



IEDB

Immune Epitope Database & Tools

Next Generation Tool Pipelines Cluster & PEPMatch

nextgen-tools.iedb.org

Presented by: Dr. Bjoern Peters, Professor

IEDB Tools

Analysis Resource & Next-Generation Tools

Epitope Prediction and Analysis Tools

Welcome to the Immune Epitope Database Analysis Resource. This site provides a collection of tools for the prediction and analysis of immune epitopes. It serves as a companion site to the [Immune Epitope Database \(IEDB\)](#), a manually curated database of experimentally characterized immune epitopes.

The tools contained fall into the following categories:

T Cell Epitope Prediction Tools

This set of tools includes MHC class I & II binding predictions, as well as peptide processing predictions and immunogenicity predictions.

B Cell Epitope Prediction Tools

The tools here are intended to predict regions of proteins that are likely to be recognized as epitopes in the context of a B cell response.

Analysis Tools

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

Analysis Resource:

- T cell epitope prediction
- B cell epitope prediction
- Analysis tools

tools.iedb.org

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

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYYPDKVFRSSVLHSTQDLFLPFFSNVTWF

HAIHVSNGTNGTKRFDNPNVLPFNDGVYFASTEKSNIIIRGWIFGTTLDSKTQSLIIVNINATNVVIVK

CEFQFCNDPFLGVVYHKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREF

MHC
Allele(s)

Ex: HLA-A*02:01

0



Next-Generation Tools:

- Re-implementing existing tools with a focus on improving usability and function
- Launched in 2023
- More tools to be added

nextgen-tools.iedb.org

IEDB Tools

Analysis Resource & Next-Generation Tools

Epitope Prediction and Analysis Tools

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>SARS2 spike glycoprotein

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYYPDKVFRSSVLHSTQDLFLPFFSNVTWF

HAIHVSNGTNGTKRFDNPVLPFNDGVYFASTEKSNIIIRGWIFGTLLDSKTQSLILIVNINATNVVIVK

CEFQFCNDPFLGVVYHKNKNSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLR

MHC
Allele(s)

Ex: HLA-A*02:01

0



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Let's pick up where we left off...



- **Unput Sequence:** Dengue virus envelope protein (type 1-4)
- **Peptide Lengths:** 8-10
- **MHC Alleles:** 27 allele panel
- **Prediction Methods:**
 1. MHC-I Binding – NetMHCpan 4.1 EL (recommended epitope predictor-2023.09)
 2. MHC-I Processing – Basic Processing Predictions
 3. MHC-I Binding Methods – NetMHCpan 4.1 BA (recommended binding predictor-2023.09)
 4. Class I pMHC Immunogenicity – 1,2,C Terminal (Default)

>NP_722460.2 envelope protein [dengue virus type 1]

MRCVVGIGNRDFVEGLSGATWVDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTTDSRCPTQGEATLVEEQDNTFVCRRTFVDRGWGNGCGLFGKGSGLITCAKFK
CVTKLEGIKIVQYENLKYSVIVTVHTGDQHQQVGNETTEHGTTATITPQAPTSEIQLTDYGALTDLDCSPRTGLDFNEMVLLTMKKKSWLVHKQWFLDLPLPWTSGASTSQETWNRQDLLVTF
KTAHAKKQEVVVLGSEQEGAMHTALTGATEIQTSGTTTIFAGHLKCRCLKMDKLKLGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTVNGRLITANPIVTDK
EKPVNIEAEPFPGESYIVVGAGEKALKLSWFKKGSIGKMFATARGARRMAILGDTAWDFGSGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTLSMTCIAVG
MVTLYLGVMMVQA

>BCG29765.1 envelope protein [dengue virus type 2]

MRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKHPATLRKYCIEAKLTNTTASRCPTQGEPSLNEEQDKRFICKHSMVDRGWGNGCGLFGKGGIVTCAMFT
CKKNMEGKVVQPENLEYTIVITPHSGEEKAVGNDTGKHGTEIKVTPQSSITEAELTYGTVTMECSPTGLDFNEMVLLQMEDKAWLVHRQWFLDLPLPWLPGADKQGSNWIKETLVT
FKNPHAKKQDVVVLGSEQEGAMHTALTGATEIQMSSGNLLFTGHLKCRCLKMDKLQKLGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPPCKIPFEIMDLEKRHLVGRITVNPVITE
KDSPVNIEAEPFPGDSYIVIGVEPGQLKLSWFKKGSIGQMFETTMRGAKRMAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAPSGVSWTMKILIGVITWIGMNSRSTLSVSLVLV
GVVTLYLGVMMVQA

>AMQ36111.1 envelope protein [dengue virus type 3]

MRCVGVGNRDFVEGLSGATWVDVLEHGSCVTTMAKNKPTLDIELKQKTEATQLATLRKLCIEGKITNITTTDSRCPTQGEAALPEEQDQNYVCKHTYVDRGWGNGCGLFGKGSGLVTCAKF
QCLEPIEGKVVQYENLKYTVIITVHTGDQHQQVGNETQGVTAETPQASTTEAILPEYGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETPTWNRKELLVTFKN
AHAKKQEVVVLGSEQEGAMHTALTGATEIQNSGGTSIFAGHLKCRCLKMDKLEKLGMSYAMCTNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTEDGQGAHNGRLITANPVVTKKEE
PVNIEAEPFPGESNIVIGIDNALKINWYKKGSSIGKMFATARGARRMAILGDTAWDFGSGVGLNSLGMVHQIFGSAYTALFSGVSWVMKIGIGVLLTWIGLNSKNTSMSFSCIAIGIITL
YLGAVVQA

>BCG29766.1 envelope protein [dengue virus type 4]

MRCVGVGNRDFVEGVSGGAWVDVLEHGSCVTTMAQKPTLDFELTKTAKVALLRKYCIEASISNITTATRCPTQGEPLYLKEEQDQQYICRRDVDRGWGNGCGLFGKGGVVTCAK
FLCSGKITGNLVQIENLEYTVVVTVHNGDTPAVGNDTSHHGVTATITPRSPSEVVKLPDYGELTLDCEPRSGIDFIEMILMKMKKKTWLVHKQWFLDLPLPWTAGADTSEVHWNHKERMV
TFKVPHAKRQDVTVLGSEQEGAMHSALAGATEVDSGDGNHMFAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTAVVVKYEGAGAPCKVPIEIRDVNKEKVVGRIISSTPF
AENTNSVTNIELEPPFGDSYIVIGVGESALTLHWFRKGSIGKMFESTYRGAKRMAILGETAWDFGSGVGLFTSLGKAVHQVFGSVYTTMFGGVSWMVRILIGFLVLWIGTNSRNTSMAMT
CIAVGGITLFLGFTVQA

T Cell Prediction – Class I

Sequence & Parameters

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Immune Epitope Database & Tools

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T Cell Prediction - Class I

T Cell Prediction - Class I

1

T Cell Prediction - Class I

Docs API Download Cite

Input Sequence(s)

```
>NP_722460.2 envelope protein [dengue virus type 1]
MRCVIGIGNRDFVEGLSGATWVDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWNGCGLFGKGSLLTCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQQVGNETTEHGTATITPQAPTSEIQLTDYGALTDLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSGEQEGAMHTALTGATEIQTSGTTTIFA
GHLKCRLLKMDKLLKGMYSVMCTGSFKLEKVAETQHGTVLVQVQYEGTDAPCKIPFSSQDEKGVTONGR
LITANPIVTDKEKPVNIEAEPFSGESYIVVGAGEKALKLWFKGSSIGKMFPEATARGARRMAILGDTAW
DFGSIGGVFTSVGLIHIQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTLSMTCIAVGMVTLVYG
VMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
```

Format: FASTA | 2,214 characters

Copy/Paste Sequence, Upload Sequence File (.txt, .json, .fasta) or Drag/Drop File

Prediction Parameters

Peptide Length(s)

MHC Allele(s)

Ex: HLA-A*02:01

Allele Finder

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)

T Cell Prediction – Class I

Sequence & Parameters

The screenshot displays the T Cell Prediction interface. On the left, a sidebar shows the pipeline steps, with 'T Cell Pred' selected. The main panel is titled 'Number of Selected Alleles: 27'. It features a list of MHC Allele(s) with checkboxes for selection. The selected alleles are: 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, and HLA-B*58:01. Below the list are buttons for '27 Allele Panel', 'Clear Selected Allele(s)', and 'Submit'. The right side of the interface shows a 'Tools' menu, 'Docs', 'API', 'Download', and 'Cite' options. A 'Download' button is visible. A text area contains a protein sequence for 'viral type 1' and 'viral type 2'. Below the text area is a slider for 'as-is' and an 'Allele Finder' button. The 'Allele Finder' button is highlighted with a red box. Below the 'Allele Finder' button is a 'Select Alleles' section with a grid of buttons for each of the 27 selected alleles. The text '27 allele(s)' is displayed at the bottom right.

Number of Selected Alleles: 27

MHC Allele(s)

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 Panel ⓘ Clear Selected Allele(s) Submit

Tools ▾ Help & Info ▾

Docs API Download Cite

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viral type 1
...SCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
...GWGNGCGLFGKGSLLTCAKFKCVTKLEGKIVQYENLKYSVI
...PTSEIQLTDYGALTDLDCSPRTGLDFNEMVLLTMKKKSWLVHK
...TFKTAHAKKQEVVVLGSGQEGAMHTALTGATEIQTSGTTTIFA
...KEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTONGR
...AGEKALKLSWFKGSSIGKMFEATARGARRMAILGDTAW
...SWTMKIGIGILLTWLGLNSRSTLSMTCIAVGMVTLYL

viral type 2

Format: FASTA | 2,214 characters

8 9 10 11 12 13 14 as-is

Ex: HLA-A*02:01

Allele Finder

Select Alleles

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)

Use 27 Allele Panel

T Cell Prediction – Class I

Prediction Models

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T Cell Prediction - Class I

+ ⓘ ▶

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)

Parameter changed since prediction.

