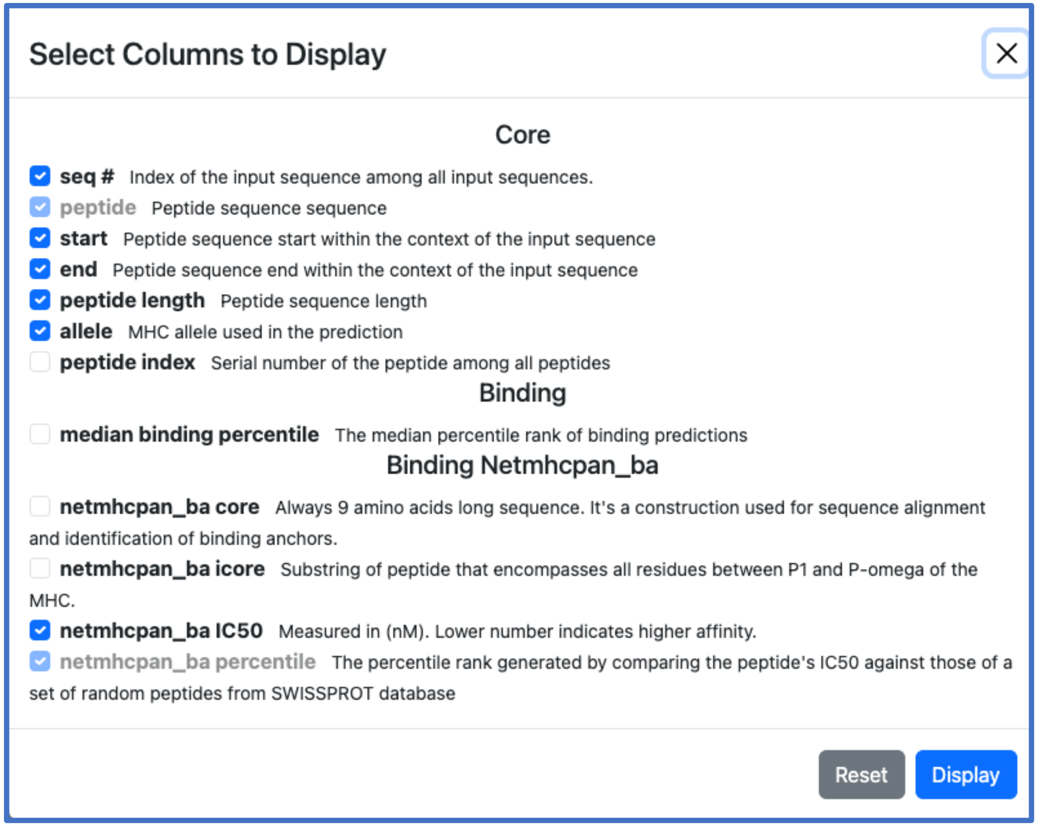
Mapping IC50 values to percentile ranks enables comparisons across alleles



Show / Hide Output Columns

'Display Columns' button





Select Columns to Display

Core

☑ **seq #** Index of the input sequence among all input sequences.

☑ **peptide** Peptide sequence sequence

☑ **start** Peptide sequence start within the context of the input sequence

☑ **end** Peptide sequence end within the context of the input sequence

☑ **peptide length** Peptide sequence length

☑ **allele** MHC allele used in the prediction

☐ **peptide index** Serial number of the peptide among all peptides

Binding

☐ **median binding percentile** The median percentile rank of binding predictions

Binding Netmhcpan_ba

☐ **netmhcpan_ba core** Always 9 amino acids long sequence. It's a construction used for sequence alignment and identification of binding anchors.

☐ **netmhcpan_ba icore** Substring of peptide that encompasses all residues between P1 and P-omega of the MHC.

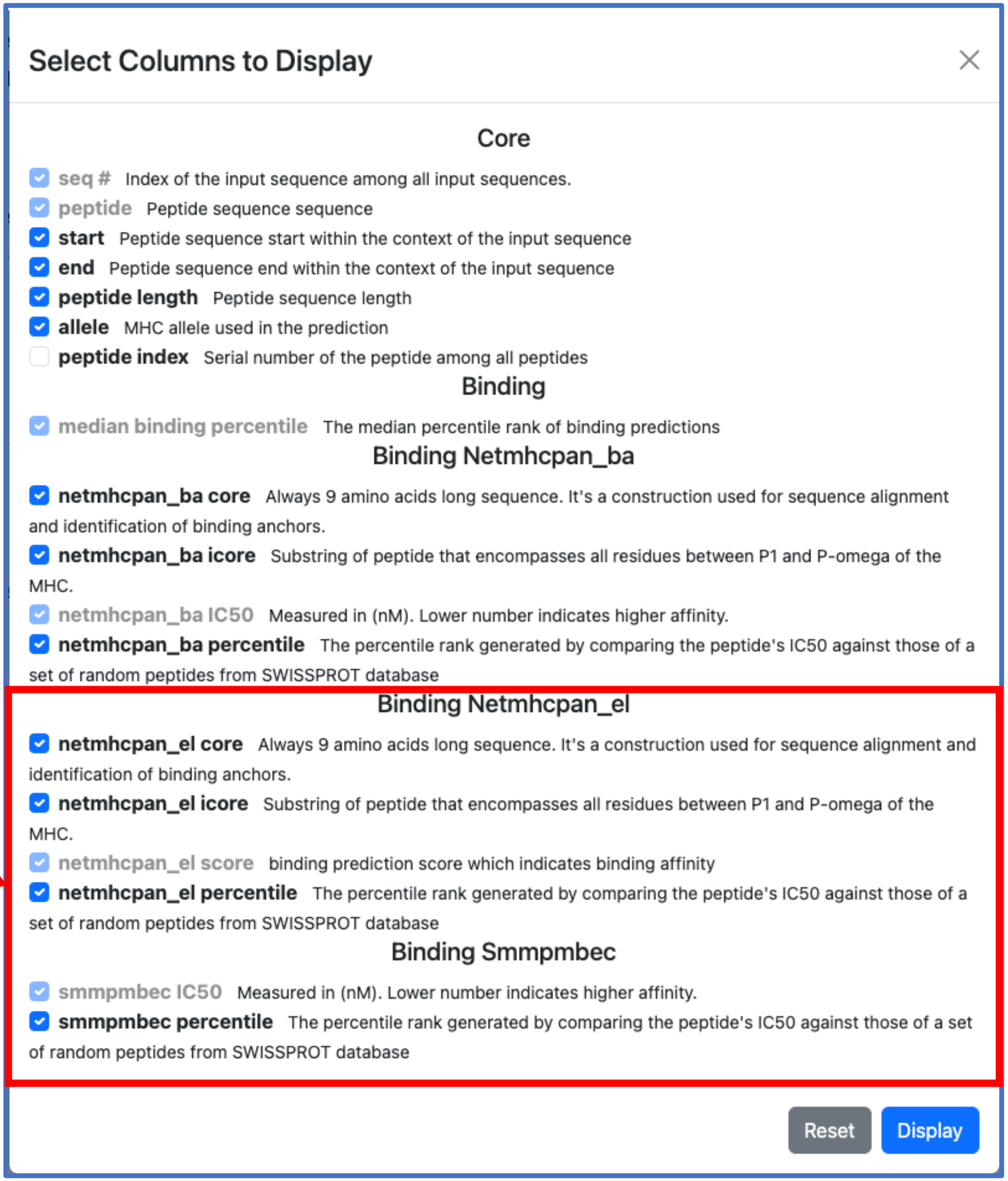
☑ **netmhcpan_ba IC50** Measured in (nM). Lower number indicates higher affinity.

☑ **netmhcpan_ba percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

With more methods, more fields are visible

(Mo methods, Mo columns)

Additional selected methods



Select Columns to Display

Core

☑ seq # Index of the input sequence among all input sequences.
☑ peptide Peptide sequence sequence
☑ **start** Peptide sequence start within the context of the input sequence
☑ **end** Peptide sequence end within the context of the input sequence
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☑ **allele** MHC allele used in the prediction
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Binding

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☑ **netmhcpan_ba core** Always 9 amino acids long sequence. It's a construction used for sequence alignment and identification of binding anchors.
☑ **netmhcpan_ba icore** Substring of peptide that encompasses all residues between P1 and P-omega of the MHC.
☑ netmhcpan_ba IC50 Measured in (nM). Lower number indicates higher affinity.
☑ **netmhcpan_ba percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

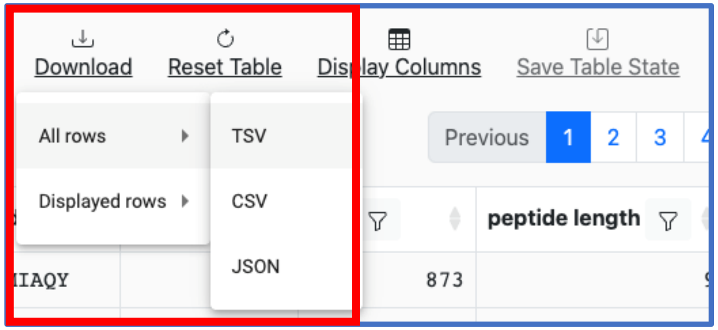
Binding Netmhcpan_el

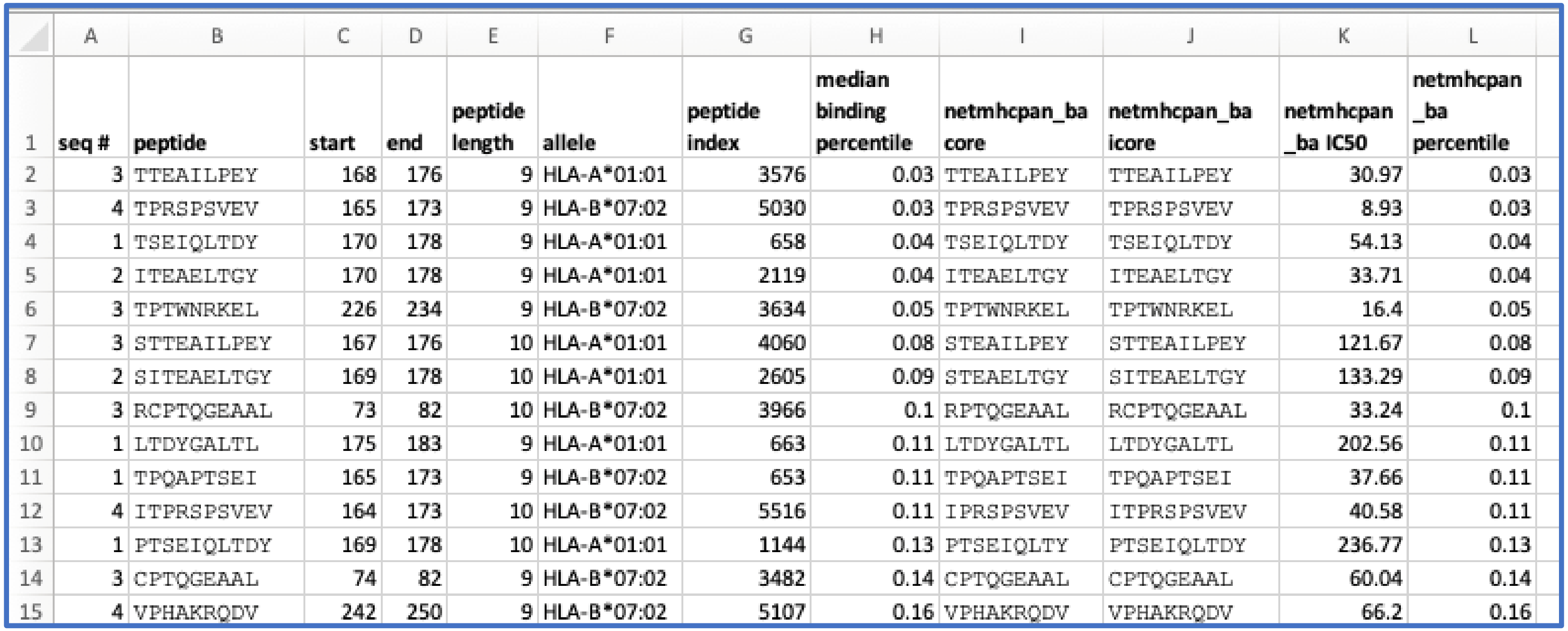
☑ **netmhcpan_el core** Always 9 amino acids long sequence. It's a construction used for sequence alignment and identification of binding anchors.
☑ **netmhcpan_el icore** Substring of peptide that encompasses all residues between P1 and P-omega of the MHC.
☑ netmhcpan_el score binding prediction score which indicates binding affinity
☑ **netmhcpan_el percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Binding Smmpmbec

