



IEDB-AR 3.0: The Future of Tools

An integrated analysis platform

Presented by: J. Greenbaum, Bioinformatics Core Director

Outline

- Motivations and vision
- Live demo
- Plans and timeline
- The team

Motivations: Why a redesign?

- Site navigation needs improvement
- No linkage between/among current tools
- Inconsistencies among tools
- Outdated layout and aesthetics
- We can do better!

What is the vision?

- **A complete re-thinking of the user experience**
 - Users should feel at home and have immediate understanding
 - Power users should be able to perform complex workflows
- **Emphasis on:**
 - Navigation
 - Simplicity
 - Consistency
 - Integration
 - Speed
- **Drawing upon familiar paradigms**
 - REST APIs
 - JSON
 - Jupyter

Live demo!

AR 3.0 prototype:

<https://iedb-ar-prototype-dev.lji.org>

Plans and timeline

- **Other planned features**
 - API access packages
 - Parity with standalone tools
 - Curated pipelines
 - High performance cluster backend and queuing system
- **Key dates**
 - Cluster backend and beta release – Early 2023
 - Remaining tools to follow

IEDB AR Redesign Team

Lead developers

Front end: Kevin Kim

Back end: Zhen (Jason) Yan

Core contributors

Haeuk Kim

Brendan Ha

Anaïs Gambiez

Team lead

Jason Greenbaum

Project owner

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UI/UX consultants

Ali Haskins-Lisle

Joe Gabbard

Project management

Nina Blazeska

Additional contributors

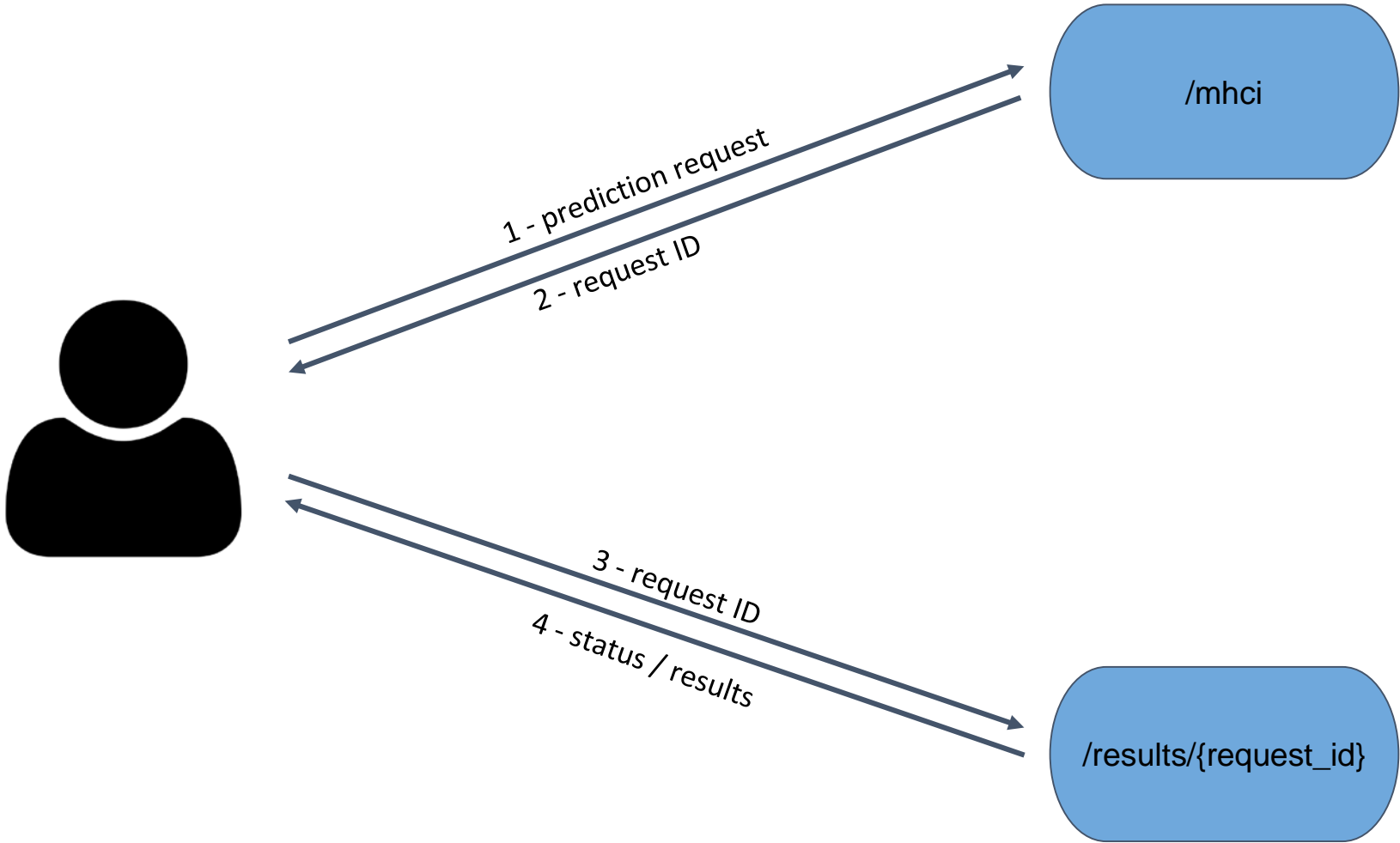
Morten Nielsen

Michael Talbott

Dan Marrama

Backup API slides

Complex jobs with simple API calls



'/mhci' endpoint allows for multiple predictors and returns request ID

POST

```
{
  "input_sequence_object_id": "",
  "input_peptide_object_id": "",
  "input_sequence_text": ">LCMV Armstrong, Prot",
  "alleles": "HLA-A*02:01,HLA-A*03:01",
  "lengths": "8,9,10,11",
  "predictors": [
    {
      "type": "binding",
      "method": "smmpmbec"
    },
    {
      "type": "binding",
      "method": "smm"
    },
    {
      "type": "processing",
      "method": "immuno",
      "max_precursor_extension": 2,
      "alpha_factor": 2
    },
    {
      "type": "immunogenicity",
      "position_to_mask": "2,5,9"
    }
  ]
}
```

Success! 🙌

```
{
  "request_id": 1580506465,
  "results_uri": "https://api.iedb.org/get_results/1580506465",
  "data": {
    "allele_list_id": 1580506466,
    "sequence_list_id": 1580506467,
    "parameter_set_id": 1580506468,
    "peptide_list_id": 1580506469,
