IEDB
Immune Epitope Database & Tools

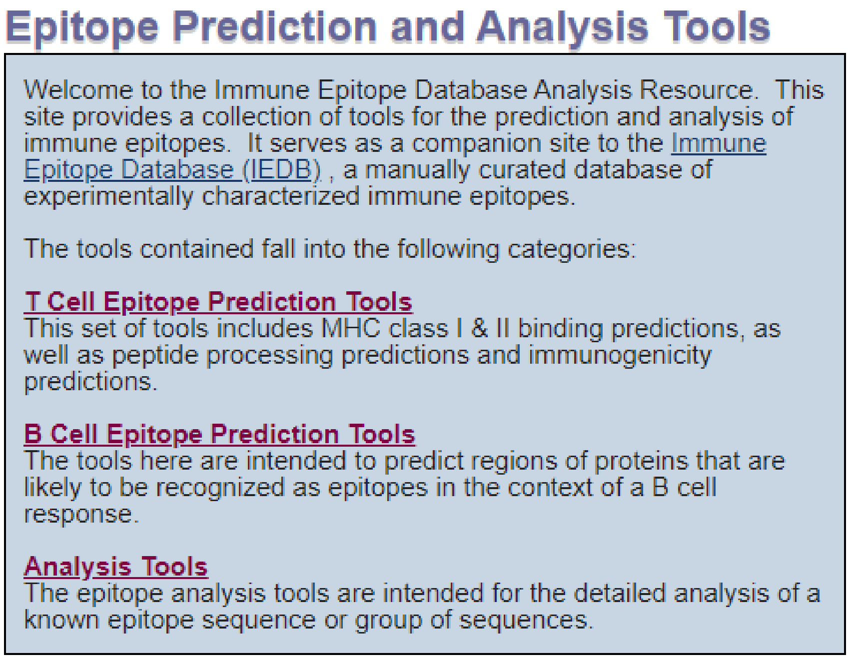
Next Generation Tool Pipelines
Cluster & PEPMatch

nextgen-tools.iedb.org

Presented by: Dr. Bjoern Peters, Professor

IEDB Tools

Analysis Resource & Next-Generation Tools



Epitope Prediction and Analysis Tools

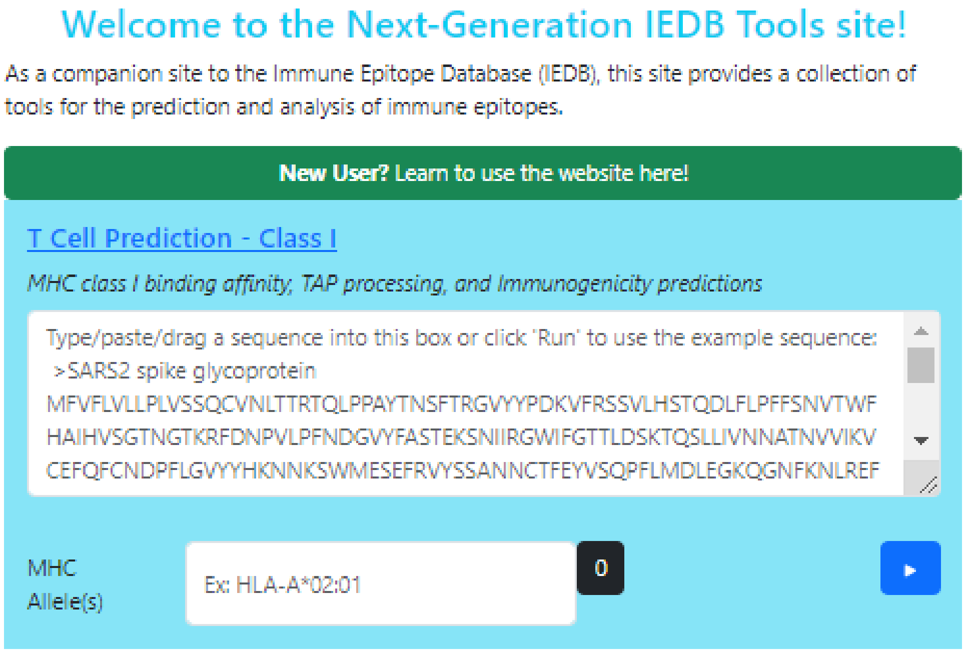
Welcome to the Immune Epitope Database Analysis Resource. This site provides a collection of tools for the prediction and analysis of immune epitopes. It serves as a companion site to the Immune Epitope Database (IEDB) , a manually curated database of experimentally characterized immune epitopes.

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.



Welcome to the Next-Generation IEDB Tools site!

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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
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWF
HAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKV
CEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREF

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

Analysis Resource:

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

tools.iedb.org

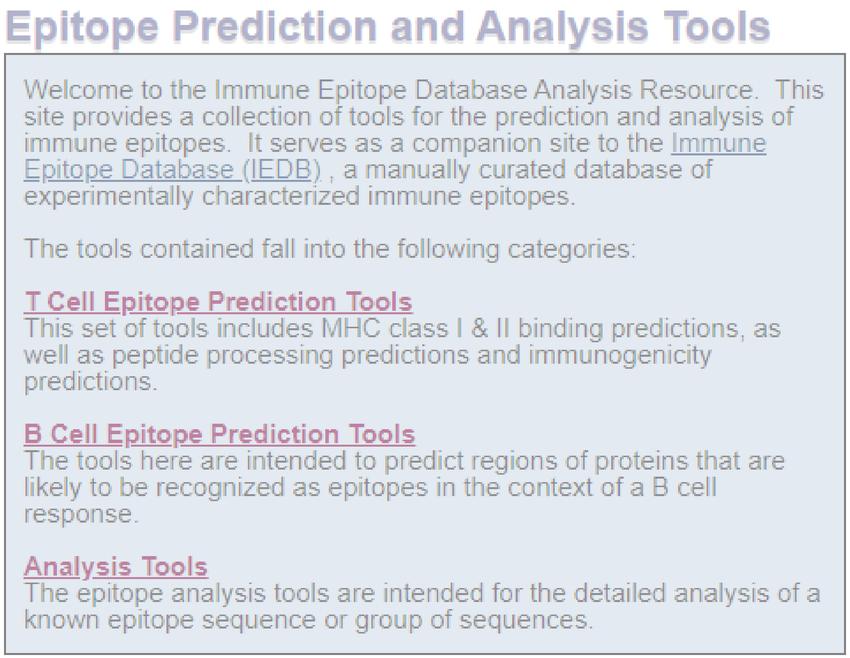
Next-Generation Tools:

- 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



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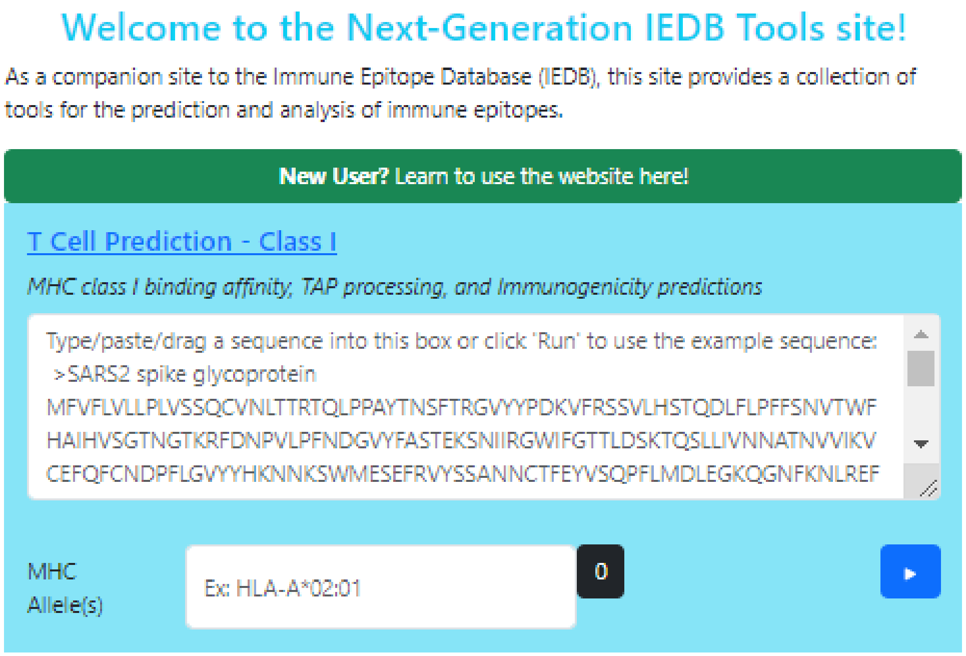

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MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWF
HAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKV
CEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREF

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

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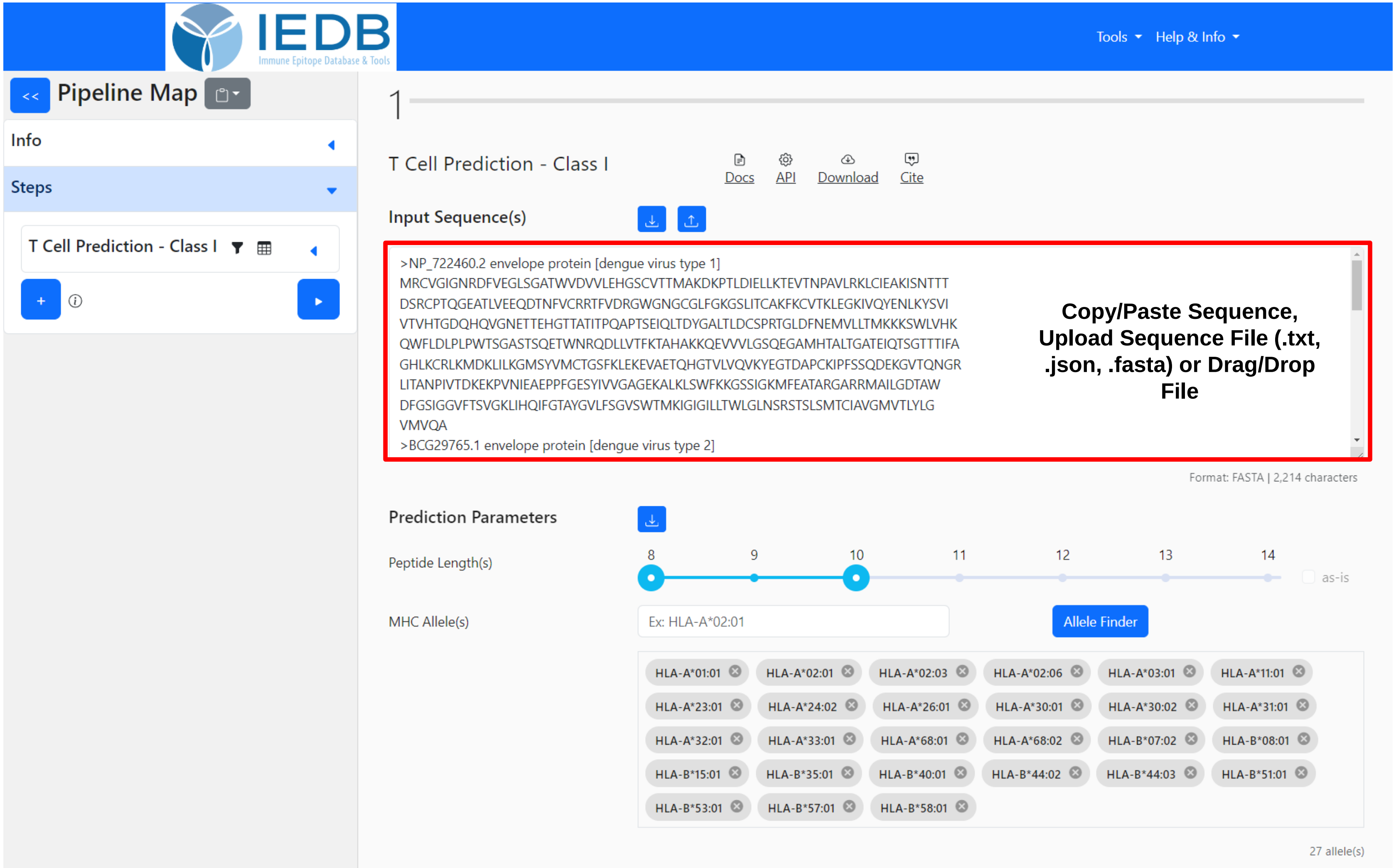
Let’s pick up where we left off…

- **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]
MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFK
CVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHKQWFLDLPLPWTSGASTSQETWNRQDLLVTF
KTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAGHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGRLITANPIVTDK
EKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAWDFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVG
MVTLYLGVMVQA
>BCG29765.1 envelope protein [dengue virus type 2]
MRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKHPATLRKYCIEAKLTNTTTASRCPTQGEPSLNEEQDKRFICKHSMVDRGWGNGCGLFGKGGIVTCAMFT
CKKNMEGKVVQPENLEYTIVITPHSGEEKAVGNDTGKHGTEIKVTPQSSITEAELTGYGTVTMECSPRTGLDFNEMVLLQMEDKAWLVHRQWFLDLPLPWLPGADKQGSNWIQKETLVT
FKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTE
KDSPVNIEAEPPFGDSYIVIGVEPGQLKLSWFKKGSSIGQMFETTMRGAKRMAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWTMKILIGVVITWIGMNSRSTSLSVSLVLV
GVVTLYLGVMVQA
>AMQ36111.1 envelope protein [dengue virus type 3]
MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLATLRKLCIEGKITNITTDSRCPTQGEAALPEEQDQNYVCKHTYVDRGWGNGCGLFGKGSLVTCAKF
QCLEPIEGKVVQYENLKYTVIITVHTGDQHQVGNETQGVTAEITPQASTTEAILPEYGTLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETPTWNRKELLVTFKN
AHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHLKCRLKMDKLELKGMSYAMCTNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTEDGQGKAHNGRLITANPVVTKKEE
PVNIEAEPPFGESNIVIGIGDNALKINWYKKGSSIGKMFEATARGARRMAILGDTAWDFGSVGGVLNSLGKMVHQIFGSAYTALFSGVSWVMKIGIGVLLTWIGLNSKNTSMSFSCIAIGIITL
YLGAVVQA
>BCG29766.1 envelope protein [dengue virus type 4]
MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVALLRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKGGVVTCAK
FLCSGKITGNLVQIENLEYTVVVTVHNGDTPAVGNDTSHHGVTATITPRSPSVEVKLPDYGELTLDCEPRSGIDFIEMILMKMKKKTWLVHKQWFLDLPLPWTAGADTSEVHWNHKERMV
TFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTAVVKVKYEGAGAPCKVPIEIRDVNKEKVVGRIISSTPF
AENTNSVTNIELEPPFGDSYIVIGVGESALTLHWFRKGSSIGKMFESTYRGAKRMAILGETAWDFGSVGGLFTSLGKAVHQVFGSVYTTMFGGVSWMVRILIGFLVLWIGTNSRNTSMAMT
CIAVGGITLFLGFTVQA

T Cell Prediction – Class I

Sequence & Parameters



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]
```

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

Format: FASTA | 2,214 characters

Prediction Parameters

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

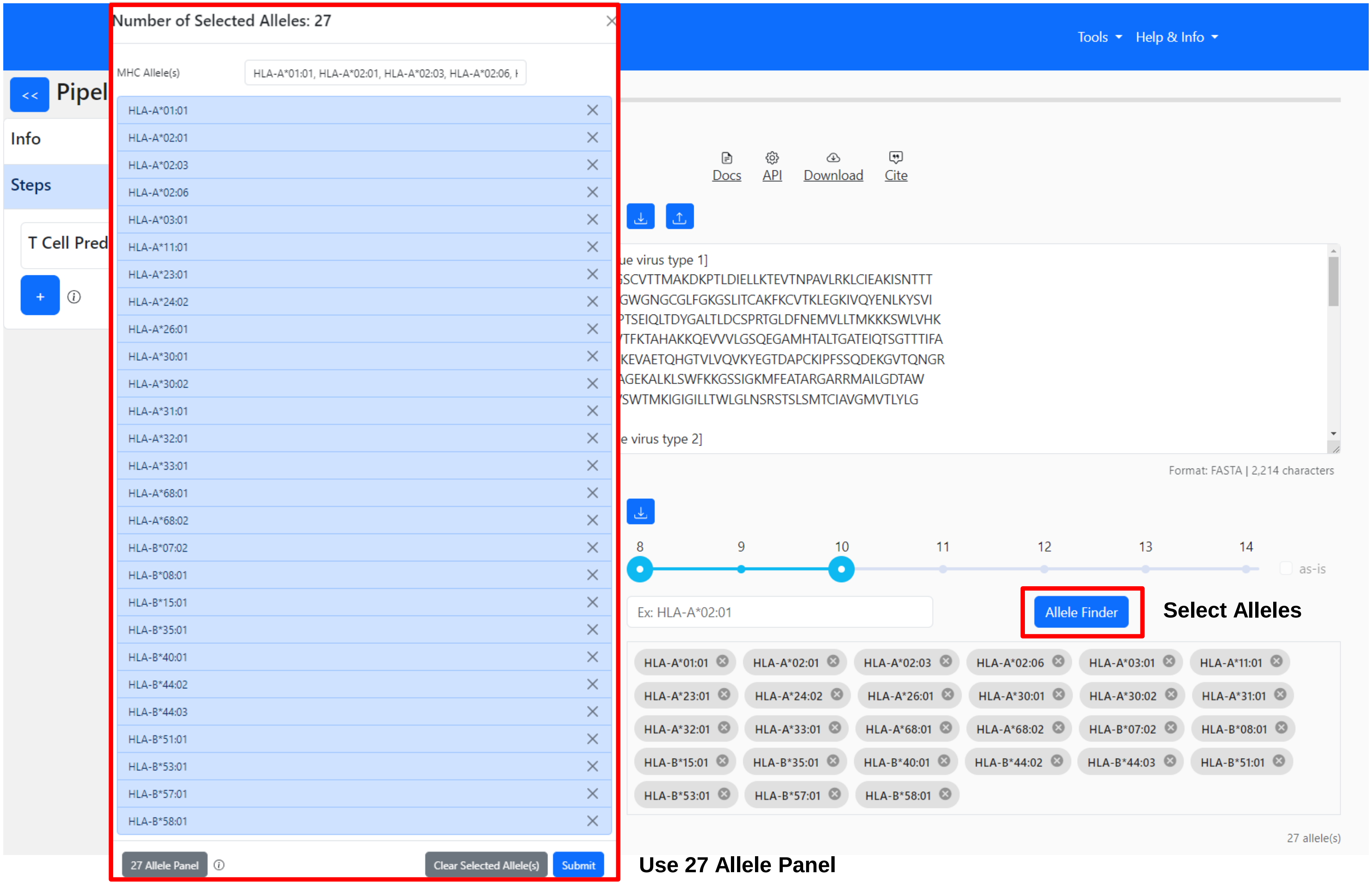
MHC Allele(s): Ex: HLA-A*02:01 Allele Finder

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)

T Cell Prediction – Class I

Sequence & Parameters



Number of Selected Alleles: 27

MHC Allele(s): HLA-A*01:01, HLA-A*02:01, HLA-A*02:03, HLA-A*02:06, H

- 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