☑ smmpmbec IC50 Measured in (nM). Lower number indicates higher affinity.
☑ **smmpmbec percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

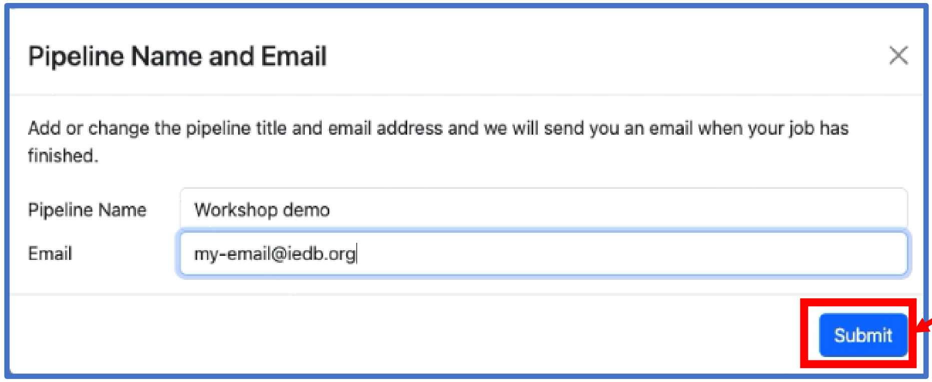
Downloaded Prediction Results





	A	B	C	D	E	F	G	H	I	J	K	L
1	seq #	peptide	start	end	peptide length	allele	peptide index	median binding percentile	netmhcpan_ba core	netmhcpan_ba icore	netmhcpan _ba IC50	netmhcpan _ba percentile
2	3	TTEAILPEY	168	176	9	HLA-A*01:01	3576	0.03	TTEAILPEY	TTEAILPEY	30.97	0.03
3	4	TPRSPSVEV	165	173	9	HLA-B*07:02	5030	0.03	TPRSPSVEV	TPRSPSVEV	8.93	0.03
4	1	TSEIQLTDY	170	178	9	HLA-A*01:01	658	0.04	TSEIQLTDY	TSEIQLTDY	54.13	0.04
5	2	ITEAELTGY	170	178	9	HLA-A*01:01	2119	0.04	ITEAELTGY	ITEAELTGY	33.71	0.04
6	3	TPTWNRKEL	226	234	9	HLA-B*07:02	3634	0.05	TPTWNRKEL	TPTWNRKEL	16.4	0.05
7	3	STTEAILPEY	167	176	10	HLA-A*01:01	4060	0.08	STEAILPEY	STTEAILPEY	121.67	0.08
8	2	SITEAELTGY	169	178	10	HLA-A*01:01	2605	0.09	STEAELTGY	SITEAELTGY	133.29	0.09
9	3	RCPTQGEAAL	73	82	10	HLA-B*07:02	3966	0.1	RPTQGEAAL	RCPTQGEAAL	33.24	0.1
10	1	LTDYGALTL	175	183	9	HLA-A*01:01	663	0.11	LTDYGALTL	LTDYGALTL	202.56	0.11
11	1	TPQAPTSEI	165	173	9	HLA-B*07:02	653	0.11	TPQAPTSEI	TPQAPTSEI	37.66	0.11
12	4	ITPRSPSVEV	164	173	10	HLA-B*07:02	5516	0.11	IPRSPSVEV	ITPRSPSVEV	40.58	0.11
13	1	PTSEIQLTDY	169	178	10	HLA-A*01:01	1144	0.13	PTSEIQLTY	PTSEIQLTDY	236.77	0.13
14	3	CPTQGEAAL	74	82	9	HLA-B*07:02	3482	0.14	CPTQGEAAL	CPTQGEAAL	60.04	0.14
15	4	VPHAKRQDV	242	250	9	HLA-B*07:02	5107	0.16	VPHAKRQDV	VPHAKRQDV	66.2	0.16

Emailed Prediction Results and Link



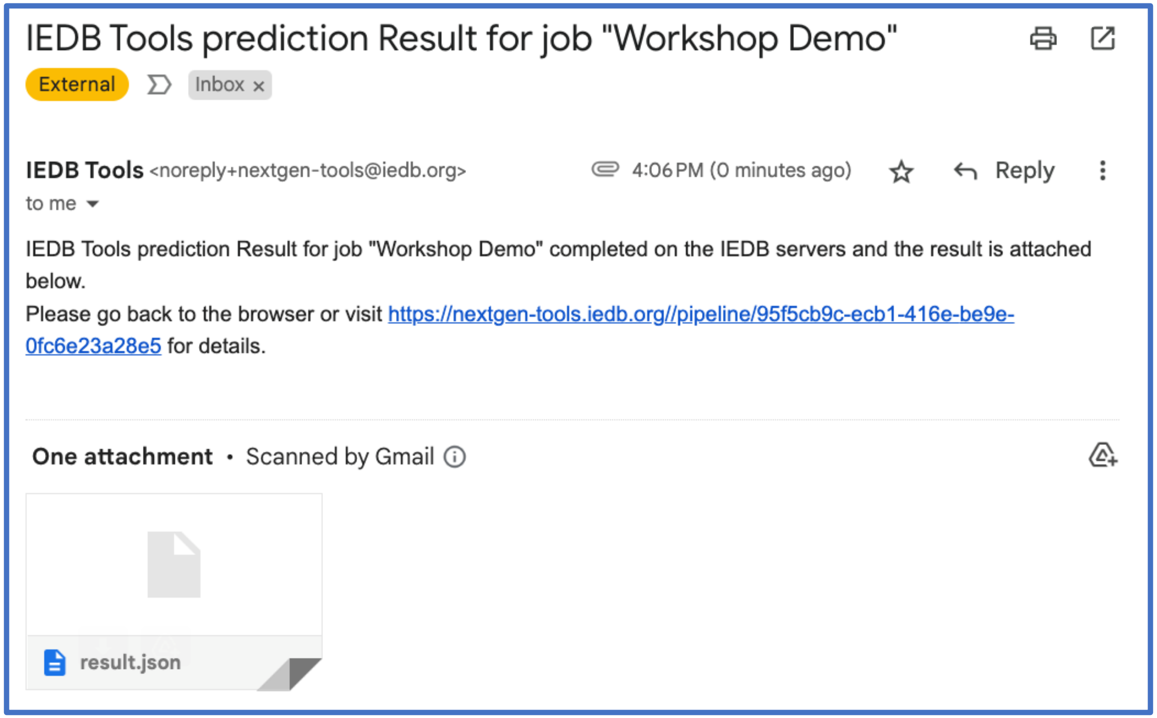
Pipeline Name and Email

Add or change the pipeline title and email address and we will send you an email when your job has finished.

Pipeline Name: Workshop demo

Email: my-email@iedb.org

Fill in details and click Submit



IEDB Tools prediction Result for job "Workshop Demo"

IEDB Tools <noreply+nextgen-tools@iedb.org> 4:06 PM (0 minutes ago)

to me

IEDB Tools prediction Result for job "Workshop Demo" completed on the IEDB servers and the result is attached below.
Please go back to the browser or visit https://nextgen-tools.iedb.org//pipeline/95f5cb9c-ecb1-416e-be9e-0fc6e23a28e5 for details.

One attachment • Scanned by Gmail

Selection of “Binders”

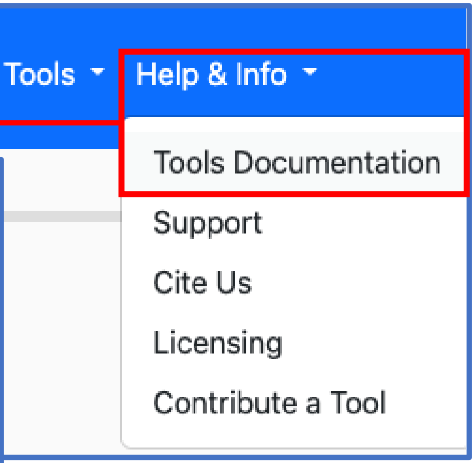
- Pick peptides **below percentile rank 1.0**

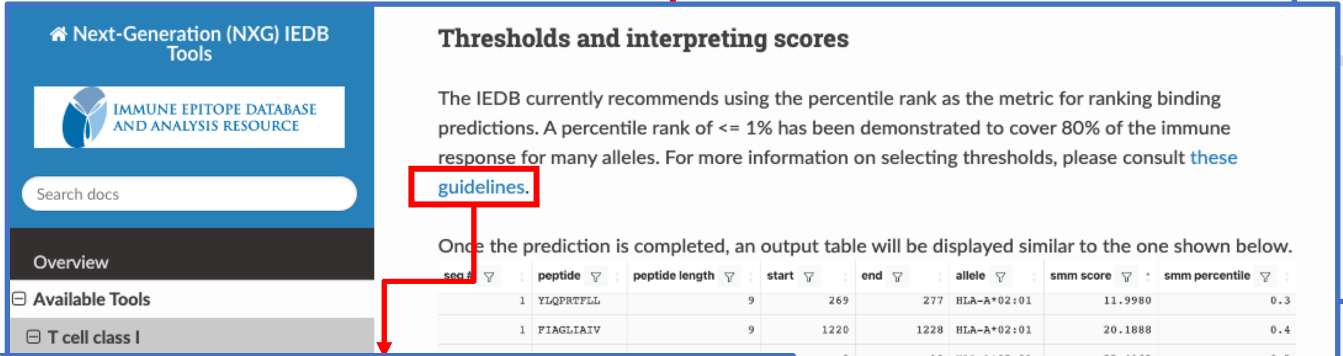
- Pick peptides **below predicted binding affinity of 500 nM**
  - IC50 < 50 nM - high affinity
  - IC50 < 500 nM - intermediate affinity
  - IC50 < 5000 nM - low affinity
  - Sette et al. 1994, J. Immunology (PMID: 7527444)
  - Ensures that all peptides have reasonable affinity