    "allele_list_uri": "https://api.iedb.org/get_object/1580506466",
    "sequence_list_uri": "https://api.iedb.org/get_object/1580506467",
    "parameter_set_uri": "https://api.iedb.org/get_object/1580506468",
    "peptide_list_uri": "https://api.iedb.org/get_object/1580506469",
  }
}
```

Validation error 😞

```
{
  "request_id": 1580506465,
  "error": [
    "sequence 2 contains X in postion 56",
    "allele name 'HLA-S-8282' is invalid"
  ]
}
```

Request status and results retrieved through 'get_results/' endpoint

Nice! 😊

Waiting... 🕒

```
{
  "request_id": 1580506465,
  "results_uri": "https://api.iedb.org/get_results/1580506465",
  "warning": "",
  "error": "",
  "status": "queued",
  "results": {}
}
```

Error 🚫

```
{
  "request_id": 1580506465,
  "results_uri": "https://api.iedb.org/get_results/1580506465",
  "warning": "",
  "error": "Execution failed for unknown reason. If the issue pe",
  "status": "error",
  "results": {}
}
```

```
{
  "request_id": 1580506465,
  "results_uri": "https://api.iedb.org/get_results/1580506465",
  "warning": "",
  "error": "",
  "status": "completed",
  "results": {
    "columns": [
      { "name": "sequence_number", "type": "int", "source": "core",
      { "name": "peptide", "type": "text", "source": "core", "sort_o
      { "name": "stop", "type": "int", "source": "core", "sort_order
      { "name": "start", "type": "int", "source": "core", "sort_orde
      { "name": "score", "type": "float", "source": "binding.smm", "
      { "name": "percentile", "type": "float", "source": "binding.sm
      { "name": "allele", "type": "text", "source": "core", "sort_or
    ],
    "peptide_table": [
      [ "GQIVTMFEA", 10, 2, 398.20, 4.2, "HLA-A*02:01", 1 ],
      [ "VTMFEALPH", 13, 5, 1904.58, 4.2, "HLA-A*03:01", 1 ],
      [ "QIVTMFEAL", 11, 3, 2449.68, 13, "HLA-A*02:01", 1 ],
      [ "IVTMFEALP", 12, 4, 23648.30, 21, "HLA-A*03:01", 1 ],
      [ "VTMFEALPH", 13, 5, 35901.28, 36, "HLA-A*02:01", 1 ],
      [ "IVTMFEALP", 12, 4, 36317.00, 36, "HLA-A*02:01", 1 ],
      [ "MGQIVTMFE", 9, 1, 84878.95, 38, "HLA-A*03:01", 1 ],
      [ "QIVTMFEAL", 11, 3, 24108.06, 45, "HLA-A*03:01", 1 ],
      [ "GQIVTMFEA", 10, 2, 265338.33, 57, "HLA-A*03:01", 1 ],
      [ "MGQIVTMFE", 9, 1, 483181.16, 68, "HLA-A*02:01", 1 ]
    ],
    "allele_confidence_score": [
      { "allele": "HLA-A*02:01", "netmhcpan_confidence": 25},
      { "allele": "HLA-A*03:01", "netmhcpan_confidence": 325}
    ]
  }
}
```

Backup Screenshots Below

Welcome to the Immune Epitope Analysis Resource!