```
ue virus type 1]
SCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTT
GWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVI
PTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHK
TFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFA
KEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGR
AGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAW
SWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLG

e virus type 2]
```

Format: FASTA | 2,214 characters

Ex: HLA-A*02:01

Select Alleles

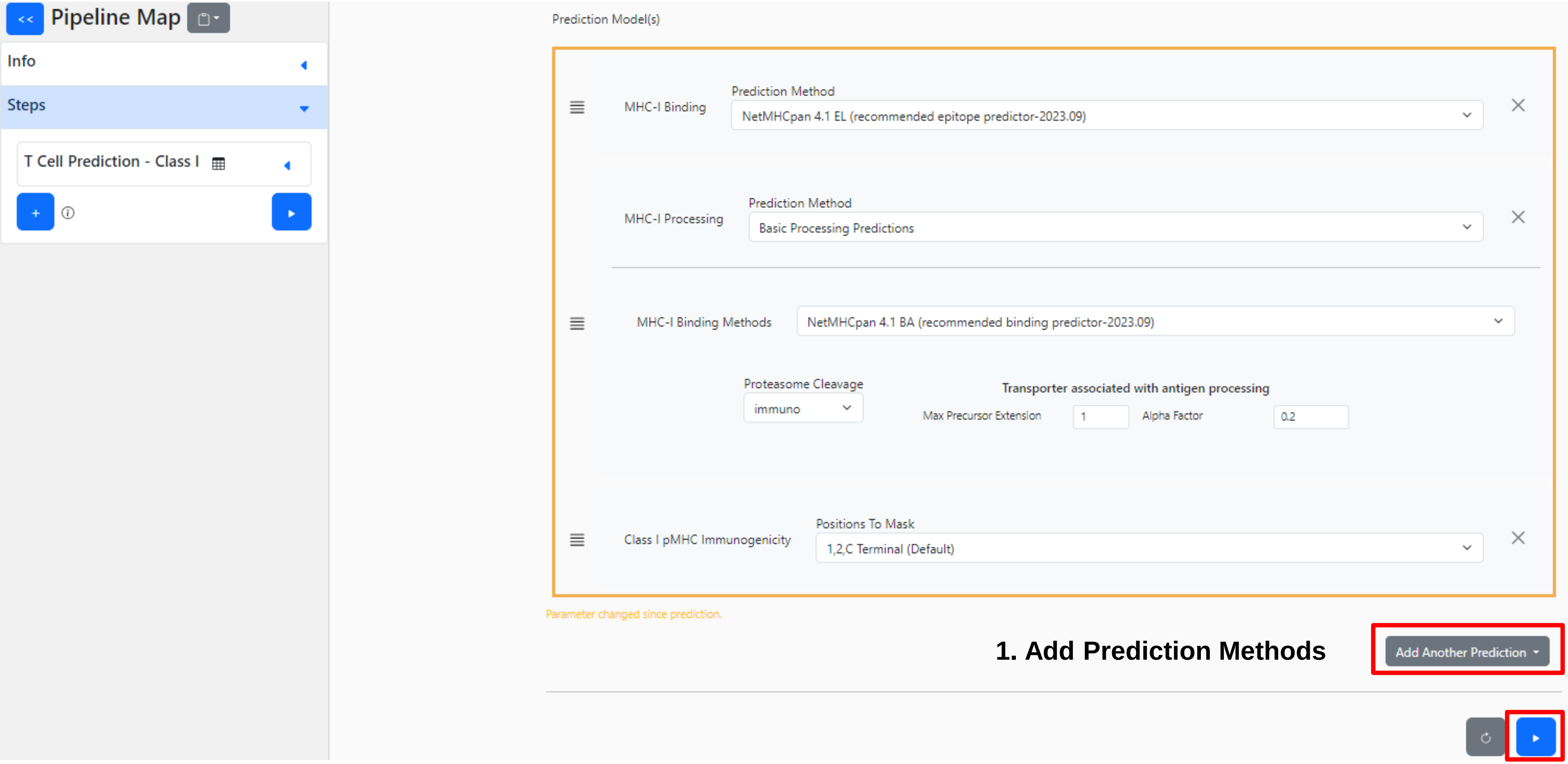
HLA-A*01:01, HLA-A*02:01, HLA-A*02:03, HLA-A*02:06, HLA-A*03:01, HLA-A*11:01, HLA-A*23:01, HLA-A*24:02, HLA-A*26:01, HLA-A*30:01, HLA-A*30:02, HLA-A*31:01, HLA-A*32:01, HLA-A*33:01, HLA-A*68:01, HLA-A*68:02, HLA-B*07:02, HLA-B*08:01, HLA-B*15:01, HLA-B*35:01, HLA-B*40:01, HLA-B*44:02, HLA-B*44:03, HLA-B*51:01,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



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)

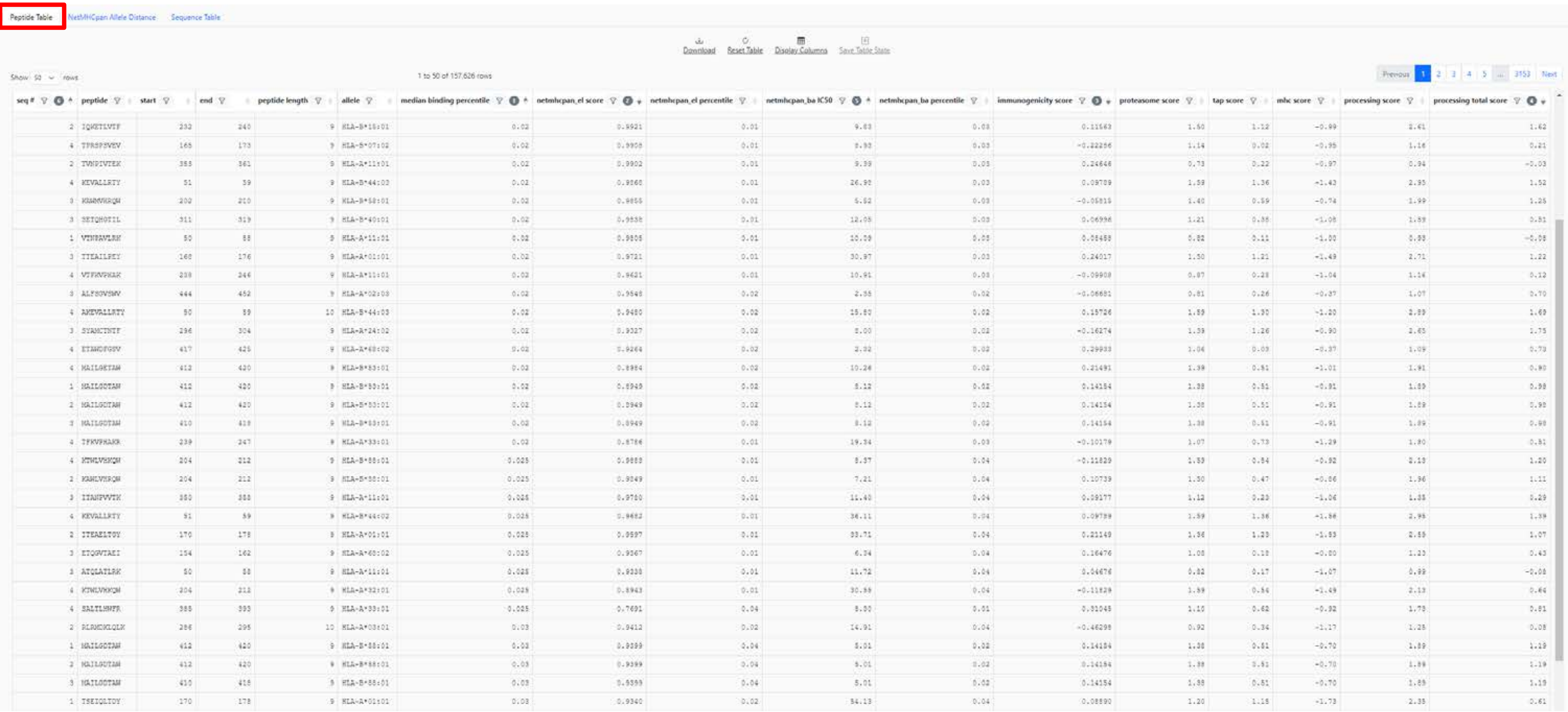
Parameter changed since prediction.

1. Add Prediction Methods

2. Click Run!

T Cell Prediction – Class I

Results – Peptide Table

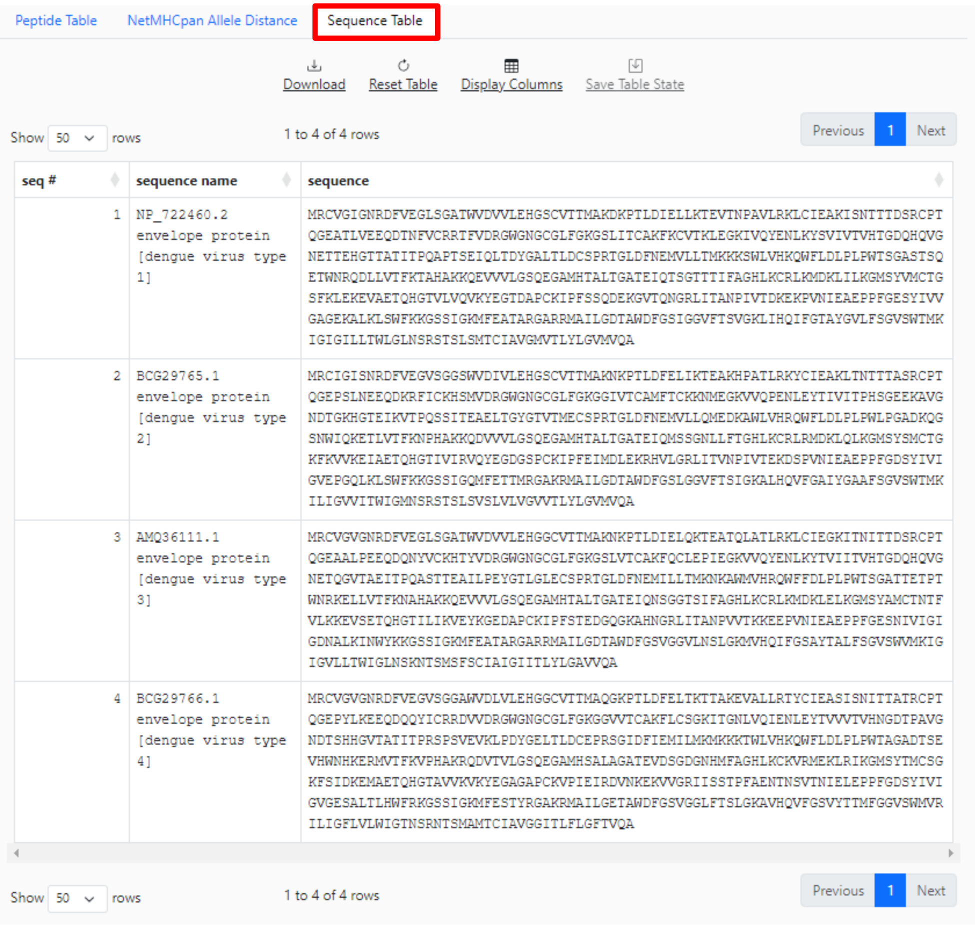


1 to 50 of 157,626 rows

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	IQKETLVIF	232	240	9	HLA-B*15:01	0.02	0.9921	0.01	9.83	0.03	0.11563	1.50	1.12	-0.99	2.61	1.62
4	TPRSPSVEV	165	173	9	HLA-B*07:02	0.02	0.9908	0.01	8.93	0.03	-0.22256	1.14	0.02	-0.95	1.16	0.21
2	TVNPIVTEK	353	361	9	HLA-A*11:01	0.02	0.9902	0.01	9.39	0.03	0.24646	0.73	0.22	-0.97	0.94	-0.03
4	KEVALLRTY	51	59	9	HLA-B*44:03	0.02	0.9868	0.01	26.98	0.03	0.09789	1.59	1.36	-1.43	2.95	1.52
3	KAWMVHRQW	202	210	9	HLA-B*58:01	0.02	0.9855	0.01	5.82	0.03	-0.05815	1.40	0.59	-0.74	1.99	1.25
3	SEIQHGTIL	311	319	9	HLA-B*40:01	0.02	0.9538	0.01	12.05	0.03	0.06996	1.21	0.38	-1.08	1.59	0.51
1	VINPAVLRK	50	58	9	HLA-A*11:01	0.02	0.9805	0.01	10.09	0.05	0.05458	0.82	0.11	-1.00	0.93	-0.08
3	ITEAILPEY	168	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	VTFKVPHAK	238	246	9	HLA-A*11:01	0.02	0.9621	0.01	10.91	0.03	-0.09908	0.87	0.28	-1.04	1.16	0.12
3	ALFSGVSWV	444	452	9	HLA-A*02:03	0.02	0.9548	0.02	2.55	0.02	-0.06681	0.81	0.26	-0.37	1.07	0.70
4	AKEVALLRTY	50	59	10	HLA-B*44:03	0.02	0.9480	0.02	15.80	0.02	0.15726	1.59	1.30	-1.20	2.89	1.69
3	SYAMCTNTF	296	304	9	HLA-A*24:02	0.02	0.9327	0.02	5.00	0.02	-0.16274	1.39	1.26	-0.90	2.65	1.75
4	ETAWDFGSV	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	2.32	0.02	0.29933	1.06	0.03	-0.37	1.09	0.73
4	MAILGETAW	412	420	9	HLA-B*53:01	0.02	0.8984	0.02	10.24	0.02	0.21491	1.39	0.51	-1.01	1.91	0.90
1	MAILGDTAW	412	420	9	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	MAILGDTAW	412	420	9	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
3	MAILGDTAW	410	418	9	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
4	TFKVPHAKR	239	247	9	HLA-A*33:01	0.02	0.8786	0.01	19.34	0.03	-0.10179	1.07	0.73	-1.29	1.80	0.51
4	KTWLVHKQW	204	212	9	HLA-B*58:01	0.025	0.9889	0.01	8.37	0.04	-0.11829	1.59	0.54	-0.92	2.13	1.20
2	KAWLVHRQW	204	212	9	HLA-B*58:01	0.025	0.9849	0.01	7.21	0.04	0.10739	1.50	0.47	-0.86	1.96	1.11
3	ITANFVVTK	380	388	9	HLA-A*11:01	0.025	0.9780	0.01	11.40	0.04	0.09177	1.12	0.23	-1.06	1.35	0.29
4	KEVALLRTY	51	59	9	HLA-B*44:02	0.025	0.9682	0.01	36.11	0.04	0.09789	1.59	1.36	-1.56	2.95	1.39
2	ITEAELTGY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	93.71	0.04	0.21149	1.36	1.23	-1.53	2.59	1.07
3	ETQGVTAEI	154	162	9	HLA-A*68:02	0.025	0.9367	0.01	6.34	0.04	0.16476	1.08	0.18	-0.80	1.23	0.43
3	ATQLATLRK	50	58	9	HLA-A*11:01	0.025	0.9338	0.01	11.72	0.04	0.04676	0.82	0.17	-1.07	0.99	-0.08
4	KTWLVHKQW	204	212	9	HLA-A*32:01	0.025	0.8943	0.01	30.99	0.04	-0.11829	1.59	0.56	-1.49	2.13	0.66
4	SALTLHWFR	385	393	9	HLA-A*33:01	0.025	0.7691	0.04	8.80	0.01	0.31045	1.10	0.62	-0.32	1.73	0.81
2	RLRMDKLQLK	286	295	10	HLA-A*03:01	0.03	0.9412	0.02	14.91	0.04	-0.46298	0.92	0.34	-1.17	1.25	0.08
1	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
2	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