- Pick **top 1% of peptides** for each allele/length combination to cover most of immune responses
  - Moutaftsi et al. 2006 (PMID: 16767078)
  - Kotturi et al. 2007 (PMID: 17329346)
  - Ensures equal number of peptides per allele

- Select based on **allele specific binding affinity** threshold

Allele-specific Thresholds



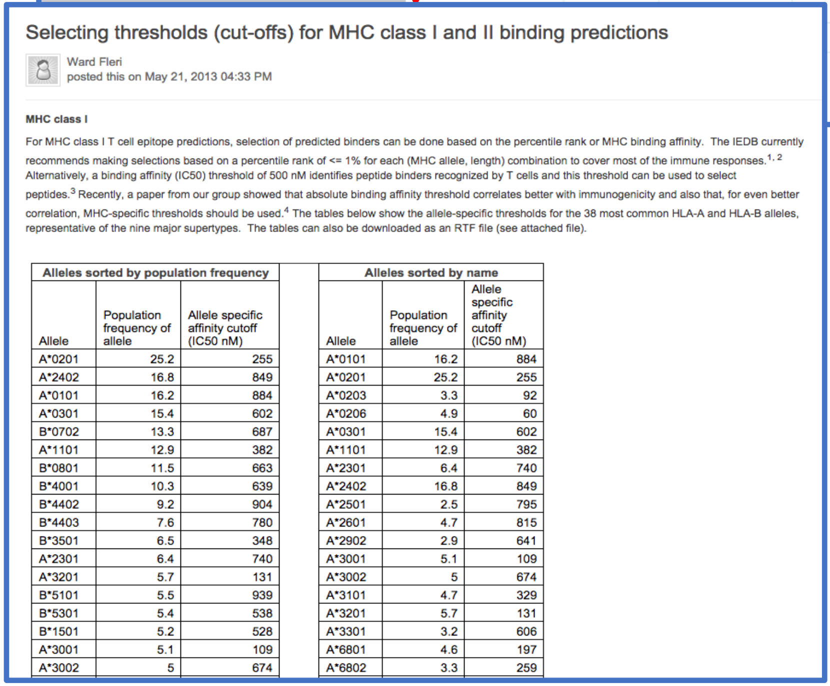


Thresholds and interpreting scores

The IEDB currently recommends using the percentile rank as the metric for ranking binding predictions. A percentile rank of <= 1% has been demonstrated to cover 80% of the immune response for many alleles. For more information on selecting thresholds, please consult these guidelines.

Once the prediction is completed, an output table will be displayed similar to the one shown below.

seq #	peptide	peptide length	start	end	allele	smm score	smm percentile
1	YLQPRTFLL	9	269	277	HLA-A*02:01	11.9980	0.3
1	FIAGLIAIV	9	1220	1228	HLA-A*02:01	20.1888	0.4
			2	10	HLA-A*02:01	25.4162	0.5
			1000	1008	HLA-A*02:01	36.7375	0.7
			417	425	HLA-A*02:01	38.8249	0.7



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	25.2	255
A*2402	16.8	849
A*0101	16.2	884
A*0301	15.4	602
B*0702	13.3	687
A*1101	12.9	382
B*0801	11.5	663
B*4001	10.3	639
B*4402	9.2	904
B*4403	7.6	780
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

J Immunol. 2013 Dec 15;191(12):5831-9. doi: 10.4049/jimmunol.1302101. Epub 2013 Nov 4.

HLA class I alleles are associated with peptide-binding repertoires of different size, affinity, and immunogenicity.

Paul S[#1], Weiskopf D[#1], Angelo MA[1], Sidney J[1], Peters B[1], Sette A[1].

PMID: 24190657 PMCID: PMC3872965 DOI: 10.4049/jimmunol.1302101

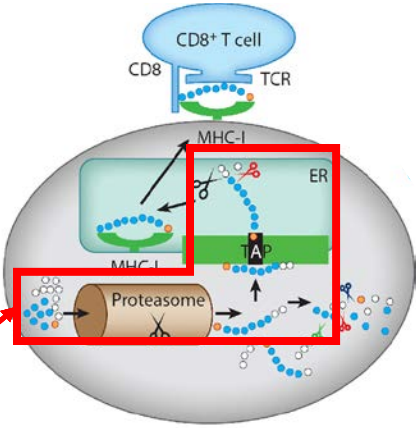
https://doi.org/10.4049/jimmunol.1302101

Recommendations

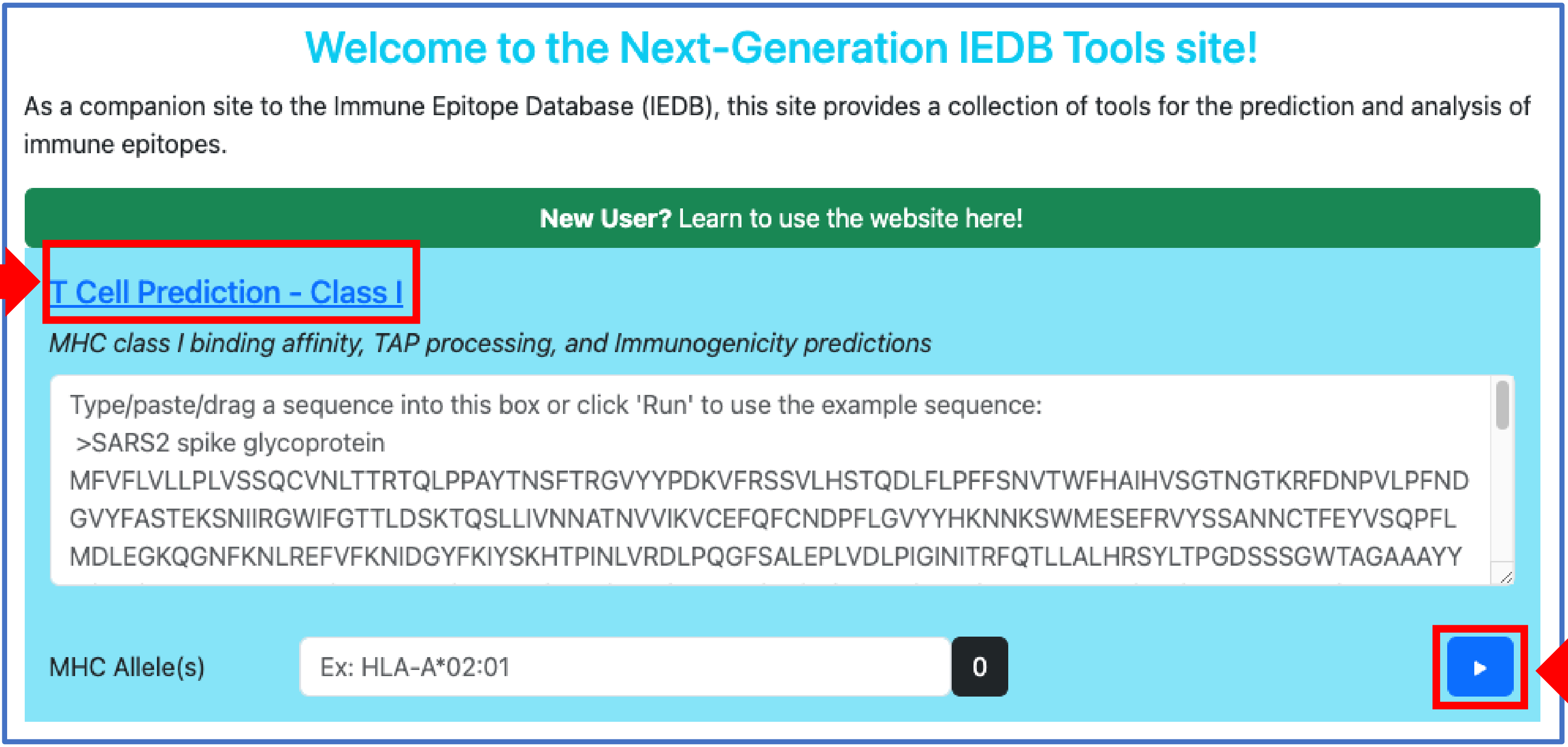
- All approaches (affinity and ranking) are reasonable, and have been applied in numerous studies
- Thresholds can be combined (peptides in top 1% and IC50 <500nM)
- Current studies suggest that allele specific thresholds can be derived

Class I processing prediction

nextgen-tools.iedb.org/tc1



Processing



Welcome to the Next-Generation IEDB Tools site!

As a companion site to the Immune Epitope Database (IEDB), this site provides a collection of tools for the prediction and analysis of immune epitopes.

New User? Learn to use the website here!

T Cell Prediction - Class I

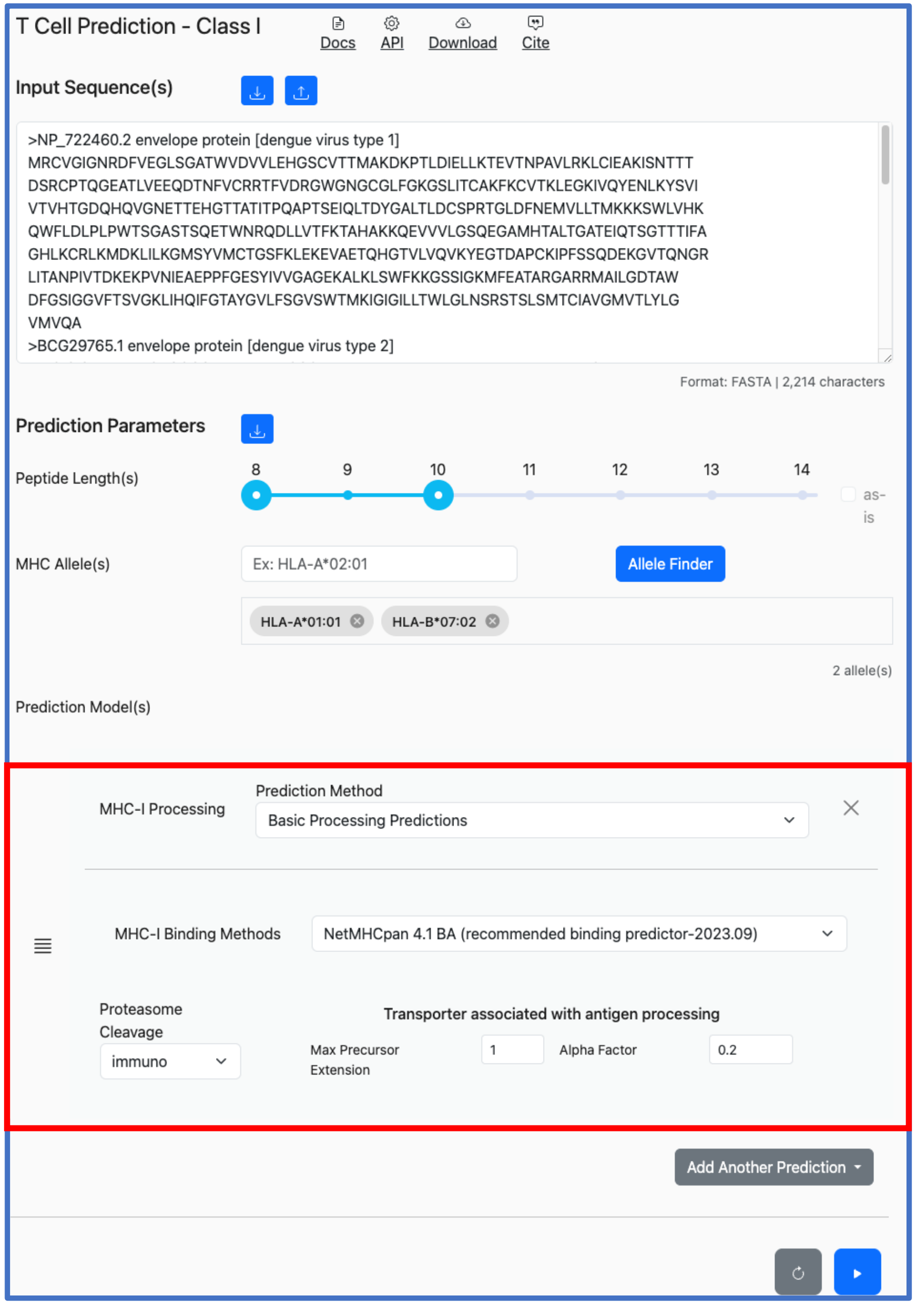
MHC class I binding affinity, TAP processing, and Immunogenicity predictions

Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFND
GVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL
MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYY

MHC Allele(s) Ex: HLA-A*02:01

Class I Processing ‘Combined Predictor’

nextgen-tools.iedb.org/tc1



T Cell Prediction - Class I

Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 9 10 11 12 13 14 ☐ as-is

MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01 HLA-B*07:02

2 allele(s)

Prediction Model(s)

MHC-I Processing — Prediction Method: Basic Processing Predictions

MHC-I Binding Methods: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

Proteasome Cleavage: immuno

Transporter associated with antigen processing

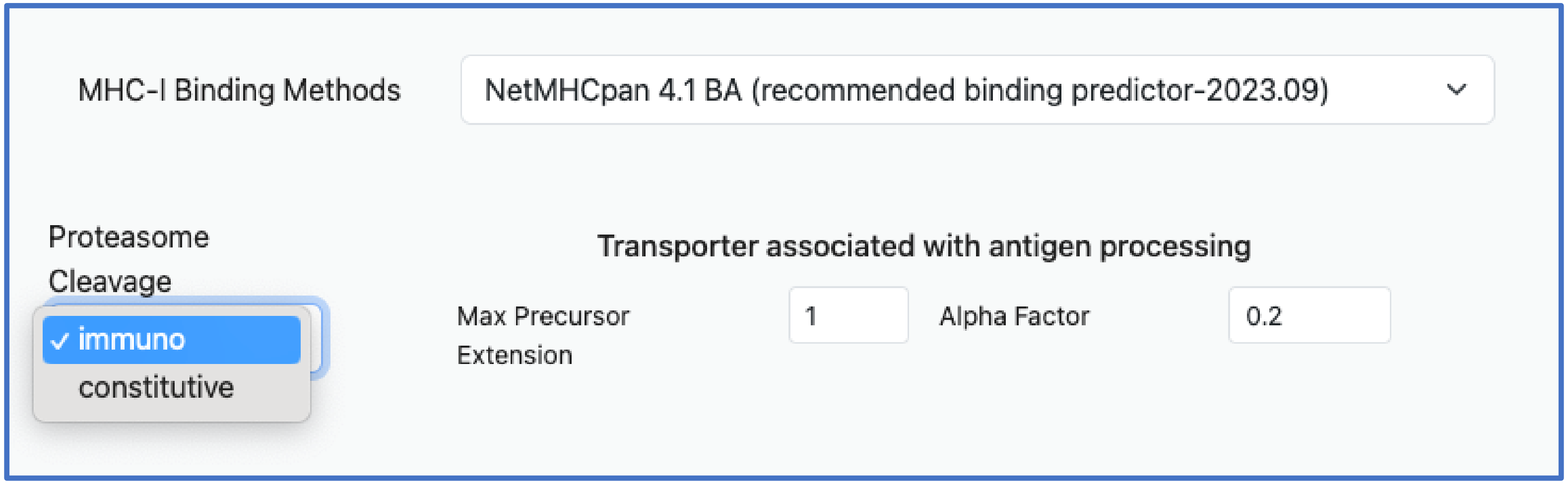
Max Precursor Extension: 1

Alpha Factor: 0.2

- Combines predictions for:
  - MHC binding
  - proteasomal cleavage
  - TAP transport
- Trained on specific *in vitro* datasets

Proteasomal Cleavage & TAP Transport Parameters

nextgen-tools.iedb.org/tc1



MHC-I Binding Methods: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

Proteasome Cleavage: ✓ immuno

Transporter associated with antigen processing

Max Precursor Extension: 1

Alpha Factor: 0.2

Proteasomal Cleavage

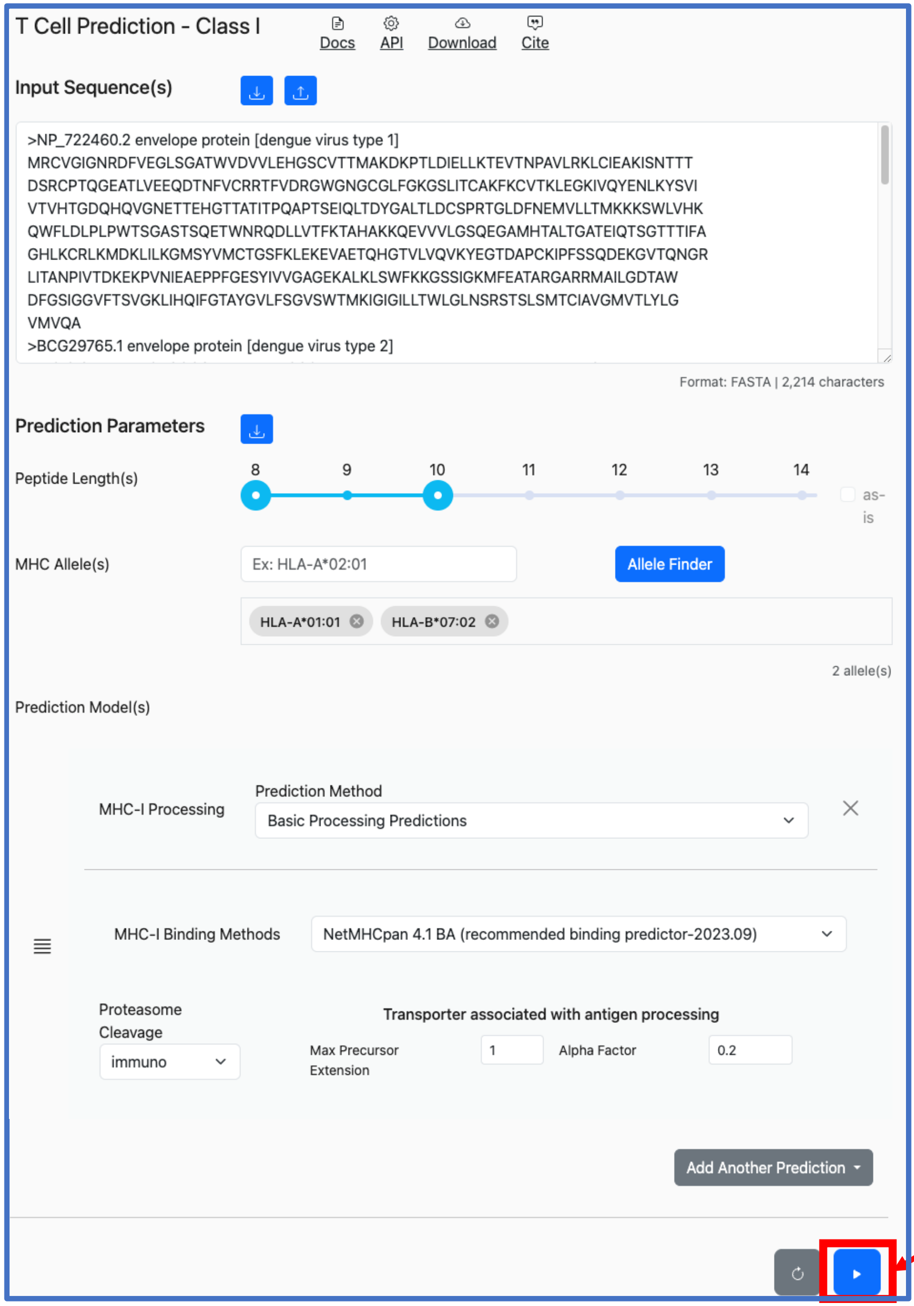
- Proteasomes create the C-terminal end of peptides
- Prediction looks for sequence motif up and downstream of potential cleavage site
- Cells may switch between immuno and constitutive proteasome machinery depending upon state

TAP Transport

- TAP transport efficiency of peptides is sequence dependent; motif derived based on *in vitro* assays
- Overall TAP transport efficiency of a presented MHC ligand can be result of a collection of precursors
- Unless paper thoroughly read and details about the precursor length distribution are known, **keep parameters unchanged**

Class I 'Combined Predictor' – Example

nextgen-tools.iedb.org/tc1



Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 – 10 (scale 8, 9, 10, 11, 12, 13, 14; ☐ as-is)

MHC Allele(s): Ex: HLA-A*02:01 — Allele Finder

HLA-A*01:01 ⊗ HLA-B*07:02 ⊗

2 allele(s)

Prediction Model(s)

MHC-I Processing — Prediction Method: Basic Processing Predictions

MHC-I Binding Methods: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

Proteasome Cleavage: immuno

Transporter associated with antigen processing

Max Precursor Extension: 1

Alpha Factor: 0.2

Run!