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

Predicts binding affinity between T cells and MHC



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

```
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFND
GVYFASTKSNIRGWIFGTTLDSKTQSLIVNATNVVIKVEFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL
MDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLTGPDSSSGWTAGAAAAY
```

MHC Allele(s)

Ex: HLA-A*02:01

0



B Cell Prediction

Predicts antibody epitopes from protein sequences



Announcements

AR v2.21 Release Notes
Publication

Appearances & Events

User Workshop Nov 7-8
Antibody Society Dec 9-13
AAAAI 2020 Mar 11-15
AAI 2020 May 13-16

Additional Resources

API

Benchmarking

Downloads

1

T Cell Prediction - Class I

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

Input Sequence(s)



```
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCIVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNAT
NVVIVKCEQFCNDPFLGVVYHKNKNSWMESEFRVYSSANNCTFEYVQPFMDLEGKQGNFNKLNREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYL
TPGDSSSGWTAGAAAYVGYLQPRTEFLLYKYNENGTITDAVDCALDPLSETKCTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSAS
FSTFKCYGVSPKLNLDLCTNVYADSFVIRGDEVRQIAPGQTKIADYNYKLPDDFTGCVIAWNSNLDLDSKVGNNYNYLRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYG
FQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
VPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPRRARSVASQSIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGD
STECNLLLLQYGSFCTQLNRALTGIAVEQDKNTQEVAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLCAQKFNGTLVLPPLLTDEMAIQ
YTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAIGIKQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLDILSRLDKVEAEVQIDRLI
TGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSMFPQSAPHGVVFLHVTVVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDN
```

1 sequence, 1,273 aa

Prediction Parameters



Peptide Length(s)



MHC Allele(s)

Ex: HLA-A*02:01

Allele Finder

HLA-A*02:01

1 allele(s)

Prediction Model(s)

Prediction Model(s)



MHC-I Binding

Prediction Method

IEDB recommended 2020.04 (NetMHCpan EL 4.1)



Add Another Prediction

Reset

Run

Peptide Table

NetMHCpan Allele Distance

Sequence Table

Download

Reset Table

Display Columns

Save Table State

Show 50 rows

1 to 50 of 1,265 rows

Previous 1 2 3 4 5 ... 26 Next

seq #	peptide	peptide length	start	end	allele	netmhcpa_n_el core	netmhcpa_n_el icore	netm
1	YLQPRTFLL	9	269	277	HLA-A*02:01	YLQPRTFLL	YLQPRTFLL	
1	VLNDILSRL	9	976	984	HLA-A*02:01	VLNDILSRL	VLNDILSRL	
1	TLDSKTQSL	9	109	117	HLA-A*02:01	TLDSKTQSL	TLDSKTQSL	
1	RLQSLQTYV	9	1000	1008	HLA-A*02:01	RLQSLQTYV	RLQSLQTYV	
1	KIADYNYKL	9	417	425	HLA-A*02:01	KIADYNYKL	KIADYNYKL	

T Cell Prediction - Class I

Input Sequence(s)



Download as: [JSON](#) [FASTA](#) [Original](#)

```
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSF...HVSGTNG
NVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNID
TPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKGIYQTSNFRVQPTES
FSTFKCYGVSPTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGN
FQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIAD
VPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYT
STECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLF
YTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKL
TGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQI
```

```
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNV
TWFAIHVSGTNGTKRFDNPLPFNDGVYFASTEKSNIIIRGWFISGTTLDLSDKTSLLIVNNT
NVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNF
KNLREFVFNIDGYFKIYKHTPTINLVRDLPGFSALEPLVDLPIGINITRFQTLALHRSY
LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEK
GIYQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLYNSA
SFSTFKCYGVSPTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVI
AWNSNNLDSKVGGNYNYLYRLFRKSNLKPFFERDITSTEIYQAGSTPCNGVEGFNCYFPLQSYG
FQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKK
FLPFQFGRDIADTTDAVRDPQTLILDITPCSFGGVSVITPGTNTSNQVAVLYQDNCVTEF
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPR
RARSVASQSIIAYTMSLGAENSVAYSNSIAIPNFTISVTTTEILPVSMTKTSVDCTMYICG
DSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQIL
PDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDI AARDL ICAQKFNGLTVLPLL TDE
MIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSA
IGKIQDLSSTASALGKLQDVVNQAALNLTVKQLSSNFGAISSVLNDILSRLDKVEAEVQ
IDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQ
SAPHGVVFLHVTYVPAQEKNFPTTAPAICHGDKAHPREGVYVSNGTHWFVTRQNFYEPQIIT
TDNTFVSGNCDVVI GIVNNTVYDPLQPELDSFKEELDKYFNHTSPDVLGDISGINASVNV
IQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT
```


Prediction Parameters

Peptide Length(s)



8

9



```
{
  "alleles": "HLA-A*02:01",
  "peptide_length_range": [
    9,
    9
  ],
  "predictors": [
    {
      "type": "binding",
      "method": "netmhcpan_el"
    }
  ]
}
```

