IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

IEDB-AR 3.0: The Future of Tools

An integrated analysis platform

Presented by: J. Greenbaum, Bioinformatics Core Director

Outline

- Motivations and vision
- Lifecycle of a mhci prediction request
- Live demo!
- Tool integration (pipelines)
- Plans and timeline

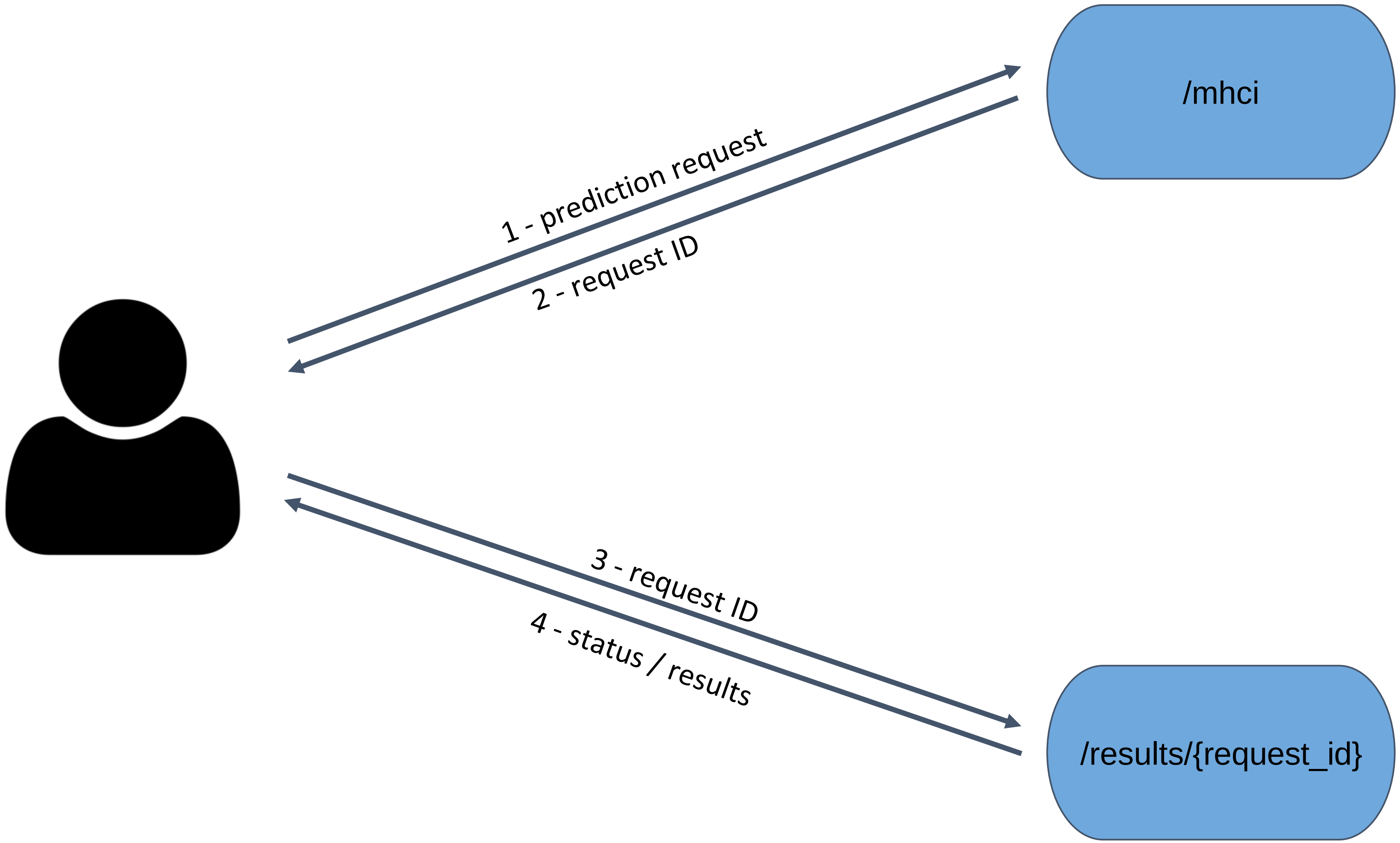
Motivations: Why a redesign?

- 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- Outdated layout and aesthetics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

Lifecycle of a mhci prediction request



/mhci

1 - prediction request

2 - request ID

3 - request ID

4 - status / results

/results/{request_id}

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

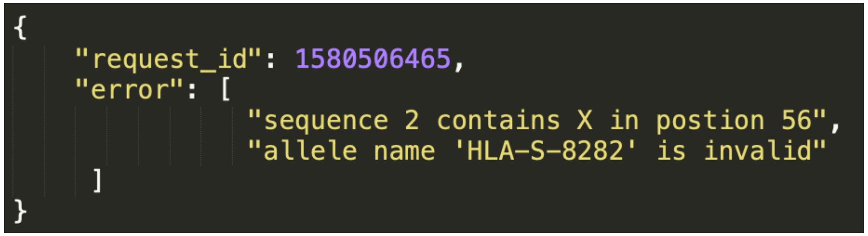
POST

```
{
    "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

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": {}
}
```

Nice! 😎

```
{
    "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}
                                  ]
   }

}
```

Live demo!

Clean and consistent APIs with interactive documentation:

https://iedb-ar-prototype.lji.org/docs/api/

T cell tool prototype:

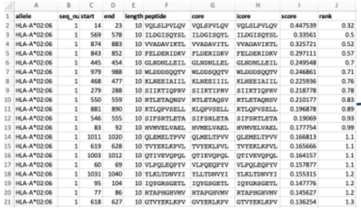
https://iedb-ar-prototype.lji.org/t-cell-prediction

Pipelines will allow for tool integration

```
>lcl|NC_045512.2_prot_YP_009724389.1_1 [gene=ORF1ab] [locus_tag=GU280_g
db_xref=GeneID:43740578] [protein=ORF1ab polyprotein] [exception=riboso
protein_id=YP_009724389.1] [location=join(266..13468,13468..21555)] [gb
MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSVEEVLSEARQHLKDGTCGLVEVEKGVLPQLEQPYVF
IKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPHVGEIPVAYRKVLLRKNGNKGAGGHSYGADL
KSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGK
ASCTLSEQLDFIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVFPLNSI
IKTIQPRVEKKKLDGFMGRIRSVYPVASPNECNQMCLSTLMKCDHCGETSWQTGDFVKATCEFCGTENLT
KEGATTCGYLPQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVFSYVGCHNKC
AYWVPRASANIGCNHTGVVGEGSEGLNDNLLEILQKEKVNINIVGDFKLNEEIAIILASFSASTSAFVET
VKGLDYKAFKQIVESCGNFKVTKGKAKKGAWNIGEQKSILSPLYAFASEAARVVRSIFSRTLETAQNSVR
VLQKAAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDW
LEEKFKEGVEFLRDGWEIVKFISTCACEIVGGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKL
KALNLGETFVTHSKGLYRKCVKSREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT
SEAVEAPLVGTPVCINGLMLLEIKDTEKYCALAPNMMVTNNTFTLKGGAPTKVTFGDDTVIEVQGYKSVN
ITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVIKTLQPVSELLTPLGIDLDEWSMATYYLFDE
```

fasta file with 12 proteins

MHC I binding tool

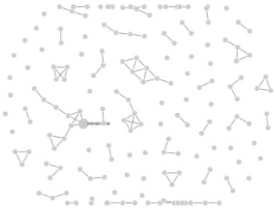


allele	seq_nu	start	end	length	peptide	core	icore	score	rank
HLA-A*02:06	1	14	23	10	VQLSLPVLQV	VQLSPVLQV	VQLSLPVLQV	0.447539	0.32
HLA-A*02:06	1	569	578	10	ILDGISQYSL	ILDGISQYL	ILDGISQYSL	0.33561	0.5
HLA-A*02:06	1	874	883	10	VVADAVIKTL	VVADAVITL	VVADAVIKTL	0.325721	0.52
HLA-A*02:06	1	843	852	10	FELDERIDKV	FLDERIDKV	FELDERIDKV	0.297111	0.57
HLA-A*02:06	1	445	454	10	GLNDNLLEIL	GLNDNLLEL	GLNDNLLEIL	0.249548	0.7
HLA-A*02:06	1	979	988	10	WLDDDSQQTV	WLDDSQQTV	WLDDDSQQTV	0.246861	0.71
HLA-A*02:06	1	468	477	10	KLNEEIAIIL	KLNEEIIIL	KLNEEIAIIL	0.225936	0.76
HLA-A*02:06	1	279	288	10	SIIKTIQPRV	SIIKTIPRV	SIIKTIQPRV	0.218778	0.78
HLA-A*02:06	1	550	559	10	RTLETAQNSV	RTLETAQSV	RTLETAQNSV	0.210177	0.83
HLA-A*02:06	1	881	890	10	KTLQPVSELL	KLQPVSELL	KTLQPVSELL	0.196878	0.89
HLA-A*02:06	1	546	555	10	SIFSRTLETA	SIFSRLETA	SIFSRTLETA	0.19069	0.93
HLA-A*02:06	1	83	92	10	HVMVELVAEL	HVMELVAEL	HVMVELVAEL	0.177754	0.99
HLA-A*02:06	1	1011	1020	10	QLEMELTPVV	QLMELTPVV	QLEMELTPVV	0.166813	1.1
HLA-A*02:06	1	619	628	10	TVYEKLKPVL	TVYEKLPVL	TVYEKLKPVL	0.165666	1.1
HLA-A*02:06	1	1003	1012	10	QTIVEVQPQL	QTIEVQPQL	QTIVEVQPQL	0.164157	1.1
HLA-A*02:06	1	60	69	10	VLPQLEQPYV	VLPQEQPYV	VLPQLEQPYV	0.157877	1.1
HLA-A*02:06	1	1031	1040	10	YLKLTDNVYI	YLLTDNVYI	YLKLTDNVYI	0.155315	1.2
HLA-A*02:06	1	95	104	10	IQYGRSGETL	IQYGSGETL	IQYGRSGETL	0.147776	1.2
HLA-A*02:06	1	77	86	10	RTAPHGHVMV	RTAPGHVMV	RTAPHGHVMV	0.145627	1.2
HLA-A*02:06	1	618	627	10	GTVYEKLKPV	GVYEKLKPV	GTVYEKLKPV	0.136254	1.3

14,053 peptide:MHC binding predictions

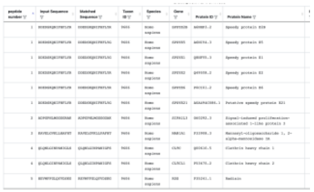
1,500 top predicted binders

Clustering tool



126 peptide clusters

Pepmatch



Identify related hits in other species

Plans and timeline

- **Other planned features**
  - API access packages
  - Customizable output formats
  - Data and pipeline shareability
  - Curated pipelines
  - High performance cluster backend and queuing system

- **Key dates**
  - 3 step pipeline support – Early 2022
  - Cluster backend and beta release – Mid 2022
  - 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