3	MAILGDTAW	410	418	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
1	TSEIQLTGY	170	178	9	HLA-A*01:01	0.03	0.9340	0.02	54.13	0.04	0.08890	1.20	1.15	-1.73	2.35	0.61

T Cell Prediction – Class I

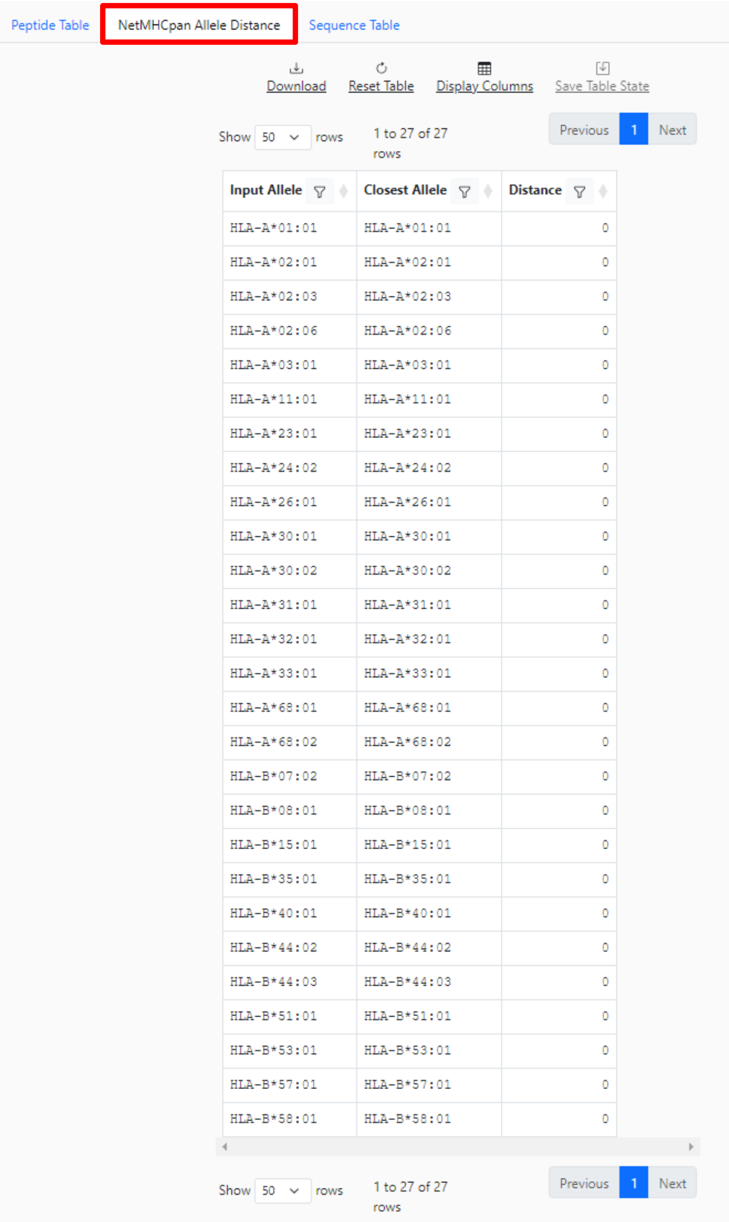
Results – NetMHCpan Allele Distance & Sequence Table



1 to 4 of 4 rows

seq #	sequence name	sequence
1	NP_722460.2 envelope protein [dengue virus type 1]	MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVLRKLCIEAKISNTTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDCSPRTGLDFNEMVLLTMKKKSWLVHKQWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAGHLKCRLKMDKLILKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAWDFGSIGGVFTSVGKLIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLGVMVQA
2	BCG29765.1 envelope protein [dengue virus type 2]	MRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKHPATLRKYCIEAKLTNTTTASRCPTQGEPSLNEEQDKRFICKHSMVDRGWGNGCGLFGKGGIVTCAMFTCKKNMEGKVVQPENLEYTIVITPHSGEEKAVGNDTGKHGTEIKVTPQSSITEAELTGYGTVTMECSPRTGLDFNEMVLLQMEDKAWLVHRQWFLDLPLPWLPGADKQGSNWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEPPFGDSYIVIGVEPGQLKLSWFKKGSSIGQMFETTMRGAKRMAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWTMKILIGVVITWIGMNSRSTSLSVSLVLVGVVTLYLGVMVQA
3	AMQ36111.1 envelope protein [dengue virus type 3]	MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLATLRKLCIEGKITNITTDSRCPTQGEAALPEEQDQNYVCKHTYVDRGWGNGCGLFGKGSLVTCAKFQCLEPIEGKVVQYENLKYTVIITVHTGDQHQVGNETQGVTAEITPQASTTEAILPEYGTLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHLKCRLKMDKLELKGMSYAMCTNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTEDGQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDNALKINWYKKGSSIGKMFEATARGARRMAILGDTAWDFGSVGGVLNSLGKMVHQIFGSAYTALFSGVSWVMKIGIGVLLTWIGLNSKNTSMSFSCIAIGIITLYLGAVVQA
4	BCG29766.1 envelope protein [dengue virus type 4]	MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVALLRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKGGVVTCAKFLCSGKITGNLVQIENLEYTVVVTVHNGDTPAVGNDTSHHGVTATITPRSPSVEVKLPDYGELTLDCEPRSGIDFIEMILMKMKKKTWLVHKQWFLDLPLPWTAGADTSEVHWNHKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTAVVKVKYEGAGAPCKVPIEIRDVNKEKVVGRIISSTPFAENTNSVTNIELEPPFGDSYIVIGVGESALTLHWFRKGSSIGKMFESTYRGAKRMAILGETAWDFGSVGGLFTSLGKAVHQVFGSVYTTMFGGVSWMVRILIGFLVLWIGTNSRNTSMAMTCIAVGGITLFLGFTVQA

1 to 4 of 4 rows



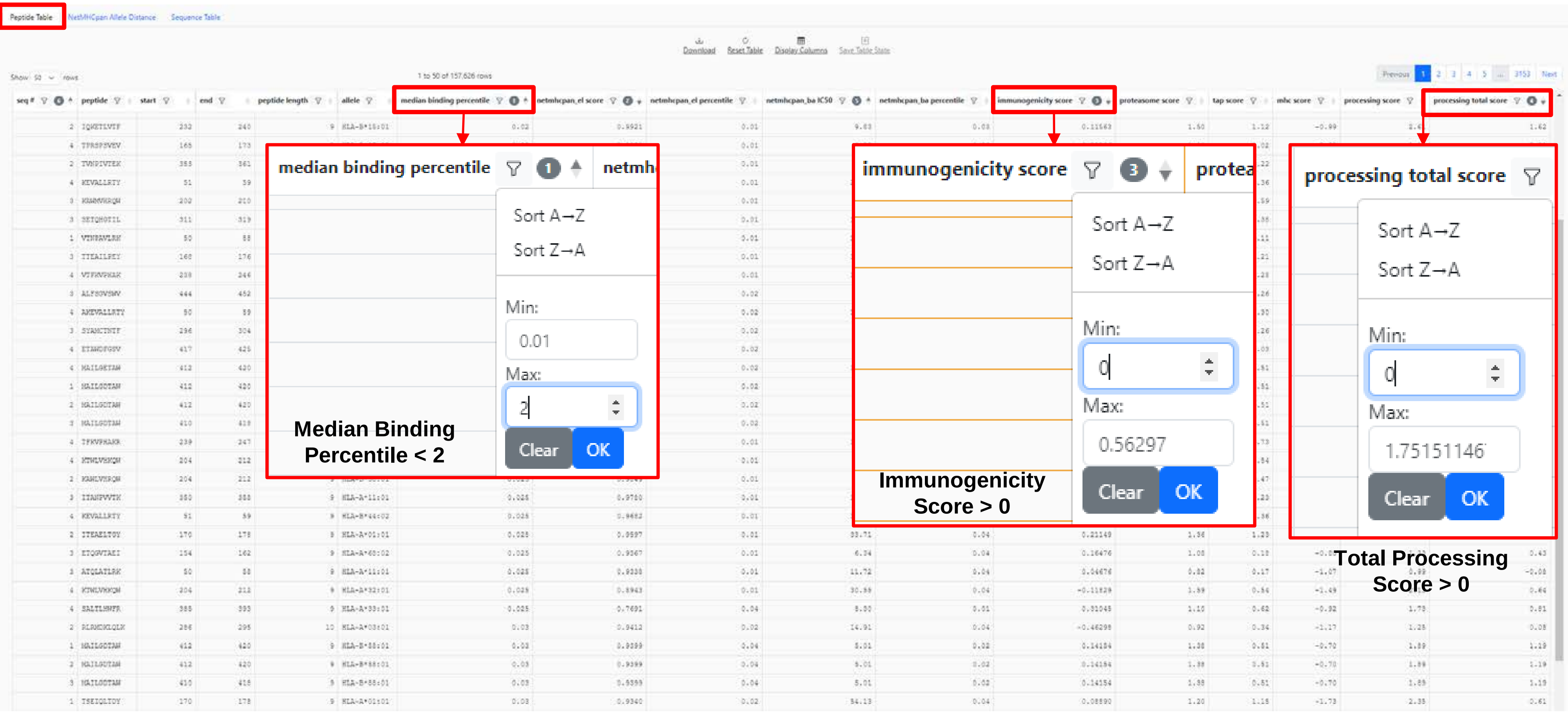
1 to 27 of 27 rows

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

1 to 27 of 27 rows

T Cell Prediction – Class I

Results – Applying Filters to Peptide Table



median binding percentile
Min: 0.01
Max: 2

Median Binding Percentile < 2

immunogenicity score
Min: 0
Max: 0.56297

Immunogenicity Score > 0

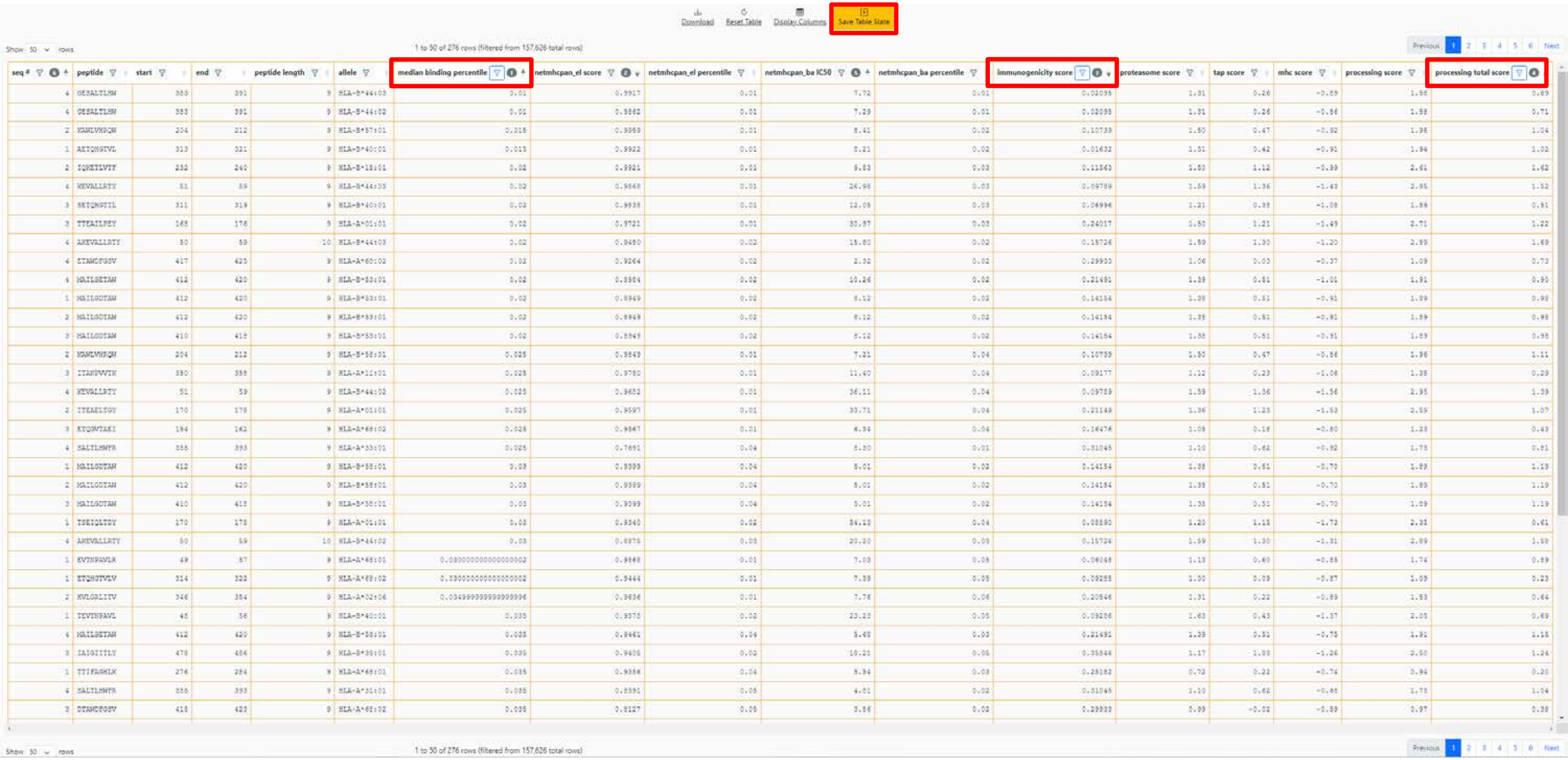
processing total score
Min: 0
Max: 1.75151146

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.



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

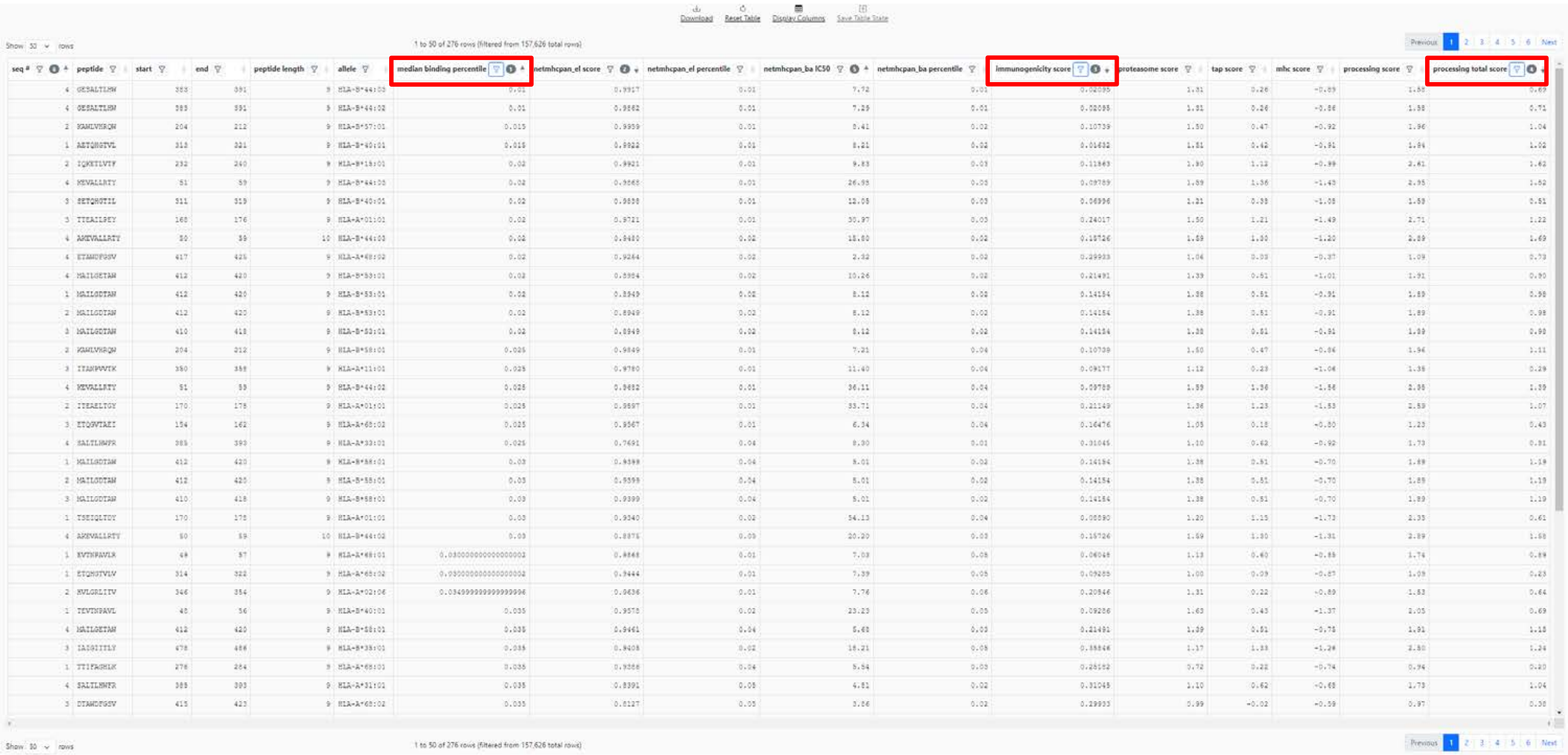
seq #	peptide	start	end	peptide length	allele	median binding percentile	netmhcpan_el score	netmhcpan_el percentile	netmhcpan_ba IC50	netmhcpan_ba percentile	immunogenicity score	proteasome score	tap score	mhc score	processing score	processing total score
4	GESALTLHW	383	391	9	HLA-B*44:03	0.01	0.9917	0.01	7.72	0.01	0.02095	1.31	0.26	-0.69	1.58	0.69
4	GESALTLHW	383	391	9	HLA-B*44:02	0.01	0.9862	0.01	7.29	0.01	0.02095	1.31	0.26	-0.86	1.58	0.71
2	KAWLVHRQW	204	212	9	HLA-B*57:01	0.015	0.9969	0.01	8.41	0.02	0.10739	1.50	0.47	-0.92	1.96	1.04
1	AETQHGTVL	313	321	9	HLA-B*40:01	0.015	0.9922	0.01	8.21	0.02	0.01632	1.51	0.42	-0.91	1.94	1.02
2	IQHETLVTF	232	240	9	HLA-B*15:01	0.02	0.9921	0.01	9.83	0.03	0.11563	1.80	1.12	-0.99	2.61	1.62
4	KEVALLRTY	51	59	9	HLA-B*44:03	0.02	0.9848	0.01	26.98	0.03	0.09789	1.59	1.36	-1.43	2.95	1.52
3	SETQHGTIL	311	319	9	HLA-B*40:01	0.02	0.9838	0.01	12.05	0.03	0.06996	1.21	0.38	-1.08	1.59	0.51
3	TTEAILFEY	168	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	AKEVALLRTY	50	59	10	HLA-B*44:03	0.02	0.9480	0.02	15.80	0.02	0.15726	1.59	1.30	-1.20	2.89	1.69
4	ETAWDFGSV	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	2.32	0.02	0.29933	1.06	0.03	-0.37	1.09	0.73