T Cell Prediction - Class I

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

Input Sequence(s)



```
>gi|9626686|ref|NP_059433.1| polyprotein [Dengue virus 1]
MNNQRKKTGRPSFNMLKRARNRVSTVSQLAKRFSKGLLSGQGPMKLVMAFIAFLRFLAIPPTAGILARWG
SFKKNGAIKVLRGFKKEISNMLNIMNRRKRSVTMLLMLLPTALAFHLTTRGGEPHMIVSKQERGKSLLFK
TSAGVNMCTLIAMD LGELCEDTMYKCPRITETEPDDVDCWCNATETWVTYGTCSQTGEHRRDKRSVALA
>gi|319748454|gb|ADV71219.1| polyprotein, partial [Dengue virus 2]
MNNQRKKARSTPFNMLKRERNRVSTVQQLTKRFSGLMLQGRGPLKLFMALVAFLRFLTIPPTAGILKRWG
TIKSKAINVLRGFRKEIGRMLNILNRRRTAGVIIMLIPTAMAFHLTTRNGEPHMIVGRQEKGKSLLFK
TEDGVNMCTLMAIDL GELCEDTITYKCPLLRQNEPEDIDCWCNSTSTWVTYGTCTTTGEHRRKRSVALV
>gi|163644369|ref|YP_001621843.1| polyprotein [Dengue virus 3]
MNNQRKKTGKPSINMLKRVRNRVSTGSQLAKRFSKGLLNGQGPMKLVMAFIAFLRFLAIPPTAGVRLARWG
```

4 sequence, 840 aa

Parameter changed since prediction.

Prediction Parameters



Peptide Length(s)



MHC Allele(s)

Ex: HLA-A*02:01

Allele Finder

Parameter changed since prediction.

HLA-A*02:01 HLA-A*01:01

2 allele(s)

☰ MHC-I Binding Prediction Method SMMPMBEC ✕

☰ MHC-I Binding Prediction Method CombLib_Sidney2008 ✕

☰ Class I pMHC Immunogenicity Positions To Mask 1,2,C Terminal (Default) ✕

MHC-I Processing Prediction Method NetCTLpan ✕

☰ Weight on C terminal cleavage 0.000 0.225 0.500 1.000

Weight on TAP transport efficiency 0.025 0.000 0.500 1.000

Percentile Rank Threshold 1.0 0.0 50.0 100.0

Reset

Cancel Run

Warnings (1)

1. allele HLA-A*01:01 is not available for method complib_sidney2008



Calculating results, please wait... Click [here](#) to receive email.

Download Reset Table Display Columns Save Table State

Show 10 rows 1 to 10 of 1,616 rows

Previous 1 2 3 4 5 ... 162 Next

seq #	peptide	peptide length	start	end	allele	median binding percentile	complib_sidney2008 score	complib_sidney2008 percentile	smpmbec score	smpmbec percentile
2	NSTSTWVTY	9	183	191	HLA-A*01:01	0.3			319.4626	
4	TLCLLIPTV	9	103	111	HLA-A*02:01	0.4	0.0000	0.5	10.2903	
3	CLMMILPAA	9	104	112	HLA-A*02:01	1.15	0.0000	1.8	25.7887	
1	LVMAPIAFL	9	46	54	HLA-A*02:01	1.15	0.0000	1.8	24.4023	
3	LVMAPIAFL	9	46	54	HLA-A*02:01	1.15	0.0000	1.8	24.4023	
4	NLTSTWVHY	9	182	190	HLA-A*01:01	1.2			1192.3946	
4	LFTSTWVHYG	9	183	191	HLA-A*01:01	1.3			1347.1625	
2	LLFKYEDCV	9	137	145	HLA-A*02:01	1.55	0.0000	1.5	95.1546	
1	NATETWVTY	9	183	191	HLA-A*01:01	1.6			1699.8868	

mmpmbec score	smpmbec percentile	immunogenicity score	NetCTLpan cleavage prediction score	NetCTLpan combined score	NetCTLpan MHC score	NetCTLpan percentile rank	NetCTLpan tap score
319.4626	0.3	0.14996	0.97363	0.69204	0.39900	0.30	2.95900
10.2903	0.3	0.06995	0.95595	1.09626	0.87200	0.10	0.36700
25.7887	0.5	-0.10104	0.06596	0.58974	0.58600	4.00	-0.44400
24.4023	0.5	0.32307	0.91289	1.02897	0.79200	0.15	1.26300
24.4023	0.5	0.32307	0.91289	1.02897	0.79200	0.15	1.26300
1192.3946	1.2	0.02468	0.97687	0.53725	0.24400	0.80	2.93800
1347.1625	1.3	0.08956	0.29092	0.18856	0.15500	32.00	-1.27600
95.1546	1.6	-0.00843	0.49290	0.72950	0.60600	2.00	0.50400
1699.8868	1.6	0.41718	0.97826	0.47738	0.18300	1.50	2.97100
1821.4615	1.7	0.27052	0.25266	0.14195	0.11700	50.00	-1.27600

Pipeline Name and Email



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

Pipeline Name

workshop demo

Email

jgbaum@lji.org

Submit

	median binding percentile	comblib_
01		
01		
01		
01		
01		
01		
01		

Sort A→Z

Sort Z→A

Min:

Max:

Clear OK

Select Columns to Display



Core

- seq #** the index of sequence
- peptide** peptide sequence
- peptide length** The length of peptide
- start** The peptide's starting point from the sequence
- end** The peptide's stop point from the sequence
- allele** one of two, or more, forms of a given gene variant
- peptide index** the index of peptide

Binding

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

Binding Comblib_sidney2008

- comblib_sidney2008 score** binding prediction score which indicates binding affinity
- comblib_sidney2008 percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Binding Smpmbec

- smpmbec score** binding prediction score which indicates binding affinity
- smpmbec percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Immunogenicity

- immunogenicity score** The higher score indicates a greater probability of eliciting an immune response.