Class I ‘Combined Predictor’ – Example

nextgen-tools.iedb.org/tc1

seq #	peptide	allele	netmhcpan_ba IC50	proteasome score	tap score	mhc score	processing score	processing total score
3	TTEAILPEY	HLA-A*01:01	30.97	1.50	1.21	-1.49	2.71	1.22
2	ITEAELTGY	HLA-A*01:01	33.71	1.36	1.23	-1.53	2.59	1.07
3	STTEAILPEY	HLA-A*01:01	121.67	1.50	1.33	-2.09	2.84	0.75
1	TSEIQLTDY	HLA-A*01:01	54.13	1.20	1.15	-1.73	2.35	0.61
2	SITEAELTGY	HLA-A*01:01	133.29	1.36	1.36	-2.12	2.72	0.59
3	TPTWNRKEL	HLA-B*07:02	16.40	1.43	0.19	-1.21	1.62	0.40
3	RCPTQGEAAL	HLA-B*07:02	33.24	1.26	0.55	-1.52	1.81	0.29
4	TPRSPSVEV	HLA-B*07:02	8.93	1.14	0.02	-0.95	1.16	0.21
2	VVQPENLEY	HLA-A*01:01	677.26	1.50	1.39	-2.83	2.89	0.06
4	LVQIENLEY	HLA-A*01:01	469.87	1.33	1.38	-2.67	2.71	0.04

- Higher scores = higher efficiency for MHC-I presentation
- MHC binding score = –log10(IC50) (sign change)
- Combined scores are additive
  - Processing = proteasome + TAP
  - Total = proteasome + TAP + MHC

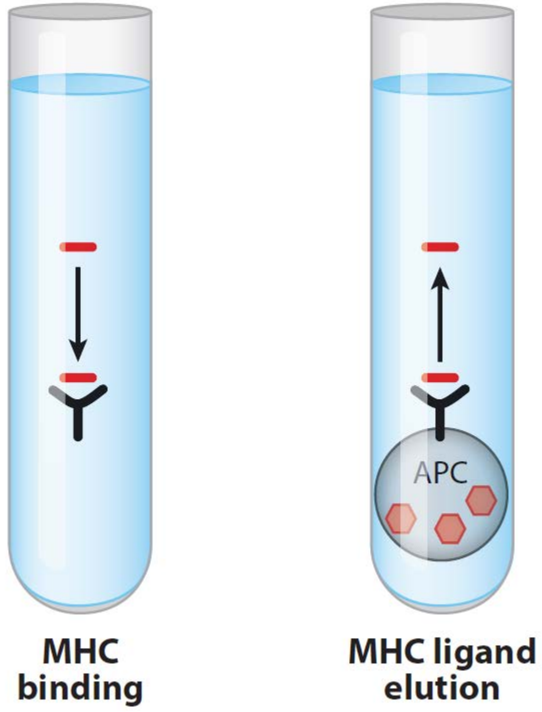
Caveats / Performance of Processing Predictions

- Predictions help understand why a given peptide may not be a good MHC ligand, despite strong predicted binding

- Most high-affinity binders are also efficiently processed due to co-evolution of MHC molecules with the proteosome and TAP

- Total processing score can be used as an additional filter for peptide selection, but should not be used without also considering binding independently

Recommended Alternative: Use Predictors Directly Trained on Eluted Ligand Data

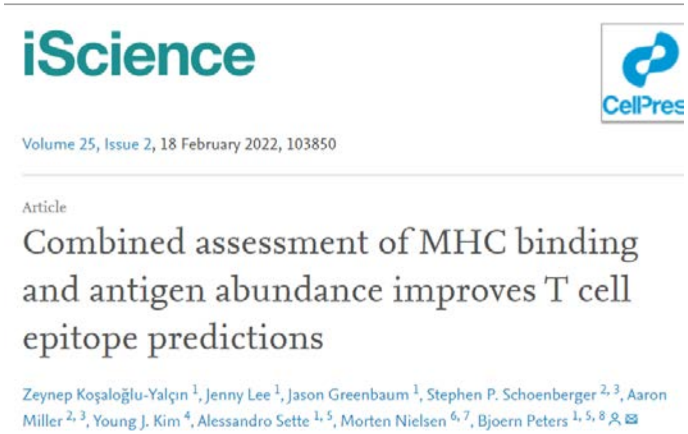


- Mass spectrometry of eluted ligands allows for the identification of a very large number of ligands in a single experiments
- Ligand sequences contain signals from both binding and processing
- **NetMHCPan EL** predictions (trained on eluted ligands) performs excellent, and can be used just like a regular MHC binding prediction

Incorporating Antigen Expression: Axel-F

tools.iedb.org/axelf

- Increased expression of an antigen in a cell increases the likelihood that peptides derived from it are processed and presented
- Axel-F tool integrates expression data into MHC ligand predictions



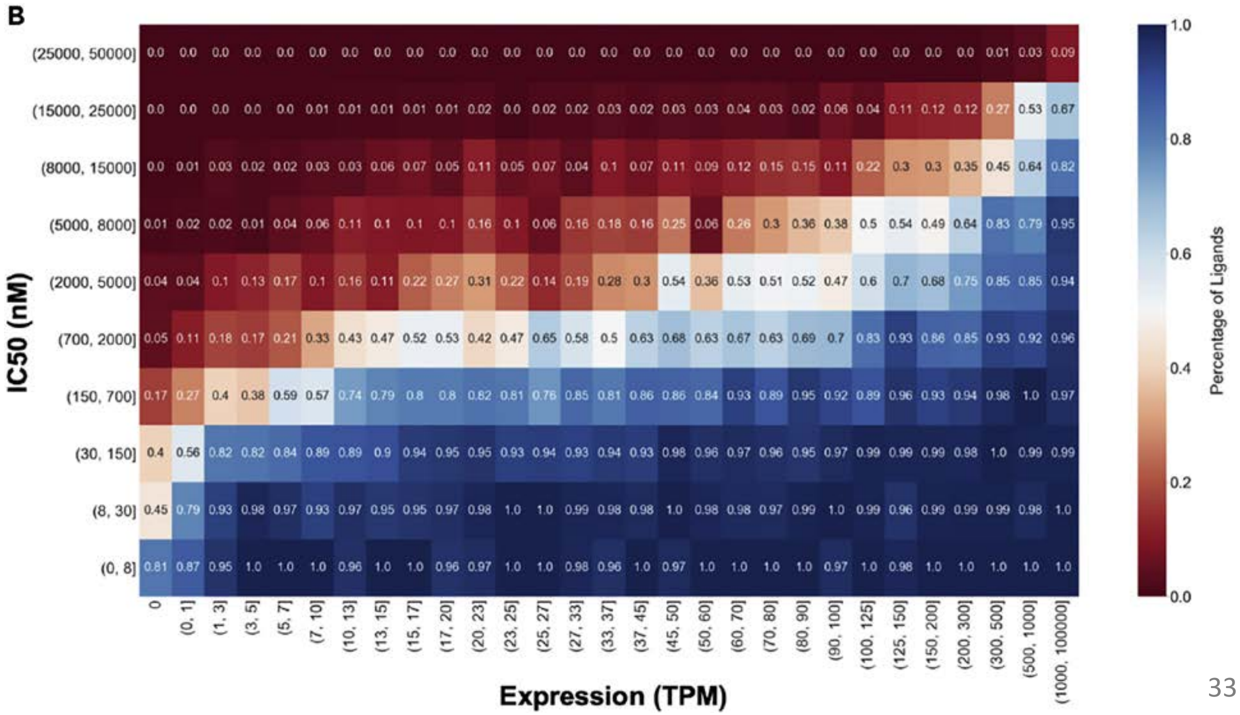
iScience

Volume 25, Issue 2, 18 February 2022, 103850

Article

Combined assessment of MHC binding and antigen abundance improves T cell epitope predictions

Zeynep Koşaloğlu-Yalçın [1], Jenny Lee [1], Jason Greenbaum [1], Stephen P. Schoenberger [2, 3], Aaron Miller [2, 3], Young J. Kim [4], Alessandro Sette [1, 5], Morten Nielsen [6, 7], Bjoern Peters [1, 5, 8]

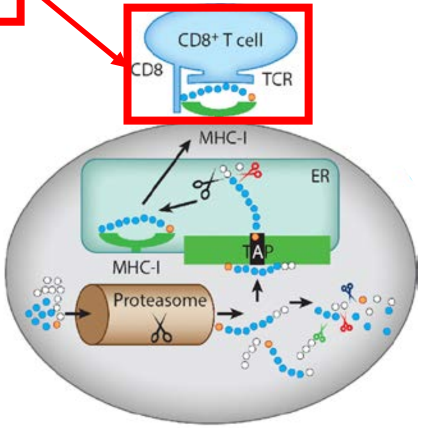


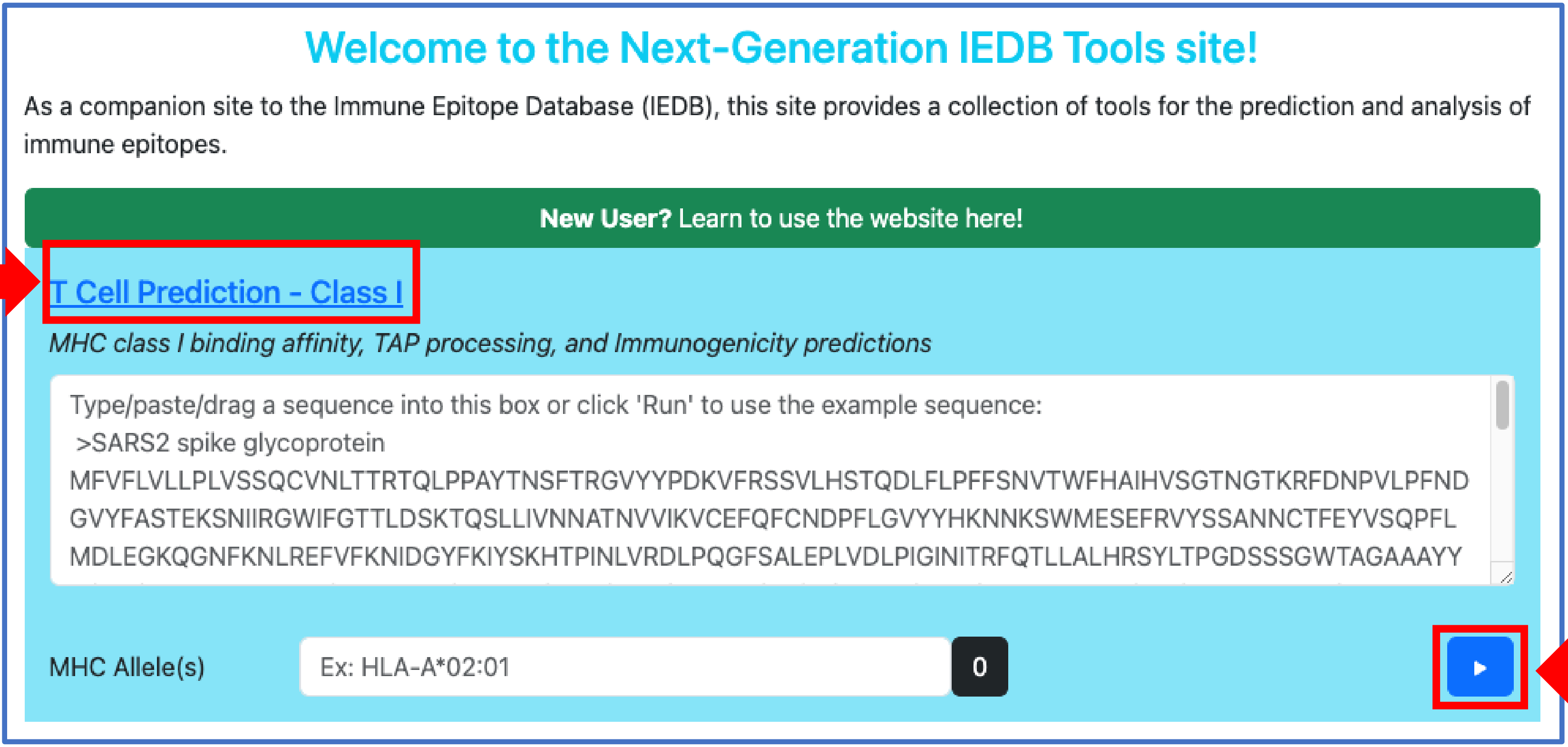
	0	(0, 1]	(1, 3]	(3, 5]	(5, 7]	(7, 10]	(10, 13]	(13, 15]	(15, 17]	(17, 20]	(20, 23]	(23, 25]	(25, 27]	(27, 33]	(33, 37]	(37, 45]	(45, 50]	(50, 60]	(60, 70]	(70, 80]	(80, 90]	(90, 100]	(100, 125]	(125, 150]	(150, 200]	(200, 300]	(300, 500]	(500, 1000]	(1000, 100000]
(25000, 50000]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.01	0.03	0.09
(15000, 25000]	0.0	0.0	0.0	0.0	0.0	0.01	0.01	0.01	0.01	0.01	0.02	0.0	0.02	0.02	0.03	0.02	0.03	0.03	0.04	0.03	0.02	0.06	0.04	0.11	0.12	0.12	0.27	0.53	0.67
(8000, 15000]	0.0	0.01	0.03	0.02	0.02	0.03	0.03	0.06	0.07	0.05	0.11	0.05	0.07	0.04	0.1	0.07	0.11	0.09	0.12	0.15	0.15	0.11	0.22	0.3	0.3	0.35	0.45	0.64	0.82
(5000, 8000]	0.01	0.02	0.02	0.01	0.04	0.06	0.11	0.1	0.1	0.1	0.16	0.1	0.06	0.16	0.18	0.16	0.25	0.06	0.26	0.3	0.36	0.38	0.5	0.54	0.49	0.64	0.83	0.79	0.95
(2000, 5000]	0.04	0.04	0.1	0.13	0.17	0.1	0.16	0.11	0.22	0.27	0.31	0.22	0.14	0.19	0.28	0.3	0.54	0.36	0.53	0.51	0.52	0.47	0.6	0.7	0.68	0.75	0.85	0.85	0.94
(700, 2000]	0.05	0.11	0.18	0.17	0.21	0.33	0.43	0.47	0.52	0.53	0.42	0.47	0.65	0.58	0.5	0.63	0.68	0.63	0.67	0.63	0.69	0.7	0.83	0.93	0.86	0.85	0.93	0.92	0.96
(150, 700]	0.17	0.27	0.4	0.38	0.59	0.57	0.74	0.79	0.8	0.8	0.82	0.81	0.76	0.85	0.81	0.86	0.86	0.84	0.93	0.89	0.95	0.92	0.89	0.96	0.93	0.94	0.98	1.0	0.97
(30, 150]	0.4	0.56	0.82	0.82	0.84	0.89	0.89	0.9	0.94	0.95	0.95	0.93	0.94	0.93	0.94	0.93	0.98	0.96	0.97	0.96	0.95	0.97	0.99	0.99	0.99	0.98	1.0	0.99	0.99
(8, 30]	0.45	0.79	0.93	0.98	0.97	0.93	0.97	0.95	0.95	0.97	0.98	1.0	1.0	0.99	0.98	0.98	1.0	0.98	0.98	0.97	0.99	1.0	0.99	0.96	0.99	0.99	0.99	0.98	1.0
(0, 8]	0.81	0.87	0.95	1.0	1.0	1.0	0.96	1.0	1.0	0.96	0.97	1.0	1.0	0.98	0.96	1.0	0.97	1.0	1.0	1.0	1.0	0.97	1.0	0.98	1.0	1.0	1.0	1.0	1.0