4	MAILGETAW	412	420	9	HLA-B*53:01	0.02	0.8984	0.02	10.26	0.02	0.21491	1.39	0.51	-1.01	1.91	0.90
1	MAILGDTAW	412	420	9	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	MAILGDTAW	412	420	9	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
3	MAILGDTAW	410	418	9	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	KAWLVHRQW	204	212	9	HLA-B*58:01	0.025	0.9849	0.01	7.21	0.04	0.10739	1.50	0.47	-0.86	1.96	1.11
3	ITANPVVTK	350	358	9	HLA-A*11:01	0.025	0.9780	0.01	11.40	0.04	0.09177	1.12	0.23	-1.06	1.35	0.29
4	KEVALLRTY	51	59	9	HLA-B*44:02	0.025	0.9682	0.01	36.11	0.04	0.09789	1.59	1.36	-1.56	2.95	1.39
2	ITEAELTGY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	33.71	0.04	0.21149	1.36	1.23	-1.53	2.59	1.07
3	KTQGVTAKI	154	162	9	HLA-A*68:02	0.025	0.9867	0.01	4.34	0.04	0.16476	1.05	0.18	-0.80	1.23	0.43
4	SALTLHWFR	385	393	9	HLA-A*33:01	0.025	0.7691	0.04	8.30	0.01	0.31045	1.10	0.62	-0.92	1.73	0.81
1	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
2	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
3	MAILGDTAW	410	418	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
1	TSEIQLTDY	170	178	9	HLA-A*01:01	0.03	0.9340	0.02	54.13	0.04	0.08890	1.20	1.15	-1.73	2.35	0.61
4	AKEVALLRTY	50	59	10	HLA-B*44:02	0.03	0.8875	0.03	20.20	0.03	0.15726	1.59	1.30	-1.31	2.89	1.58
1	EVTNPAVLR	49	57	9	HLA-A*68:01	0.030000000000000002	0.9868	0.01	7.03	0.05	0.06048	1.13	0.60	-0.85	1.74	0.89
1	ETQHGTVLV	314	322	9	HLA-A*68:02	0.030000000000000002	0.9444	0.01	7.39	0.05	0.09285	1.00	0.09	-0.87	1.09	0.23
2	KVLGRLITV	346	354	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	TEVTNPAVL	48	56	9	HLA-B*40:01	0.035	0.9578	0.02	23.23	0.05	0.09286	1.63	0.43	-1.37	2.05	0.69
4	MAILGETAW	412	420	9	HLA-B*58:01	0.035	0.8461	0.04	5.48	0.03	0.21491	1.39	0.51	-0.75	1.91	1.16
3	IAIGIITLY	478	486	9	HLA-B*35:01	0.035	0.9405	0.02	10.21	0.05	0.35846	1.17	1.33	-1.26	2.50	1.24
1	TTIFAGHLK	276	284	9	HLA-A*68:01	0.035	0.9386	0.04	5.34	0.03	0.25182	0.72	0.22	-0.74	0.94	0.20
4	SALTLHWFR	385	393	9	HLA-A*31:01	0.035	0.8391	0.05	4.61	0.02	0.31045	1.10	0.62	-0.66	1.73	1.04
3	DTAWDFGSV	415	423	9	HLA-A*68:02	0.035	0.8127	0.05	3.86	0.02	0.29933	0.99	-0.02	-0.59	0.97	0.38

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

T Cell Prediction – Class I

Filtered Results

Table state has been saved – can proceed with analyses

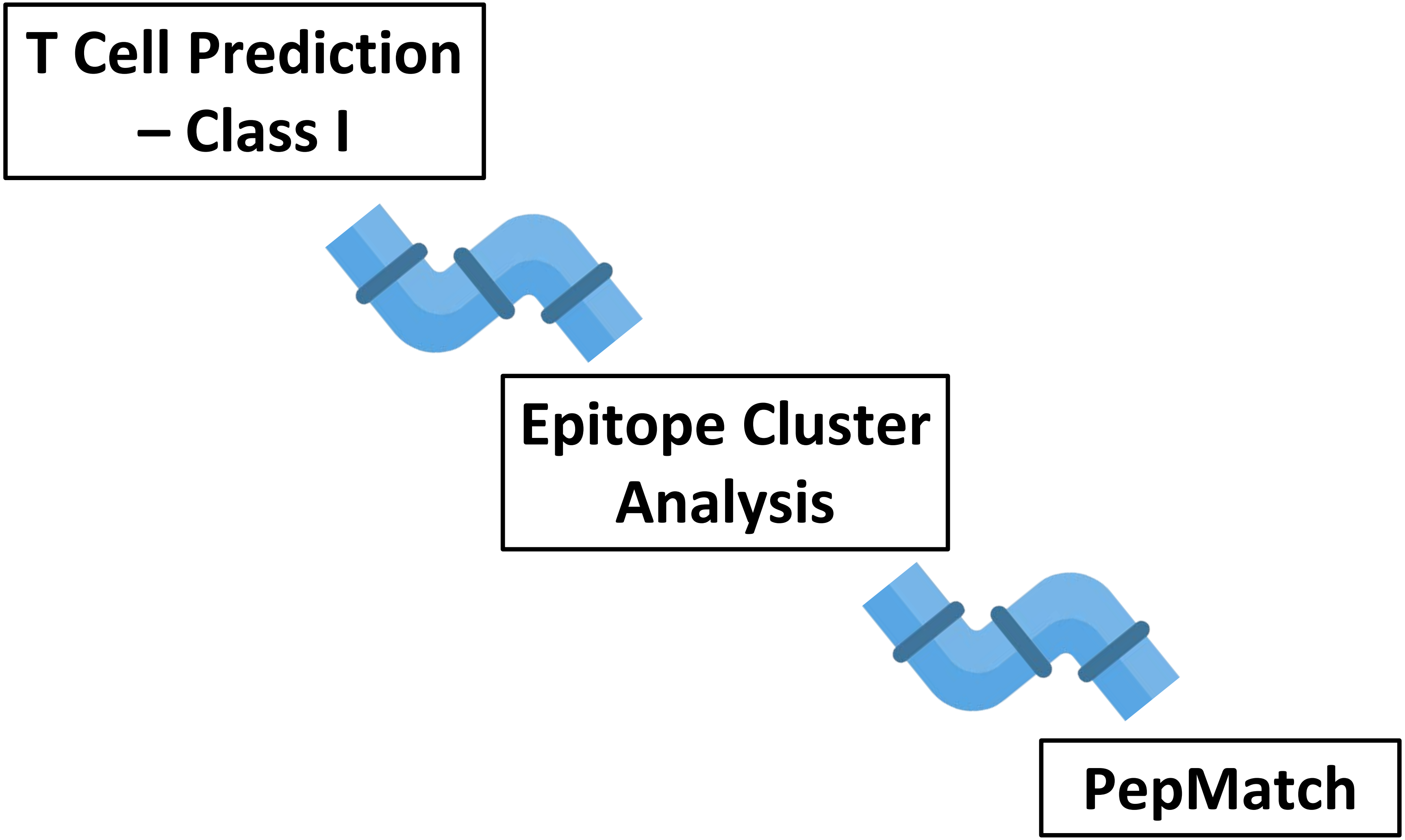


1 to 50 of 276 rows (filtered from 157,626 total rows)

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	GESALTLHW	383	391	9	HLA-B*44:03	0.01	0.9917	0.01	7.72	0.01	0.02095	1.31	0.26	-0.89	1.58	0.69
4	GESALTLHW	383	391	9	HLA-B*44:02	0.01	0.9862	0.01	7.29	0.01	0.02095	1.31	0.26	-0.86	1.58	0.71
2	KAWLVHRQW	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	AETQHGTVL	313	321	9	HLA-B*40:01	0.015	0.9922	0.01	8.21	0.02	0.01632	1.51	0.42	-0.91	1.94	1.02
2	IQKETLVTF	232	240	9	HLA-B*15:01	0.02	0.9921	0.01	9.83	0.03	0.11863	1.30	1.12	-0.99	2.41	1.62
4	MEVALLRTY	51	59	9	HLA-B*44:03	0.02	0.9868	0.01	26.95	0.03	0.09789	1.59	1.36	-1.43	2.95	1.52
3	SETQHGTIL	311	319	9	HLA-B*40:01	0.02	0.9858	0.01	12.05	0.03	0.06996	1.21	0.38	-1.08	1.59	0.51
3	TTEAILPEY	168	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	AMEVALLRTY	50	59	10	HLA-B*44:03	0.02	0.9480	0.02	18.80	0.02	0.15726	1.59	1.30	-1.20	2.89	1.69
4	ETAWDFGSV	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	2.32	0.02	0.29933	1.04	0.05	-0.37	1.09	0.73
4	MAILGETAW	412	420	9	HLA-B*53:01	0.02	0.8984	0.02	10.26	0.02	0.21491	1.39	0.51	-1.01	1.91	0.90
1	MAILGDTAW	412	420	9	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	MAILGDTAW	412	420	9	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
3	MAILGDTAW	410	418	9	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	KAWLVHRQW	204	212	9	HLA-B*58:01	0.025	0.9849	0.01	7.21	0.04	0.10739	1.50	0.47	-0.86	1.96	1.11
3	ITANPVVTK	350	358	9	HLA-A*11:01	0.025	0.9780	0.01	11.40	0.04	0.09177	1.12	0.23	-1.06	1.35	0.29
4	MEVALLRTY	51	59	9	HLA-B*44:02	0.025	0.9682	0.01	36.11	0.04	0.09789	1.59	1.36	-1.56	2.95	1.39