Processing Netctlpan

- NetCTLpan cleavage prediction score**
- NetCTLpan combined score** This score combines the proteasomal cleavage, TAP transport and MHC binding predictions.
- NetCTLpan MHC score** The MHC binding prediction is identical to the Class-I. And the output is $-\log(\text{IC}_{50})$ values.
- NetCTLpan percentile rank**
- NetCTLpan tap score** The TAP score estimates an effective $-\log(\text{IC}_{50})$ values for the binding to TAP of a peptide or its N-terminal prolonged precursors.

Reset

Display

Select Columns to Display



Core

- seq #** the index of sequence
- peptide** peptide sequence
- peptide length** The length of peptide
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Binding

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

Binding Comblib_sidney2008

- comblib_sidney2008 score** binding prediction score which indicates binding affinity
- comblib_sidney2008 percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Binding Smpmbec

- smpmbec score** binding prediction score which indicates binding affinity
- smpmbec percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Immunogenicity

- immunogenicity score** The higher score indicates a greater probability of eliciting an immune response.

Processing Netctlpan

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- NetCTLpan percentile rank**
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Reset

Display

seq #	peptide	peptide length	start	end	allele	median binding percentile	comblib_sidney2008 score	co
2	NSTSTWVTY	9	183	191	HLA-A*01:01	0.3		
4	TLLCLIPTV	9	103	111	HLA-A*02:01	0.4	0.0000	
3	CLMMILPAA	9	104	112	HLA-A*02:01	1.15	0.0000	
1	LVMAFIAFL	9	46	54	HLA-A*02:01	1.15	0.0000	
3	LVMAFIAFL	9	46	54	HLA-A*02:01	1.15	0.0000	
4	NLTSTWVMY	9	182	190	HLA-A*01:01	1.2		
4	LTSTWVMYG	9	183	191	HLA-A*01:01	1.3		
2	LLFKTEDGV	9	137	145	HLA-A*02:01	1.55	0.0000	
1	NATETWVTY	9	183	191	HLA-A*01:01	1.6		
3	LTSTWVTYG	9	184	192	HLA-A*01:01	1.7		

peptide	peptide length	allele	median binding percentile	comblib_sidney2008 score	smpmpec score	immunogenicity score
NSTSTWVTY	9	HLA-A*01:01	0.3		319.4626	
TLLCLIPTV	9	HLA-A*02:01	0.4	0.0000	10.2903	
CLMMILPAA	9	HLA-A*02:01	1.15	0.0000	25.7887	
LVMAFIAFL	9	HLA-A*02:01	1.15	0.0000	24.4023	
LVMAFIAFL	9	HLA-A*02:01	1.15	0.0000	24.4023	
NLTSTWVMY	9	HLA-A*01:01	1.2		1192.3946	
LTSTWVMYG	9	HLA-A*01:01	1.3		1347.1625	
LLFKTEDGV	9	HLA-A*02:01	1.55	0.0000	95.1546	
NATETWVTY	9	HLA-A*01:01	1.6		1699.8868	