Systems architecture
Jason Greenbaum

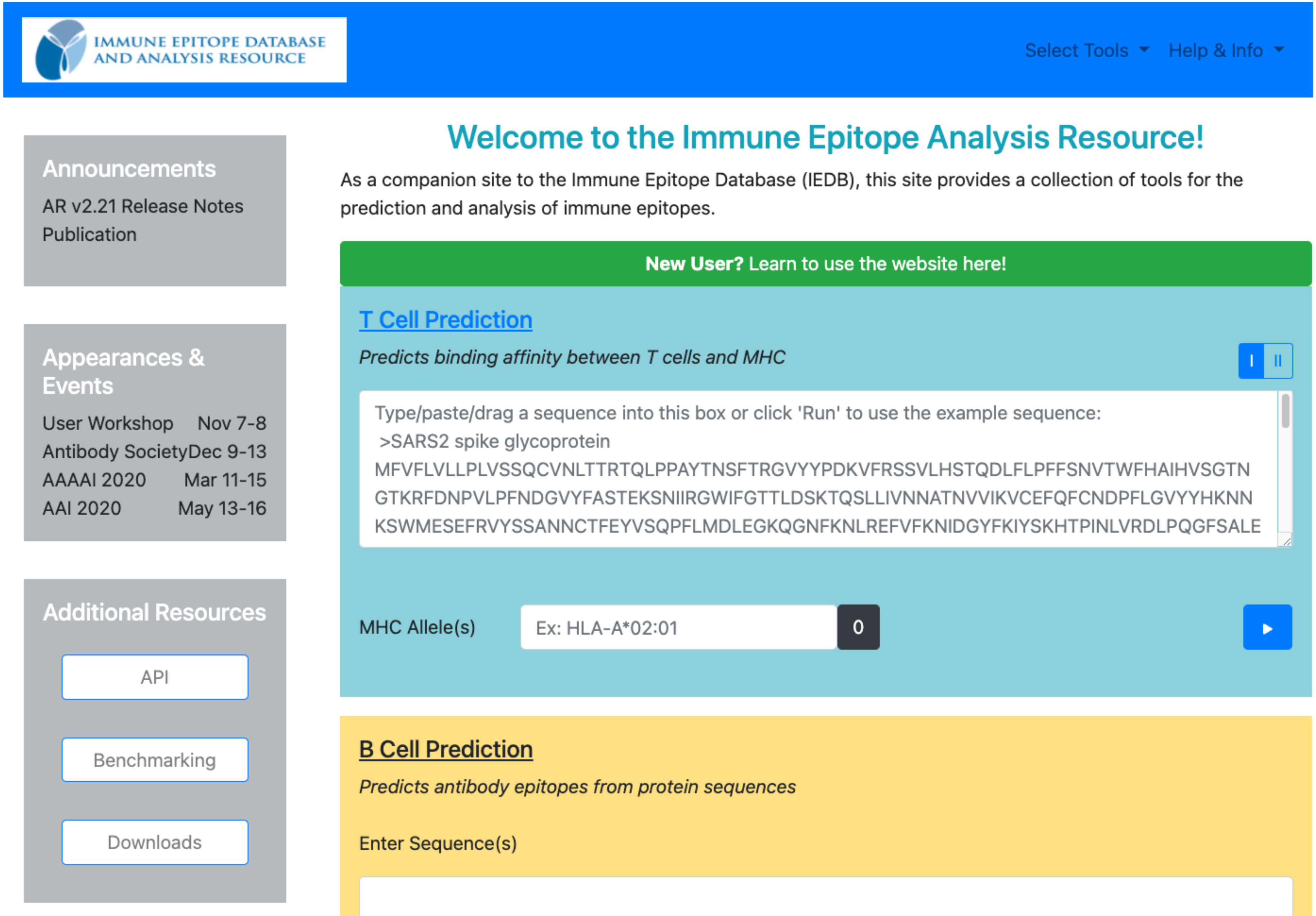
Project owner
Bjoern Peters

UI/UX consultants
Ali Haskins-Lisle
Joe Gabbard

Project management
Nina Blazeska

Additional contributors
Morten Nielsen
Michael Talbott
Dan Marrama
Apurva Mody

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!

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

T Cell Prediction

Predicts binding affinity between T cells and MHC

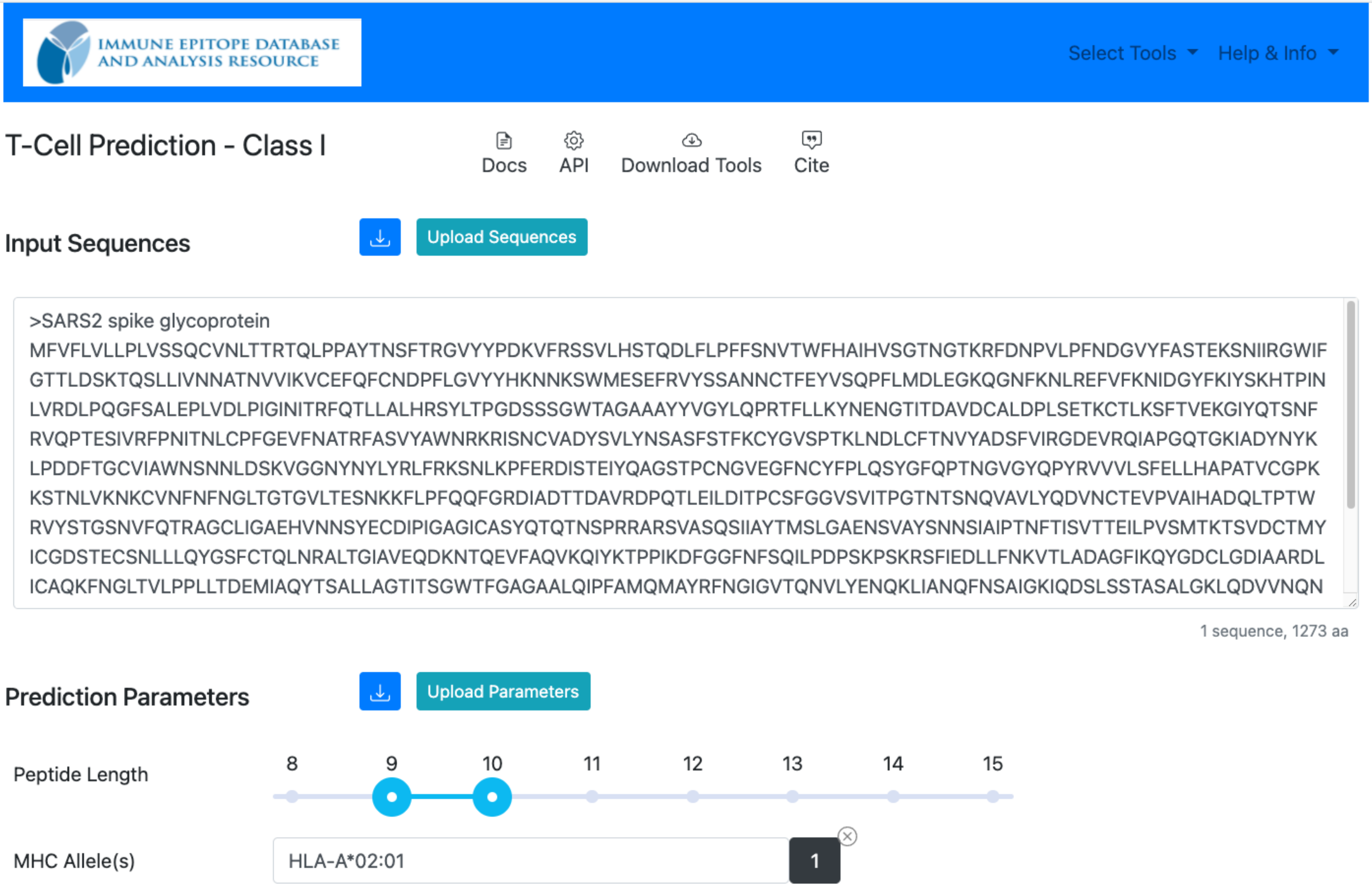
Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTN
GTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNN
KSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALE

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

B Cell Prediction

Predicts antibody epitopes from protein sequences

Enter Sequence(s)



T-Cell Prediction - Class I

Input Sequences

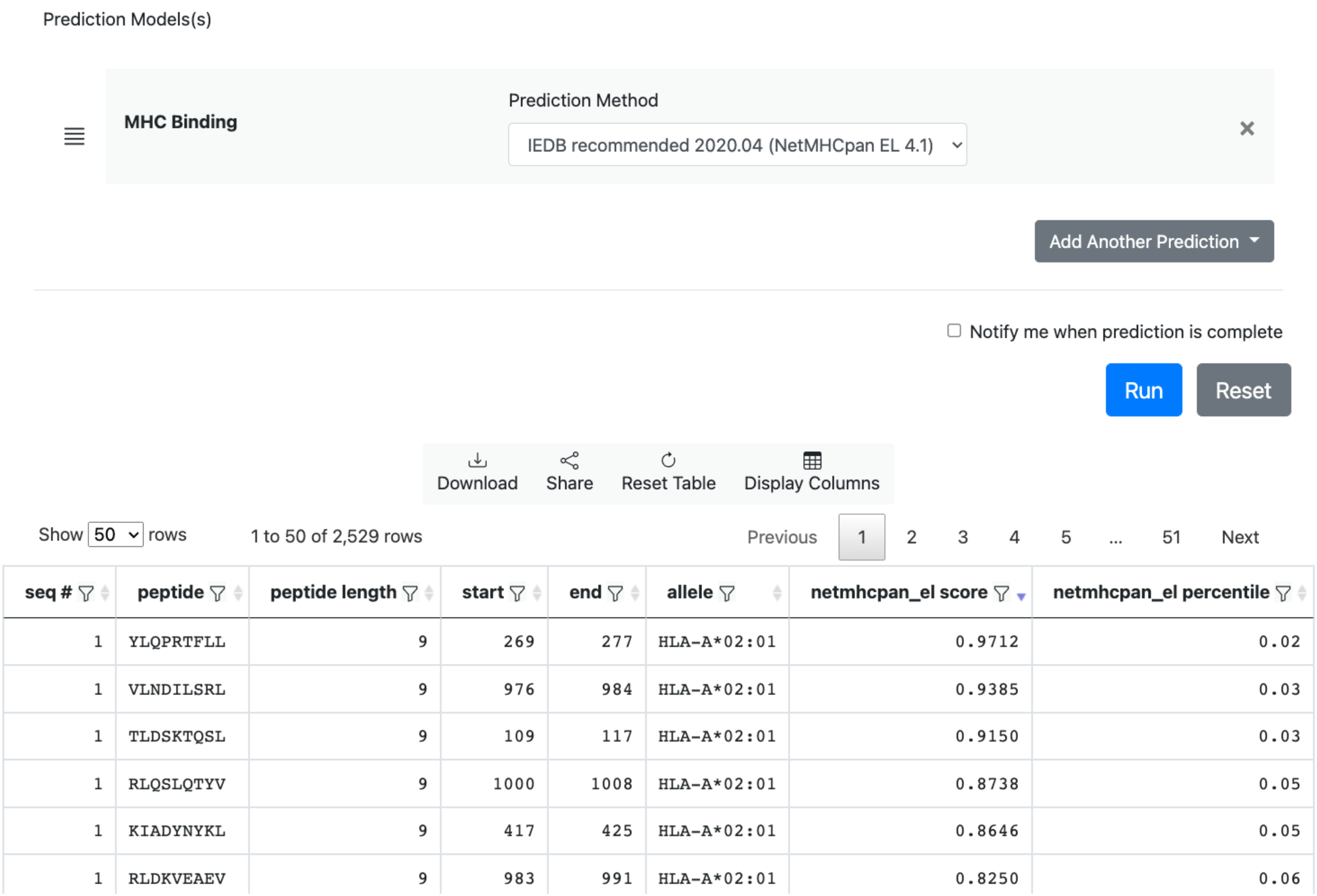
```
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIF
GTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPIN
LVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNF
RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYK
LPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPK
KSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTW
RVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMY
ICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDL
ICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQN
```

1 sequence, 1273 aa

Prediction Parameters

Peptide Length: 9 – 10

MHC Allele(s): HLA-A*02:01 1



Prediction Models(s)