1. Add Prediction Methods

Add Another Prediction



2. Click Run!

T Cell Prediction – Class I

Results – Peptide Table

Peptide Table | NetMHCpan Allele Distance | Sequence Table

Download | Reset Table | Display Columns | Save Table State

Show 50 rows | 1 to 50 of 157,626 rows

Previous | 1 | 2 | 3 | 4 | 5 | ... | 3153 | Next

seq #	peptide	start	end	peptide length	allele	median binding percentile	netmhcpan_e1 score	netmhcpan_e1 percentile	netmhcpan_ha IC50	netmhcpan_ha percentile	immunogenicity score	proteasome score	tap score	mhc score	processing score	processing total score
2	IQDITIVTF	232	240	9	HLA-B*16:01	0.02	0.9921	0.01	9.83	0.03	0.11563	1.50	1.12	-0.99	2.41	1.42
4	TPRSPFVEV	165	173	9	HLA-B*07:02	0.02	0.9908	0.01	9.92	0.03	-0.22256	1.14	0.02	-0.95	1.16	0.21
2	TVNSIVIEK	383	381	9	HLA-A*11:01	0.02	0.9902	0.01	9.99	0.03	0.24648	0.73	0.22	-0.97	0.94	-0.03
4	KEVALLETY	51	59	9	HLA-B*44:02	0.02	0.9260	0.01	26.92	0.03	0.09709	1.53	1.36	-1.43	2.93	1.52
3	KMANVGRQK	202	210	9	HLA-B*58:01	0.02	0.9855	0.01	5.82	0.03	-0.05915	1.40	0.59	-0.74	1.99	1.25
3	SEIQHDTIL	311	319	9	HLA-B*40:01	0.02	0.9838	0.01	12.08	0.03	0.04996	1.21	0.35	-1.08	1.89	0.81
1	VHFWVLRK	80	88	9	HLA-A*11:01	0.02	0.9808	0.01	10.70	0.03	0.05489	0.82	0.11	-1.00	0.89	-0.08
3	ITGALLETY	160	176	9	HLA-A*01:01	0.02	0.9721	0.03	30.97	0.03	0.24017	1.50	1.21	-1.49	2.71	1.22
4	VFIRVSRK	238	244	9	HLA-A*11:01	0.02	0.9621	0.01	10.91	0.03	-0.09908	0.87	0.28	-1.04	1.14	0.12
3	ALFQVSRV	444	452	9	HLA-A*02:08	0.02	0.9549	0.02	2.95	0.02	-0.06801	0.81	0.26	-0.37	1.07	0.70
4	KMEVALLETY	50	59	10	HLA-B*44:02	0.02	0.9450	0.02	15.80	0.02	0.15726	1.59	1.90	-1.20	2.89	1.49
3	SYANCTNYF	296	304	9	HLA-A*24:02	0.02	0.9327	0.02	5.00	0.02	-0.16274	1.39	1.16	-0.90	2.65	1.75
4	ETMGVGVV	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	2.32	0.02	0.29933	1.04	0.03	-0.37	1.09	0.73
4	HALLDGTAK	412	420	9	HLA-B*83:01	0.02	0.9864	0.02	10.24	0.02	0.21491	1.39	0.81	-1.01	1.91	0.90
1	HALLDGTAK	412	420	9	HLA-B*83:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.39	0.81	-0.91	1.89	0.98
2	HALLDGTAK	412	420	9	HLA-B*83:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.00	0.51	-0.91	1.89	0.90
3	HALLDGTAK	410	418	9	HLA-B*83:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.39	0.81	-0.91	1.89	0.90
4	TFKVFHAKK	239	247	9	HLA-A*33:01	0.02	0.8764	0.03	19.34	0.03	-0.10179	1.07	0.73	-1.29	1.90	0.81
4	KYWLVRQK	204	212	9	HLA-B*88:01	0.025	0.9889	0.01	8.97	0.04	-0.11829	1.89	0.84	-0.92	2.19	1.20
2	KHLYVSRK	204	212	9	HLA-B*88:01	0.025	0.9049	0.01	7.21	0.04	0.10739	1.50	0.47	-0.86	1.96	1.11
3	ITANFVPTK	380	388	9	HLA-A*11:01	0.025	0.9750	0.01	11.40	0.04	0.09177	1.12	0.23	-1.04	1.88	1.29
4	KEVALLETY	51	59	9	HLA-B*44:02	0.025	0.9882	0.01	36.11	0.04	0.09799	1.89	1.36	-1.86	2.95	1.89
2	ITKSLTQV	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	33.71	0.04	0.22149	1.54	1.23	-1.83	2.55	1.07
3	ITQGVTAET	154	162	9	HLA-A*60:02	0.025	0.9267	0.01	6.74	0.04	0.16476	1.00	0.19	-0.20	1.23	0.43
3	ATQGLSRK	50	58	9	HLA-A*11:01	0.025	0.8033	0.01	11.72	0.04	0.04676	0.82	0.17	-1.07	0.89	-0.08
4	KYWLVRQK	204	212	9	HLA-B*83:01	0.025	0.8943	0.01	30.89	0.04	-0.11829	1.89	0.84	-1.49	2.19	0.44
4	SALLSHFFK	388	396	9	HLA-A*33:01	0.025	0.7691	0.04	8.00	0.01	0.30245	1.10	0.62	-0.32	1.79	0.81
2	ELKMKLQK	286	296	10	HLA-A*03:01	0.03	0.9412	0.02	14.91	0.04	-0.46298	0.92	0.34	-1.17	1.28	0.08
1	HALLDGTAK	412	420	9	HLA-B*88:01	0.03	0.9299	0.04	5.01	0.02	0.14154	1.89	0.81	-0.70	1.89	1.29
2	HALLDGTAK	412	420	9	HLA-B*88:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.89	0.81	-0.70	1.89	1.19
3	HALLDGTAK	410	418	9	HLA-B*88:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.89	0.81	-0.70	1.89	1.19
1	TRKGLTQV	170	178	9	HLA-A*01:01	0.03	0.9240	0.02	84.13	0.04	0.08890	1.20	1.18	-1.73	2.35	0.61

T Cell Prediction – Class I

Results – NetMHCpan Allele Distance & Sequence Table

Peptide Table NetMHCpan Allele Distance **Sequence Table**

Download Reset Table Display Columns Save Table State

Show 50 rows 1 to 4 of 4 rows Previous 1 Next

seq #	sequence name	sequence
1	NP_722460.2 envelope protein [dengue virus type 1]	MRCVGINRDFVEGLSGATWVDVLEHGSCVITMAKDKPTLDIELLKTVEINPAVLRKLCIEAKISNTITDSRCPT QGEATLVEEQDINFCVRRFTVDRGWGNGCGLFGKGSLLITCAKFCVTKLEGKIVQYENLKYSVIIVTHIGDQHQVQ NETTEHGTATITPQAPTSEIQLTDYDGLTLDLDCSPRTGLDFNEMVLLTMKRSWLVHKQWFLDPLFPWTS EITWNRQLLVTFKTAHAKKQEVVWVLSQEGAMHTALTGATEIQTSGTTIFAGHLKRLKMDKLLKMGMSYV SFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVQNGRLITANPVIIVTEKSPVNIIEAEP GAGEKALKSWFKGSSIGKMFETARGARRMAILGDTAWDFGSGVGVFTSVGKLHQIFGTAYGVLFSGVSW IGIGILLIWLGLNSRSTLSMTCIAVGMVTLVYLGVMVQA
2	BCG29765.1 envelope protein [dengue virus type 2]	MRCIGISNRDFVEGVSQSWVDIVLEHGSCVITMAKDKPTLDFELIKTEAKHPATLRKYIEAKLINTITASRCPT QGEPSLNEEQDKRFICKHSMVDRGWGNGCGLFGKGGIVTCAMFTCKNMEGKVVQENLETVITVPHSGEEKAVG NDTGHGTEIKVT PQSSITEAELTYGVTMECSPTGLDFNEMVLLQMEDKAWLVHRQWFLDPLFPWLGADQK SNWIKETLVTFKNPHAKKQDQVWVLSQEGAMHTALTGATEIQMSGNLLFTGHLKRLKMDKLLKMGMSYV KFKVVKIEAETQHGTVIVRVQYEGDGSFCCKIPFEMDLEKRVHLGRLITVNPVIVTEKSPVNIIEAEP GVEPGQLKSWFKGSSIGKMFETMRGAKRMAILGDTAWDFGSGVGVFTSIGKALHQVFGAIFYGAAFGVSW ILIGVVIWIGLNSRSTLSVSLVVLVGVVTLVYLGVMVQA
3	AMQ36111.1 envelope protein [dengue virus type 3]	MRCVGVGNRDFVEGLSGATWVDVLEHGSCVITMAKDKPTLDIELQKTEATQLATLRKLCIEGKININTITDSRCPT QGEAALPEEQDQNVVCKHTYVDRGWGNGCGLFGKGSLLITCAKFCQCLEPIEGKVVQYENLKYTVIIVTHIGDQHQVQ NETQGVTAELITPQASTTEALPEYGTGLGECSPRTGLDFNEMVLLTMKRSWLVHRQWFLDPLFPWTS WNRKELLVTFKNAHAKKQEVVWVLSQEGAMHTALTGATEIQNSGGTIFAGHLKRLKMDKLELKGMSYV VLKKEVSETQHGTVILIKVEYKGEDAPCKIPFSTEDGQKAGHNGRLITANPVIIVTEKSPVNIIEAEP GDNALKINWYKGSISGKMFETARGARRMAILGDTAWDFGSGVGVFLNSLGMVHQIFGSAITYALFSGVSW IGVLLIWLGLNSRSTLSMFSFCIAIGITLILYLGAVVQA
4	BCG29766.1 envelope protein [dengue virus type 4]	MRCVGVGNRDFVEGVSQSWVDIVLEHGSCVITMAKDKPTLDFELIKTITAKEVALLRKYIERASINNTITASRCPT QGEPSLKEEQDQYICRRDWDVDRGWGNGCGLFGKGGVITCAKFLCSGKITGNLVQIENLETVVTVHNGDTPAVG NDTSHHGVTATITPRPSVEVVKLPDYGELTLDLDCSPRSGIDFEMIIMKMKKKTWLVHKQWFLDPLFPW VHNMKERMVTFKVPFAKQDQVWVLSQEGAMHSLALGATEVDSGDGNHMFAGHLKRLKMDKLELKGMSYV KFSIDKEMAEQHGTAWVVKYEGAGAPCKVPIEIRDVNEKVVGRISSTPFAENTNSVNIIELEPPGDSYV GVGESALTLHWFRKGSISGKMFESTYRGAKRMAILGETAWDFGSGVGLFTSLGKAVHQVQVGSVYITMFGVSW ILIGVLLIWLGLNSRSTLSMAMTCIAVGGITLFLGFTVQA