Seq #

2

Allele

HLA-A*01:01

Length

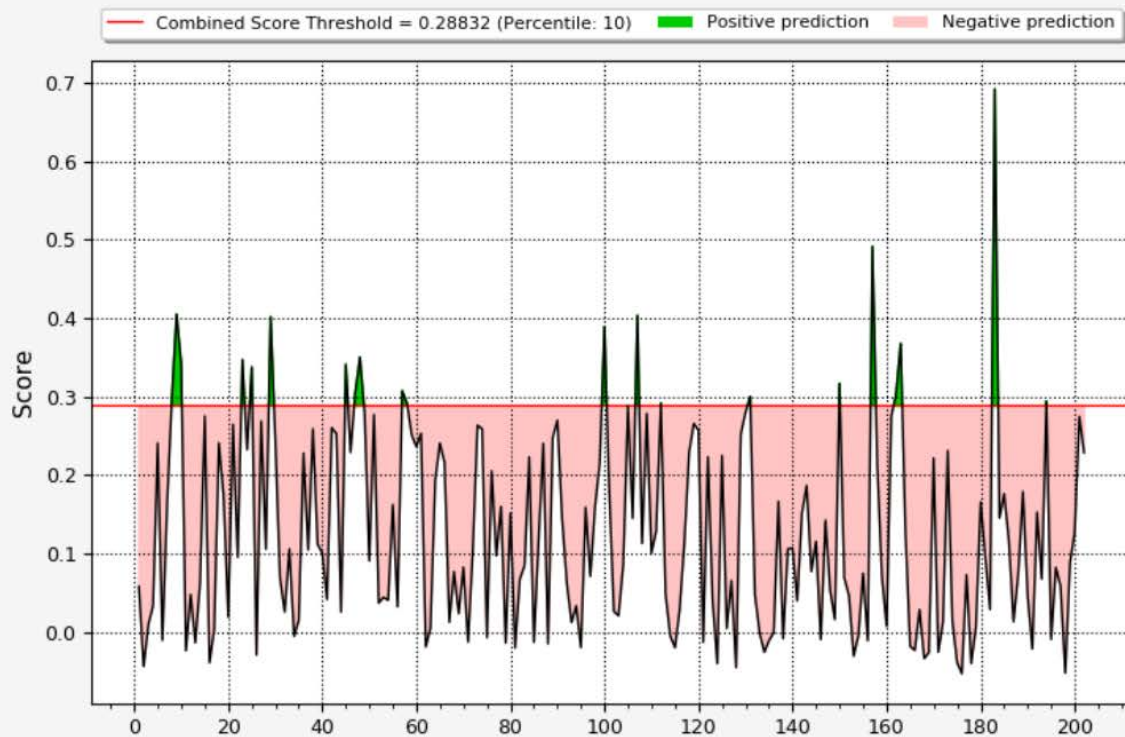
9

processing.netctpan





Percentile Threshold 10

submit

processing.netctpan Prediction



Peptide Table Processing Plots **Sequence Table**

 [Download](#)
 [Reset Table](#)
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Show rows

1 to 4 of 4 rows

Previous **1** Next

seq #	sequence name	sequence
1	gi 9626686 ref NP_059433.1 polyprotein [Dengue virus 1]	MNNQRKKTGRPSFNMLKRARNRVSTVSQLAKRFSKGLLSGQGPMLVMAFIAFLRFLAIPPTAGILARWGSFKKNGAIKVLGRFKKEISNMLNIMNRRKRSVTMLMLLPTA LAFHLTRRGEPHMIVSKQERGKSLLFKTSAGVNMCTLIAMDGLGELCEDTMTYKCPRIETETEPDDVDCWCNATETWVTYGTCSTQTEHRRDKRSVALA
2	gi 319748454 gb ADV71219.1 polyprotein, partial [Dengue virus 2]	MNNQRKKARSTPFNMLKRERNRVSTVQQLTKRFSGLMLQGRGPLKLFMALVAFLRFLTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLNILNRRRRTAGVIIMLIPTA MAFHLTRNGEPHMIVGRQEKGSLLFKTEDGVNMCTLMAIDLGELCEDTITYKPLLRQNEPEDIDWCNSTSTWVTYGTCSTTTEHRRDKRSVALV
3	gi 163644369 ref YP_001621843.1 polyprotein [Dengue virus 3]	MNNQRKKTGKPSINMLKRVRNRVSTGSQLAKRFSKGLLNGQGPMLVMAFIAFLRFLAIPPTAGVLARWGTFFKSGAIKVLKGFKEISNMLSIIINQRKTSLSCLMMILPAA LAFHLTSRDGEPRMIVGKNERGKSLLFKTSAGINMCTLIAMDGEMCDDTIVTYKCPHITVEPEPIDWCNLTSTWVTYGTCNQAGEHRRDKRSVALA
4	gi 444892655 gb AGE13482.1 polyprotein [Dengue virus 4]	MNQRKKVVRPPFNMLKRERNRVSTPQGLVKRFSTGLFSGKPLRMVLAFITFLRVLSIPPTAGILKRWGQLKKNKAIKILIGFRKEIGRMLNILNRRRRTMTLLCLIPTVM AFHLSTRDGEPLMIVAKHERGRPLLFKTTTEGINKCTLIAMDGEMCEDTIVTYKPLLVTNEPEPIDWCNLTSTWVMYGTCTQSGERRREKRSVALTP

Show rows

1 to 4 of 4 rows

Previous **1** Next

<< Pipeline Map

Info

Steps

T Cell Prediction - Class I

+ add a step to the pipeline

Reset Run

Warnings (1)

Peptide Table Processing Plots Sequence Table

Download
 Reset Table
 Display Columns
 Save Table State

Show 50 rows 1 to 50 of 1,616 rows Previous 1 2 3 4 5 ... 33 Next

seq #	peptide	peptide length	start	end	allele	median binding percentile	comblib_s
2	NSTSTWVTY	9	183	191	HLA-A*01:01	0.3	
4	TLLCLIPTV	9	103	111	HLA-A*02:01	0.4	
3	CLMMILPAA	9	104	112	HLA-A*02:01	1.15	
1	LVMAFIAFL	9	46	54	HLA-A*02:01	1.15	