Class I immunogenicity prediction

nextgen-tools.iedb.org/tc1

Immunogenicity





Welcome to the Next-Generation IEDB Tools site!

As a companion site to the Immune Epitope Database (IEDB), this site provides a collection of tools for the prediction and analysis of immune epitopes.

New User? Learn to use the website here!

T Cell Prediction - Class I

MHC class I binding affinity, TAP processing, and Immunogenicity predictions

Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFND
GVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL
MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYY

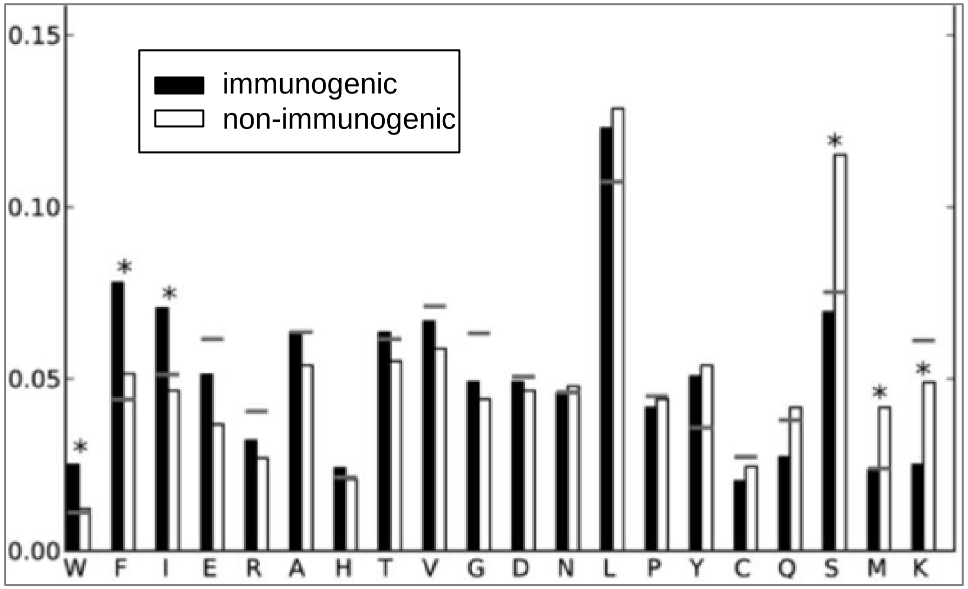
MHC Allele(s) Ex: HLA-A*02:01 0

Class I Immunogenicity Prediction

- Approach: Assemble two datasets of peptides with similar MHC binding affinity, that are (i) recognized or (ii) not recognized by T cells

- Enrichment of W,F,I and depletion of S,M,K in immunogenic peptides

- Use enrichments to calculate propensity scores




PLoS Comput Biol. 2013 Oct;9(10):e1003266. doi: 10.1371/journal.pcbi.1003266. Epub 2013 Oct 24.

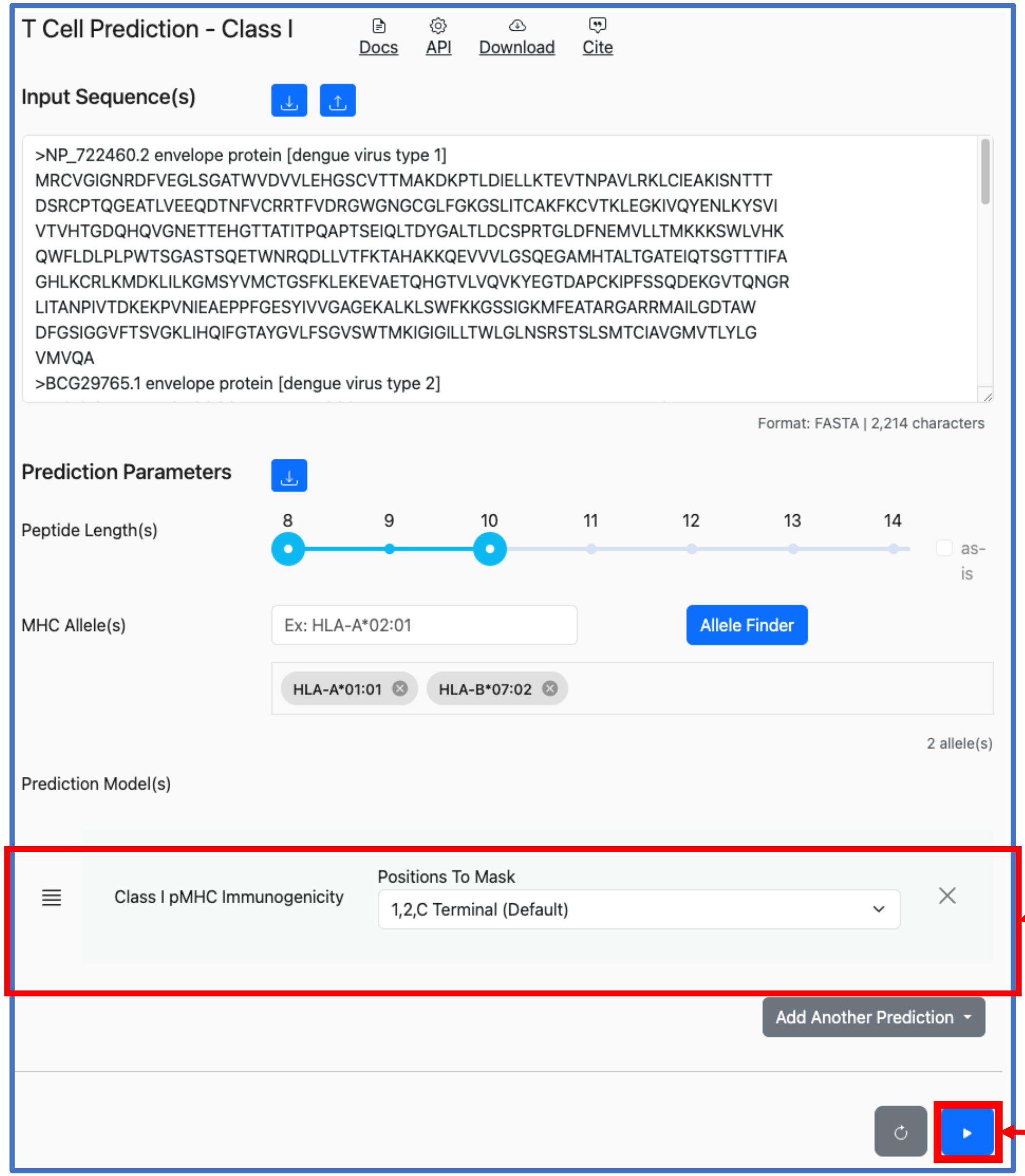
Properties of MHC class I presented peptides that enhance immunogenicity.

Calis JJ[1], Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Keşmir C, Peters B.