Show 50 rows 1 to 4 of 4 rows Previous 1 Next

Peptide Table **NetMHCpan Allele Distance** Sequence Table

Download Reset Table Display Columns Save Table State

Show 50 rows 1 to 27 of 27 rows Previous 1 Next

Input Allele	Closest Allele	Distance
HLA-A*01:01	HLA-A*01:01	0
HLA-A*02:01	HLA-A*02:01	0
HLA-A*02:03	HLA-A*02:03	0
HLA-A*02:06	HLA-A*02:06	0
HLA-A*03:01	HLA-A*03:01	0
HLA-A*11:01	HLA-A*11:01	0
HLA-A*23:01	HLA-A*23:01	0
HLA-A*24:02	HLA-A*24:02	0
HLA-A*26:01	HLA-A*26:01	0
HLA-A*30:01	HLA-A*30:01	0
HLA-A*30:02	HLA-A*30:02	0
HLA-A*31:01	HLA-A*31:01	0
HLA-A*32:01	HLA-A*32:01	0
HLA-A*33:01	HLA-A*33:01	0
HLA-A*68:01	HLA-A*68:01	0
HLA-A*68:02	HLA-A*68:02	0
HLA-B*07:02	HLA-B*07:02	0
HLA-B*08:01	HLA-B*08:01	0
HLA-B*15:01	HLA-B*15:01	0
HLA-B*35:01	HLA-B*35:01	0
HLA-B*40:01	HLA-B*40:01	0
HLA-B*44:02	HLA-B*44:02	0
HLA-B*44:03	HLA-B*44:03	0
HLA-B*51:01	HLA-B*51:01	0
HLA-B*53:01	HLA-B*53:01	0
HLA-B*57:01	HLA-B*57:01	0
HLA-B*58:01	HLA-B*58:01	0

Show 50 rows 1 to 27 of 27 rows Previous 1 Next

T Cell Prediction – Class I

Results – Applying Filters to Peptide Table

Peptide Table | NetMHCpan Allele Distance | Sequence Table

Download | Reset Table | Display Columns | Save Table State

Show: 50 | 1 to 50 of 157,626 rows

seq #	peptide	start	end	peptide length	allele	median binding percentile	netmhcpan, el score	netmhcpan, el percentile	netmhcpan, ba IC50	netmhcpan, ba percentile	immunogenicity score	proteasome score	tap score	mhc score	processing score	processing total score
2	IQDITVTF	232	240	9	HLA-B*15:01	0.02	0.9921	0.01	9.83	0.03	0.11543	1.50	1.12	-0.99	1.6	1.42
4	TPSPFPEV	165	173	9	HLA-B*44:02	0.02	0.9750	0.01	6.74	0.04	0.16476	1.00	0.19	-0.07	0.99	-0.08
2	TVADIVTEK	383	381	3	HLA-A*01:01	0.025	0.9882	0.01	11.72	0.04	0.34676	0.82	0.17	-0.32	1.79	0.91
4	KEVALLETY	51	59	9	HLA-A*01:01	0.025	0.9597	0.01	93.71	0.04	0.22149	1.34	1.23	-0.01	1.43	0.43
3	KMANVGRQI	202	210	9	HLA-B*44:02	0.025	0.9367	0.01	6.04	0.04	0.16476	1.00	0.19	-0.07	0.99	-0.08
3	SEIQHDTIL	311	319	9	HLA-A*01:01	0.025	0.9038	0.01	11.72	0.04	0.34676	0.82	0.17	-0.32	1.79	0.91
1	VHRAWLRFI	90	88	3	HLA-B*32:01	0.025	0.8942	0.01	30.89	0.04	-0.11829	1.89	0.64	-1.49	1.28	-0.08
3	TTEALLREY	160	176	17	HLA-A*03:01	0.025	0.7691	0.04	8.00	0.01	0.32048	1.10	0.60	-0.32	1.79	0.91
4	VFIRVPEAK	238	244	7	HLA-A*03:01	0.03	0.9412	0.02	14.91	0.04	-0.46098	0.92	0.34	-1.17	1.28	-0.08
3	ALPSONVMV	444	452	9	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
4	KMEVALLETY	90	89	1	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
3	SYANCTINT	296	304	9	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
4	ETMDFQGVV	417	425	9	HLA-A*01:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
6	HALISGETAH	412	420	9	HLA-A*01:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
1	HALISQDTAH	412	420	9	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
2	HALISQDTAH	412	419	8	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
3	HALISQDTAH	412	419	8	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
4	TFKVFPAKQ	239	247	9	HLA-A*01:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
4	KYWLVRQKH	204	212	9	HLA-B*32:01	0.025	0.8942	0.01	30.89	0.04	-0.11829	1.89	0.64	-1.49	1.28	-0.08
2	KMHLVYERQ	204	212	9	HLA-B*32:01	0.025	0.8942	0.01	30.89	0.04	-0.11829	1.89	0.64	-1.49	1.28	-0.08
3	IITNPFVTH	380	388	9	HLA-A*01:01	0.025	0.9750	0.01	6.74	0.04	0.16476	1.00	0.19	-0.07	0.99	-0.08
4	KEVALLETY	51	59	9	HLA-A*01:01	0.025	0.9882	0.01	11.72	0.04	0.34676	0.82	0.17	-0.32	1.79	0.91
2	ITREALTOY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	93.71	0.04	0.22149	1.34	1.23	-0.01	1.43	0.43
3	ETQGVTAET	154	162	9	HLA-A*60:02	0.025	0.9367	0.01	6.04	0.04	0.16476	1.00	0.19	-0.07	0.99	-0.08
3	ATQGLALRK	50	58	9	HLA-A*11:01	0.025	0.9038	0.01	11.72	0.04	0.34676	0.82	0.17	-0.32	1.79	0.91
4	KYWLVRQKH	204	212	9	HLA-B*32:01	0.025	0.8942	0.01	30.89	0.04	-0.11829	1.89	0.64	-1.49	1.28	-0.08
4	SALLLHFFA	388	393	6	HLA-A*03:01	0.025	0.7691	0.04	8.00	0.01	0.32048	1.10	0.60	-0.32	1.79	0.91
2	RLMCKLQKQ	286	295	10	HLA-A*03:01	0.03	0.9412	0.02	14.91	0.04	-0.46098	0.92	0.34	-1.17	1.28	-0.08
1	HALISQDTAH	412	420	9	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
2	HALISQDTAH	412	420	9	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
3	HALISQDTAH	412	419	8	HLA-B*08:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19
1	TRKIGLTOY	170	178	9	HLA-A*01:01	0.03	0.9289	0.04	9.01	0.02	0.14354	1.88	0.61	-0.70	1.89	1.19

1 to 50 of 157,626 rows

Previous | 1 | 2 | 3 | 4 | 5 | ... | 3153 | Next

median binding percentile 1

Sort A→Z
Sort Z→A

Min: 0.01

Max: 2

Clear OK

Median Binding Percentile < 2

immunogenicity score 3

Sort A→Z
Sort Z→A

Min: d

Max: 0.56297

Clear OK

Immunogenicity Score > 0

processing total score

Sort A→Z
Sort Z→A

Min: d

Max: 1.75151146

Clear OK

Total Processing Score > 0

T Cell Prediction – Class I

Results – Applying Filters to Peptide Table

Yellow indicates changes have been made to table. Select “Save Table State” to proceed.

Download Reset Table Display Columns **Save Table State**

Show: 50 rows 1 to 50 of 276 rows (filtered from 157,626 total rows)

seq #	peptide	start	end	peptide length	allele	median binding percentile	netmhcpan_el score	netmhcpan_el percentile	netmhcpan_el IC50	netmhcpan_el percentile	immunogenicity score	proteasome score	tap score	mhc score	processing score	processing total score
6	DESAITISM	353	391	39	HLA-B*44:03	0.01	0.9917	0.01	7.72	0.01	0.02035	1.91	0.26	+0.69	1.93	0.69
4	DESAITISM	353	391	39	HLA-B*44:02	0.01	0.9942	0.01	7.29	0.01	0.02035	1.91	0.26	+0.66	1.93	0.71
2	YAKLWVDM	204	212	9	HLA-B*57:01	0.018	0.9899	0.01	8.41	0.02	0.10739	1.80	0.47	+0.90	1.96	1.04
1	ATQGVNVL	313	321	9	HLA-B*40:01	0.013	0.9923	0.01	0.21	0.02	0.01632	1.51	0.42	+0.91	1.94	1.02
2	IQNSIVVF	292	290	8	HLA-B*18:01	0.02	0.9921	0.01	8.83	0.02	0.11863	1.80	1.12	+0.89	2.61	1.62
4	NEVALISTY	51	59	9	HLA-B*44:03	0.02	0.9848	0.01	26.98	0.03	0.09789	1.59	1.36	+1.49	2.95	1.92
3	REYKQVIL	311	319	9	HLA-B*40:01	0.02	0.9938	0.01	12.08	0.03	0.04996	1.21	0.38	+1.08	1.99	0.81
3	TEALISFY	168	176	9	HLA-A*01:01	0.02	0.9721	0.01	30.87	0.03	0.26017	1.80	1.21	+1.49	2.71	1.22
4	AEVALLISTY	50	59	10	HLA-B*44:03	0.02	0.9460	0.02	15.80	0.02	0.18726	1.89	1.30	+1.20	2.83	1.69
4	STAMDFGVY	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	2.02	0.02	0.29933	1.06	0.03	+0.27	1.09	0.73
4	HALLOSTAM	412	420	9	HLA-B*58:01	0.02	0.9394	0.02	10.26	0.02	0.21491	1.38	0.51	+1.01	1.91	0.90
1	HALLOSTAM	412	420	9	HLA-B*53:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.39	0.51	+0.91	1.89	0.90
2	HALLOSTAM	412	420	9	HLA-B*59:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.38	0.51	+0.91	1.89	0.98
3	HALLOSTAM	412	418	7	HLA-B*53:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.38	0.51	+0.91	1.89	0.98
2	YAKLWVDM	204	212	9	HLA-B*58:01	0.025	0.9848	0.01	7.23	0.04	0.10739	1.80	0.47	+0.86	1.96	1.11
3	ITAMFVWR	350	358	9	HLA-A*11:01	0.028	0.9780	0.01	11.40	0.04	0.09177	1.12	0.23	+1.08	1.35	0.29
4	NEVALISTY	51	59	9	HLA-B*44:02	0.029	0.9632	0.01	36.11	0.04	0.09789	1.59	1.36	+1.56	2.95	1.59
2	TEALISFY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	39.71	0.04	0.21189	1.36	1.23	+1.63	2.56	1.07
3	RYQMTAKE	184	182	9	HLA-A*68:02	0.028	0.9867	0.01	4.34	0.04	0.14676	1.08	0.18	+0.80	1.23	0.43
4	HALTMWR	355	393	39	HLA-A*03:01	0.025	0.7691	0.04	8.00	0.01	0.31045	1.10	0.68	+0.90	1.73	0.81
1	HALLOSTAM	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.02	0.03	0.14154	1.38	0.51	+0.70	1.89	1.23
2	HALLOSTAM	412	420	9	HLA-B*59:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	+0.70	1.89	1.19
3	HALLOSTAM	410	418	9	HLA-B*59:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	+0.70	1.89	1.19
1	TEALISFY	170	178	9	HLA-A*01:01	0.03	0.9340	0.02	34.15	0.04	0.08890	1.20	1.15	+1.73	2.35	0.41
4	AEVALLISTY	50	59	10	HLA-B*44:02	0.03	0.8875	0.03	20.20	0.03	0.18726	1.59	1.30	+1.31	2.89	1.59
1	EVYFAWER	49	57	9	HLA-A*68:01	0.030000000000000002	0.9368	0.01	7.03	0.08	0.04028	1.13	0.40	+0.88	1.74	0.89
1	ETQVWVW	314	322	9	HLA-A*68:02	0.030000000000000002	0.9444	0.01	7.39	0.08	0.09285	1.00	0.09	+0.87	1.09	0.23
2	RYQNSIVVF	346	354	9	HLA-A*02:06	0.034999999999999996	0.9836	0.01	7.76	0.06	0.20546	1.01	0.22	+0.89	1.03	0.44
1	TEVINAVL	45	56	9	HLA-B*40:01	0.035	0.9076	0.02	23.23	0.05	0.09206	1.63	0.43	+1.37	2.03	0.69
4	HALLOSTAM	412	420	9	HLA-B*58:01	0.035	0.9461	0.04	8.40	0.03	0.21491	1.38	0.51	+0.75	1.91	1.15
3	YAGIVIL	478	486	9	HLA-B*39:01	0.035	0.9405	0.02	10.21	0.05	0.35848	1.17	1.09	+1.26	2.50	1.24
1	ITFAKSLK	276	284	9	HLA-A*69:01	0.035	0.9386	0.04	8.34	0.03	0.28182	0.70	0.22	+0.74	0.94	0.20
4	HALTMWR	355	393	39	HLA-A*01:01	0.035	0.8391	0.08	4.01	0.02	0.31045	1.10	0.68	+0.88	1.73	1.04
3	STAMDFGVY	418	423	6	HLA-A*68:02	0.035	0.8127	0.08	9.66	0.02	0.29933	0.99	+0.02	+0.89	0.97	0.38