T Cell Prediction - Class I

+

- Cluster
 - Peptide
- Pepmatch

T Cell Prediction - Class I

Epitope Cluster Analysis

Down

Show 50 rows 1 to 50 c

seq #	peptide	peptide length
2	NSTSTWVTY	
4	TLLCLIPTV	
3	CLMMILPAA	
1	LVMAFIAFL	
3	LVMAFIAFL	
4	NSTSTWVTY	

<< Pipeline Map

Info

Steps

T Cell Prediction - Class I

Epitope Cluster Analysis

4	MVLAFITFL	9	45	53	HLA-A*02:01	2.2
1	LLFKTSAGV	9	137	145	HLA-A*02:01	2.35
1	ELCEDIMTY	9	157	165	HLA-A*01:01	2.4
2	ALVAFRLFL	9	49	57	HLA-A*02:01	2.5
4	EMCEDTPTY	9	156	164	HLA-A*01:01	2.6
2	ELCEDITY	9	157	165	HLA-A*01:01	2.7

Show rows 1 to 50 of 1,616 rows Previous **1** 2 3 4 5 ... 33 Next

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Cluster [Docs](#) [API](#) [Download Tools](#) [Cite](#)

Prediction Parameters

Sequence Identity Threshold





Peptide Length(s)

Cluster Method

Results will load once step is run

Peptide Table

Visualization

 Download
  Reset Table
  Display Columns
  Save Table State

Show rows

1 to 50 of 118 rows

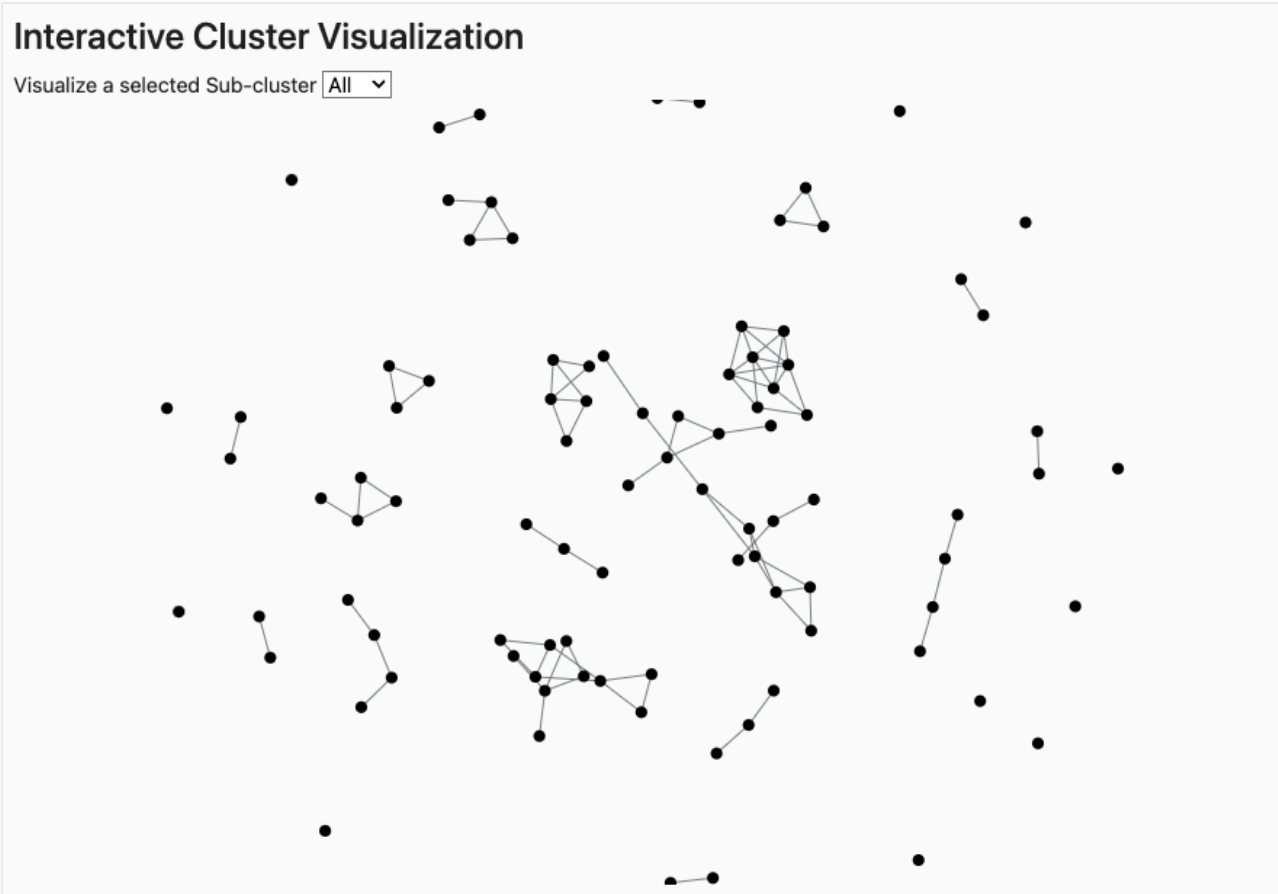
Previous **1** 2 3 Next

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	input seq #	Peptide	Cluster Consensus
1.1	Consensus	RSVTMLLMLLPTALAF	-	-	-	RSVTMLLMLLPTALAF
1.1	1	RSVTMLLM-----	1	57	RSVTMLLM	RSVTMLLMLLPTALAF
1.1	2	-SVTMLLM-----	2	94	SVTMLLM	RSVTMLLMLLPTALAF
1.1	3	--VTMLMLLP-----	3	80	VTMLMLLP	RSVTMLLMLLPTALAF
1.1	4	---TMLMLLP-----	4	28	TMLMLLP	RSVTMLLMLLPTALAF
1.1	5	----MLMLLP-----	5	12	MLMLLP	RSVTMLLMLLPTALAF
1.1	6	-----LLMLLP-----	6	33	LLMLLP	RSVTMLLMLLPTALAF
1.1	7	-----MLLP-----	8	49	MLLP	RSVTMLLMLLPTALAF
1.1	8	-----MLIPTAMAF	8	48	MLIPTAMAF	RSVTMLLMLLPTALAF
1.2	Singleton	CLIPTVMAF	-	71	CLIPTVMAF	CLIPTVMAF

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Interactive Cluster Visualization

Visualize a selected Sub-cluster



Steps

T Cell Prediction - Class I

Epitope Cluster Analysis

+

T Cell Prediction - Class I

- Pepmatch
- Peptide
- Cluster Consensus

20.1	Consensus	ISNMLXIXN	-	-	-	ISNMLXIXN
21.1	Consensus	LXIPPPTAGX	-	-	-	LXIPPPTAGX
22.1	Consensus	LSTRDGEPLMI	-	-	-	LSTRDGEPLMI

Show 50 rows

1 to 22 of 22 rows (filtered from 118 total rows)

Previous 1 Next

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Pepmatch

[Docs](#)
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Prediction Parameters



Maximum number of mismatches



Proteome

Human

Include all matches or best match per peptide

- Best match per peptide
- All matches

Reset

Run

Results will load once step is run

IEDB-AR API Documentation v1.0.0

[Base URL: api-iedb-ar-prototype-dev.lji.org/]
<https://api-iedb-ar-prototype-dev.lji.org/swagger?format=openapi>

Contact Yan

Schemes
HTTPS

Django Login

Authorize

Filter by tag