MHC Binding

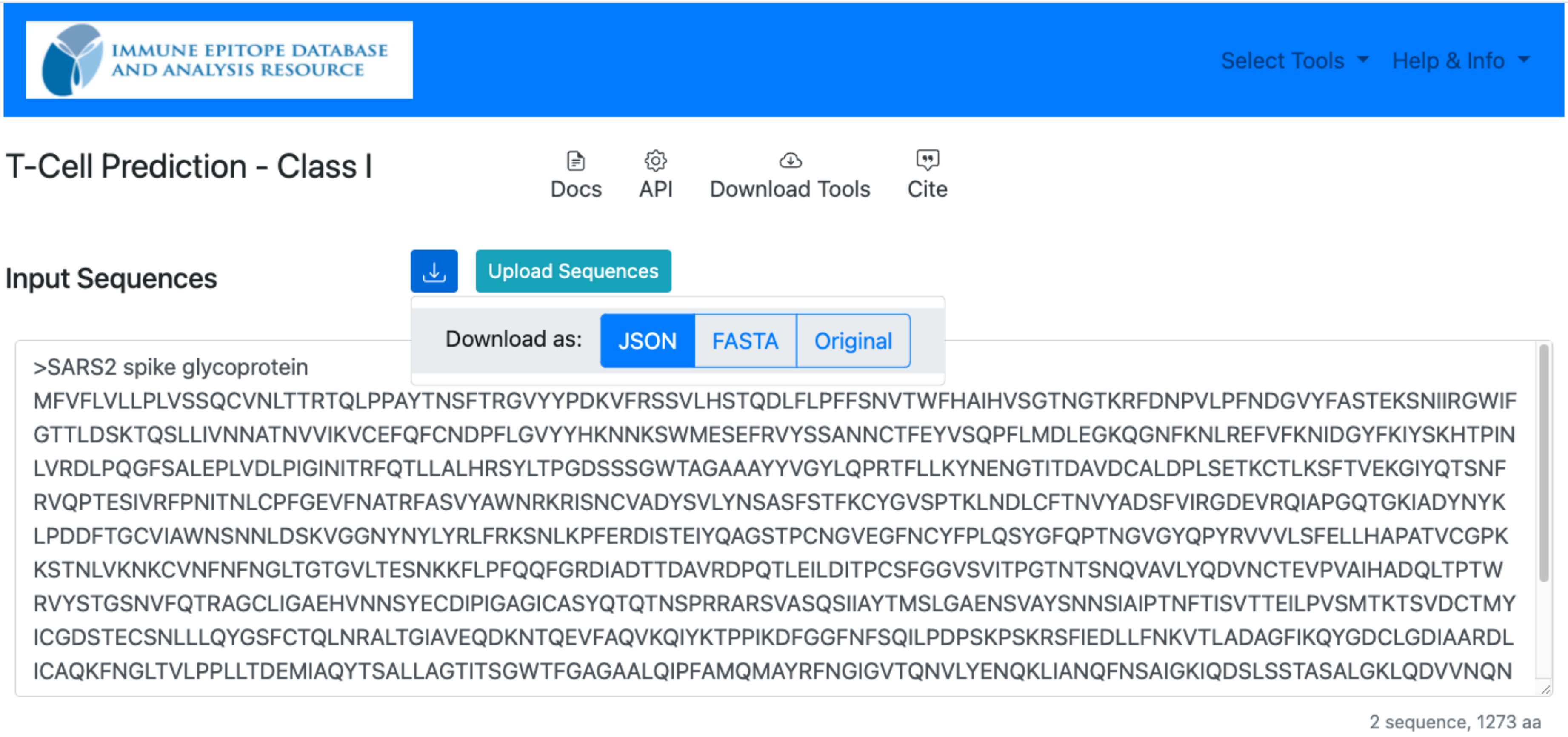
Prediction Method: IEDB recommended 2020.04 (NetMHCpan EL 4.1)

☐ Notify me when prediction is complete

Show 50 rows

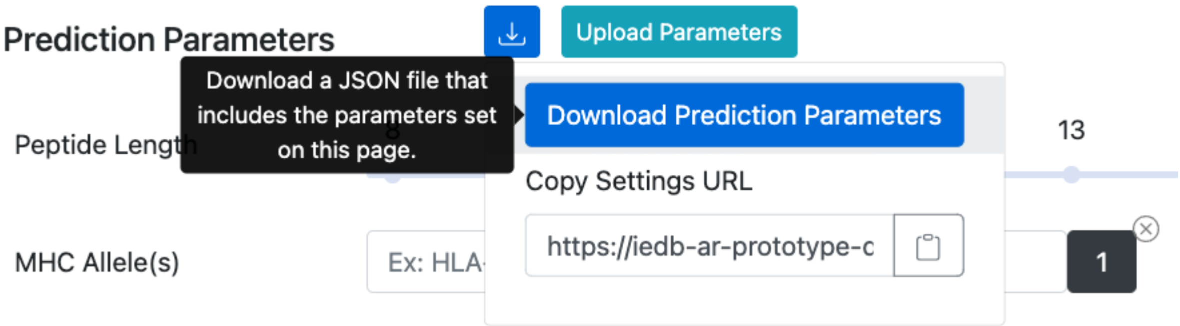
1 to 50 of 2,529 rows

seq #	peptide	peptide length	start	end	allele	netmhcpan_el score	netmhcpan_el percentile
1	YLQPRTFLL	9	269	277	HLA-A*02:01	0.9712	0.02
1	VLNDILSRL	9	976	984	HLA-A*02:01	0.9385	0.03
1	TLDSKTQSL	9	109	117	HLA-A*02:01	0.9150	0.03
1	RLQSLQTYV	9	1000	1008	HLA-A*02:01	0.8738	0.05
1	KIADYNYKL	9	417	425	HLA-A*02:01	0.8646	0.05
1	RLDKVEAEV	9	983	991	HLA-A*02:01	0.8250	0.06



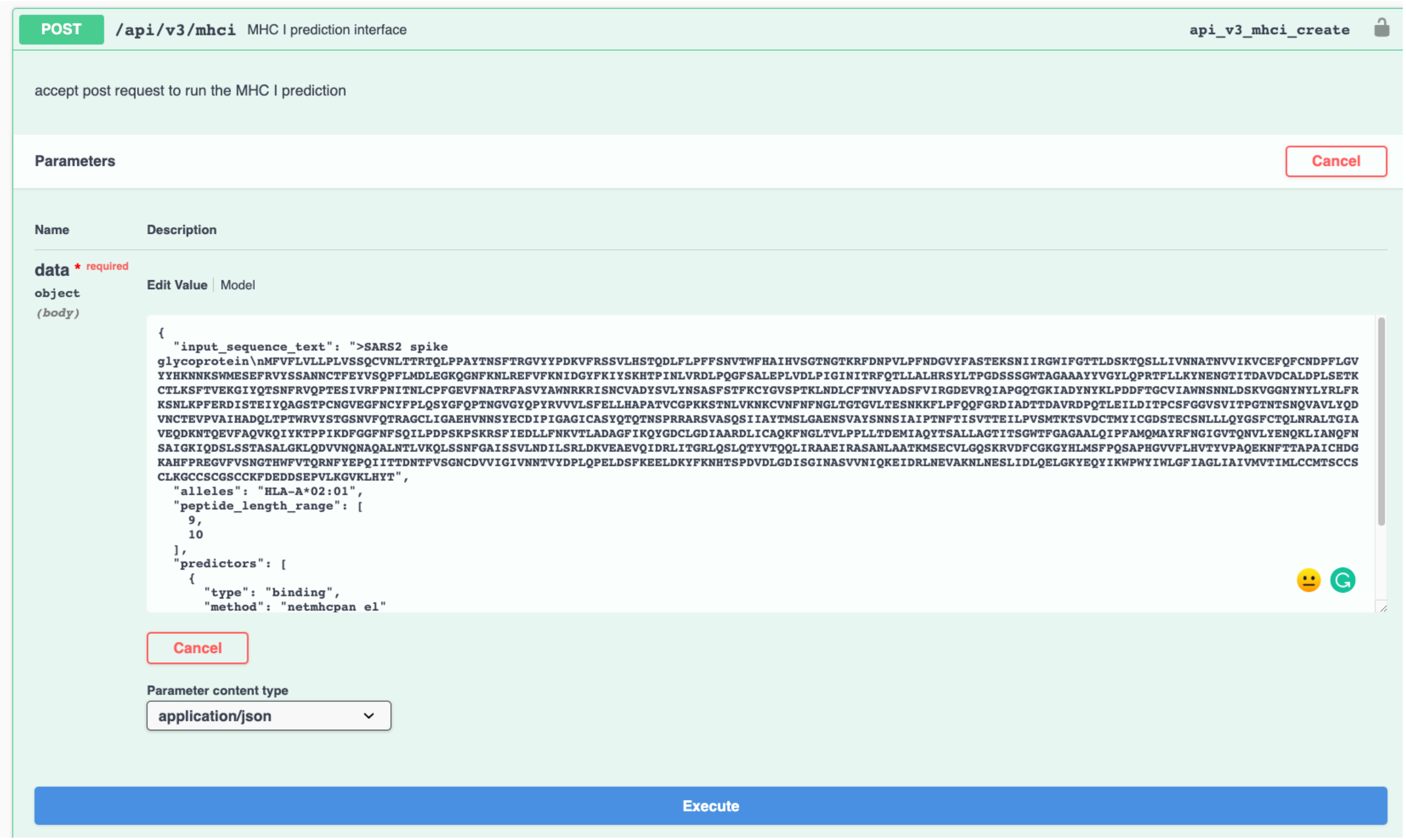
```
>SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIF
GTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPIN
LVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNF
RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYK
LPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPK
KSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTW
RVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMY
ICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDL
ICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQN
```

2 sequence, 1273 aa



Download a JSON file that includes the parameters set on this page.

```
{
  "input_sequence_text": ">SARS2 spike glycoprotein\nMFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDK
  VFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEF
  QFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEP
  LVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSN
  FRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQ
  IAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTN
  GVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFG
  GVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRAR
  SVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
  TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEM
  IAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNT
  LVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFP
  QSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPEL
  DSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCM
  TSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT",
  "alleles": "HLA-A*02:01",
  "peptide_length_range": [
    9,
    10
  ],
  "predictors": [
    {
      "type": "binding",
      "method": "netmhcpan_el"
    }
  ]
}
```



POST `/api/v3/mhci` MHC I prediction interface

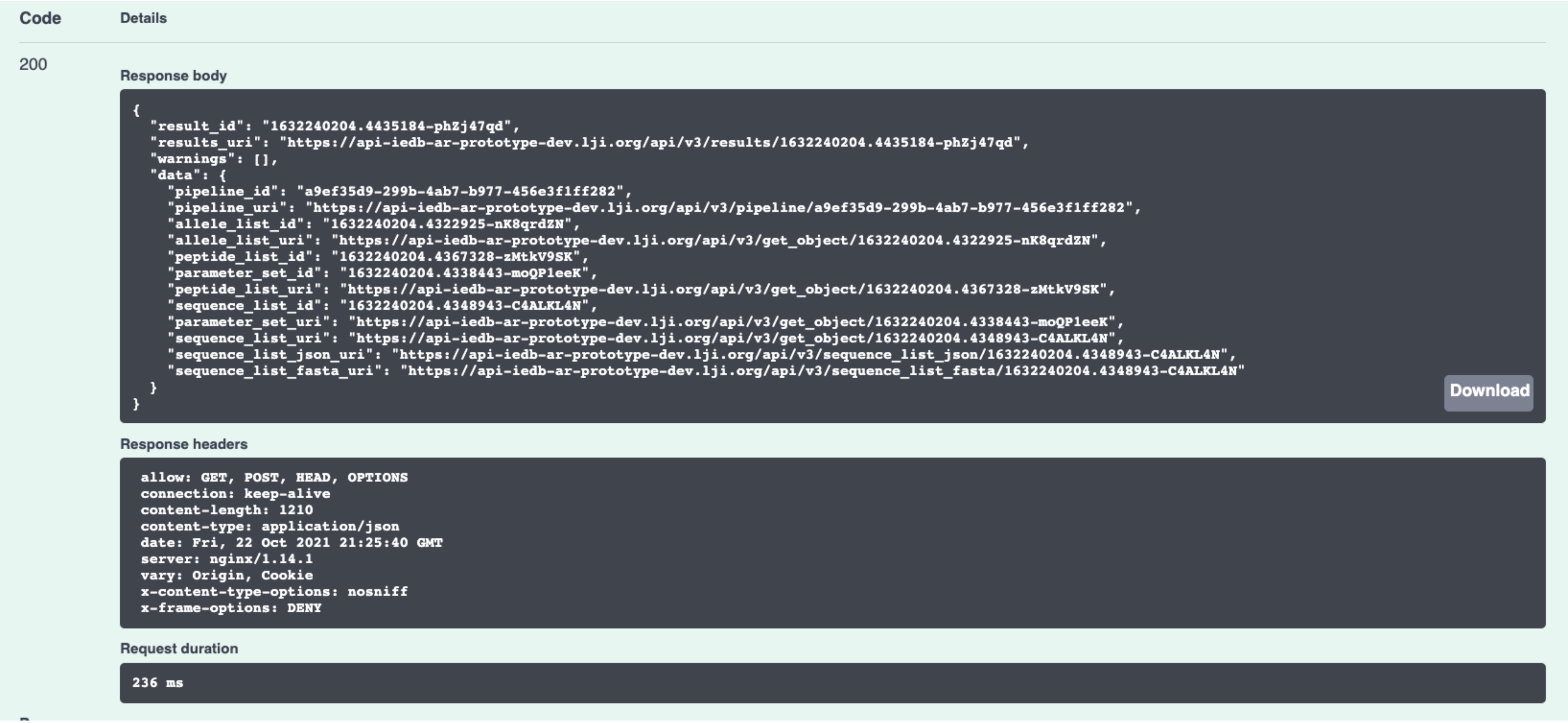
accept post request to run the MHC I prediction