Show: 50 rows 1 to 50 of 276 rows (filtered from 157,626 total rows)

Previous 1 2 3 4 5 6 Next

T Cell Prediction – Class I

Filtered Results

Table state has been saved – can proceed with analyses

Download Reset Table Display Columns Save Table State

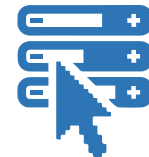
Show 50 rows 1 to 50 of 276 rows (filtered from 157,626 total rows)

seq #	peptide	start	end	peptide length	allele	median binding percentile	netmhcpan_el score	netmhcpan_el percentile	netmhcpan_ba IC50	netmhcpan_ba percentile	immunogenicity score	proteasome score	tap score	mhc score	processing score	processing total score
4	QSSALTIEM	383	391	9	HLA-B*44:02	0.01	0.9917	0.01	7.72	0.01	0.02055	1.81	0.26	-0.89	1.88	0.69
4	QSSALTIEM	383	391	9	HLA-B*44:02	0.01	0.9882	0.01	7.29	0.01	0.02055	1.81	0.26	-0.88	1.88	0.71
2	SKMLVNSM	204	212	9	HLA-B*57:01	0.015	0.9959	0.01	8.41	0.02	0.10739	1.50	0.47	+0.92	1.96	1.04
1	ASTQNSVL	313	321	9	HLA-B*40:01	0.015	0.9922	0.01	8.21	0.02	0.01632	1.81	0.42	-0.91	1.94	1.52
2	IQMIVLTF	232	240	9	HLA-B*18:01	0.02	0.9921	0.01	9.83	0.01	0.11863	1.90	1.12	+0.99	2.61	1.62
4	VEVALIET	51	59	9	HLA-B*44:02	0.02	0.9885	0.01	26.95	0.02	0.09769	1.89	1.56	-1.43	2.95	1.52
3	ETQNTIIL	511	519	9	HLA-B*40:01	0.02	0.9838	0.01	12.05	0.02	0.06936	1.21	0.38	-1.03	1.59	0.91
3	TEALISEY	160	176	9	HLA-A*01:01	0.02	0.9721	0.01	30.97	0.03	0.24017	1.50	1.21	+1.49	2.71	1.22
4	AMVALLRT	30	39	10	HLA-B*44:02	0.02	0.9402	0.02	18.80	0.02	0.18726	1.68	1.20	-1.20	2.88	1.69
4	ETAMDPSV	417	425	9	HLA-A*68:02	0.02	0.9284	0.02	2.32	0.02	0.29933	1.04	0.39	-0.37	1.09	0.73
4	HALLOGTM	412	420	9	HLA-B*59:01	0.02	0.9264	0.02	10.26	0.02	0.21491	1.39	0.61	+1.01	1.91	0.90
1	HALLOGTM	412	420	9	HLA-B*59:01	0.02	0.9249	0.02	8.12	0.02	0.14154	1.38	0.61	-0.91	1.89	0.98
2	HALLOGTM	412	420	9	HLA-B*59:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.38	0.61	-0.91	1.89	0.98
3	HALLOGTM	410	418	9	HLA-B*53:01	0.02	0.8949	0.02	8.12	0.02	0.14154	1.38	0.61	-0.91	1.89	0.90
2	SKMLVNSM	204	212	9	HLA-B*58:01	0.025	0.9849	0.01	7.21	0.04	0.10739	1.60	0.47	-0.84	1.94	1.11
3	ITAMPAVK	350	358	9	HLA-A*11:01	0.025	0.9780	0.01	11.40	0.04	0.09177	1.12	0.28	+1.04	1.36	0.29
4	VEVALIET	51	59	9	HLA-B*44:02	0.025	0.9882	0.01	36.11	0.04	0.09769	1.99	1.56	-1.54	2.98	1.89
2	TEALISEY	170	178	9	HLA-A*01:01	0.025	0.9697	0.01	33.71	0.04	0.21149	1.36	1.23	-1.53	2.89	1.07
3	ETQNTIIL	154	162	9	HLA-A*68:02	0.025	0.9567	0.01	6.34	0.04	0.16476	1.05	0.18	-0.50	1.23	0.43
4	HALIHWK	383	393	9	HLA-A*30:01	0.025	0.7691	0.04	8.30	0.01	0.31045	1.10	0.62	-0.92	1.73	0.91
1	HALLOGTM	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	8.01	0.02	0.14154	1.38	0.61	-0.70	1.89	1.19
2	HALLOGTM	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	8.01	0.02	0.14154	1.38	0.61	-0.70	1.89	1.19
3	HALLOGTM	410	418	9	HLA-B*58:01	0.03	0.9399	0.04	8.01	0.02	0.14154	1.38	0.61	-0.70	1.89	1.19
1	TSBQETLV	170	178	9	HLA-A*01:01	0.03	0.9240	0.02	54.13	0.04	0.00590	1.20	1.15	+1.73	2.39	0.61
4	AMVALLRT	30	39	10	HLA-B*44:02	0.03	0.8975	0.09	20.29	0.02	0.15726	1.69	1.80	-1.31	2.89	1.68
1	EVNFWK	49	57	9	HLA-A*68:01	0.030000000000000003	0.8848	0.01	7.03	0.08	0.04048	1.18	0.60	+0.88	1.74	0.89
1	ETQNTIIL	314	322	9	HLA-A*68:02	0.0300000000000000052	0.9444	0.01	7.39	0.08	0.09205	1.00	0.39	-0.87	1.09	0.43
2	IVGRLIIV	146	154	9	HLA-A*02:06	0.034999999999999996	0.9636	0.01	7.76	0.06	0.20546	1.31	0.22	-0.89	1.53	0.64
1	TEVDFKVL	40	56	9	HLA-B*40:01	0.035	0.9570	0.03	23.23	0.03	0.09206	1.63	0.43	-1.37	2.05	0.69
4	HALLOGTM	412	420	9	HLA-B*58:01	0.035	0.9461	0.04	6.48	0.03	0.21491	1.39	0.61	-0.71	1.91	1.13
3	IASRITLL	478	486	9	HLA-B*38:01	0.035	0.9408	0.02	18.21	0.03	0.89848	1.37	1.33	-1.24	2.80	1.24
1	ITFWRK	278	284	9	HLA-A*69:01	0.035	0.9358	0.04	9.94	0.03	0.28192	0.72	0.28	-0.74	0.94	0.20
4	HALIHWK	383	393	9	HLA-A*31:01	0.035	-0.8391	0.08	4.81	0.02	0.31245	1.10	0.62	-0.68	1.73	1.04
3	ETAMDPSV	415	423	9	HLA-A*68:02	0.035	0.8127	0.03	3.86	0.02	0.29933	0.99	-0.02	+0.59	0.97	0.30

Show 50 rows 1 to 50 of 276 rows (filtered from 157,626 total rows)

Previous 1 2 3 4 5 6 Next

Now let's build the rest of the pipeline...



**T Cell Prediction
– Class I**



**Epitope Cluster
Analysis**



PepMatch

Add Cluster Tool (Peptide)

The screenshot displays the IEDB Pipeline Map interface. On the left, a sidebar shows the 'Pipeline Map' with a 'Steps' list containing 'T Cell Prediction - Class I'. A red box highlights a '+' button in the sidebar, which has opened a dropdown menu with options: 'Cluster', 'Peptide', and 'Pepmatch'. A red arrow points from the text '1. Add Cluster to Pipeline' to this '+' button. The main interface shows the 'T Cell Prediction - Class I' step with various controls and input fields.

1. Add Cluster to Pipeline

IEDB Immune Epitope Database & Tools

Tools ▾ Help & Info ▾

<< Pipeline Map

Info

Steps

T Cell Prediction - Class I

+

Cluster Peptide

Pepmatch

1

T Cell Prediction - Class I

Docs API Download Cite

Input Sequence(s)

>NP_722460.2 envelope protein [dengue virus type 1]
MRCVIGIGNRDFVEGLSGATWVDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPVLRKLCIEAKISNTTT
DSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGLSITCAKFKCVTKLEGKIVQYENLKYSVI
VTVHTGDQHQVGNETTEHGTATITPQAPTSEIQLTDYGALTDLDCSPRTGLDFNEMVLLTMKKKSWLVHK
QWFLDLPLPWTSGASTSQTWNRQDLLVTFKTAHAKKQEVVVLGSGEQAMHTALTGATEIQTSGTTTIFA
GHLKCRLLKMDKLLKGMYSVMCTGSFKLEKVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTONGR
LITANPIVTDKEKPVNIEAEPFSGESYVVGAGEKALKLSWFKKGGSIGKMFATARGARRMAILGDTAW
DFGSGIGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTLSMTCIAVGMVTLYL
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-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 Cluster Tool (Peptide)

The screenshot shows the IEDB web interface with a table of peptide data. The table has columns for seq #, peptide, start, end, peptide length, allele, median binding percentile, netmhcpan_el score, netmhcpan_el percentile, and netmhcpan. The peptide column is highlighted with a red box, and a red arrow points from a text box to it.