2	ITEAELTGY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	33.71	0.04	0.21149	1.36	1.23	-1.53	2.59	1.07
3	ETQGVTAEI	154	162	9	HLA-A*68:02	0.025	0.9567	0.01	6.34	0.04	0.16476	1.05	0.18	-0.80	1.23	0.43
4	SALTLHWFR	385	393	9	HLA-A*33:01	0.025	0.7691	0.04	8.30	0.01	0.31045	1.10	0.62	-0.92	1.73	0.81
1	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
2	MAILGDTAW	412	420	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
3	MAILGDTAW	410	418	9	HLA-B*58:01	0.03	0.9399	0.04	5.01	0.02	0.14154	1.38	0.51	-0.70	1.89	1.19
1	TSEIQLTDY	170	178	9	HLA-A*01:01	0.03	0.9340	0.02	54.13	0.04	0.08890	1.20	1.15	-1.73	2.35	0.61
4	AMEVALLRTY	50	59	10	HLA-B*44:02	0.03	0.8875	0.03	20.20	0.03	0.15726	1.59	1.30	-1.31	2.89	1.58
1	EVTNPAVLR	49	57	9	HLA-A*68:01	0.030000000000000002	0.8848	0.01	7.03	0.05	0.06048	1.13	0.60	-0.85	1.74	0.89
1	ETQHGTVLV	314	322	9	HLA-A*68:02	0.030000000000000002	0.9444	0.01	7.39	0.05	0.09285	1.00	0.09	-0.87	1.09	0.23
2	HVLGRLITV	346	354	9	HLA-A*02:06	0.034999999999999996	0.9636	0.01	7.76	0.06	0.20946	1.31	0.22	-0.89	1.53	0.64
1	TEVTNPAVL	48	56	9	HLA-B*40:01	0.035	0.9578	0.02	23.23	0.05	0.09286	1.63	0.43	-1.37	2.05	0.69
4	MAILGETAW	412	420	9	HLA-B*58:01	0.035	0.9461	0.04	5.68	0.03	0.21491	1.39	0.51	-0.78	1.91	1.18
3	IASGIITLY	478	486	9	HLA-B*35:01	0.035	0.9408	0.02	18.21	0.05	0.35846	1.17	1.33	-1.26	2.50	1.24
1	TTIFAGHLK	276	284	9	HLA-A*68:01	0.035	0.9366	0.04	5.54	0.03	0.26182	0.72	0.22	-0.74	0.94	0.20
4	SALTLHWFR	385	393	9	HLA-A*31:01	0.035	0.8391	0.05	4.81	0.02	0.31045	1.10	0.62	-0.68	1.73	1.04
3	DTAWDFGSV	415	423	9	HLA-A*68:02	0.035	0.8127	0.05	3.86	0.02	0.29933	0.99	-0.02	-0.59	0.97	0.38

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

Now let's build the rest of the pipeline…

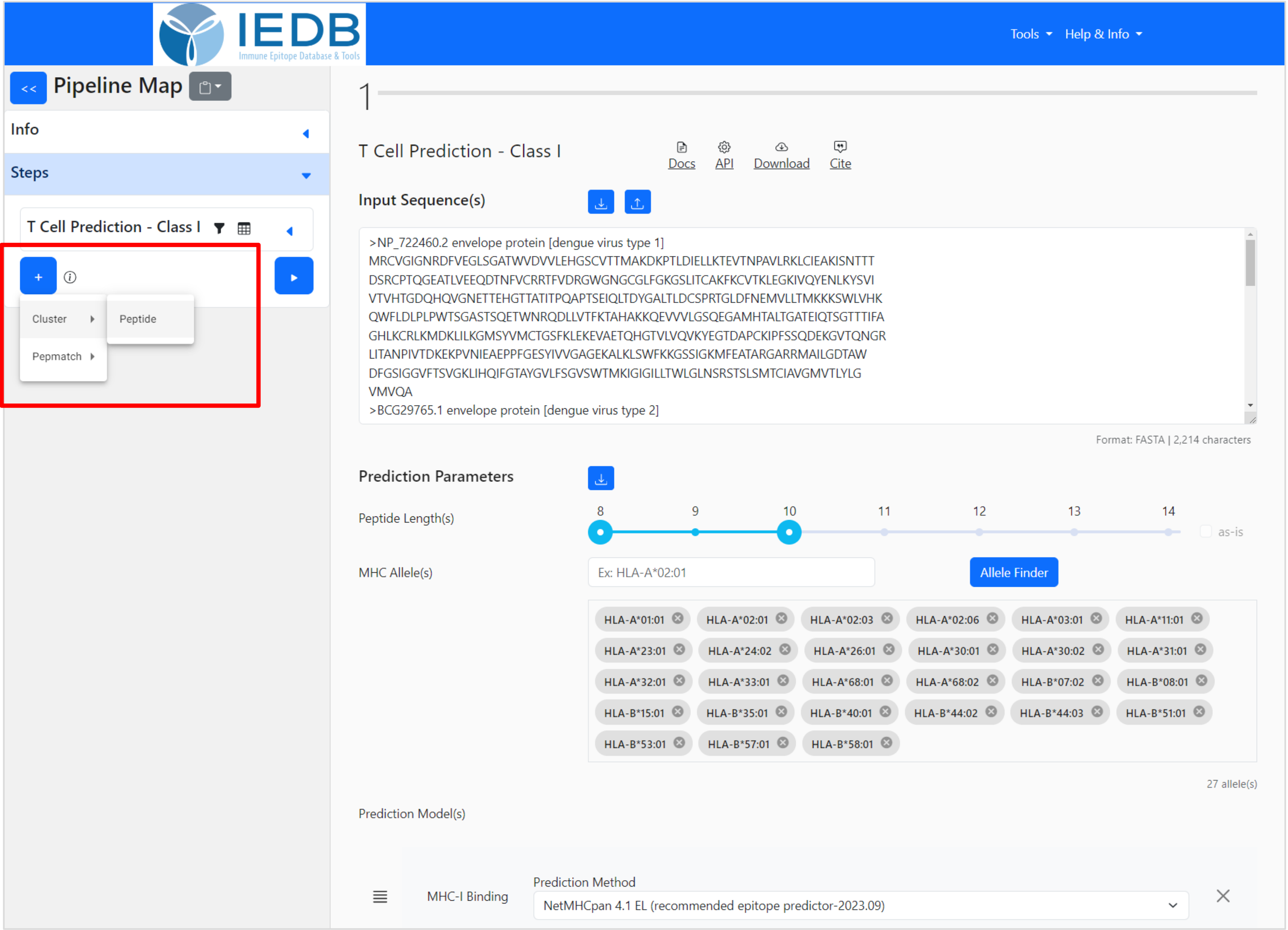


T Cell Prediction – Class I

Epitope Cluster Analysis

PepMatch

Add Cluster Tool (Peptide)



1. Add Cluster to Pipeline

T Cell Prediction - Class I

Input Sequence(s)

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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

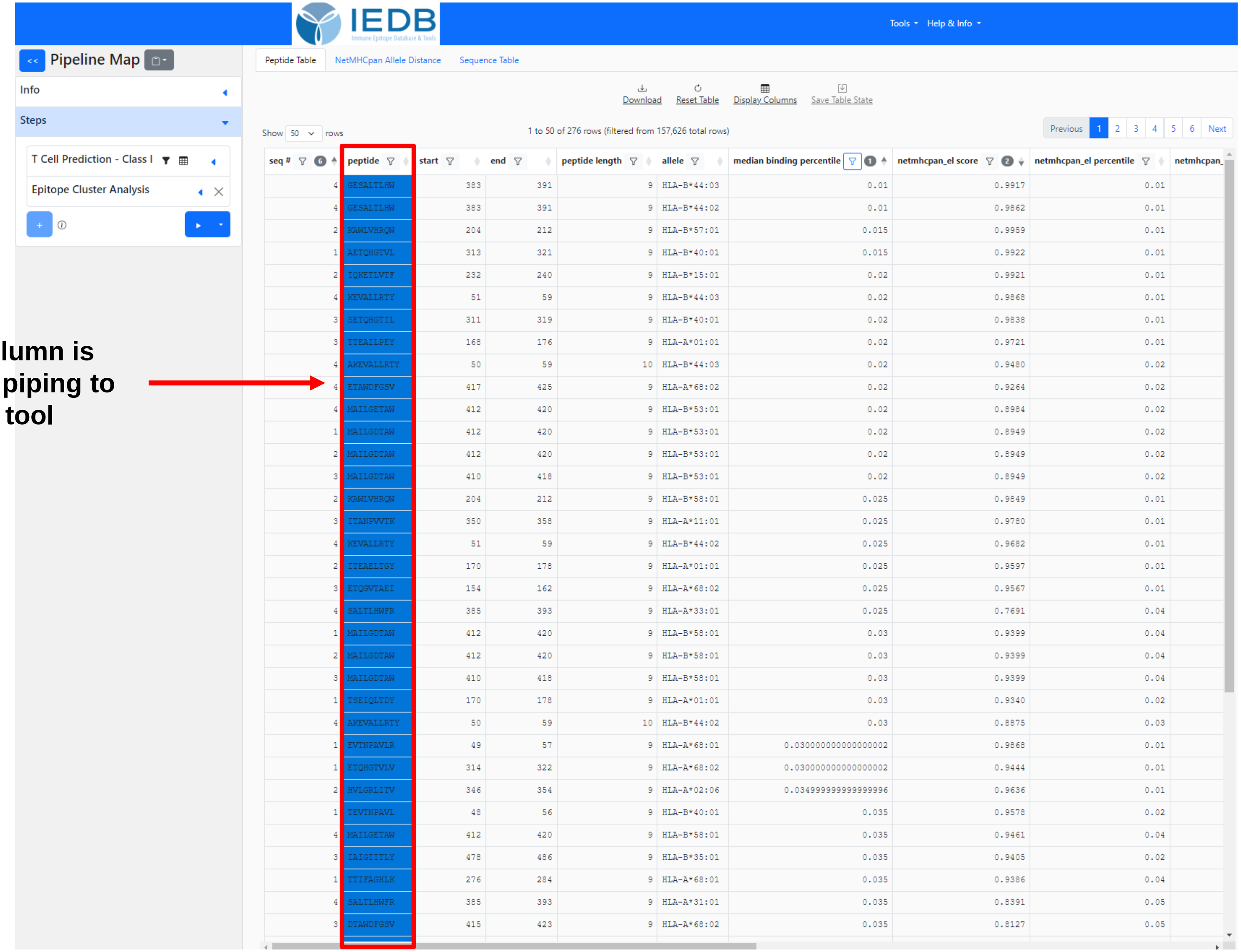
27 allele(s)

Prediction Model(s)

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

Add Cluster Tool (Peptide)

Peptide column is selected for piping to Cluster tool

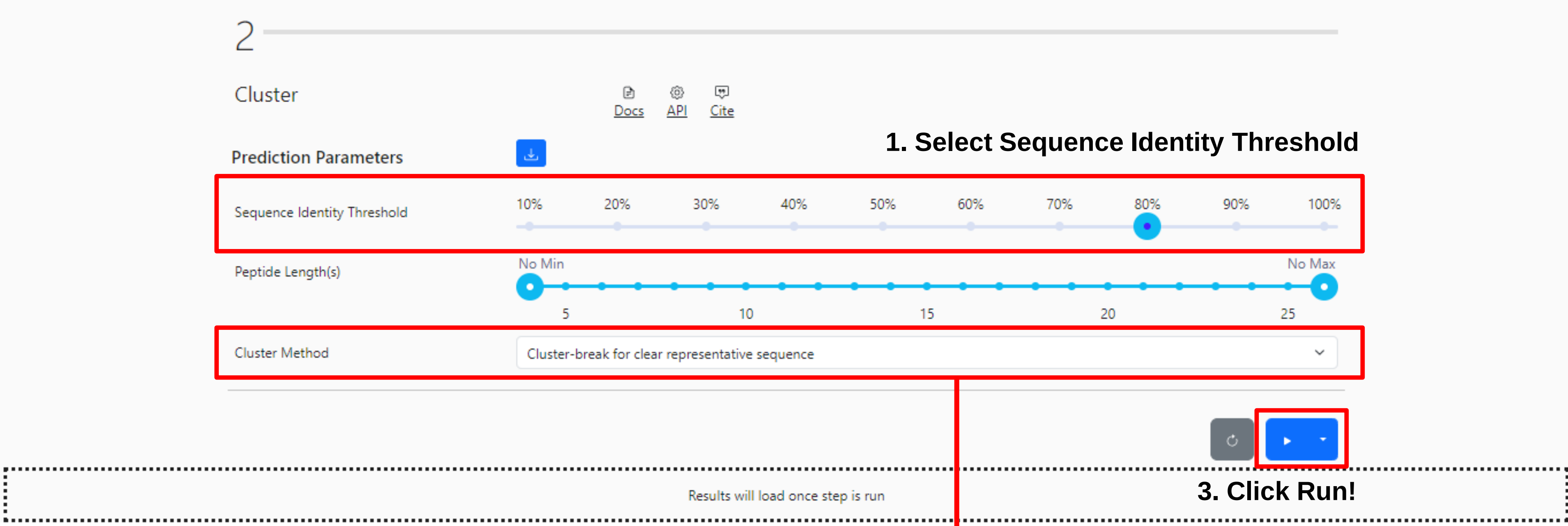


Show 50 rows

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_
4	GESALTLHW	383	391	9	HLA-B*44:03	0.01	0.9917	0.01	
4	GESALTLHW	383	391	9	HLA-B*44:02	0.01	0.9862	0.01	
2	KAWLVHRQW	204	212	9	HLA-B*57:01	0.015	0.9959	0.01	
1	AETQHGTVL	313	321	9	HLA-B*40:01	0.015	0.9922	0.01	
2	IQKETLVTF	232	240	9	HLA-B*15:01	0.02	0.9921	0.01	
4	KEVALLRTY	51	59	9	HLA-B*44:03	0.02	0.9868	0.01	
3	SETQHGTIL	311	319	9	HLA-B*40:01	0.02	0.9838	0.01	
3	TTEAILPEY	168	176	9	HLA-A*01:01	0.02	0.9721	0.01	
4	AKEVALLRTY	50	59	10	HLA-B*44:03	0.02	0.9480	0.02	
4	ETAWDFGSV	417	425	9	HLA-A*68:02	0.02	0.9264	0.02	
4	MAILGETAW	412	420	9	HLA-B*53:01	0.02	0.8984	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	KAWLVHRQW	204	212	9	HLA-B*58:01	0.025	0.9849	0.01	
3	ITANPVVTK	350	358	9	HLA-A*11:01	0.025	0.9780	0.01	
4	KEVALLRTY	51	59	9	HLA-B*44:02	0.025	0.9682	0.01	
2	ITEAELTGY	170	178	9	HLA-A*01:01	0.025	0.9597	0.01	
3	ETQGVTAEI	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	TSEIQLTDY	170	178	9	HLA-A*01:01	0.03	0.9340	0.02	
4	AKEVALLRTY	50	59	10	HLA-B*44:02	0.03	0.8875	0.03	
1	EVTNPAVLR	49	57	9	HLA-A*68:01	0.030000000000000002	0.9868	0.01	
1	ETQHGTVLV	314	322	9	HLA-A*68:02	0.030000000000000002	0.9444	0.01	
2	HVLGRLITV	346	354	9	HLA-A*02:06	0.034999999999999996	0.9636	0.01	
1	TEVTNPAVL	48	56	9	HLA-B*40:01	0.035	0.9578	0.02	
4	MAILGETAW	412	420	9	HLA-B*58:01	0.035	0.9461	0.04	
3	IAIGIITLY	478	486	9	HLA-B*35:01	0.035	0.9405	0.02	
1	TTIFAGHLK	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	DTAWDFGSV	415	423	9	HLA-A*68:02	0.035	0.8127	0.05	

Select Cluster Parameters



Cluster

Prediction Parameters

1. Select Sequence Identity Threshold

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

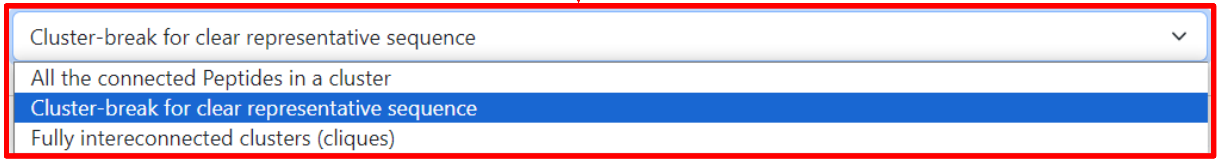