data * required
object
(body)

```
{
  "input_sequence_text": ">SARS2 spike
glycoprotein\nMFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGV
YYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK
CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFR
KSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQD
VNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIA
VEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDG
KAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCS
CLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT",
  "alleles": "HLA-A*02:01",
  "peptide_length_range": [
    9,
    10
  ],
  "predictors": [
    {
      "type": "binding",
      "method": "netmhcpan el"
```

Parameter content type

application/json



200

Response body

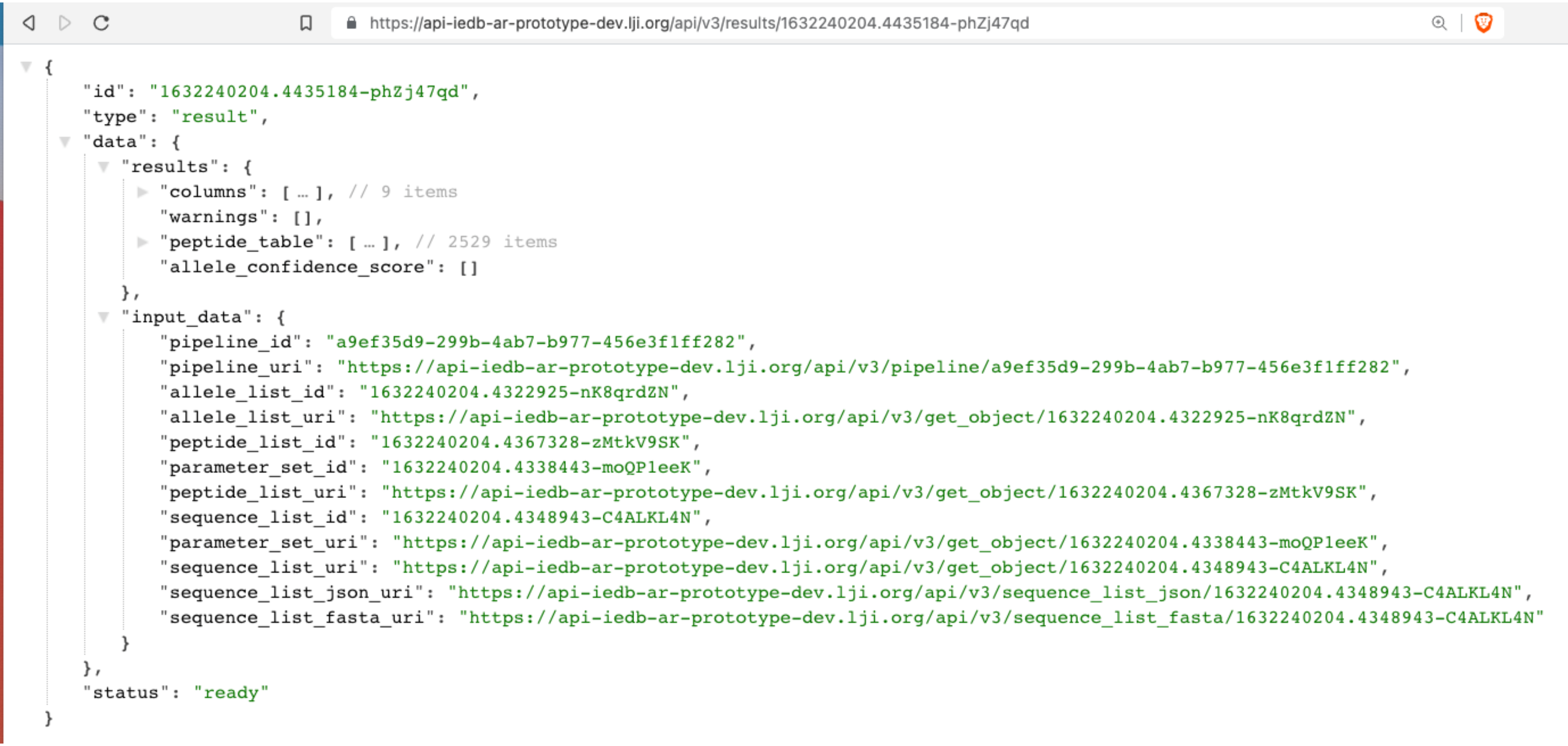
```
{
  "result_id": "1632240204.4435184-phZj47qd",
  "results_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/results/1632240204.4435184-phZj47qd",
  "warnings": [],
  "data": {
    "pipeline_id": "a9ef35d9-299b-4ab7-b977-456e3f1ff282",
    "pipeline_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/pipeline/a9ef35d9-299b-4ab7-b977-456e3f1ff282",
    "allele_list_id": "1632240204.4322925-nK8qrdZN",
    "allele_list_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4322925-nK8qrdZN",
    "peptide_list_id": "1632240204.4367328-zMtkV9SK",
    "parameter_set_id": "1632240204.4338443-moQPleeK",
    "peptide_list_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4367328-zMtkV9SK",
    "sequence_list_id": "1632240204.4348943-C4ALKL4N",
    "parameter_set_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4338443-moQPleeK",
    "sequence_list_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4348943-C4ALKL4N",
    "sequence_list_json_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/sequence_list_json/1632240204.4348943-C4ALKL4N",
    "sequence_list_fasta_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/sequence_list_fasta/1632240204.4348943-C4ALKL4N"
  }
}
```

Response headers

```
allow: GET, POST, HEAD, OPTIONS
connection: keep-alive
content-length: 1210
content-type: application/json
date: Fri, 22 Oct 2021 21:25:40 GMT
server: nginx/1.14.1
vary: Origin, Cookie
x-content-type-options: nosniff
x-frame-options: DENY
```

Request duration

```
236 ms
```

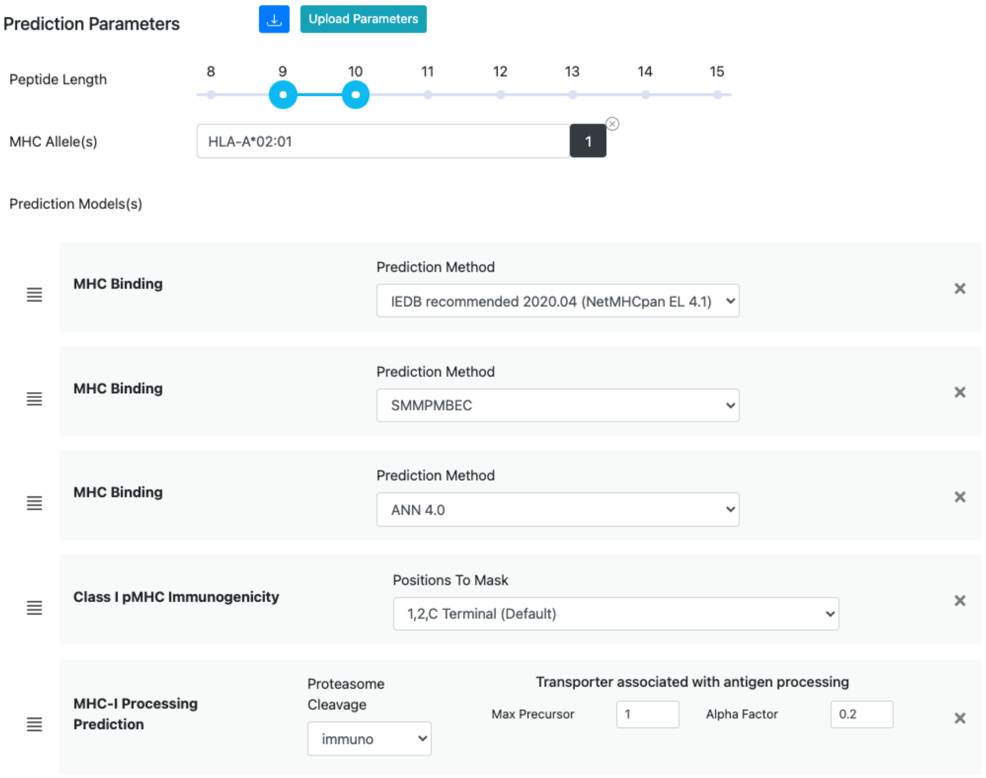


https://api-iedb-ar-prototype-dev.lji.org/api/v3/results/1632240204.4435184-phZj47qd

```
{
    "id": "1632240204.4435184-phZj47qd",
    "type": "result",
    "data": {
        "results": {
            "columns": [ … ], // 9 items
            "warnings": [],
            "peptide_table": [ … ], // 2529 items
            "allele_confidence_score": []
        },
        "input_data": {
            "pipeline_id": "a9ef35d9-299b-4ab7-b977-456e3f1ff282",
            "pipeline_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/pipeline/a9ef35d9-299b-4ab7-b977-456e3f1ff282",
            "allele_list_id": "1632240204.4322925-nK8qrdZN",
            "allele_list_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4322925-nK8qrdZN",
            "peptide_list_id": "1632240204.4367328-zMtkV9SK",
            "parameter_set_id": "1632240204.4338443-moQPleeK",
            "peptide_list_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4367328-zMtkV9SK",
            "sequence_list_id": "1632240204.4348943-C4ALKL4N",
            "parameter_set_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4338443-moQPleeK",
            "sequence_list_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/get_object/1632240204.4348943-C4ALKL4N",
            "sequence_list_json_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/sequence_list_json/1632240204.4348943-C4ALKL4N",
            "sequence_list_fasta_uri": "https://api-iedb-ar-prototype-dev.lji.org/api/v3/sequence_list_fasta/1632240204.4348943-C4ALKL4N"
        }
    },
    "status": "ready"
}
```

Prediction Parameters

```
{
  "input_sequence_text": ">SARS2 spike glycoprotein\nMFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDK
  VFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEF
  QFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEP
  LVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSN
  FRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQ
  IAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTN
  GVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFG
  GVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRAR
  SVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
  TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEM
  IAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNT
  LVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFP
  QSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPEL
  DSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCM
  TSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT",
  "alleles": "HLA-A*02:01",
  "peptide_length_range": [
    9,
    10
  ],
  "predictors": [
    {
      "type": "binding",
      "method": "netmhcpan_el"
    },
    {
      "type": "binding",
      "method": "smmpmbec"
    },
    {
      "type": "binding",
      "method": "ann"
    },
    {
      "type": "immunogenicity",
      "mask_choice": "default",
      "position_to_mask": "2,5,9"
    },
    {
      "type": "processing",
      "proteasome": "immuno",
      "tap_precursor": 1,
      "tap_alpha": 0.2
    }
  ]
}
```