Peptide column is selected for piping to Cluster tool

seq #	peptide	start	end	peptide length	allele	median binding percentile	netmhcpan_el score	netmhcpan_el percentile	netmhcpan
4	GESALLLW	383	391	9	HLA-B*44:03	0.01	0.9917	0.01	
4	GESALLLW	383	391	9	HLA-B*44:02	0.01	0.9862	0.01	
2	KMWLVRQW	204	212	9	HLA-B*57:01	0.015	0.9959	0.01	
2	ASTDSTVL	313	321	9	HLA-B*40:01	0.015	0.9922	0.01	
2	TKKTHLTF	232	240	9	HLA-B*15:01	0.02	0.9921	0.01	
4	KEVALLRY	51	59	9	HLA-B*44:03	0.02	0.9868	0.01	
3	SETDSTIL	311	319	9	HLA-B*40:01	0.02	0.9838	0.01	
3	ITFALLRY	168	176	9	HLA-A*01:01	0.02	0.9721	0.01	
4	AKEVALLRY	50	59	10	HLA-B*44:03	0.02	0.9480	0.02	
4	ETAMDPSV	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	
4	MAILGDTAW	412	420	9	HLA-B*53:01	0.02	0.8944	0.02	
1	MAILGDTAW	412	420	9	HLA-B*53:01	0.02	0.8949	0.02	
2	MAILGDTAW	412	420	9	HLA-B*53:01	0.02	0.8949	0.02	
3	MAILGDTAW	410	418	9	HLA-B*53:01	0.02	0.8949	0.02	
2	KMWLVRQW	204	212	9	HLA-B*58:01	0.025	0.9849	0.01	
3	ITANPQVVK	350	358	9	HLA-A*11:01	0.025	0.9780	0.01	
4	KEVALLRY	51	59	9	HLA-B*44:02	0.025	0.9682	0.01	
2	ITSEALTSY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	
3	ETQVIREI	154	162	9	HLA-A*68:02	0.025	0.9567	0.01	
4	SALTLHWFR	385	393	9	HLA-A*33:01	0.025	0.7691	0.04	
1	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	
2	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	
3	MAILGDTAW	410	418	9	HLA-B*58:01	0.03	0.9399	0.04	
1	ITSEIGLTDY	170	178	9	HLA-A*01:01	0.03	0.9340	0.02	
4	AKEVALLRY	50	59	10	HLA-B*44:02	0.03	0.8875	0.03	
2	EVTNPAVLR	49	57	9	HLA-A*68:01	0.030000000000000002	0.9868	0.01	
1	ETQNSTVIV	314	322	9	HLA-A*68:02	0.030000000000000002	0.9444	0.01	
2	MVLGRLLIV	346	354	9	HLA-A*02:06	0.034999999999999996	0.9636	0.01	
2	IEVINEAVL	48	56	9	HLA-B*40:01	0.035	0.9578	0.02	
4	MAILGDTAW	412	420	9	HLA-B*58:01	0.035	0.9461	0.04	
3	LAIGLLTLV	478	486	9	HLA-B*35:01	0.035	0.9405	0.02	
2	ITIFAGRLK	276	284	9	HLA-A*68:01	0.035	0.9386	0.04	
4	SALTLHWFR	385	393	9	HLA-A*31:01	0.035	0.8391	0.05	
3	ETAMDPSV	415	423	9	HLA-A*68:02	0.035	0.8127	0.05	

Select Cluster Parameters

2

Cluster

[Docs](#) [API](#) [Cite](#)

Prediction Parameters



1. Select Sequence Identity Threshold

Sequence Identity Threshold



Peptide Length(s)



Cluster Method

Cluster-break for clear representative sequence



3. Click Run!

Results will load once step is run

2. Select Cluster Method

Cluster-break for clear representative sequence

All the connected Peptides in a cluster

Cluster-break for clear representative sequence

Fully intereconnected clusters (cliques)

Cluster Results – Warnings

IEDB
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Tools ▾ Help & Info ▾

<< Pipeline Map 📄

Info ▾

Steps ▾

T Cell Prediction - Class I ▾ 📅

Epitope Cluster Analysis 📅 ▾ ✕

+ ⓘ ▶

2 Cluster

📄 Docs 🔗 API 📄 Cite

Prediction Parameters 📄

Sequence Identity Threshold 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%

Peptide Length(s) No Min 5 10 15 20 25 No Max

Cluster Method Cluster-break for clear representative sequence ▾

🔄 ▶

Warnings (68) 📄

Peptide Table Visualization

📄 Download 🔄 Reset Table 📄 Display Columns 📄 Save Table State

Show 50 rows 1 to 50 of 182 rows
Previous 1 2 3 4 Next

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	1	NKAWMVHRQW--	1	seq174	NKAWMVHRQW	NKAWXVHRQWFX
1.1	2	--KAWLVHRQWF-	2	seq73	KAWLVHRQWF	NKAWXVHRQWFX
1.1	3	--KAWMVHRQWF-	2	seq156	KAWMVHRQWF	NKAWXVHRQWFX
1.1	4	--KAWLVHRQW--	2	seq71	KAWLVHRQW	NKAWXVHRQWFX
1.1	5	--AWMVHRQWFF	3	seq135	AWMVHRQWFF	NKAWXVHRQWFX
1.1	6	--AWLVHRQWF-	3	seq52	AWLVHRQWF	NKAWXVHRQWFX
1.1	7	--AWMVHRQWF-	3	seq133	AWMVHRQWF	NKAWXVHRQWFX
1.1	8	--WLVHRQWFL	4	seq124	WLVHRQWFL	NKAWXVHRQWFX
1.1	Consensus	NKAWXVHRQWFX	-	-	-	NKAWXVHRQWFX
1.2	Singleton	KNKAWMVHR	-	seq163	KNKAWMVHR	KNKAWMVHR

Cluster Results – Warnings

The screenshot displays a software interface for a pipeline. On the left, a sidebar shows a 'Pipeline Map' with steps: 'T Cell Prediction - Class I' and 'Epitope Cluster Analysis'. The main area is titled 'Cluster' and shows 'Prediction Parameters' for 'Sequence Identity Threshold' (set to 80%), 'Peptide Length(s)' (set to 5-25), and 'Cluster Method' (set to 'Cluster-break for clear representative sequence'). Below this, a 'Warnings (68)' section is highlighted with a red border, containing a list of 44 items. Each item indicates the number of duplicates found for a specific input sequence. A large text overlay on the right of the warnings section reads: 'Warnings indicate removal of duplicate inputs'.

Cluster

Prediction Parameters

Sequence Identity Threshold: 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%

Peptide Length(s): No Min 5 10 15 20 25 No Max

Cluster Method: Cluster-break for clear representative sequence

Warnings (68)

- 4 duplicates found of input sequence: "GLDFNEMVLL"
- 2 duplicates found of input sequence: "GMVTLYLGV"
- 2 duplicates found of input sequence: "IFGTAYGVLF"
- 2 duplicates found of input sequence: "IGIGILLTW"
- 3 duplicates found of input sequence: "KIGIGILLTW"
- 4 duplicates found of input sequence: "KQWFLDLPL"
- 2 duplicates found of input sequence: "LHQIFGTAY"
- 12 duplicates found of input sequence: "MAILGDTAW"
- 2 duplicates found of input sequence: "QTSGETTIF"
- 9 duplicates found of input sequence: "RMAILGDTAW"
- 2 duplicates found of input sequence: "RTFVDRGW"
- 2 duplicates found of input sequence: "SIGGVFTSV"
- 2 duplicates found of input sequence: "ALHQVFGAIY"
- 3 duplicates found of input sequence: "AMHTALTGA"
- 2 duplicates found of input sequence: "AWLVHRQWF"
- 2 duplicates found of input sequence: "FLDLPLPWL"
- 2 duplicates found of input sequence: "GTIVIRVQY"
- 2 duplicates found of input sequence: "HVLGRLLTV"
- 2 duplicates found of input sequence: "ITEAELTGY"
- 2 duplicates found of input sequence: "KAWLVHRQWF"
- 2 duplicates found of input sequence: "KAWLVHRQWF"
- 2 duplicates found of input sequence: "KILVGVVITW"
- 3 duplicates found of input sequence: "KVVQPENLEY"
- 2 duplicates found of input sequence: "LQMEDKAWLV"
- 2 duplicates found of input sequence: "LNTNTTASR"
- 2 duplicates found of input sequence: "LVLVGVVITW"
- 3 duplicates found of input sequence: "QWFLDLPLPW"
- 4 duplicates found of input sequence: "RQWFLDLPL"
- 2 duplicates found of input sequence: "SLVLVGVVITL"
- 3 duplicates found of input sequence: "SVSLVLVGV"
- 2 duplicates found of input sequence: "VFGAIGAAF"
- 2 duplicates found of input sequence: "VLVGVVITL"
- 2 duplicates found of input sequence: "VLVGVVITL"
- 5 duplicates found of input sequence: "VVQPENLEY"
- 4 duplicates found of input sequence: "WLVHRQWF"
- 2 duplicates found of input sequence: "ALFSGVSWWF"
- 2 duplicates found of input sequence: "AWMVHRQWF"
- 2 duplicates found of input sequence: "AWMVHRQWF"
- 2 duplicates found of input sequence: "CIAIGITLY"
- 4 duplicates found of input sequence: "IAIGITLY"
- 2 duplicates found of input sequence: "IGIGVLLTW"
- 2 duplicates found of input sequence: "ILPEYGLGL"
- 4 duplicates found of input sequence: "KAWMVHRQWF"
- 3 duplicates found of input sequence: "KIGIGVLLTW"