Peptide Length(s): No Min – No Max (5, 10, 15, 20, 25)

Cluster Method: Cluster-break for clear representative sequence

Results will load once step is run

3. Click Run!

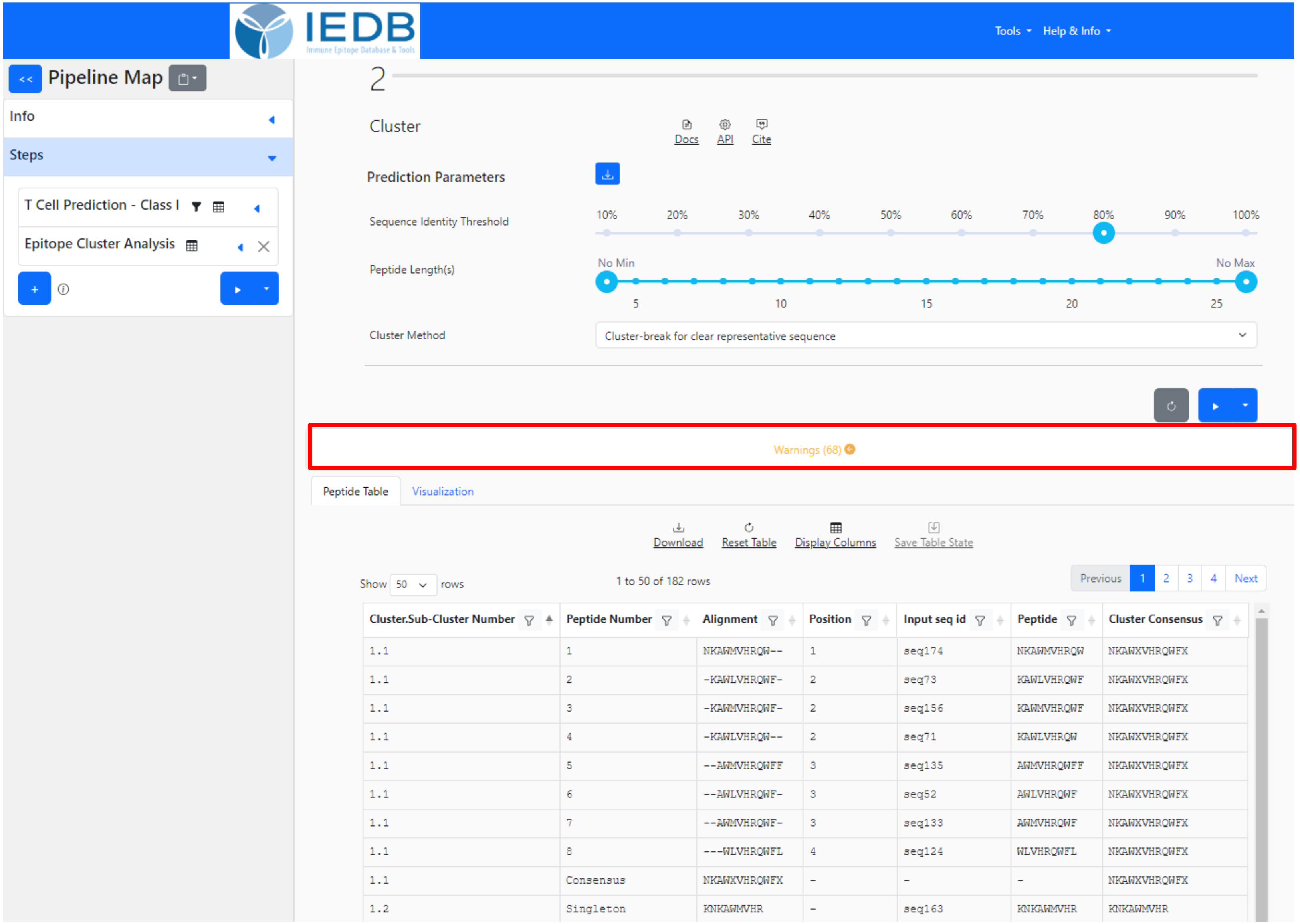
2. Select Cluster Method



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



Prediction Parameters

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

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

Cluster Method: Cluster-break for clear representative sequence

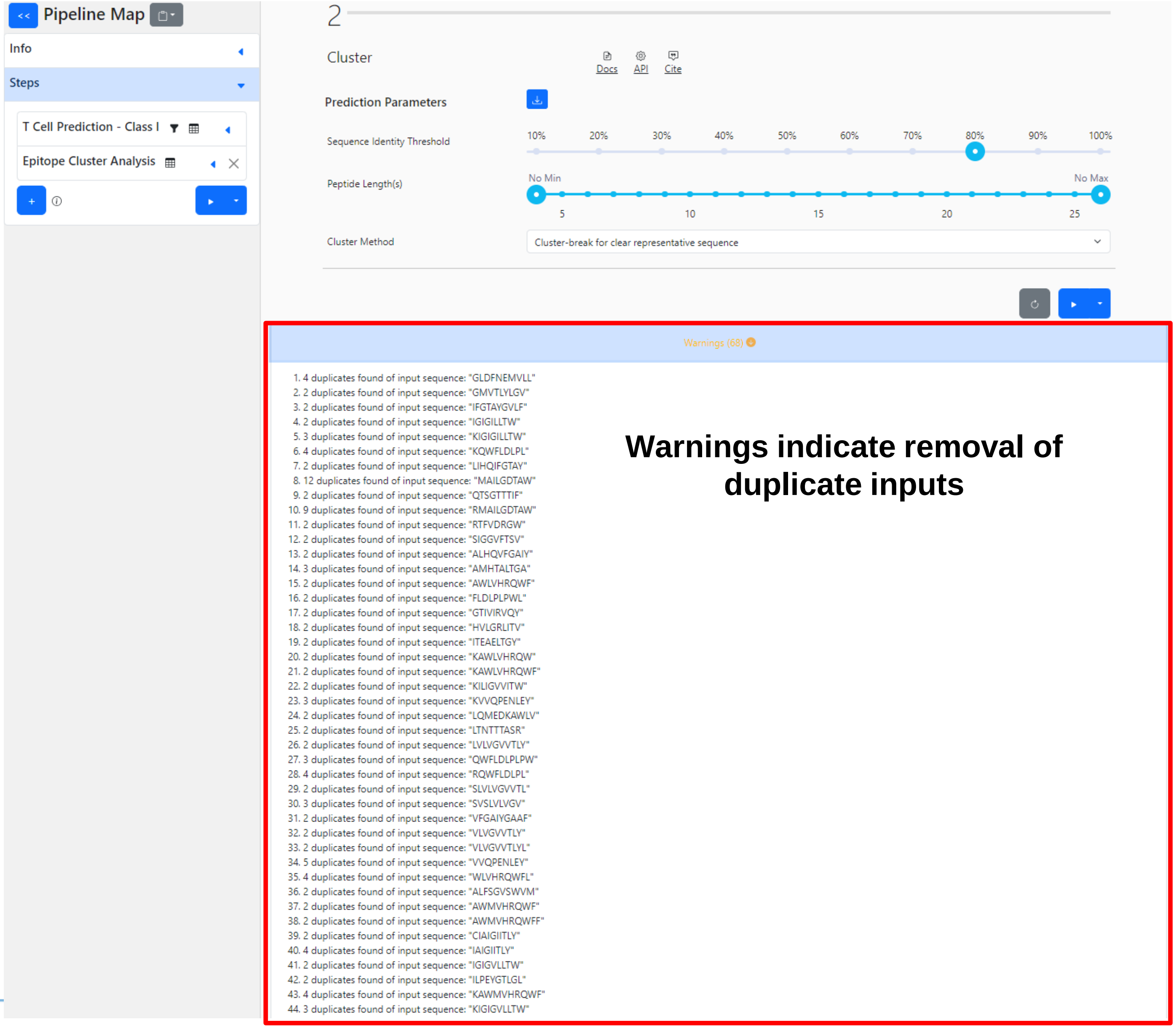
Warnings (68)

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	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



Prediction Parameters

Sequence Identity Threshold: 80%

Peptide Length(s): No Min – No Max

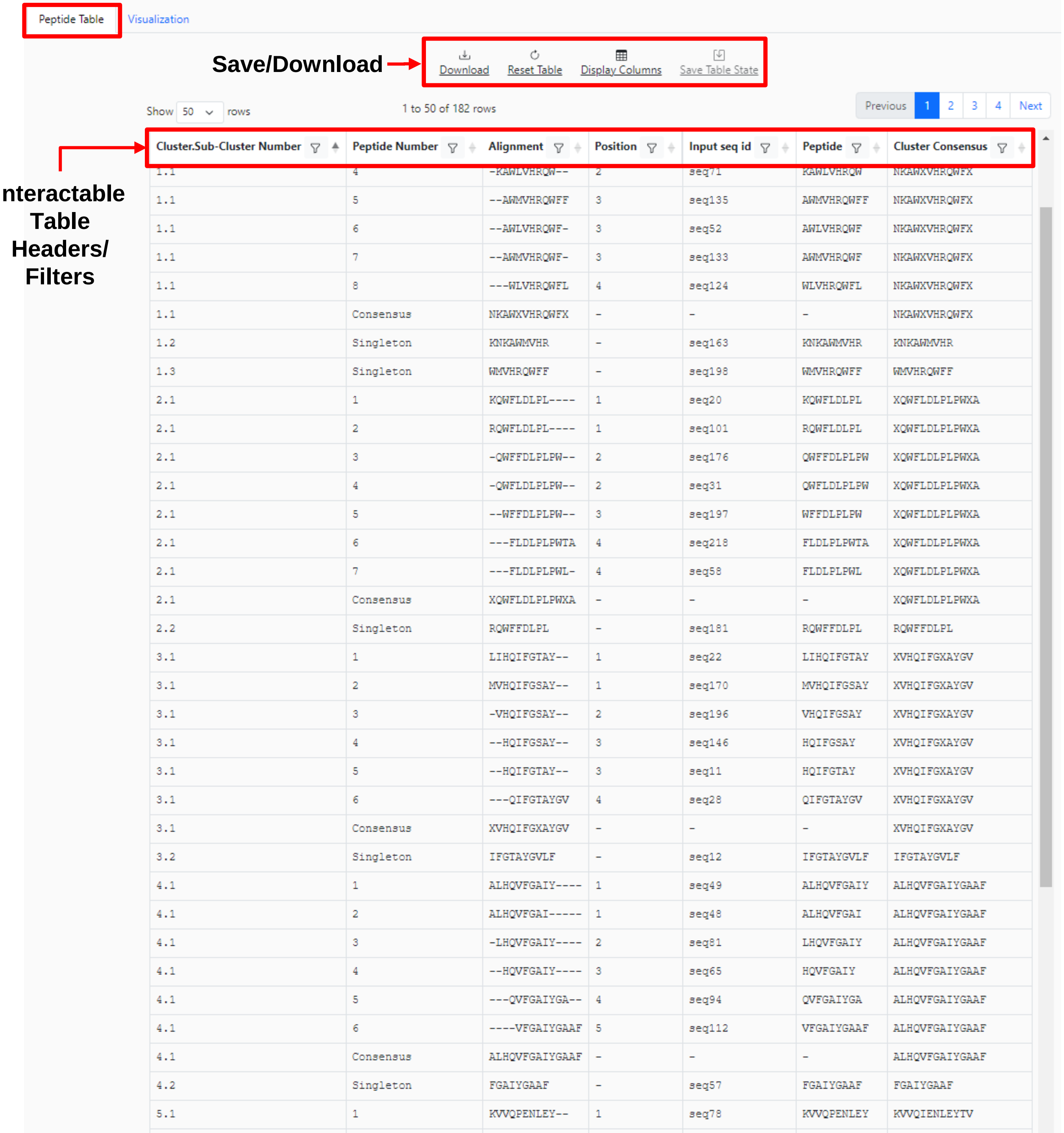
Cluster Method: Cluster-break for clear representative sequence

Warnings (68)

1. 4 duplicates found of input sequence: "GLDFNEMVLL"
2. 2 duplicates found of input sequence: "GMVTLYLGV"
3. 2 duplicates found of input sequence: "IFGTAYGVLF"
4. 2 duplicates found of input sequence: "IGIGILLTW"
5. 3 duplicates found of input sequence: "KIGIGILLTW"
6. 4 duplicates found of input sequence: "KQWFLDLPL"
7. 2 duplicates found of input sequence: "LIHQIFGTAY"
8. 12 duplicates found of input sequence: "MAILGDTAW"
9. 2 duplicates found of input sequence: "QTSGTTTIF"
10. 9 duplicates found of input sequence: "RMAILGDTAW"
11. 2 duplicates found of input sequence: "RTFVDRGW"
12. 2 duplicates found of input sequence: "SIGGVFTSV"
13. 2 duplicates found of input sequence: "ALHQVFGAIY"
14. 3 duplicates found of input sequence: "AMHTALTGA"
15. 2 duplicates found of input sequence: "AWLVHRQWF"
16. 2 duplicates found of input sequence: "FLDLPLPWL"
17. 2 duplicates found of input sequence: "GTIVIRVQY"
18. 2 duplicates found of input sequence: "HVLGRLITV"
19. 2 duplicates found of input sequence: "ITEAELTGY"
20. 2 duplicates found of input sequence: "KAWLVHRQW"
21. 2 duplicates found of input sequence: "KAWLVHRQWF"
22. 2 duplicates found of input sequence: "KILIGVVITW"
23. 3 duplicates found of input sequence: "KVVQPENLEY"
24. 2 duplicates found of input sequence: "LQMEDKAWLV"
25. 2 duplicates found of input sequence: "LTNTTTASR"
26. 2 duplicates found of input sequence: "LVLVGVVTLY"
27. 3 duplicates found of input sequence: "QWFLDLPLPW"
28. 4 duplicates found of input sequence: "RQWFLDLPL"
29. 2 duplicates found of input sequence: "SLVLVGVVTL"
30. 3 duplicates found of input sequence: "SVSLVLVGV"
31. 2 duplicates found of input sequence: "VFGAIYGAAF"
32. 2 duplicates found of input sequence: "VLVGVVTLY"
33. 2 duplicates found of input sequence: "VLVGVVTLYL"
34. 5 duplicates found of input sequence: "VVQPENLEY"
35. 4 duplicates found of input sequence: "WLVHRQWFL"
36. 2 duplicates found of input sequence: "ALFSGVSWVM"
37. 2 duplicates found of input sequence: "AWMVHRQWF"
38. 2 duplicates found of input sequence: "AWMVHRQWFF"
39. 2 duplicates found of input sequence: "CIAIGIITLY"
40. 4 duplicates found of input sequence: "IAIGIITLY"
41. 2 duplicates found of input sequence: "IGIGVLLTW"
42. 2 duplicates found of input sequence: "ILPEYGTLGL"
43. 4 duplicates found of input sequence: "KAWMVHRQWF"
44. 3 duplicates found of input sequence: "KIGIGVLLTW"

Warnings indicate removal of duplicate inputs

Cluster Results – Table



Save/Download

Interactable Table Headers/ Filters

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
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
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	---FLDLPLPWTA	4	seq218	FLDLPLPWTA	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	ALHQVFGAI-----	1	seq48	ALHQVFGAI	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

Interactive Cluster Visualization

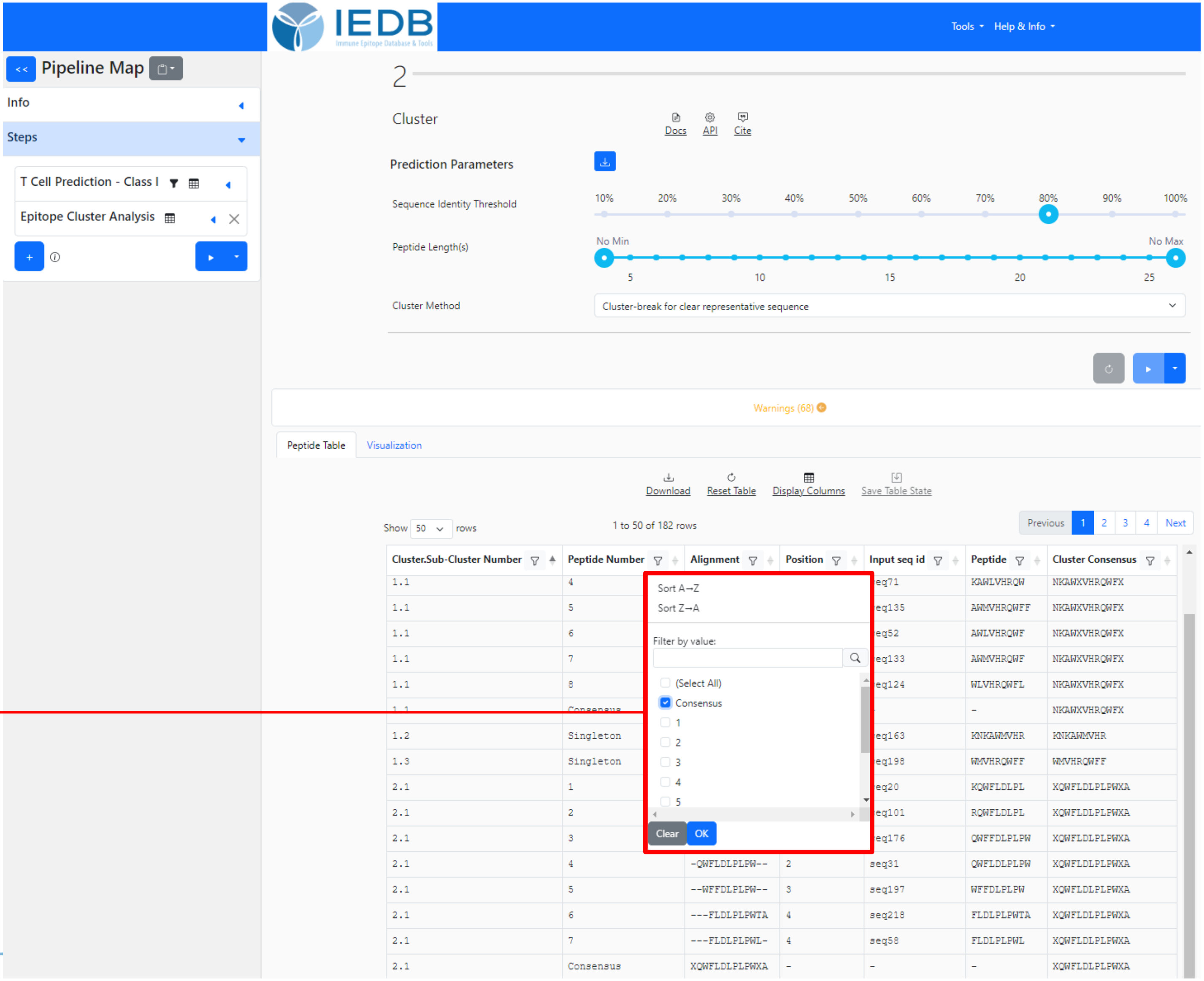
Visualize a selected Sub-cluster All

Interactive Cluster Visualization

Visualize a selected Sub-cluster 1.1

Cluster Results

Applying Filters to Peptide Table



2

Cluster

Prediction Parameters