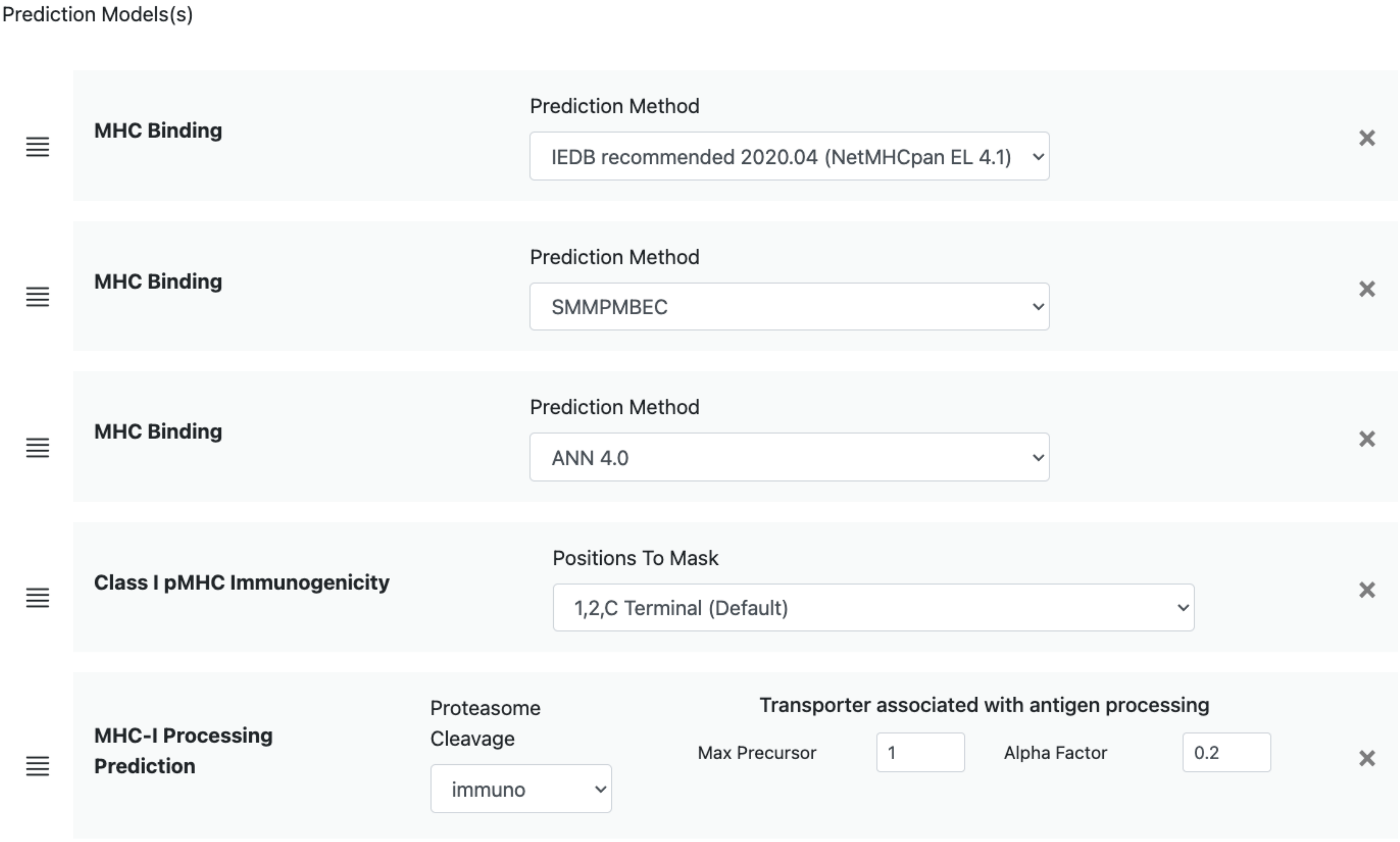


Peptide Length: 9, 10

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

Prediction Models(s)

- MHC Binding — Prediction Method: IEDB recommended 2020.04 (NetMHCpan EL 4.1)
- MHC Binding — Prediction Method: SMMPMBEC
- MHC Binding — Prediction Method: ANN 4.0
- Class I pMHC Immunogenicity — Positions To Mask: 1,2,C Terminal (Default)
- MHC-I Processing Prediction — Proteasome Cleavage: immuno; Transporter associated with antigen processing: Max Precursor 1, Alpha Factor 0.2



Prediction Models(s)

MHC Binding

Prediction Method: IEDB recommended 2020.04 (NetMHCpan EL 4.1)

MHC Binding

Prediction Method: SMMPMBEC

MHC Binding

Prediction Method: ANN 4.0

Class I pMHC Immunogenicity

Positions To Mask: 1,2,C Terminal (Default)