Warnings indicate removal of duplicate inputs

Cluster Results – Table

Interactable Table Headers/Filters

Peptide Table Visualization

Save/Download → Download Reset Table Display Columns Save Table State

Show 50 rows 1 to 50 of 182 rows

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	4	-KAWLVHRQW--	2	seq71	KAWLVHRQW	NKAWVHRQWFX
1.1	5	--AWMVHRQWFF	3	seq135	AWMVHRQWFF	NKAWVHRQWFX
1.1	6	--AWLVHRQWFF	3	seq52	AWLVHRQWFF	NKAWVHRQWFX
1.1	7	--AWMVHRQWFF	3	seq133	AWMVHRQWFF	NKAWVHRQWFX
1.1	8	---WLVHRQWFL	4	seq124	WLVHRQWFL	NKAWVHRQWFX
1.1	Consensus	NKAWVHRQWFX	-	-	-	NKAWVHRQWFX
1.2	Singleton	KNGAWMVHR	-	seq163	KNGAWMVHR	KNGAWMVHR
1.3	Singleton	WMVHRQWFF	-	seq198	WMVHRQWFF	WMVHRQWFF
2.1	1	KQWFLDLPL----	1	seq20	KQWFLDLPL	XQWFLDLPLPWXA
2.1	2	RQWFLDLPL----	1	seq101	RQWFLDLPL	XQWFLDLPLPWXA
2.1	3	-QWFFDLPLPW--	2	seq176	QWFFDLPLPW	XQWFLDLPLPWXA
2.1	4	-QWFLDLPLPW--	2	seq31	QWFLDLPLPW	XQWFLDLPLPWXA
2.1	5	--WFFDLPLPW--	3	seq197	WFFDLPLPW	XQWFLDLPLPWXA
2.1	6	---FLDLPLPWIA	4	seq218	FLDLPLPWIA	XQWFLDLPLPWXA
2.1	7	---FLDLPLPWL-	4	seq58	FLDLPLPWL	XQWFLDLPLPWXA
2.1	Consensus	XQWFLDLPLPWXA	-	-	-	XQWFLDLPLPWXA
2.2	Singleton	RQWFFDLPL	-	seq181	RQWFFDLPL	RQWFFDLPL
3.1	1	LIHQIFGTAY--	1	seq22	LIHQIFGTAY	XVHQIFGXAYGV
3.1	2	MVHQIFGSAY--	1	seq170	MVHQIFGSAY	XVHQIFGXAYGV
3.1	3	-VHQIFGSAY--	2	seq196	VHQIFGSAY	XVHQIFGXAYGV
3.1	4	--HQIFGSAY--	3	seq146	HQIFGSAY	XVHQIFGXAYGV
3.1	5	--HQIFGTAY--	3	seq11	HQIFGTAY	XVHQIFGXAYGV
3.1	6	---QIFGTAYGV	4	seq28	QIFGTAYGV	XVHQIFGXAYGV
3.1	Consensus	XVHQIFGXAYGV	-	-	-	XVHQIFGXAYGV
3.2	Singleton	IFGTAYGVLF	-	seq12	IFGTAYGVLF	IFGTAYGVLF
4.1	1	ALHQVFGAIY----	1	seq49	ALHQVFGAIY	ALHQVFGAIYGAAF
4.1	2	ALHQVFGAIY----	1	seq48	ALHQVFGAIY	ALHQVFGAIYGAAF
4.1	3	-LHQVFGAIY----	2	seq81	LHQVFGAIY	ALHQVFGAIYGAAF
4.1	4	--HQVFGAIY----	3	seq65	HQVFGAIY	ALHQVFGAIYGAAF
4.1	5	---QVFGAIYGA--	4	seq94	QVFGAIYGA	ALHQVFGAIYGAAF
4.1	6	---VFGAIYGAAF	5	seq112	VFGAIYGAAF	ALHQVFGAIYGAAF
4.1	Consensus	ALHQVFGAIYGAAF	-	-	-	ALHQVFGAIYGAAF
4.2	Singleton	FGAIYGAAF	-	seq57	FGAIYGAAF	FGAIYGAAF
5.1	1	KVVQPENLEY--	1	seq78	KVVQPENLEY	KVVQIENLEYTV

Cluster Results – Visualization

Peptide Table

Visualization

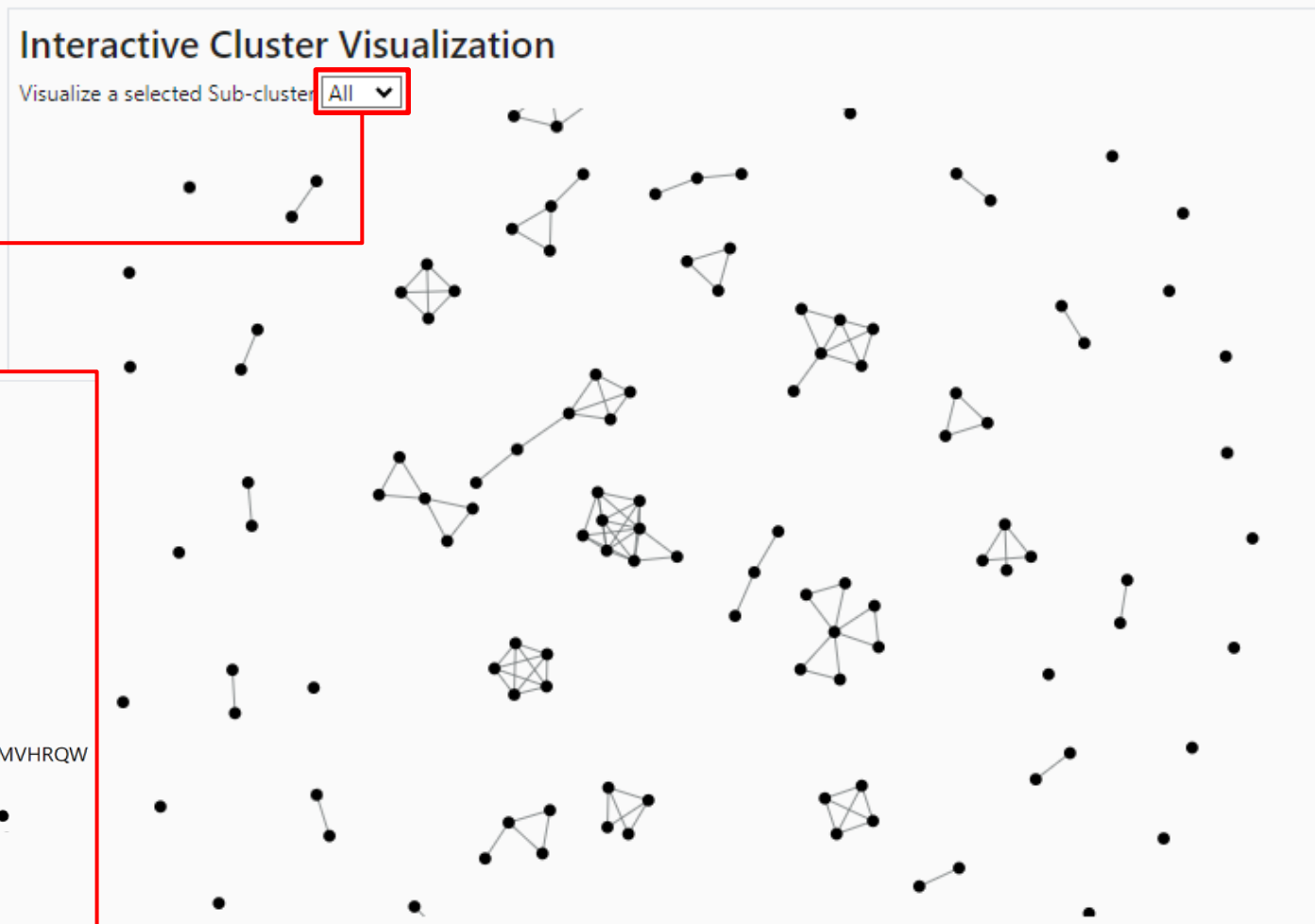
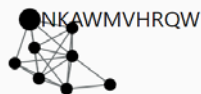
Interactive Cluster Visualization

Visualize a selected Sub-cluster: All

Interactive Cluster Visualization

Visualize a selected Sub-cluster:

- 1.1
- All
- 1.2
- 1.3
- 2.1
- 2.2
- 3.1
- 3.2
- 4.1
- 4.2
- 5.1
- 6.1
- 7.1
- 8.1
- 9.1
- 10.1
- 11.1
- 12.1
- 13.1
- 14.1



Cluster Results

Applying Filters to Peptide Table

IEDB
Immune Epitope Database & Tools

Tools - Help & Info

<< Pipeline Map

Info

Steps

T Cell Prediction - Class I

Epitope Cluster Analysis

Cluster

Prediction Parameters

Sequence Identity Threshold: 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%

Peptide Length(s): No Min 5 10 15 20 25 No Max

Cluster Method: Cluster-break for clear representative sequence

Warnings (68)

Peptide Table Visualization

Download Reset Table Display Columns Save Table State

Show 50 rows 1 to 50 of 182 rows

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	4			eq71	KGALVHRQW	NGKAVVHRQWFX
1.1	5			eq135	AMVVRQWFF	NGKAVVHRQWFX
1.1	6			eq52	ANLVHRQWF	NGKAVVHRQWFX
1.1	7			eq133	AMVVRQWFF	NGKAVVHRQWFX
1.1	8			eq124	WLVHRQWFL	NGKAVVHRQWFX
1.1	Consensus			-	-	NGKAVVHRQWFX
1.2	Singleton			eq163	RNGKAVVHR	RNGKAVVHR
1.3	Singleton			eq198	WVVRQWFF	WVVRQWFF
2.1	1			eq20	XQWFLDLPWXA	XQWFLDLPWXA
2.1	2			eq101	RQWFLDLPWXA	XQWFLDLPWXA
2.1	3			eq176	QWFFDLPWXA	XQWFLDLPWXA
2.1	4	-QWFLDLPW--	2	seq31	QWFLDLPWXA	XQWFLDLPWXA
2.1	5	--WFFDLPW--	3	seq197	WFFDLPWXA	XQWFLDLPWXA
2.1	6	---FLDLPWTA	4	seq218	FLDLPWTA	XQWFLDLPWXA
2.1	7	---FLDLPWL-	4	seq58	FLDLPWL	XQWFLDLPWXA
2.1	Consensus	XQWFLDLPWXA	-	-	-	XQWFLDLPWXA

Sort A-Z
Sort Z-A
Filter by value:
 (Select All)
 Consensus
 1
 2
 3
 4
 5
Clear OK

Filter Peptide Number = 'Consensus'

Cluster Results

Applying Filters to Peptide Table

Must save table state before next pipe step

The screenshot displays a software interface for analyzing peptide clusters. On the left, a 'Pipeline Map' sidebar shows the current step as 'Epitope Cluster Analysis'. The main area is titled 'Peptide Table' and shows a table with 32 rows and 7 columns. The columns are: Cluster.Sub-Cluster Number, Peptide Number, Alignment, Position, Input seq id, Peptide, and Cluster Consensus. The 'Peptide Number' column is highlighted with a red box, and a 'Save Table State' button is also highlighted with a red box. The table shows a list of peptides, all with a 'Consensus' alignment and a '-' in the 'Position' and 'Input seq id' columns. The 'Peptide' column contains various amino acid sequences, and the 'Cluster Consensus' column contains the same sequences. The interface includes navigation controls for rows and a 'Previous/Next' button.