Sequence Identity Threshold: 10% 20% 30% 40% 50% 60% 70% 80% 90% 100% (set to 80%)

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

Cluster Method: Cluster-break for clear representative sequence

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	KAWLVHRQW	NKAWXVHRQWFX
1.1	5			eq135	AWMVHRQWFF	NKAWXVHRQWFX
1.1	6			eq52	AWLVHRQWF	NKAWXVHRQWFX
1.1	7			eq133	AWMVHRQWF	NKAWXVHRQWFX
1.1	8			eq124	WLVHRQWFL	NKAWXVHRQWFX
1.1	Consensus				-	NKAWXVHRQWFX
1.2	Singleton			eq163	KNKAWMVHR	KNKAWMVHR
1.3	Singleton			eq198	WMVHRQWFF	WMVHRQWFF
2.1	1			eq20	KQWFLDLPL	XQWFLDLPLPWXA
2.1	2			eq101	RQWFLDLPL	XQWFLDLPLPWXA
2.1	3			eq176	QWFFDLPLPW	XQWFLDLPLPWXA
2.1	4	-QWFLDLPLPW--	2	seq31	QWFLDLPLPW	XQWFLDLPLPWXA
2.1	5	--WFFDLPLPW--	3	seq197	WFFDLPLPW	XQWFLDLPLPWXA
2.1	6	---FLDLPLPWTA	4	seq218	FLDLPLPWTA	XQWFLDLPLPWXA
2.1	7	---FLDLPLPWL-	4	seq58	FLDLPLPWL	XQWFLDLPLPWXA
2.1	Consensus	XQWFLDLPLPWXA	-	-	-	XQWFLDLPLPWXA

Sort A→Z
Sort Z→A

Filter by value:

☐ (Select All)
☑ Consensus
☐ 1
☐ 2
☐ 3
☐ 4
☐ 5

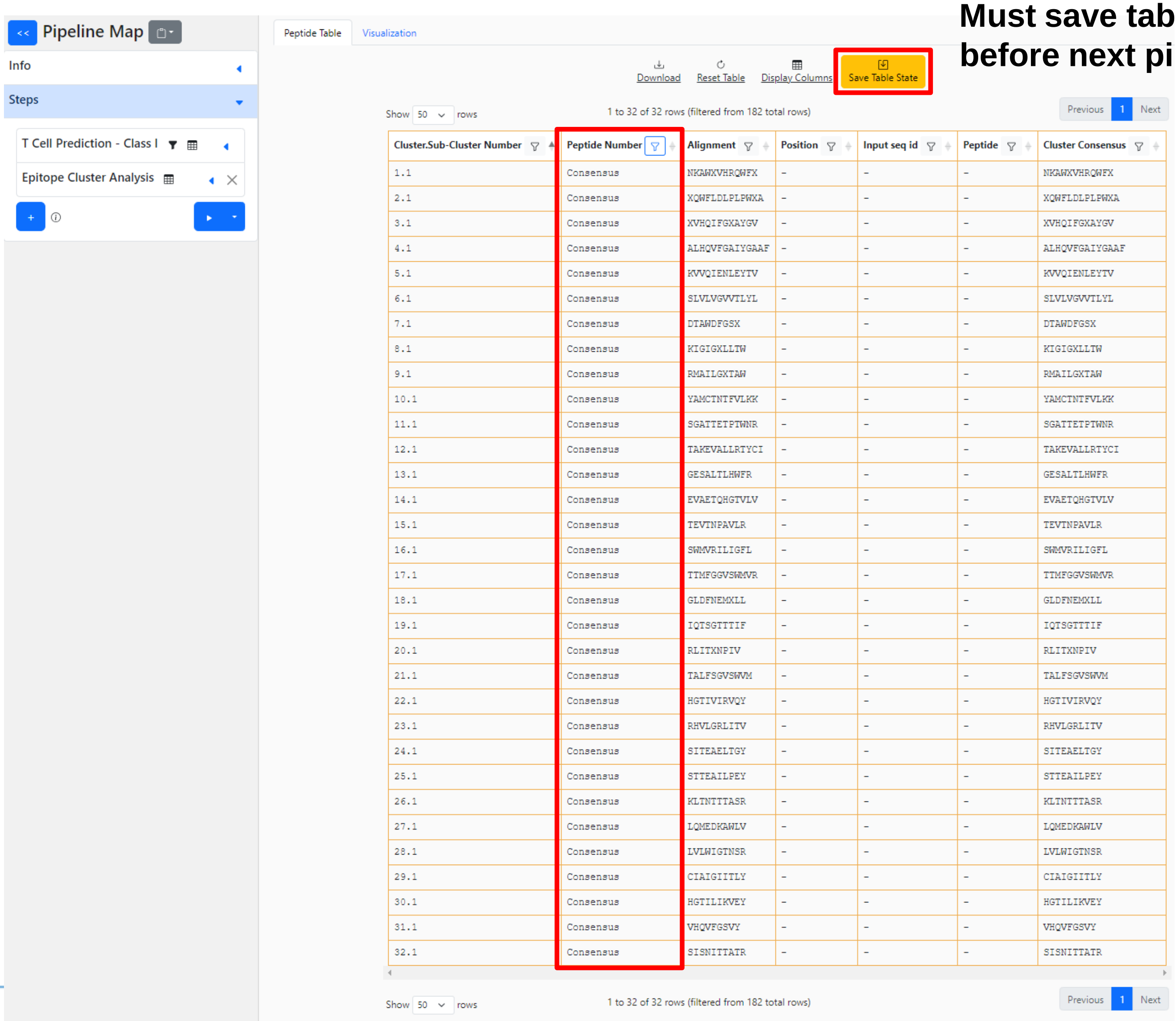
Clear OK

Filter Peptide Number = ‘Consensus’

Cluster Results

Applying Filters to Peptide Table

Must save table state before next pipe step



Show 50 rows

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

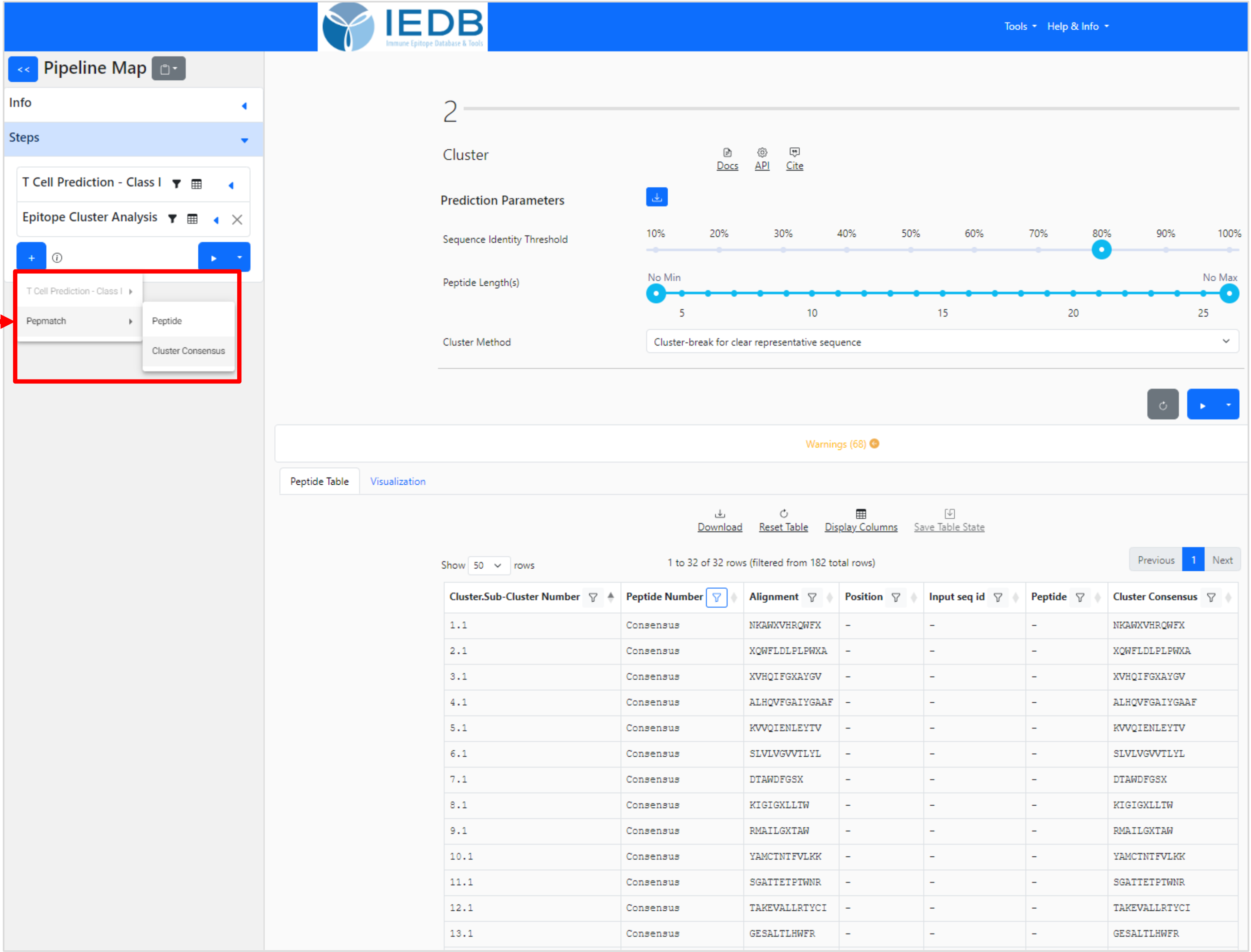
Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	Consensus	NKAWXVHRQWFX	-	-	-	NKAWXVHRQWFX
2.1	Consensus	XQWFLDLPLPWXA	-	-	-	XQWFLDLPLPWXA
3.1	Consensus	XVHQIFGXAYGV	-	-	-	XVHQIFGXAYGV
4.1	Consensus	ALHQVFGAIYGAAF	-	-	-	ALHQVFGAIYGAAF
5.1	Consensus	KVVQIENLEYTV	-	-	-	KVVQIENLEYTV
6.1	Consensus	SLVLVGVVTLYL	-	-	-	SLVLVGVVTLYL
7.1	Consensus	DTAWDFGSX	-	-	-	DTAWDFGSX
8.1	Consensus	KIGIGXLLTW	-	-	-	KIGIGXLLTW
9.1	Consensus	RMAILGXTAW	-	-	-	RMAILGXTAW
10.1	Consensus	YAMCTNTFVLKK	-	-	-	YAMCTNTFVLKK
11.1	Consensus	SGATTETPTWNR	-	-	-	SGATTETPTWNR
12.1	Consensus	TAKEVALLRTYCI	-	-	-	TAKEVALLRTYCI
13.1	Consensus	GESALTLHWFR	-	-	-	GESALTLHWFR
14.1	Consensus	EVAETQHGTVLV	-	-	-	EVAETQHGTVLV
15.1	Consensus	TEVTNPAVLR	-	-	-	TEVTNPAVLR
16.1	Consensus	SWMVRILIGFL	-	-	-	SWMVRILIGFL
17.1	Consensus	TTMFGGVSWMVR	-	-	-	TTMFGGVSWMVR
18.1	Consensus	GLDFNEMXLL	-	-	-	GLDFNEMXLL
19.1	Consensus	IQTSGTTTIF	-	-	-	IQTSGTTTIF
20.1	Consensus	RLITXNPIV	-	-	-	RLITXNPIV
21.1	Consensus	TALFSGVSWVM	-	-	-	TALFSGVSWVM
22.1	Consensus	HGTIVIRVQY	-	-	-	HGTIVIRVQY
23.1	Consensus	RHVLGRLITV	-	-	-	RHVLGRLITV
24.1	Consensus	SITEAELTGY	-	-	-	SITEAELTGY
25.1	Consensus	STTEAILPEY	-	-	-	STTEAILPEY
26.1	Consensus	KLTNTTTASR	-	-	-	KLTNTTTASR
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

Show 50 rows

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

Add PEPMatch Tool (Cluster Consensus)

1. Add PEPMatch to Pipeline as Cluster Consensus



2

Cluster

Prediction Parameters

Sequence Identity Threshold: 80% (scale 10% – 100%)

Peptide Length(s): No Min – No Max

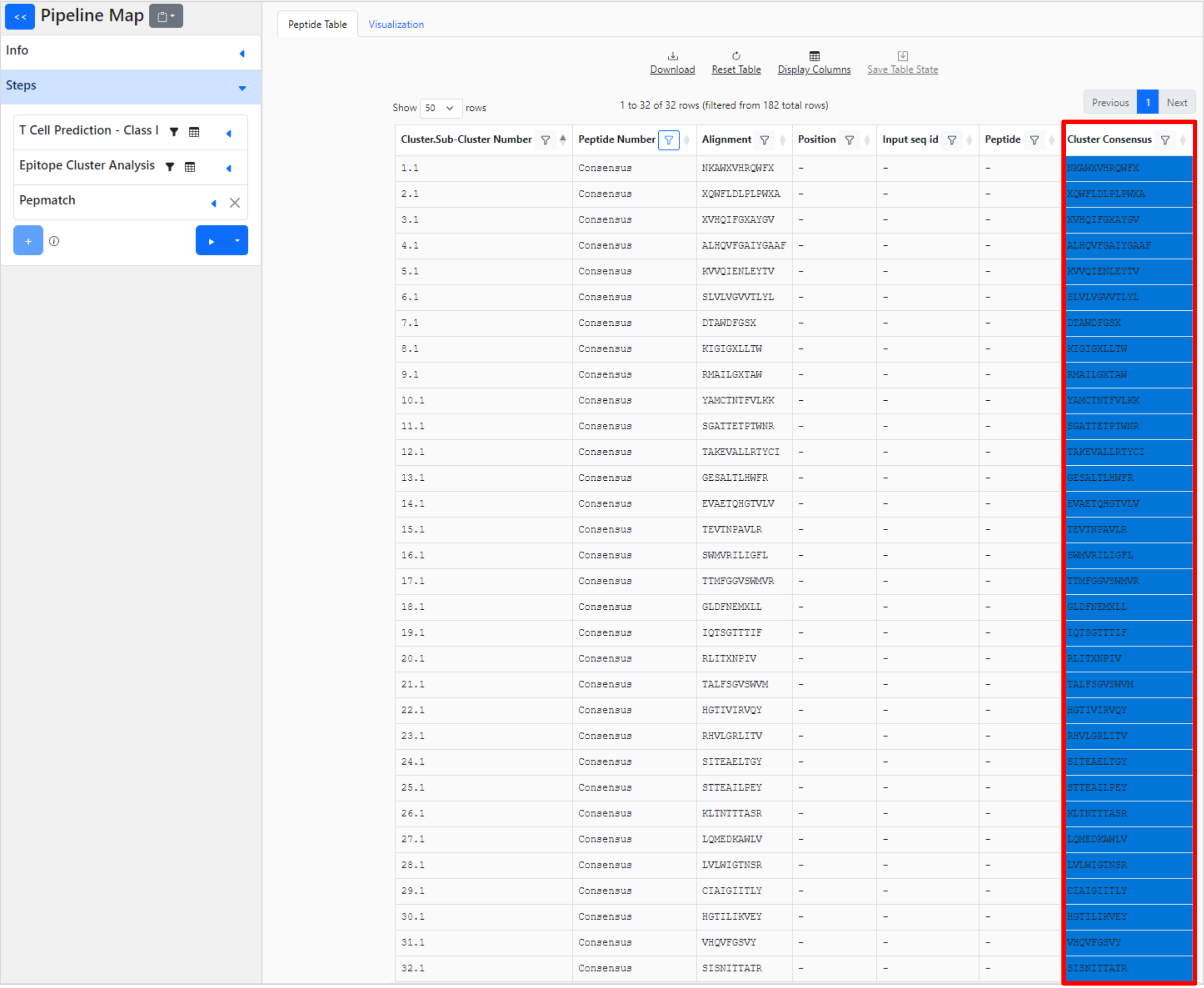
Cluster Method: Cluster-break for clear representative sequence

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	NKAWXVHRQWFX	-	-	-	NKAWXVHRQWFX
2.1	Consensus	XQWFLDLPLPWXA	-	-	-	XQWFLDLPLPWXA
3.1	Consensus	XVHQIFGXAYGV	-	-	-	XVHQIFGXAYGV
4.1	Consensus	ALHQVFGAIYGAAF	-	-	-	ALHQVFGAIYGAAF
5.1	Consensus	KVVQIENLEYTV	-	-	-	KVVQIENLEYTV
6.1	Consensus	SLVLVGVVTLYL	-	-	-	SLVLVGVVTLYL
7.1	Consensus	DTAWDFGSX	-	-	-	DTAWDFGSX
8.1	Consensus	KIGIGXLLTW	-	-	-	KIGIGXLLTW
9.1	Consensus	RMAILGXTAW	-	-	-	RMAILGXTAW
10.1	Consensus	YAMCTNTFVLKK	-	-	-	YAMCTNTFVLKK
11.1	Consensus	SGATTETPTWNR	-	-	-	SGATTETPTWNR
12.1	Consensus	TAKEVALLRTYCI	-	-	-	TAKEVALLRTYCI
13.1	Consensus	GESALTLHWFR	-	-	-	GESALTLHWFR

Add Cluster Tool (Peptide)

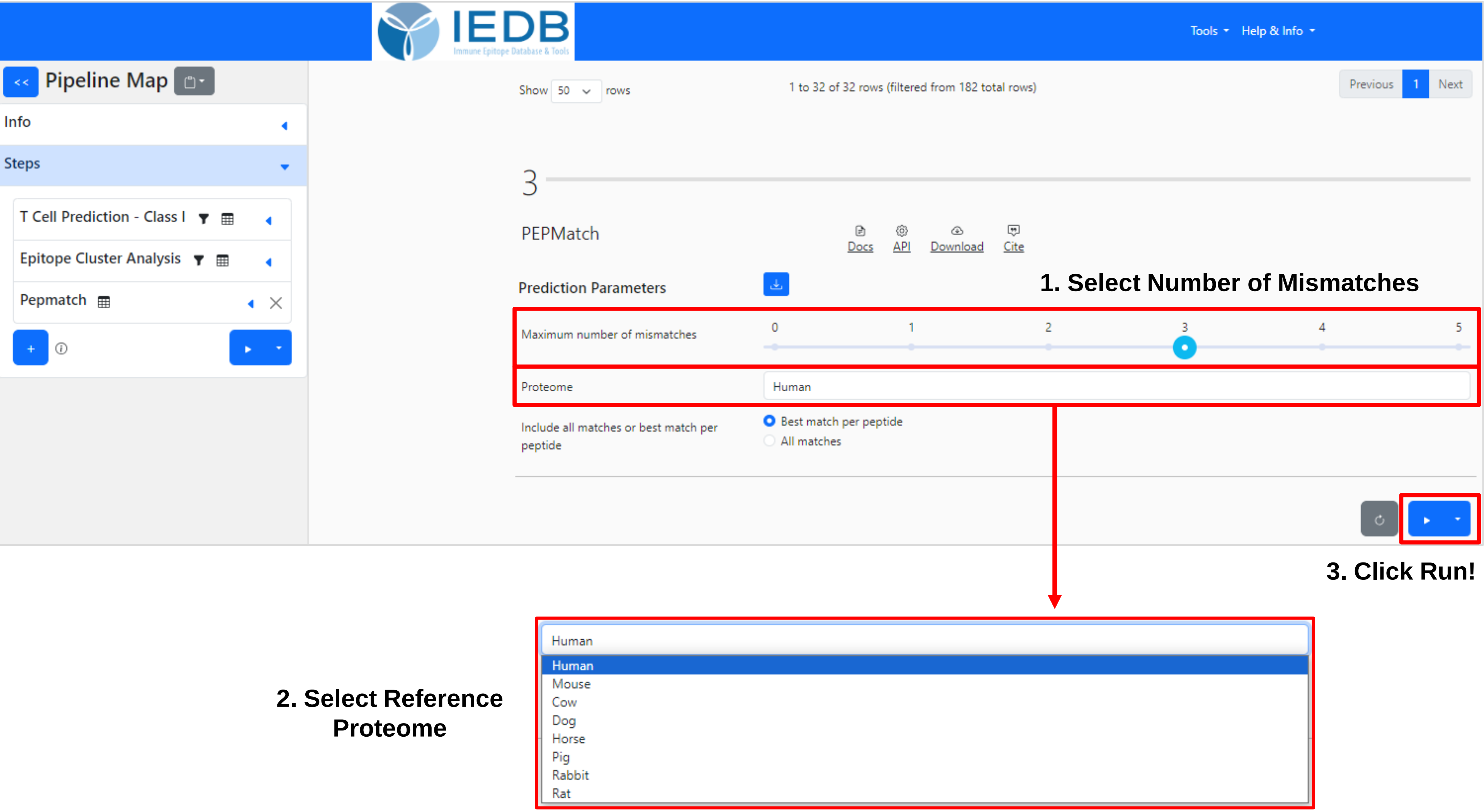


1 to 32 of 32 rows (filtered from 182 total rows)

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Input seq id	Peptide	Cluster Consensus
1.1	Consensus	NKAWXVHRQWFX	-	-	-	NKAWXVHRQWFX
2.1	Consensus	XQWFLDLPLPWXA	-	-	-	XQWFLDLPLPWXA
3.1	Consensus	XVHQIFGXAYGV	-	-	-	XVHQIFGXAYGV
4.1	Consensus	ALHQVFGAIYGAAF	-	-	-	ALHQVFGAIYGAAF
5.1	Consensus	KVVQIENLEYTV	-	-	-	KVVQIENLEYTV