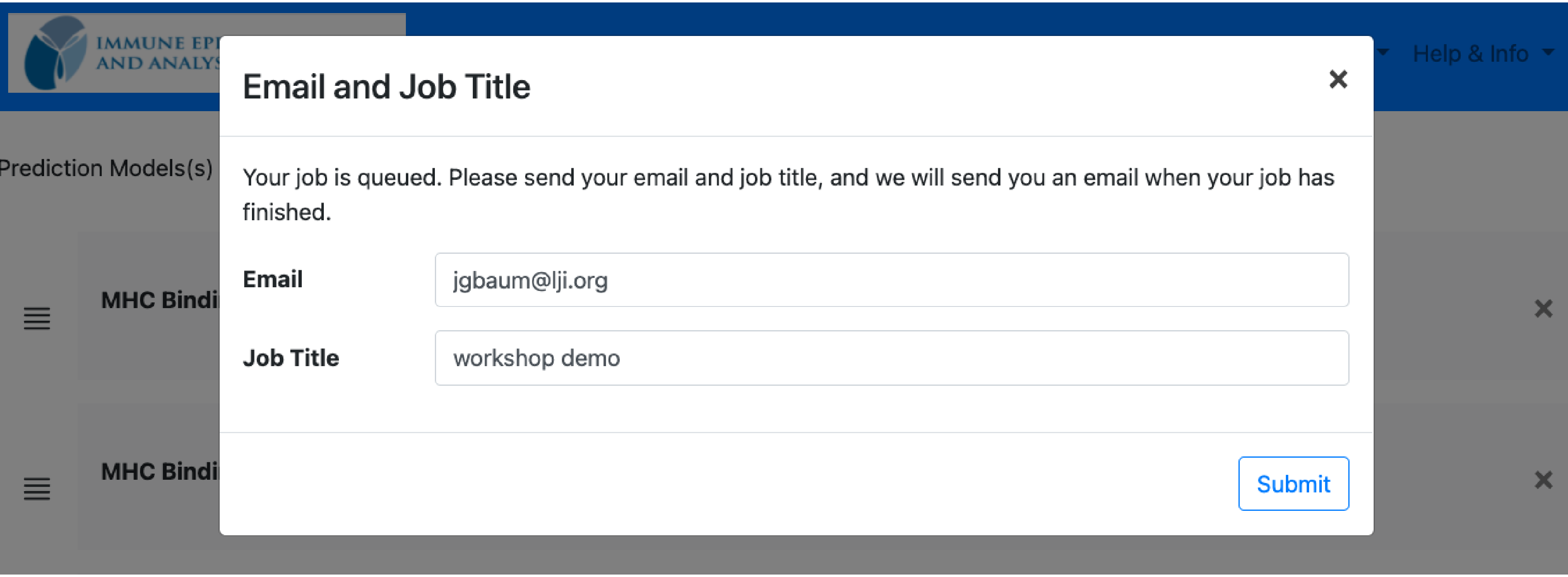
MHC-I Processing Prediction

Proteasome Cleavage: immuno

Transporter associated with antigen processing

Max Precursor: 1

Alpha Factor: 0.2

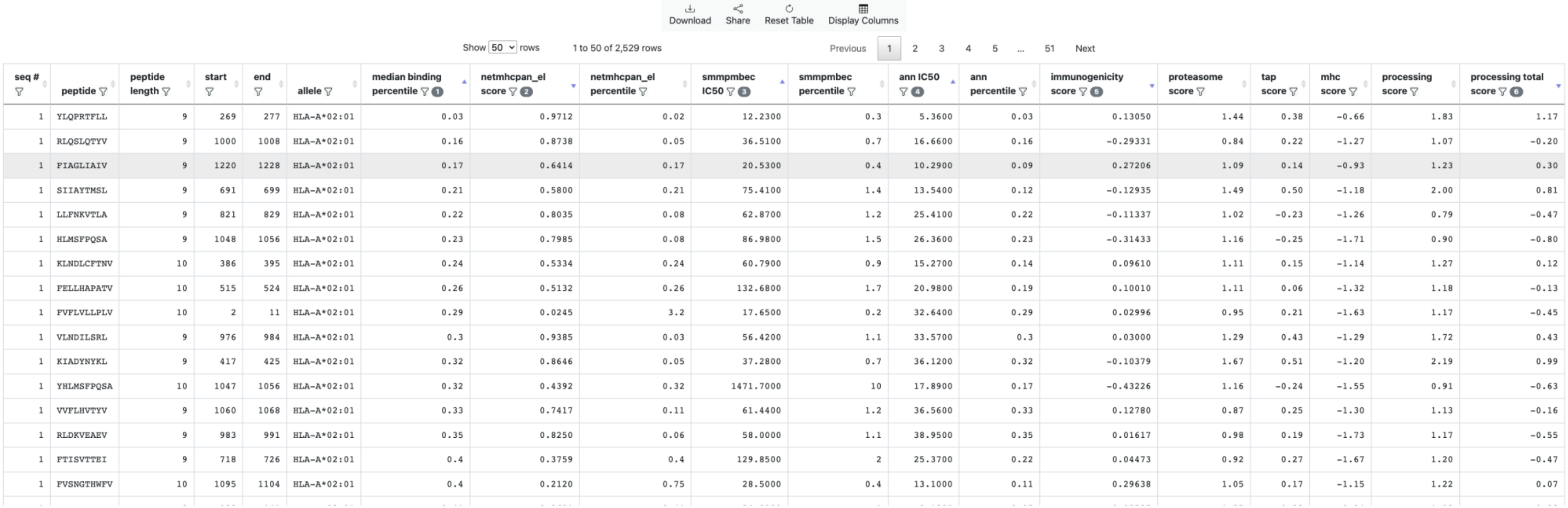


Email and Job Title

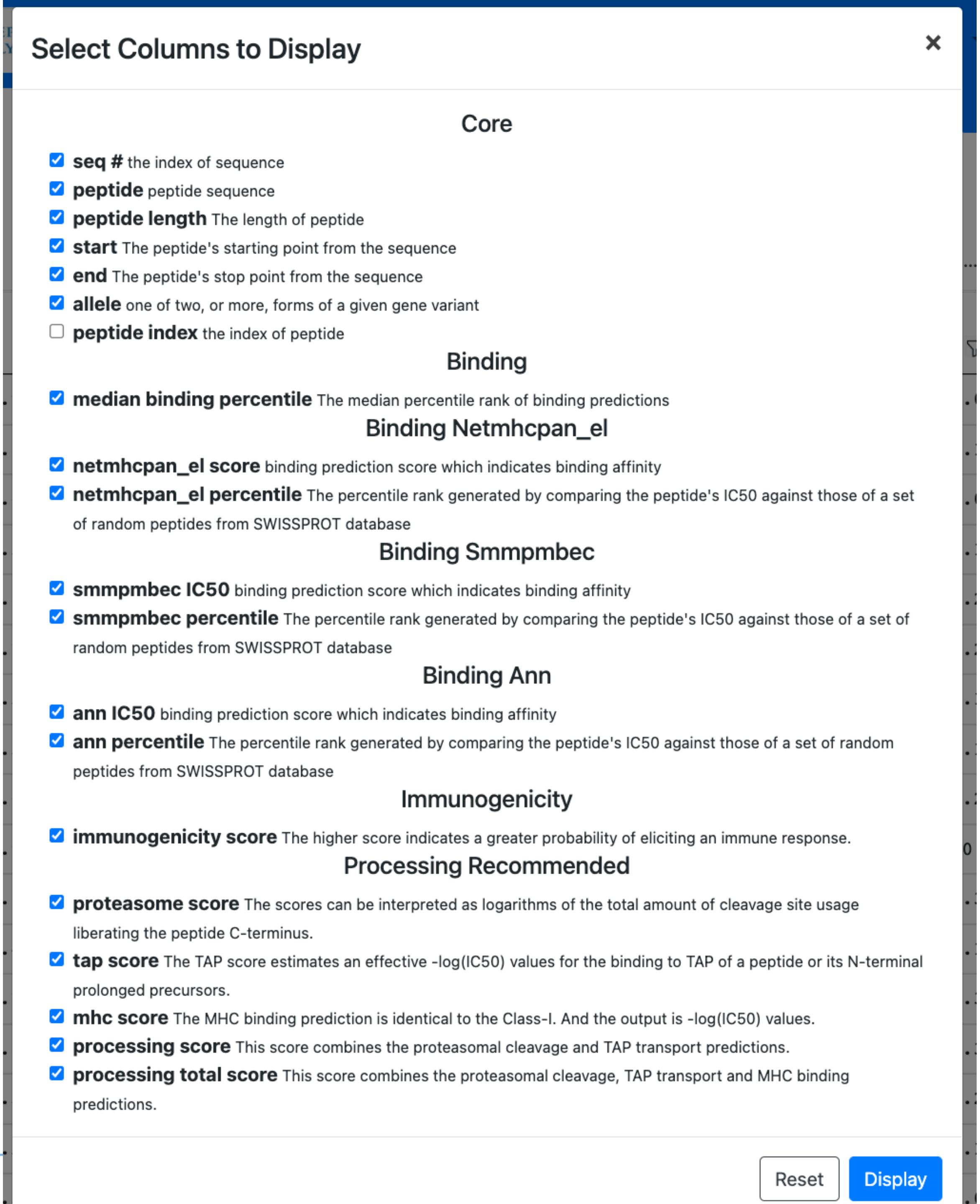
Your job is queued. Please send your email and job title, and we will send you an email when your job has finished.

Email jgbaum@lji.org

Job Title workshop demo



seq #	peptide	peptide length	start	end	allele	median binding percentile ①	netmhcpan_el score ②	netmhcpan_el percentile	smmpmbec IC50 ③	smmpmbec percentile	ann IC50 ④	ann percentile	immunogenicity score ⑤	proteasome score	tap score	mhc score	processing score	processing total score ⑥
1	YLQPRTFLL	9	269	277	HLA-A*02:01	0.03	0.9712	0.02	12.2300	0.3	5.3600	0.03	0.13050	1.44	0.38	-0.66	1.83	1.17
1	RLQSLQTYV	9	1000	1008	HLA-A*02:01	0.16	0.8738	0.05	36.5100	0.7	16.6600	0.16	-0.29331	0.84	0.22	-1.27	1.07	-0.20
1	FIAGLIAIV	9	1220	1228	HLA-A*02:01	0.17	0.6414	0.17	20.5300	0.4	10.2900	0.09	0.27206	1.09	0.14	-0.93	1.23	0.30
1	SIIAYTMSL	9	691	699	HLA-A*02:01	0.21	0.5800	0.21	75.4100	1.4	13.5400	0.12	-0.12935	1.49	0.50	-1.18	2.00	0.81
1	LLFNKVTLA	9	821	829	HLA-A*02:01	0.22	0.8035	0.08	62.8700	1.2	25.4100	0.22	-0.11337	1.02	-0.23	-1.26	0.79	-0.47
1	HLMSFPQSA	9	1048	1056	HLA-A*02:01	0.23	0.7985	0.08	86.9800	1.5	26.3600	0.23	-0.31433	1.16	-0.25	-1.71	0.90	-0.80
1	KLNDLCFTNV	10	386	395	HLA-A*02:01	0.24	0.5334	0.24	60.7900	0.9	15.2700	0.14	0.09610	1.11	0.15	-1.14	1.27	0.12
1	FELLHAPATV	10	515	524	HLA-A*02:01	0.26	0.5132	0.26	132.6800	1.7	20.9800	0.19	0.10010	1.11	0.06	-1.32	1.18	-0.13
1	FVFLVLLPLV	10	2	11	HLA-A*02:01	0.29	0.0245	3.2	17.6500	0.2	32.6400	0.29	0.02996	0.95	0.21	-1.63	1.17	-0.45
1	VLNDILSRL	9	976	984	HLA-A*02:01	0.3	0.9385	0.03	56.4200	1.1	33.5700	0.3	0.03000	1.29	0.43	-1.29	1.72	0.43
1	KIADYNYKL	9	417	425	HLA-A*02:01	0.32	0.8646	0.05	37.2800	0.7	36.1200	0.32	-0.10379	1.67	0.51	-1.20	2.19	0.99
1	YHLMSFPQSA	10	1047	1056	HLA-A*02:01	0.32	0.4392	0.32	1471.7000	10	17.8900	0.17	-0.43226	1.16	-0.24	-1.55	0.91	-0.63
1	VVFLHVTYV	9	1060	1068	HLA-A*02:01	0.33	0.7417	0.11	61.4400	1.2	36.5600	0.33	0.12780	0.87	0.25	-1.30	1.13	-0.16
1	RLDKVEAEV	9	983	991	HLA-A*02:01	0.35	0.8250	0.06	58.0000	1.1	38.9500	0.35	0.01617	0.98	0.19	-1.73	1.17	-0.55
1	FTISVTTEI	9	718	726	HLA-A*02:01	0.4	0.3759	0.4	129.8500	2	25.3700	0.22	0.04473	0.92	0.27	-1.67	1.20	-0.47
1	FVSNGTHWFV	10	1095	1104	HLA-A*02:01	0.4	0.2120	0.75	28.5000	0.4	13.1000	0.11	0.29638	1.05	0.17	-1.15	1.22	0.07



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 Netmhcpan_el

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

Binding Smmpmbec

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

Binding Ann

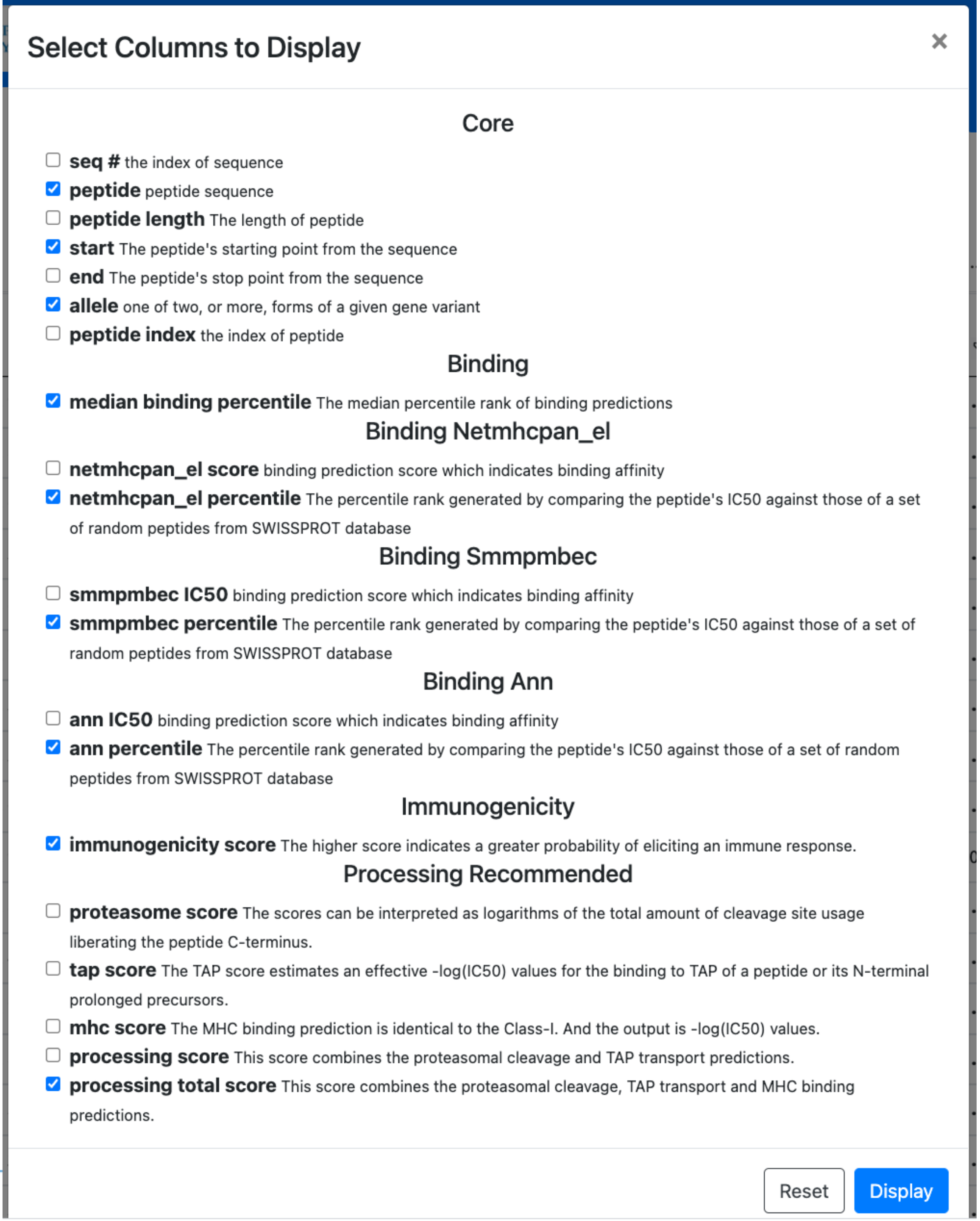
☑ **ann IC50** binding prediction score which indicates binding affinity
☑ **ann percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Immunogenicity

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

Processing Recommended

☑ **proteasome score** The scores can be interpreted as logarithms of the total amount of cleavage site usage liberating the peptide C-terminus.
☑ **tap score** The TAP score estimates an effective -log(IC50) values for the binding to TAP of a peptide or its N-terminal prolonged precursors.
☑ **mhc score** The MHC binding prediction is identical to the Class-I. And the output is -log(IC50) values.
☑ **processing score** This score combines the proteasomal cleavage and TAP transport predictions.
☑ **processing total score** This score combines the proteasomal cleavage, TAP transport and MHC binding predictions.