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	Consensus	NRKMKVHRQWFX	-	-	-	NRKMKVHRQWFX
2.1	Consensus	XQWFLDPLPWXA	-	-	-	XQWFLDPLPWXA
3.1	Consensus	XVHQIFGXAYGV	-	-	-	XVHQIFGXAYGV
4.1	Consensus	ALHQVFGAIYGAAF	-	-	-	ALHQVFGAIYGAAF
5.1	Consensus	KVQIENLEYTV	-	-	-	KVQIENLEYTV
6.1	Consensus	SLVLGVWTLYL	-	-	-	SLVLGVWTLYL
7.1	Consensus	DTAWDFGSX	-	-	-	DTAWDFGSX
8.1	Consensus	KIGIGKLLTW	-	-	-	KIGIGKLLTW
9.1	Consensus	RMAILGXTAN	-	-	-	RMAILGXTAN
10.1	Consensus	YAMCTNPFVLKK	-	-	-	YAMCTNPFVLKK
11.1	Consensus	SGATTETPTWNR	-	-	-	SGATTETPTWNR
12.1	Consensus	TAKEVALLRTYCI	-	-	-	TAKEVALLRTYCI
13.1	Consensus	GESALLHWFR	-	-	-	GESALLHWFR
14.1	Consensus	EVAETQHGIVLV	-	-	-	EVAETQHGIVLV
15.1	Consensus	TEVTNPAVLR	-	-	-	TEVTNPAVLR
16.1	Consensus	SMWRILIGFL	-	-	-	SMWRILIGFL
17.1	Consensus	ITMFGGVSMVR	-	-	-	ITMFGGVSMVR
18.1	Consensus	GLDFNEMKLL	-	-	-	GLDFNEMKLL
19.1	Consensus	IQTSGTTIF	-	-	-	IQTSGTTIF
20.1	Consensus	RLITXNPV	-	-	-	RLITXNPV
21.1	Consensus	TALFSGVSWM	-	-	-	TALFSGVSWM
22.1	Consensus	HGTIVIRVQY	-	-	-	HGTIVIRVQY
23.1	Consensus	RHVLGRLLIV	-	-	-	RHVLGRLLIV
24.1	Consensus	SITEAELTGY	-	-	-	SITEAELTGY
25.1	Consensus	SITEAILPEY	-	-	-	SITEAILPEY
26.1	Consensus	KLNTTTASR	-	-	-	KLNTTTASR
27.1	Consensus	LQMEDKRWLV	-	-	-	LQMEDKRWLV
28.1	Consensus	LVLNIGTNSR	-	-	-	LVLNIGTNSR
29.1	Consensus	CIAIGIITLY	-	-	-	CIAIGIITLY
30.1	Consensus	HGTILIKVEY	-	-	-	HGTILIKVEY
31.1	Consensus	VHQVFGSVY	-	-	-	VHQVFGSVY
32.1	Consensus	SISNITTATR	-	-	-	SISNITTATR

Add PEPMatch Tool (Cluster Consensus)

1. Add PEPMatch to Pipeline as Cluster Consensus

The screenshot shows the IEDB Pipeline Map interface. On the left, a sidebar contains a list of steps: 'T Cell Prediction - Class I' and 'Epitope Cluster Analysis'. A red box highlights the 'Add' button (+) next to 'Epitope Cluster Analysis', which has opened a dropdown menu. The menu options are 'Peptide' and 'Cluster Consensus'. A red arrow points from the text '1. Add PEPMatch to Pipeline as Cluster Consensus' to the 'Cluster Consensus' option in the dropdown.

The main interface displays the 'Cluster' tool configuration. The 'Sequence Identity Threshold' is set to 80% and the 'Peptide Length(s)' is set to 5. The 'Cluster Method' is 'Cluster-break for clear representative sequence'. Below the configuration, there are 'Warnings (68)' and tabs for 'Peptide Table' and 'Visualization'. The 'Peptide Table' tab is active, showing a table with 13 rows of consensus peptides.

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	Consensus	NGKMKVHRQWFX	-	-	-	NGKMKVHRQWFX
2.1	Consensus	XQWFLDLPLPWXA	-	-	-	XQWFLDLPLPWXA
3.1	Consensus	XVHQIFGXAYGV	-	-	-	XVHQIFGXAYGV
4.1	Consensus	ALHQVFGAIYGAAF	-	-	-	ALHQVFGAIYGAAF
5.1	Consensus	KVVQIENLEYTV	-	-	-	KVVQIENLEYTV
6.1	Consensus	SLVLGVVITLYL	-	-	-	SLVLGVVITLYL
7.1	Consensus	DTAWDFGSX	-	-	-	DTAWDFGSX
8.1	Consensus	KIGIGXLLTW	-	-	-	KIGIGXLLTW
9.1	Consensus	RMAILGXTAW	-	-	-	RMAILGXTAW
10.1	Consensus	YAMCTINFVLKQ	-	-	-	YAMCTINFVLKQ
11.1	Consensus	SGATTETPTWNR	-	-	-	SGATTETPTWNR
12.1	Consensus	TAKEVALLRITYCI	-	-	-	TAKEVALLRITYCI
13.1	Consensus	GESALTLHWFR	-	-	-	GESALTLHWFR

Add Cluster Tool (Peptide)

Pipeline Map

Info

Steps

- T Cell Prediction - Class I
- Epitope Cluster Analysis
- Pepmatch

Peptide Table Visualization

Download Reset Table Display Columns Save Table State

Show 50 rows 1 to 32 of 32 rows (filtered from 182 total rows)

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	Consensus	NGAKVHRQWFX	-	-	-	NGAKVHRQWFX
2.1	Consensus	XQWFLDLPFWKA	-	-	-	XQWFLDLPFWKA
3.1	Consensus	XVHQIFGKAYGV	-	-	-	XVHQIFGKAYGV
4.1	Consensus	ALHQVFGAIVGAAF	-	-	-	ALHQVFGAIVGAAF
5.1	Consensus	KVQIENLEYTV	-	-	-	KVQIENLEYTV
6.1	Consensus	SLVLVGVVILYL	-	-	-	SLVLVGVVILYL
7.1	Consensus	DTAWDFGSX	-	-	-	DTAWDFGSX
8.1	Consensus	KIGIGKLLTW	-	-	-	KIGIGKLLTW
9.1	Consensus	RMAILGXTAW	-	-	-	RMAILGXTAW
10.1	Consensus	YAMCTNTEFLKK	-	-	-	YAMCTNTEFLKK
11.1	Consensus	SGATTETPTWNR	-	-	-	SGATTETPTWNR
12.1	Consensus	TAKEVALLRITYCI	-	-	-	TAKEVALLRITYCI
13.1	Consensus	GESALILHWFR	-	-	-	GESALILHWFR
14.1	Consensus	EVAETQHGTVLV	-	-	-	EVAETQHGTVLV
15.1	Consensus	TEVTNPAVLR	-	-	-	TEVTNPAVLR
16.1	Consensus	SMMVRILIGFL	-	-	-	SMMVRILIGFL
17.1	Consensus	TIIFGGVSMVNR	-	-	-	TIIFGGVSMVNR
18.1	Consensus	GLDFNEMKLL	-	-	-	GLDFNEMKLL
19.1	Consensus	IQTSGITTIIF	-	-	-	IQTSGITTIIF
20.1	Consensus	RLITXNPIV	-	-	-	RLITXNPIV
21.1	Consensus	TALFSGVSMVM	-	-	-	TALFSGVSMVM
22.1	Consensus	HGTIVIRVQY	-	-	-	HGTIVIRVQY
23.1	Consensus	RHVLGRLITV	-	-	-	RHVLGRLITV
24.1	Consensus	SITEAELTGY	-	-	-	SITEAELTGY
25.1	Consensus	STTEAILPEY	-	-	-	STTEAILPEY
26.1	Consensus	KLINTTTASR	-	-	-	KLINTTTASR
27.1	Consensus	LQMEDKAWLV	-	-	-	LQMEDKAWLV
28.1	Consensus	LVLWIGTNSR	-	-	-	LVLWIGTNSR
29.1	Consensus	CIAIGIITLY	-	-	-	CIAIGIITLY
30.1	Consensus	HGTILIKVEY	-	-	-	HGTILIKVEY
31.1	Consensus	VHQVFGSVY	-	-	-	VHQVFGSVY
32.1	Consensus	SISNITTATR	-	-	-	SISNITTATR

Cluster Consensus column is selected for piping to PEPMatch tool

Select PEPMatch Parameters

The screenshot shows the IEDB PEPMatch interface. On the left is a 'Pipeline Map' sidebar with steps: 'T Cell Prediction - Class I', 'Epitope Cluster Analysis', and 'Pepmatch'. The main area displays 'PEPMatch' with a 'Prediction Parameters' section. A slider for 'Maximum number of mismatches' is set to 3. The 'Proteome' dropdown is set to 'Human'. Below, the 'Best match per peptide' radio button is selected. A red box highlights the 'Maximum number of mismatches' slider and the 'Proteome' dropdown. A red arrow points from the 'Proteome' dropdown to a separate dropdown menu at the bottom. A 'Run' button is highlighted with a red box.

IEDB Immune Epitope Database & Tools

Tools ▾ Help & Info ▾

Show 50 rows 1 to 32 of 32 rows (filtered from 182 total rows) Previous 1 Next

1. Select Number of Mismatches

Maximum number of mismatches: 0 1 2 3 4 5

Proteome: Human

Include all matches or best match per peptide: Best match per peptide All matches

Run

2. Select Reference Proteome

A dropdown menu with the following options: Human (highlighted), Mouse, Cow, Dog, Horse, Pig, Rabbit, Rat.