6.1	Consensus	SLVLVGVVTLYL	-	-	-	SLVLVGVVTLYL
7.1	Consensus	DTAWDFGSX	-	-	-	DTAWDFGSX
8.1	Consensus	KIGIGXLLTW	-	-	-	KIGIGXLLTW
9.1	Consensus	RMAILGXTAW	-	-	-	RMAILGXTAW
10.1	Consensus	YAMCTNTFVLKK	-	-	-	YAMCTNTFVLKK
11.1	Consensus	SGATTETPTWNR	-	-	-	SGATTETPTWNR
12.1	Consensus	TAKEVALLRTYCI	-	-	-	TAKEVALLRTYCI
13.1	Consensus	GESALTLHWFR	-	-	-	GESALTLHWFR
14.1	Consensus	EVAETQHGTVLV	-	-	-	EVAETQHGTVLV
15.1	Consensus	TEVTNPAVLR	-	-	-	TEVTNPAVLR
16.1	Consensus	SWMVRILIGFL	-	-	-	SWMVRILIGFL
17.1	Consensus	TTMFGGVSWMVR	-	-	-	TTMFGGVSWMVR
18.1	Consensus	GLDFNEMXLL	-	-	-	GLDFNEMXLL
19.1	Consensus	IQTSGTTTIF	-	-	-	IQTSGTTTIF
20.1	Consensus	RLITXNPIV	-	-	-	RLITXNPIV
21.1	Consensus	TALFSGVSWVM	-	-	-	TALFSGVSWVM
22.1	Consensus	HGTIVIRVQY	-	-	-	HGTIVIRVQY
23.1	Consensus	RHVLGRLITV	-	-	-	RHVLGRLITV
24.1	Consensus	SITEAELTGY	-	-	-	SITEAELTGY
25.1	Consensus	STTEAILPEY	-	-	-	STTEAILPEY
26.1	Consensus	KLTNTTTASR	-	-	-	KLTNTTTASR
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



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

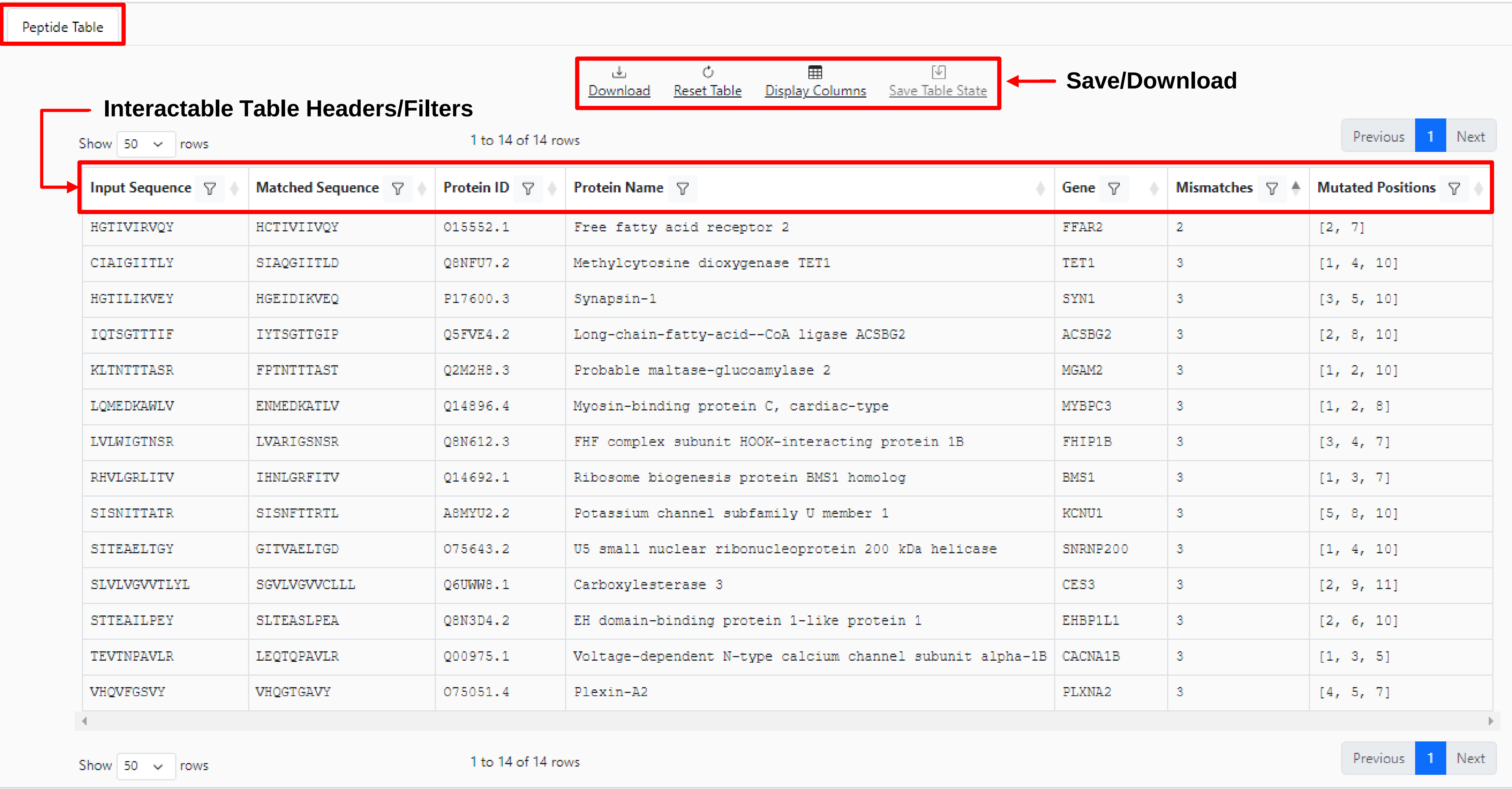
Human
- Human
- Mouse
- Cow
- Dog
- Horse
- Pig
- Rabbit
- Rat

1. Select Number of Mismatches

2. Select Reference Proteome

3. Click Run!

PEPMatch Results – Peptide Table



Save/Download

Interactable Table Headers/Filters

1 to 14 of 14 rows

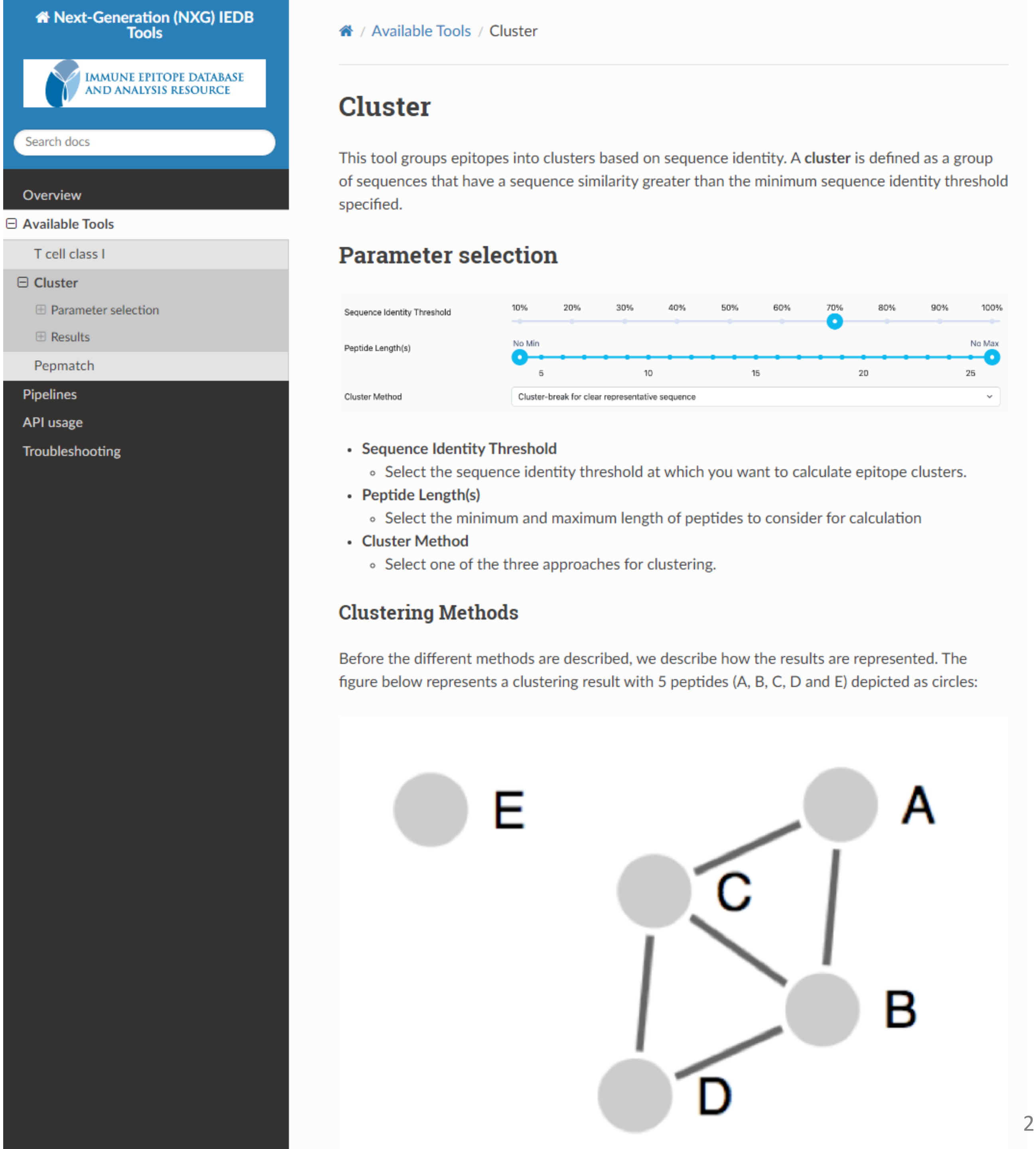
Input Sequence	Matched Sequence	Protein ID	Protein Name	Gene	Mismatches	Mutated Positions
HGTIVIRVQY	HCTIVIIVQY	O15552.1	Free fatty acid receptor 2	FFAR2	2	[2, 7]
CIAIGIITLY	SIAQGIITLD	Q8NFU7.2	Methylcytosine dioxygenase TET1	TET1	3	[1, 4, 10]
HGTILIKVEY	HGEIDIKVEQ	P17600.3	Synapsin-1	SYN1	3	[3, 5, 10]
IQTSGTTTIF	IYTSGTTGIP	Q5FVE4.2	Long-chain-fatty-acid--CoA ligase ACSBG2	ACSBG2	3	[2, 8, 10]
KLTNTTTASR	FPTNTTTAST	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	SISNFTTRTL	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]
SLVLVGVVTLYL	SGVLVGVVCLLL	Q6UWW8.1	Carboxylesterase 3	CES3	3	[2, 9, 11]
STTEAILPEY	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]

1 to 14 of 14 rows

Help Documentation

Cluster Tool

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

Available Tools / Cluster

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: 70%

Peptide Length(s): No Min – No Max

Cluster Method: Cluster-break for clear representative sequence

- **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.

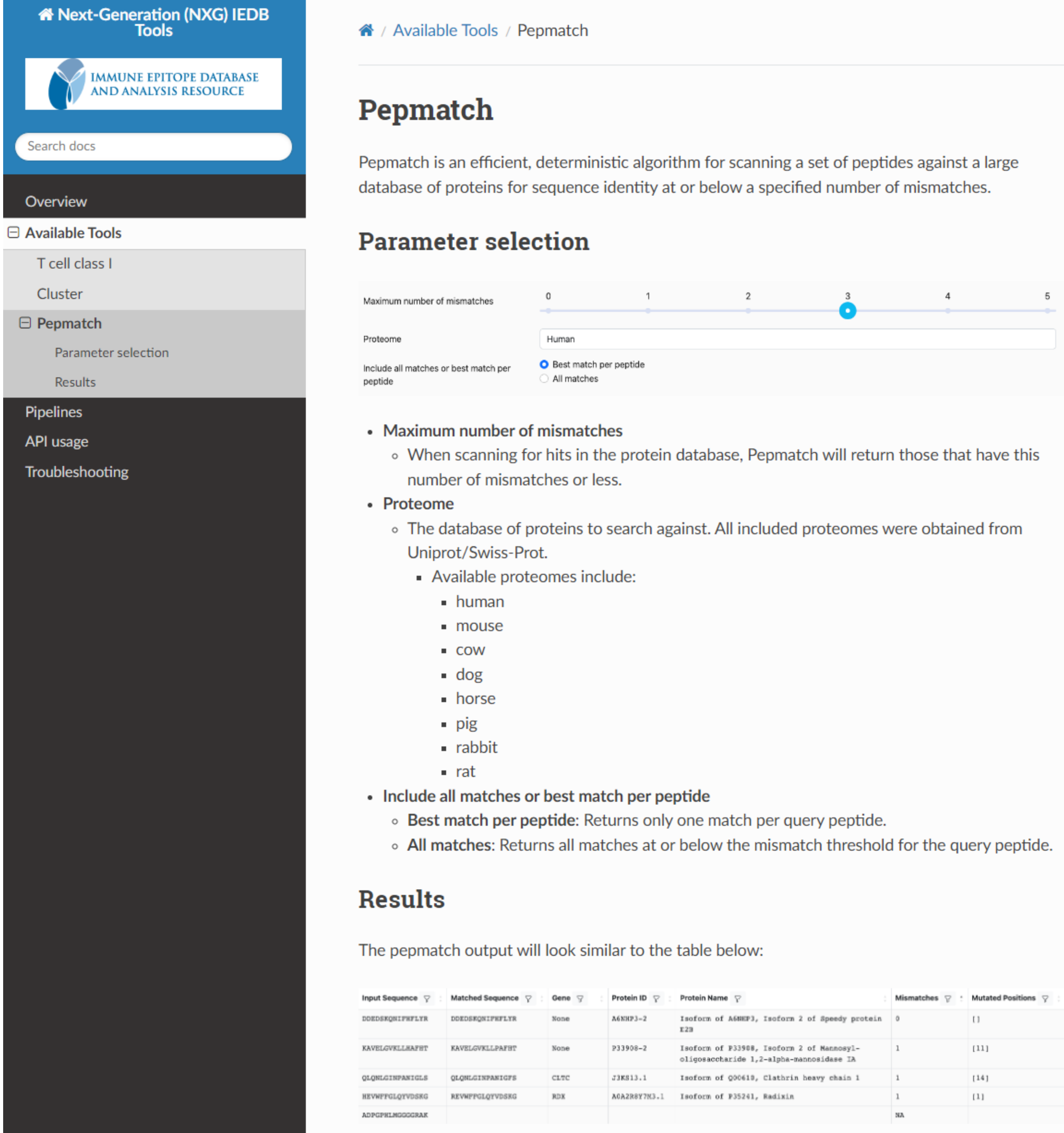
Clustering Methods

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



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
DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYR	None	A6NHP3-2	Isoform of A6NHP3, Isoform 2 of Speedy protein E2B	0	[]
KAVELGVKLLHAFHT	KAVELGVKLLPAFHT	None	P33908-2	Isoform of P33908, Isoform 2 of Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	1	[11]
QLQNLGINPANIGLS	QLQNLGINPANIGFS	CLTC	J3KS13.1	Isoform of Q00610, Clathrin heavy chain 1	1	[14]
HEVWFFGLQYVDSKG	REVWFFGLQYVDSKG	RDX	A0A2R8Y7N3.1	Isoform of P35241, Radixin	1	[1]
ADPGPHLMGGGGRAK					NA	

Plans and Timeline

Planned releases

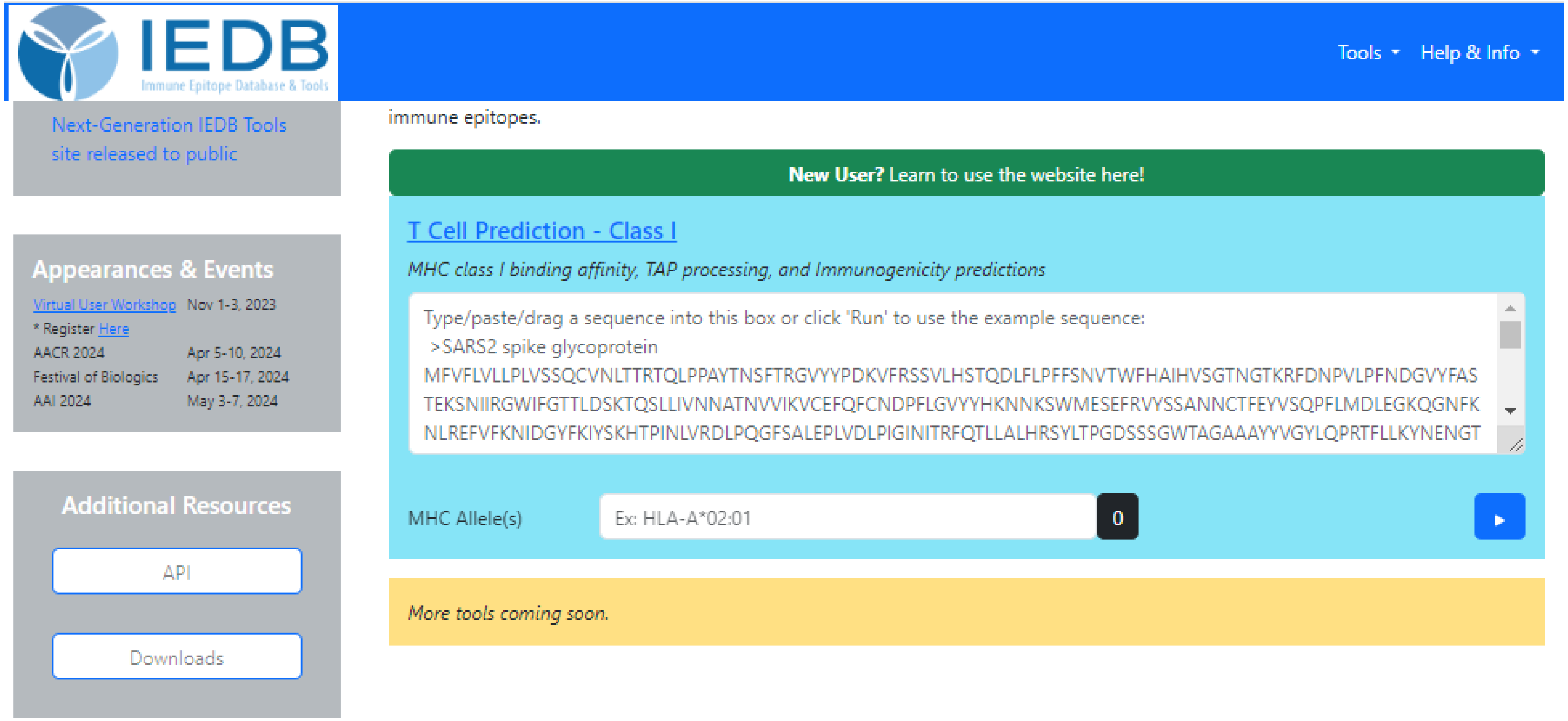
- 1.1 – completed October 2023
  - Migration of backend to a compute cluster
- 1.2 - target November 2023
  - MHC-NP integration
- 2.0 - target March 2024
  - Cancer-focused functionality
    - Peptide expression estimator (PepX)
    - Mutated peptide generation
    - Paired wild-type and mutant peptide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



Next-Generation IEDB Tools site released to public

Appearances & Events

Virtual User Workshop	Nov 1-3, 2023
* Register Here	
AACR 2024	Apr 5-10, 2024
Festival of Biologics	Apr 15-17, 2024
AAI 2024	May 3-7, 2024

Additional Resources

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
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFAS
TEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFK
NLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGT

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

More tools coming soon.