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 Netmhcpan_el

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

Binding Smmpmbec

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

Binding Ann

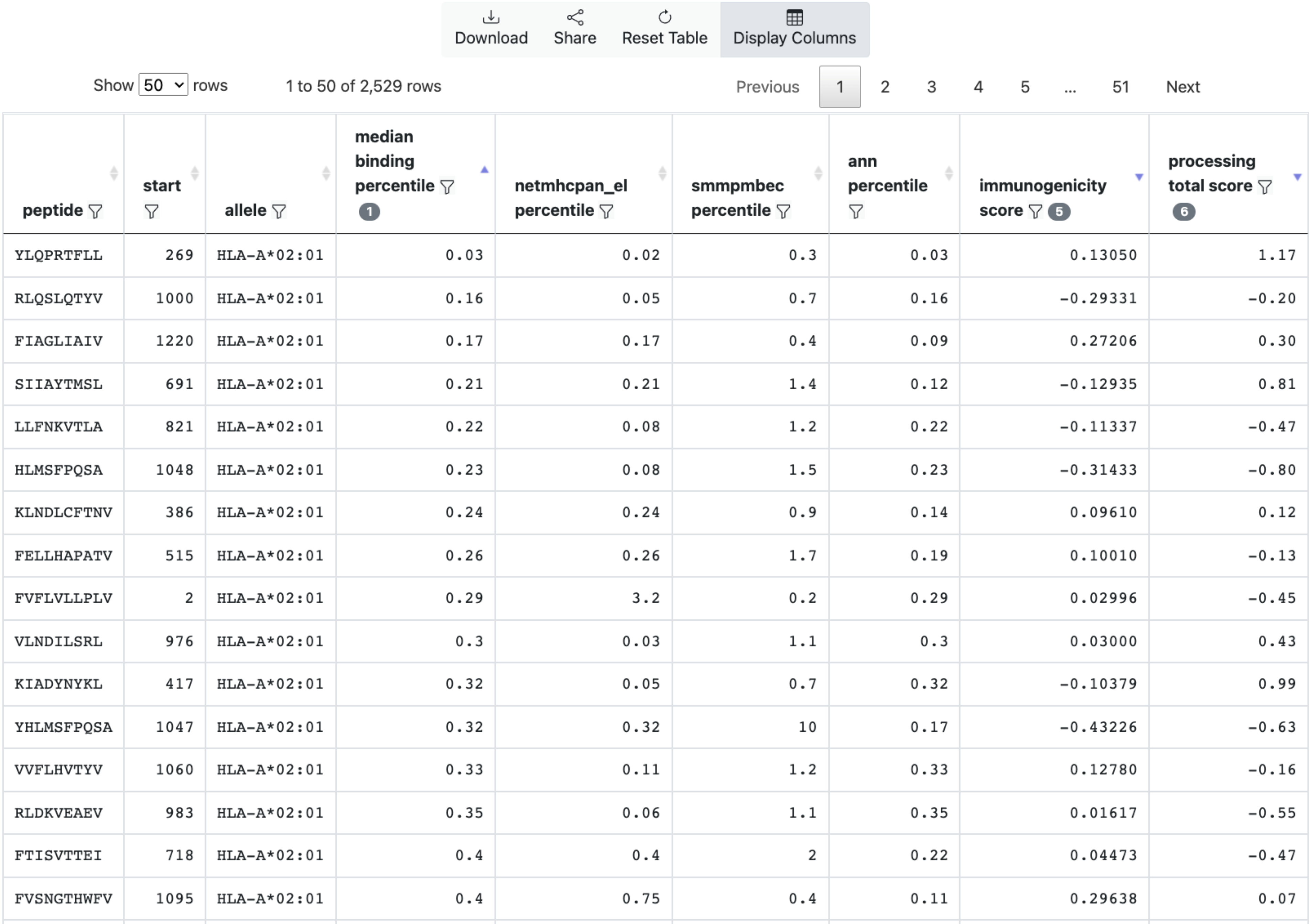
- ☐ **ann IC50** binding prediction score which indicates binding affinity
- ☑ **ann percentile** The percentile rank generated by comparing the peptide's IC50 against those of a set of random peptides from SWISSPROT database

Immunogenicity

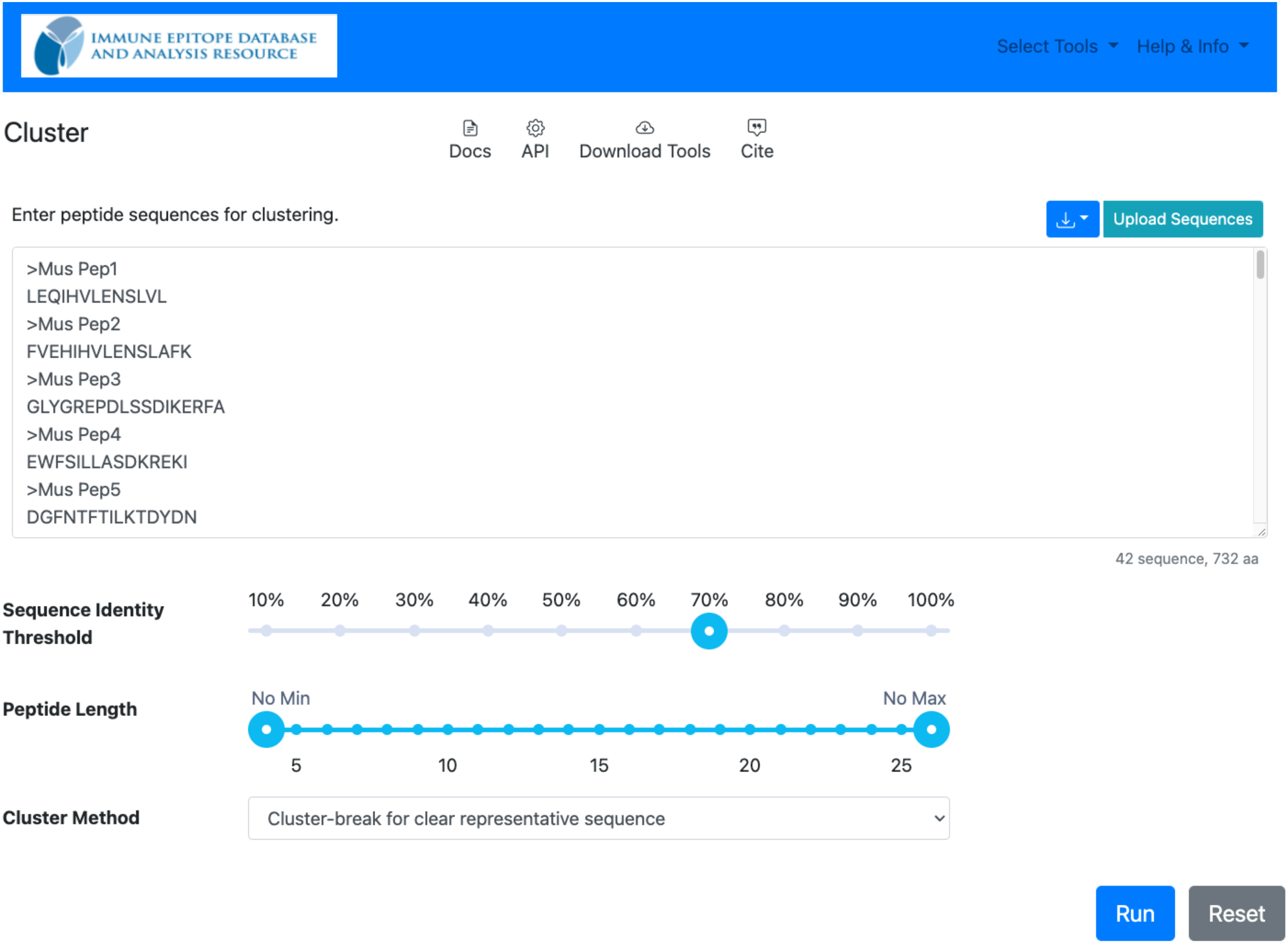
- ☑ **immunogenicity score** The higher score indicates a greater probability of eliciting an immune response.

Processing Recommended

- ☐ **proteasome score** The scores can be interpreted as logarithms of the total amount of cleavage site usage liberating the peptide C-terminus.
- ☐ **tap score** The TAP score estimates an effective -log(IC50) values for the binding to TAP of a peptide or its N-terminal prolonged precursors.
- ☐ **mhc score** The MHC binding prediction is identical to the Class-I. And the output is -log(IC50) values.
- ☐ **processing score** This score combines the proteasomal cleavage and TAP transport predictions.
- ☑ **processing total score** This score combines the proteasomal cleavage, TAP transport and MHC binding predictions.



peptide	start	allele	median binding percentile 1	netmhcpan_el percentile	smmpmbec percentile	ann percentile	immunogenicity score 5	processing total score 6
YLQPRTFLL	269	HLA-A*02:01	0.03	0.02	0.3	0.03	0.13050	1.17
RLQSLQTYV	1000	HLA-A*02:01	0.16	0.05	0.7	0.16	-0.29331	-0.20
FIAGLIAIV	1220	HLA-A*02:01	0.17	0.17	0.4	0.09	0.27206	0.30
SIIAYTMSL	691	HLA-A*02:01	0.21	0.21	1.4	0.12	-0.12935	0.81
LLFNKVTLA	821	HLA-A*02:01	0.22	0.08	1.2	0.22	-0.11337	-0.47
HLMSFPQSA	1048	HLA-A*02:01	0.23	0.08	1.5	0.23	-0.31433	-0.80
KLNDLCFTNV	386	HLA-A*02:01	0.24	0.24	0.9	0.14	0.09610	0.12
FELLHAPATV	515	HLA-A*02:01	0.26	0.26	1.7	0.19	0.10010	-0.13
FVFLVLLPLV	2	HLA-A*02:01	0.29	3.2	0.2	0.29	0.02996	-0.45
VLNDILSRL	976	HLA-A*02:01	0.3	0.03	1.1	0.3	0.03000	0.43
KIADYNYKL	417	HLA-A*02:01	0.32	0.05	0.7	0.32	-0.10379	0.99
YHLMSFPQSA	1047	HLA-A*02:01	0.32	0.32	10	0.17	-0.43226	-0.63
VVFLHVTYV	1060	HLA-A*02:01	0.33	0.11	1.2	0.33	0.12780	-0.16
RLDKVEAEV	983	HLA-A*02:01	0.35	0.06	1.1	0.35	0.01617	-0.55
FTISVTTEI	718	HLA-A*02:01	0.4	0.4	2	0.22	0.04473	-0.47
FVSNGTHWFV	1095	HLA-A*02:01	0.4	0.75	0.4	0.11	0.29638	0.07



Cluster

Enter peptide sequences for clustering.

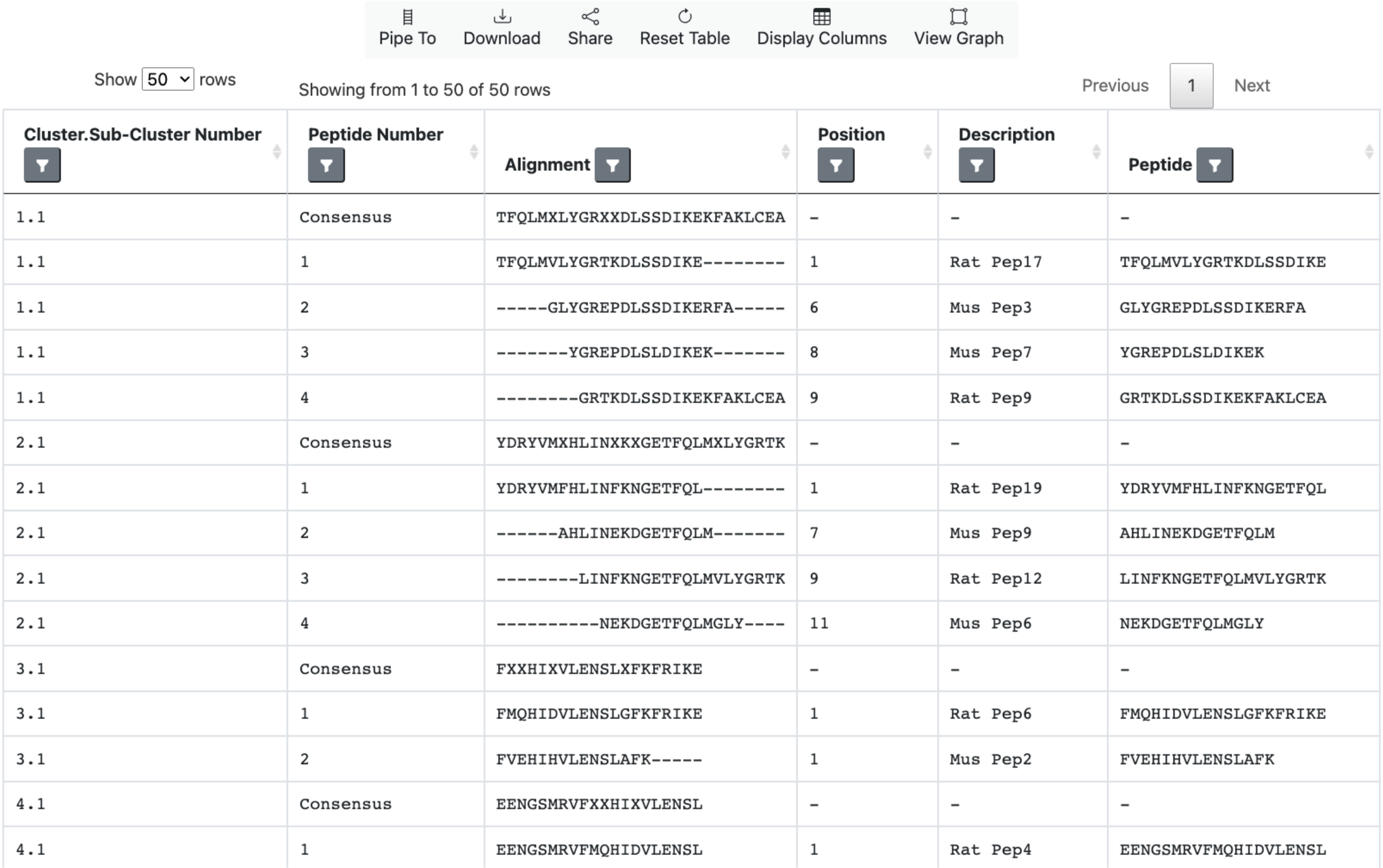
```
>Mus Pep1
LEQIHVLENSLVL
>Mus Pep2
FVEHIHVLENSLAFK
>Mus Pep3
GLYGREPDLSSDIKERFA
>Mus Pep4
EWFSILLASDKREKI
>Mus Pep5
DGFNTFTILKTDYDN
```