3. Click Run!

PEPMatch Results – Peptide Table

Peptide Table

[Download](#)
[Reset Table](#)
[Display Columns](#)
[Save Table State](#)

Save/Download

Interactive Table Headers/Filters

Show 50 rows

1 to 14 of 14 rows

Previous 1 Next

Input Sequence	Matched Sequence	Protein ID	Protein Name	Gene	Mismatches	Mutated Positions
HGTIVIRVQY	HCTIVIIIVQY	O15552.1	Free fatty acid receptor 2	FFAR2	2	[2, 7]
CIAIGIITLY	SIAQGIITLD	Q8NFU7.2	Methylcytosine dioxygenase TET1	TET1	3	[1, 4, 10]
HGTILIKVEY	HGEIDIKVEQ	P17600.3	Synapsin-1	SYN1	3	[3, 5, 10]
IQTSGTIIIF	IYTSGITGIP	Q5FVE4.2	Long-chain-fatty-acid--CoA ligase ACSBG2	ACSBG2	3	[2, 8, 10]
KLNTTTASR	FPTNTTAST	Q2M2H8.3	Probable maltase-glucoamylase 2	MGAM2	3	[1, 2, 10]
LQMEDKAWLV	ENMEDKATLV	Q14896.4	Myosin-binding protein C, cardiac-type	MYBPC3	3	[1, 2, 8]
LVLWIGTNSR	LVARIGSNSR	Q8N612.3	FHF complex subunit HOOK-interacting protein 1B	FHIP1B	3	[3, 4, 7]
RHVLGRLITV	IHNLGRFITV	Q14692.1	Ribosome biogenesis protein BMS1 homolog	BMS1	3	[1, 3, 7]
SISNITTATR	SISNFTTRL	A8MYU2.2	Potassium channel subfamily U member 1	KCNU1	3	[5, 8, 10]
SITEAELTGY	GITVAELTGD	O75643.2	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	3	[1, 4, 10]
SLVLGVVTLYL	SGVLGVVCLLL	Q6UWW8.1	Carboxylesterase 3	CES3	3	[2, 9, 11]
STEAALPEY	SLTEASLPEA	Q8N3D4.2	EH domain-binding protein 1-like protein 1	EHBP1L1	3	[2, 6, 10]
TEVTNPAVLR	LEQTQPAVLR	Q00975.1	Voltage-dependent N-type calcium channel subunit alpha-1B	CACNA1B	3	[1, 3, 5]
VHQVFGSVY	VHQGTGAVY	O75051.4	Plexin-A2	PLXNA2	3	[4, 5, 7]

Show 50 rows

1 to 14 of 14 rows

Previous 1 Next

Help Documentation Cluster Tool

[https://nextgen-
tools.iedb.org/docs/tools/cluster/index.html](https://nextgen-tools.iedb.org/docs/tools/cluster/index.html)

Next-Generation (NXG) IEDB Tools

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Search docs

Overview

Available Tools

- T cell class I
- Cluster
 - Parameter selection
 - Results
- Pepmatch

Pipelines

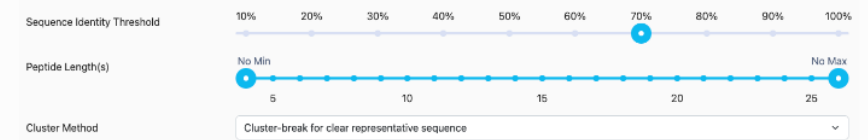
API usage

Troubleshooting

Cluster

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

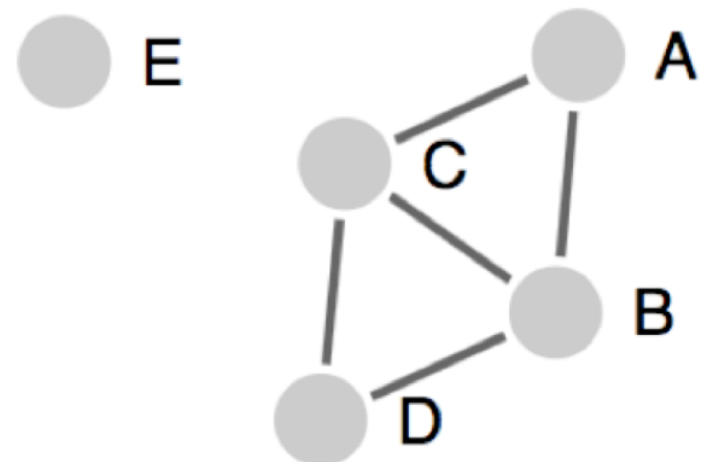
Parameter selection



- **Sequence Identity Threshold**
 - Select the sequence identity threshold at which you want to calculate epitope clusters.
- **Peptide Length(s)**
 - Select the minimum and maximum length of peptides to consider for calculation
- **Cluster Method**
 - Select one of the three approaches for clustering.

Clustering Methods

Before the different methods are described, we describe how the results are represented. The figure below represents a clustering result with 5 peptides (A, B, C, D and E) depicted as circles:



Help Documentation PEPMatch Tool

<https://nextgen-tools.iedb.org/docs/tools/pepmatch/index.html>

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- API usage
- Troubleshooting

Pepmatch

Pepmatch is an efficient, deterministic algorithm for scanning a set of peptides against a large database of proteins for sequence identity at or below a specified number of mismatches.

Parameter selection

Maximum number of mismatches: 0 1 2 3 4 5 (3 selected)

Proteome: Human

Include all matches or best match per peptide:
 Best match per peptide
 All matches

- Maximum number of mismatches**
 - When scanning for hits in the protein database, Pepmatch will return those that have this number of mismatches or less.
- Proteome**
 - The database of proteins to search against. All included proteomes were obtained from Uniprot/Swiss-Prot.
 - Available proteomes include:
 - human
 - mouse
 - cow
 - dog
 - horse
 - pig
 - rabbit
 - rat
- Include all matches or best match per peptide**
 - Best match per peptide:** Returns only one match per query peptide.
 - All matches:** Returns all matches at or below the mismatch threshold for the query peptide.

Results

The pepmatch output will look similar to the table below:

Input Sequence	Matched Sequence	Gene	Protein ID	Protein Name	Mismatches	Mutated Positions
DDEDSRQIPFELYR	DDEDSRQIPFELYR	None	A6KHP3-2	Isoform of A6KHP3, Isoform 2 of Speedy protein E2B	0	[]
KAVELGVLLAAFSIT	KAVELGVLLAAFSIT	None	P33906-2	Isoform of P33908, Isoform 2 of Mannosyl-oligosaccharide 1,2-alpha-mannosidase 2A	1	[11]
QLQRIGINPANGLS	QLQRIGINPANGFS	CLTC	J2K513.1	Isoform of Q00419, Clathrin heavy chain 1	1	[14]
REYWFYGLQTYDSRG	REYWFYGLQTYDSRG	RDX	AGA2R8Y7K3.1	Isoform of P35241, Radixin	1	[1]
ADPGFRLMGGOURAK					NA	

Plans and Timeline



Planned releases

- 1.1 – completed October 2023
 - Migration of backend to a compute cluster
- 1.2 - target November 2023
 - MHC-NP integration
- 2.0 - target March 2024
 - Cancer-focused functionality
 - Peptide expression estimator (PepX)
 - Mutated peptide generation
 - Paired wild-type and mutant peptide predictions

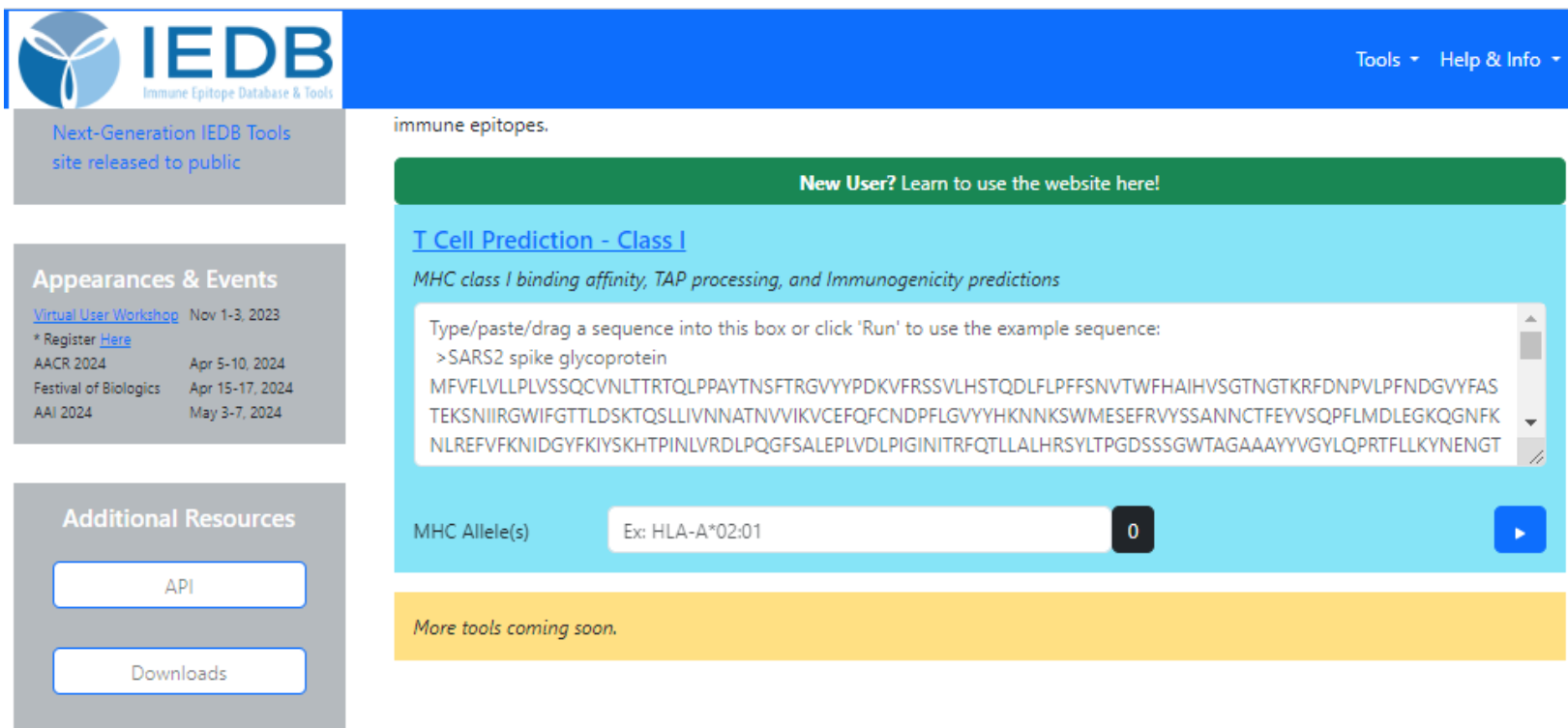
Additional plans

- All legacy tools eventually migrated to nextgen-tools
- Curated pipelines
- API access packages
- Parity with standalone tools

Test the Next-Generation Tools Now!



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



The screenshot shows the IEDB website interface. The top navigation bar is blue with the IEDB logo on the left and 'Tools' and 'Help & Info' on the right. A grey sidebar on the left contains three sections: 'Next-Generation IEDB Tools site released to public', 'Appearances & Events' (listing workshops from 2023 to 2024), and 'Additional Resources' (with buttons for 'API' and 'Downloads'). The main content area features a green banner for new users, a light blue section for 'T Cell Prediction - Class I' with a description of MHC class I binding affinity, TAP processing, and immunogenicity predictions. Below this is a text input field containing an example sequence: '>SARS2 spike glycoprotein' followed by a long amino acid sequence. Underneath the input field is a dropdown menu for 'MHC Allele(s)' with 'Ex: HLA-A*02:01' selected and a 'Run' button. A yellow banner at the bottom of the main content area says 'More tools coming soon.'