PMID: 24204222 PMCID: PMC3808449 DOI: 10.1371/journal.pcbi.1003266

Class I Immunogenicity Prediction – Example

nextgen-tools.iedb.org/tc1



Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 ● 9 10 ● 11 12 13 14 ☐ as-is

MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01 ⊗ HLA-B*07:02 ⊗

Prediction Model(s)

Class I pMHC Immunogenicity — Positions To Mask: 1,2,C Terminal (Default)

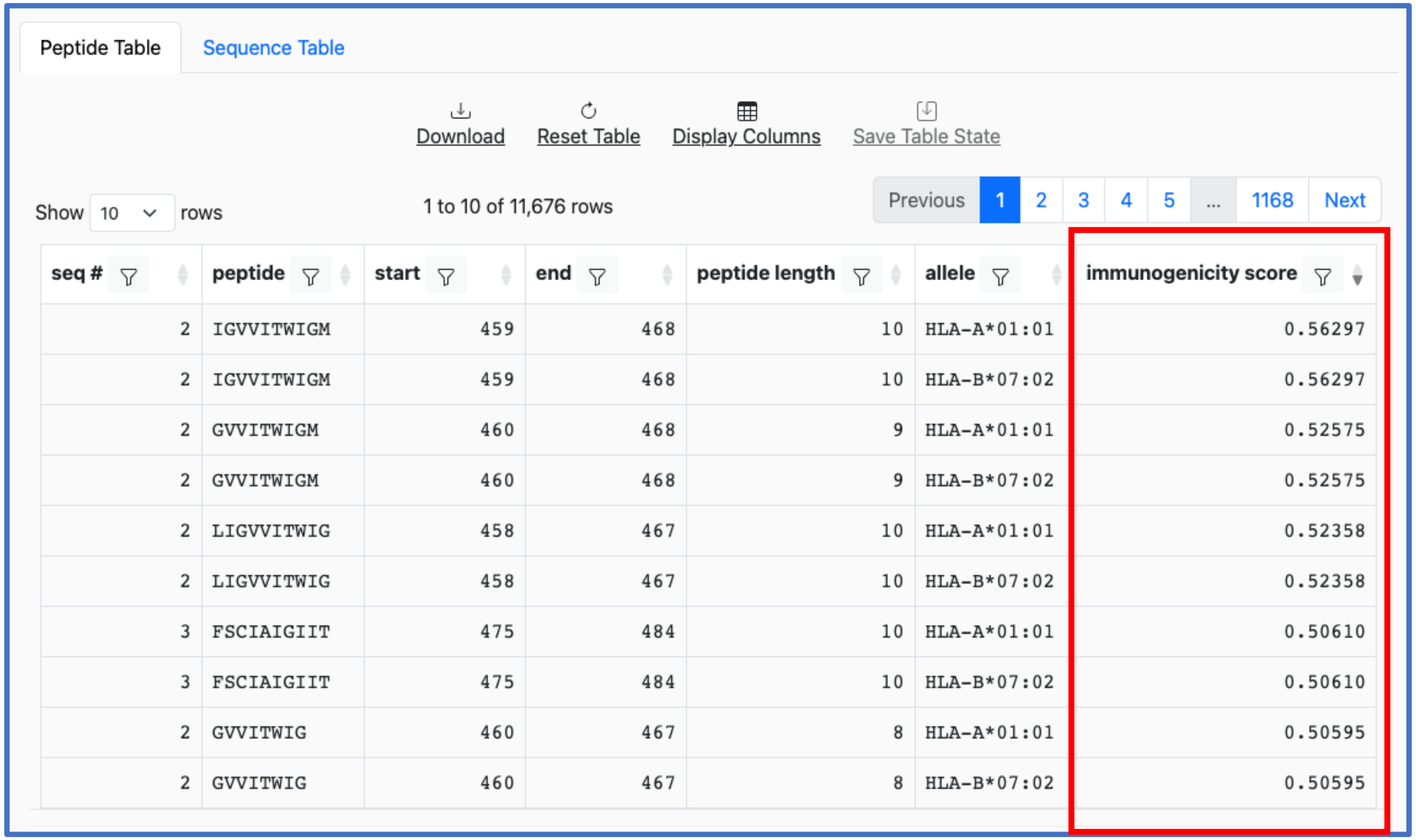
Mask positions that are MHC anchors

Run!

*Although predictions can be made for any length, this tools was only validated for 9mer peptides.

Class I Immunogenicity Prediction – Example

nextgen-tools.iedb.org/tc1



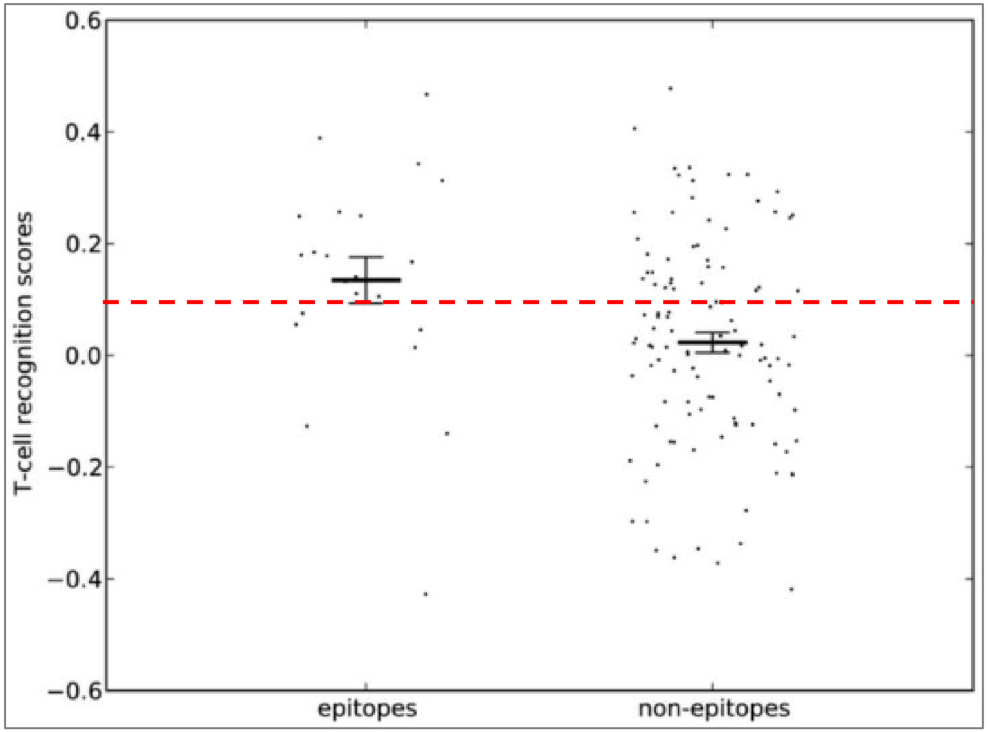
1 to 10 of 11,676 rows

seq #	peptide	start	end	peptide length	allele	immunogenicity score
2	IGVVITWIGM	459	468	10	HLA-A*01:01	0.56297
2	IGVVITWIGM	459	468	10	HLA-B*07:02	0.56297
2	GVVITWIGM	460	468	9	HLA-A*01:01	0.52575
2	GVVITWIGM	460	468	9	HLA-B*07:02	0.52575
2	LIGVVITWIG	458	467	10	HLA-A*01:01	0.52358
2	LIGVVITWIG	458	467	10	HLA-B*07:02	0.52358
3	FSCIAIGIIT	475	484	10	HLA-A*01:01	0.50610
3	FSCIAIGIIT	475	484	10	HLA-B*07:02	0.50610
2	GVVITWIG	460	467	8	HLA-A*01:01	0.50595
2	GVVITWIG	460	467	8	HLA-B*07:02	0.50595

- Scores are sums of propensity scores at all unmasked positions
- High scores = peptide is more likely to be immunogenic
- If ‘allele-specific’ is unselected, the same score will apply over all alleles

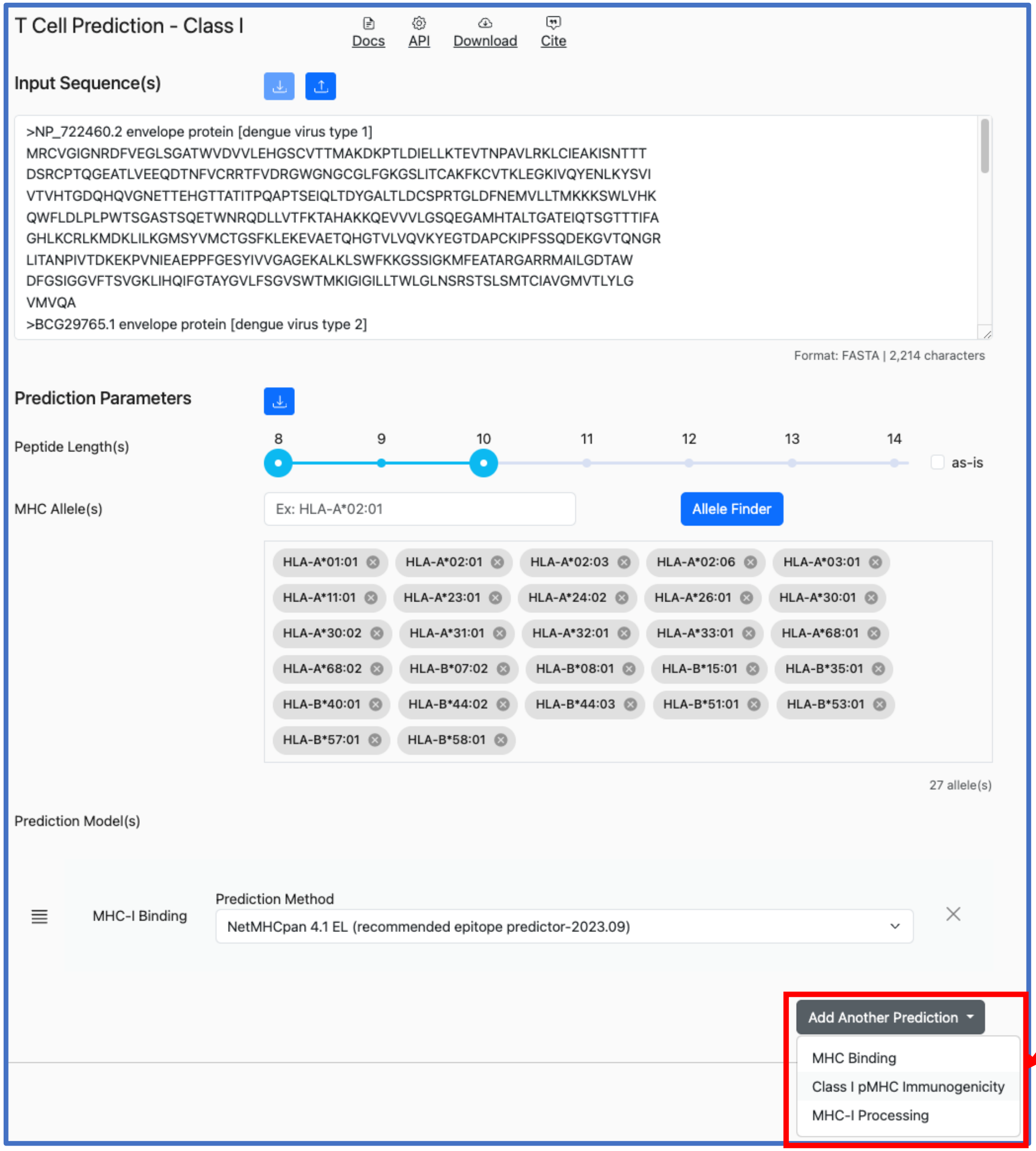
Class I Immunogenicity Prediction Caveats / Performance

- Experimentally, many MHC binding peptides can be immunogenic (~50%)
- Cross validation gave AUC values ~ 0.65. Test on independent blind set gave AUC = 0.69
- Recommendation: Use as filter (cutoff 0) if high specificity is desired.