api

- GET** /api/ api_list
- GET** /api/.*
- POST** /api/.* api_.*_create
- GET** /api/v3 api_v3_list



accept post request to run the MHC I prediction

Parameters

[Try it out](#)

Name	Description
------	-------------

data * *required*

object

(body)

Example Value | Model

```

{
  input_sequence_text string
    default: SLYNTVATLYCVHQRIDV
    input sequences

  input_sequence_format string
    default: auto
    one of these 4 format: fasta, space_separated, named_space_separated, json

  alleles string
    default: HLA-A*01:01
    input alleles

  peptide_length_range integer[]
    peptide lengths (8-15)

  predictors {
    description:
      There are 3 type of predictors "binding", "processing", and "immunogenicity".
      The available parameters for "binding" are: "type", "method".
      The available parameters for "processing" are: "type", "proteasome", "tap_precursor", "tap_alpha".
      The available parameters for "immunogenicity" are: "type", "mask_choice", "position_to_mask".

      And this is an example:
      "predictors": [
        {
          "type": "binding",
          "method": "smmpmbec"
        },
        {
          "type": "binding",
          "method": "smm"
        },
        {
          "type": "processing",
          "proteasome": "immuno",
          "tap_precursor": 1,
          "tap_alpha": 0.2
        },
        {
          "type": "immunogenicity",
          "mask_choice": "custom",
          "position_to_mask": "2,5,9"
        }
      ]
  }
}

```

Parameters

Cancel

Name	Description
------	-------------

result_id * required	
----------------------	--

string	
(path)	

1632240204.4435184-phZj47qd	
-----------------------------	--

Execute

Clear

Responses

Response content type

application/json

Curl

```
curl -X GET "https://api-iedb-ar-prototype-dev.lji.org/api/v3/results/1632240204.4435184-phZj47qd" -H "accept: application/json" -H "X-CSRFToken: fRaTg6FOUQEKOIP5bFJuDDpteAVcAtbf70WsDywNr9bNEdH0YjKZ2AuxcOpRM3TW"
```

Request URL

```
https://api-iedb-ar-prototype-dev.lji.org/api/v3/results/1632240204.4435184-phZj47qd
```

Server response

Code	Details
------	---------

200	
-----	--

Response body

```
{
  "id": "1632240204.4435184-phZj47qd",
  "type": "result",
  "data": {
    "results": {
      "columns": [
        {
          "name": "sequence_number",
          "type": "int",
          "hidden": false,
          "source": "core",
          "sort_order": 0,
          "description": "the index of sequence",
          "display_name": "seq #",
          "default_order": null,
          "row_sort_priority": null
        },
        {
          "name": "peptide",
          "type": "text",
```