Combining Multiple Predictors

nextgen-tools.iedb.org/tc1



T Cell Prediction - Class I

Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
LITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
DFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Prediction Parameters

Peptide Length(s): 8 9 10 11 12 13 14 ☐ as-is

MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01, HLA-A*02:01, HLA-A*02:03, HLA-A*02:06, HLA-A*03:01, HLA-A*11:01, HLA-A*23:01, HLA-A*24:02, HLA-A*26:01, HLA-A*30:01, HLA-A*30:02, HLA-A*31:01, HLA-A*32:01, HLA-A*33:01, HLA-A*68:01, HLA-A*68:02, HLA-B*07:02, HLA-B*08:01, HLA-B*15:01, HLA-B*35:01, HLA-B*40:01, HLA-B*44:02, HLA-B*44:03, HLA-B*51:01, HLA-B*53:01, HLA-B*57:01, HLA-B*58:01

27 allele(s)

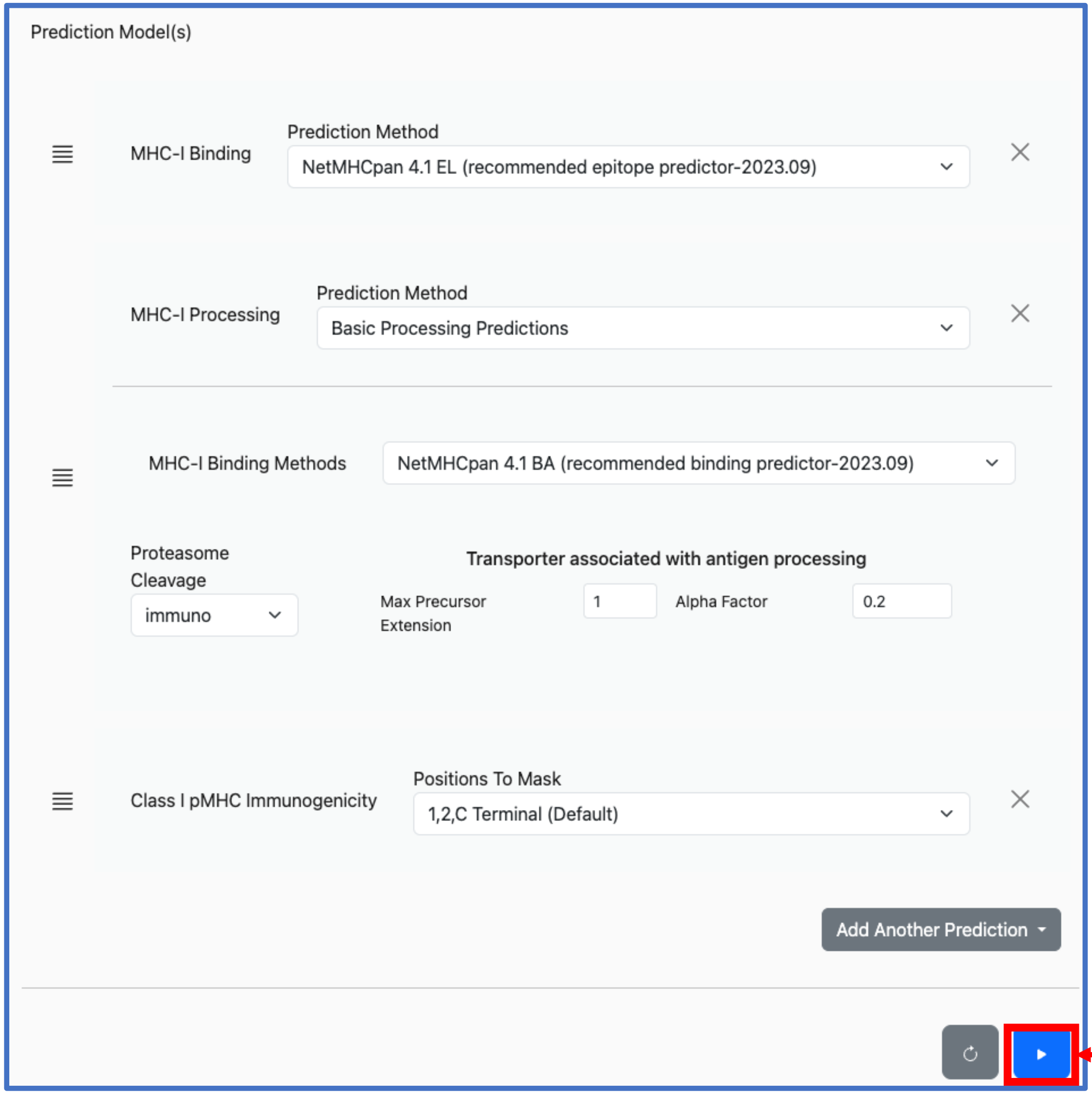
Prediction Model(s)

MHC-I Binding — Prediction Method: NetMHCpan 4.1 EL (recommended epitope predictor-2023.09)

Add another prediction

Combining Multiple Predictors

nextgen-tools.iedb.org/tc1



Prediction Model(s)

MHC-I Binding — Prediction Method: NetMHCpan 4.1 EL (recommended epitope predictor-2023.09)

MHC-I Processing — Prediction Method: Basic Processing Predictions

MHC-I Binding Methods: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

Proteasome Cleavage: immuno

Transporter associated with antigen processing

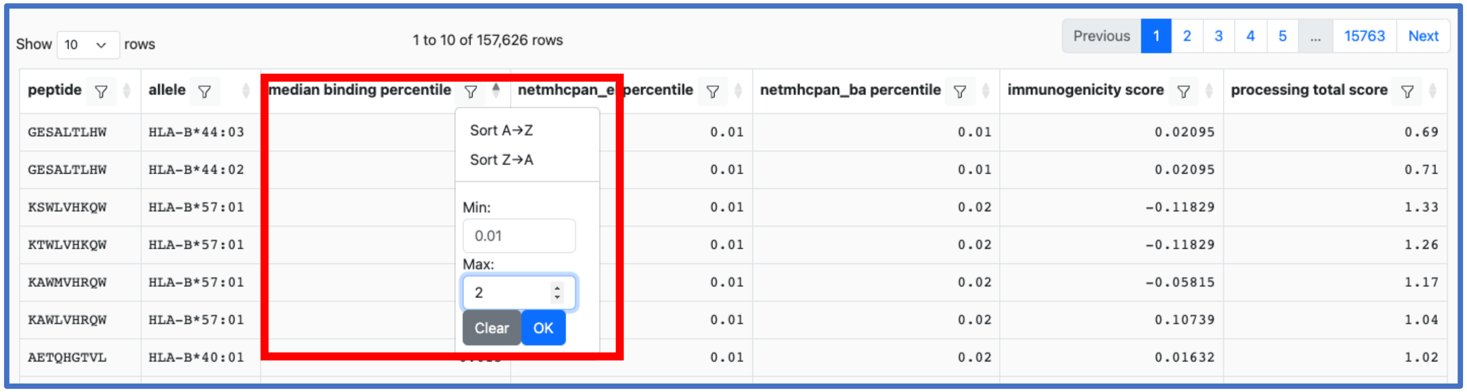
Max Precursor Extension: 1

Alpha Factor: 0.2

Class I pMHC Immunogenicity — Positions To Mask: 1,2,C Terminal (Default)

Run!

Apply Filters and Save Your Work!



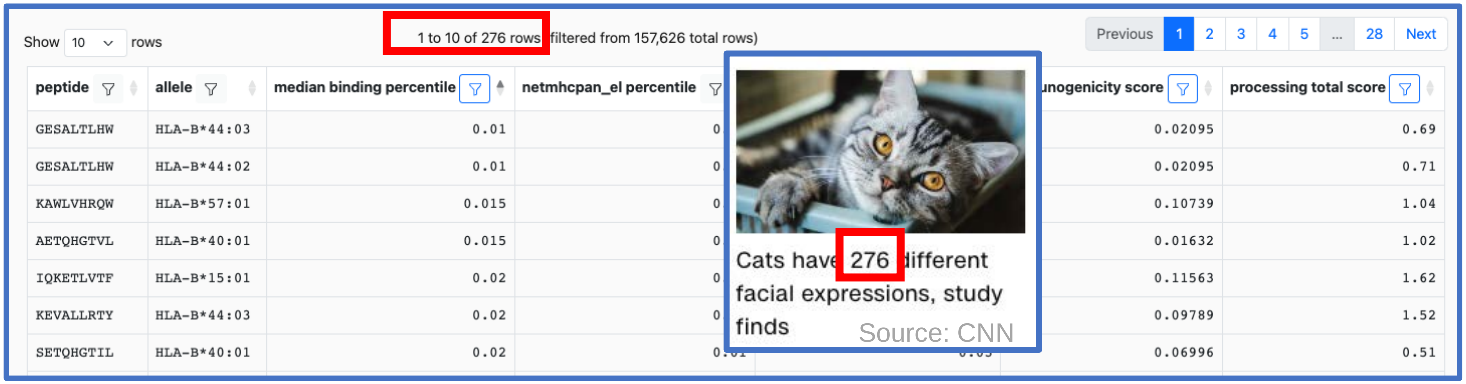
Show 10 rows

1 to 10 of 157,626 rows

peptide	allele	median binding percentile	netmhcpan_e percentile	netmhcpan_ba percentile	immunogenicity score	processing total score
GESALTLHW	HLA-B*44:03		0.01	0.01	0.02095	0.69
GESALTLHW	HLA-B*44:02		0.01	0.01	0.02095	0.71
KSWLVHKQW	HLA-B*57:01		0.01	0.02	-0.11829	1.33
KTWLVHKQW	HLA-B*57:01		0.01	0.02	-0.11829	1.26
KAWMVHRQW	HLA-B*57:01		0.01	0.02	-0.05815	1.17
KAWLVHRQW	HLA-B*57:01		0.01	0.02	0.10739	1.04
AETQHGTVL	HLA-B*40:01		0.01	0.02	0.01632	1.02

Min: 0.01

Max: 2



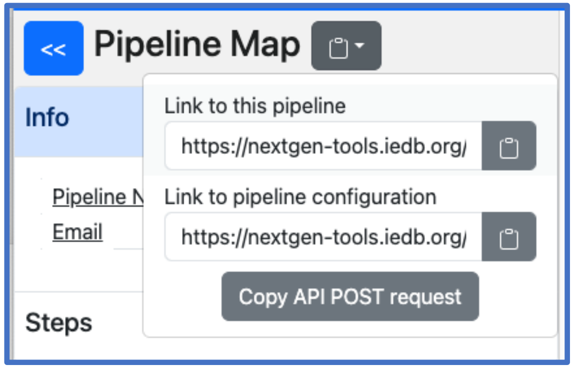
Show 10 rows

1 to 10 of 276 rows filtered from 157,626 total rows)

peptide	allele	median binding percentile	netmhcpan_el percentile	unogenicity score	processing total score
GESALTLHW	HLA-B*44:03	0.01	0	0.02095	0.69
GESALTLHW	HLA-B*44:02	0.01	0	0.02095	0.71
KAWLVHRQW	HLA-B*57:01	0.015	0	0.10739	1.04
AETQHGTVL	HLA-B*40:01	0.015	0	0.01632	1.02
IQKETLVTF	HLA-B*15:01	0.02	0	0.11563	1.62
KEVALLRTY	HLA-B*44:03	0.02	0	0.09789	1.52
SETQHGTIL	HLA-B*40:01	0.02	0.01	0.06996	0.51

Cats have 276 different facial expressions, study finds

Source: CNN



Pipeline Map

Info

Link to this pipeline

https://nextgen-tools.iedb.org/

Pipeline N

Email

Link to pipeline configuration

https://nextgen-tools.iedb.org/

Steps

- Pipeline link will include all selected parameters plus all data
- Pipeline ‘configuration’ link will only include selected parameters

Review

- Next-generation IEDB Tools website (nextgen-tools.iedb.org) hosts the complete T cell, class I suite of tools
    - MHC binding & elution
    - Antigen processing
    - Immunogenicity
- Recommended methods will continue to change as algorithms are evaluated
- No uniform threshold exists for selecting peptide candidates
- Tools may be executed simultaneously, and results can be filtered and shared