42 sequence, 732 aa

Sequence Identity Threshold: 70%

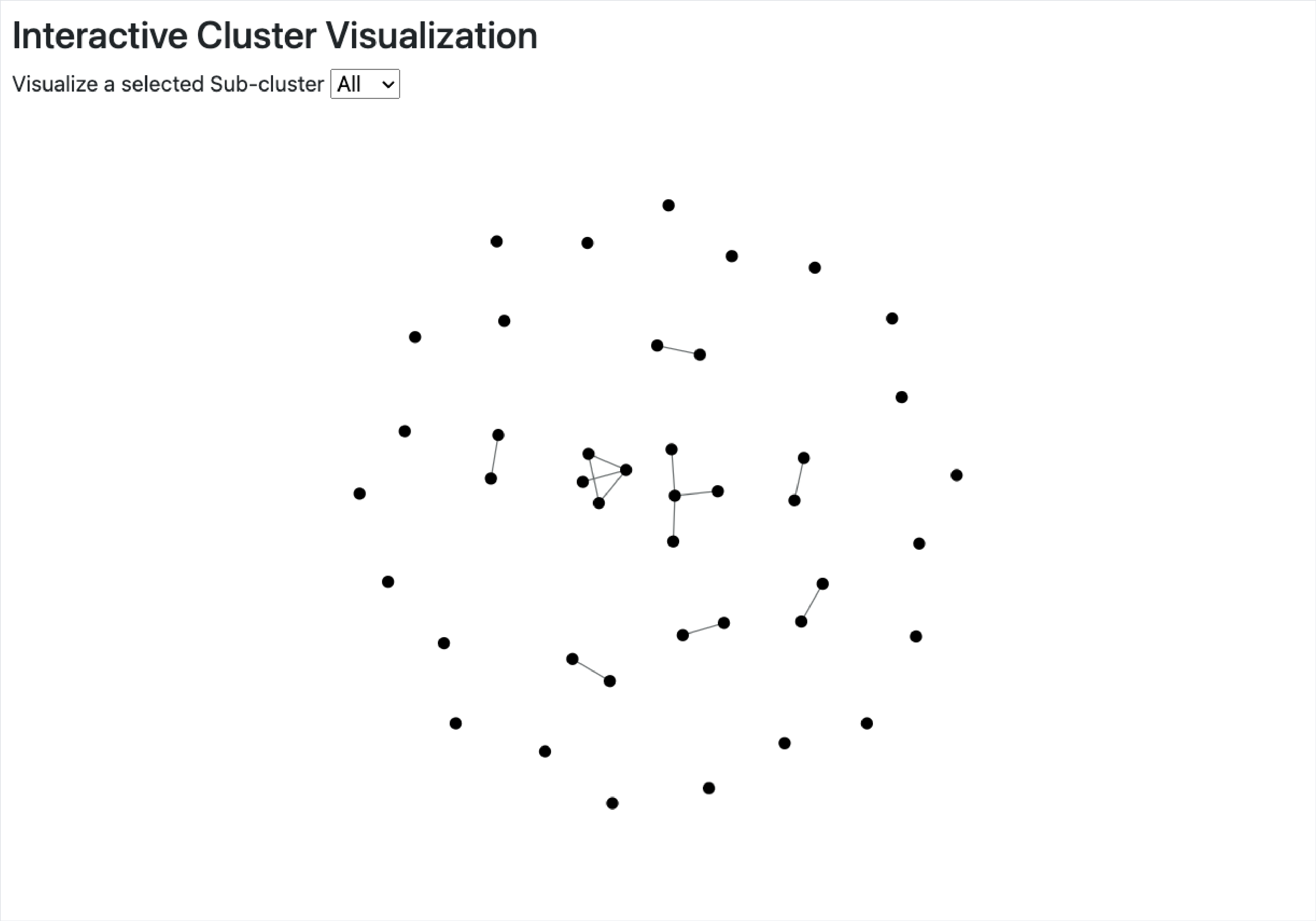
Peptide Length: No Min – No Max

Cluster Method: Cluster-break for clear representative sequence



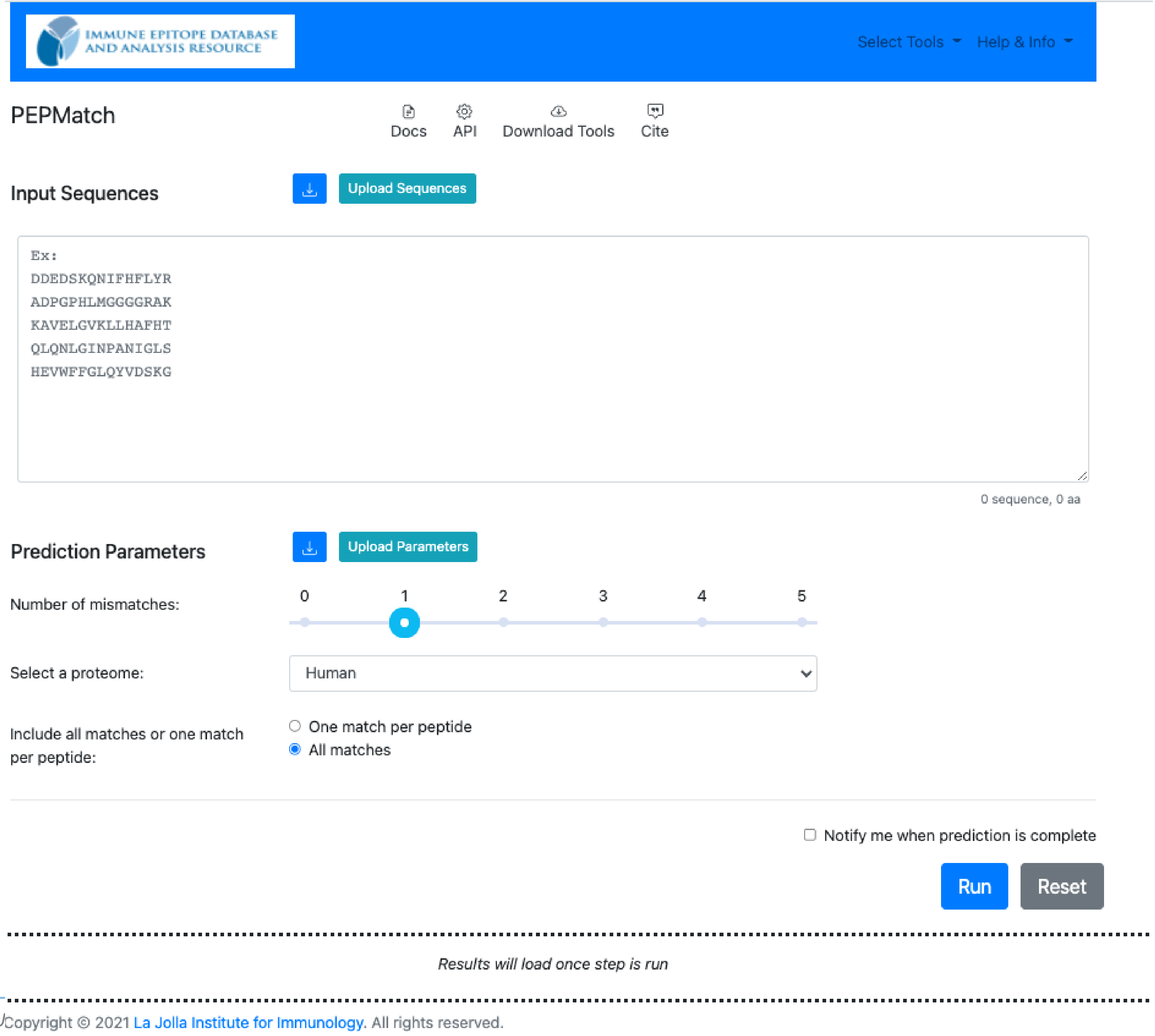
Showing from 1 to 50 of 50 rows

Cluster.Sub-Cluster Number	Peptide Number	Alignment	Position	Description	Peptide
1.1	Consensus	TFQLMXLYGRXXDLSSDIKEKFAKLCEA	-	-	-
1.1	1	TFQLMVLYGRTKDLSSDIKE--------	1	Rat Pep17	TFQLMVLYGRTKDLSSDIKE
1.1	2	-----GLYGREPDLSSDIKERFA-----	6	Mus Pep3	GLYGREPDLSSDIKERFA
1.1	3	-------YGREPDLSLDIKEK-------	8	Mus Pep7	YGREPDLSLDIKEK
1.1	4	--------GRTKDLSSDIKEKFAKLCEA	9	Rat Pep9	GRTKDLSSDIKEKFAKLCEA
2.1	Consensus	YDRYVMXHLINXKXGETFQLMXLYGRTK	-	-	-
2.1	1	YDRYVMFHLINFKNGETFQL--------	1	Rat Pep19	YDRYVMFHLINFKNGETFQL
2.1	2	------AHLINEKDGETFQLM-------	7	Mus Pep9	AHLINEKDGETFQLM
2.1	3	--------LINFKNGETFQLMVLYGRTK	9	Rat Pep12	LINFKNGETFQLMVLYGRTK
2.1	4	----------NEKDGETFQLMGLY----	11	Mus Pep6	NEKDGETFQLMGLY
3.1	Consensus	FXXHIXVLENSLXFKFRIKE	-	-	-
3.1	1	FMQHIDVLENSLGFKFRIKE	1	Rat Pep6	FMQHIDVLENSLGFKFRIKE
3.1	2	FVEHIHVLENSLAFK-----	1	Mus Pep2	FVEHIHVLENSLAFK
4.1	Consensus	EENGSMRVFXXHIXVLENSL	-	-	-
4.1	1	EENGSMRVFMQHIDVLENSL	1	Rat Pep4	EENGSMRVFMQHIDVLENSL



Interactive Cluster Visualization

Visualize a selected Sub-cluster All



PEPMatch

Input Sequences

```
Ex:
DDEDSKQNIFHFLYR
ADPGPHLMGGGGRAK
KAVELGVKLLHAFHT
QLQNLGINPANIGLS
HEVWFFGLQYVDSKG
```

0 sequence, 0 aa

Prediction Parameters

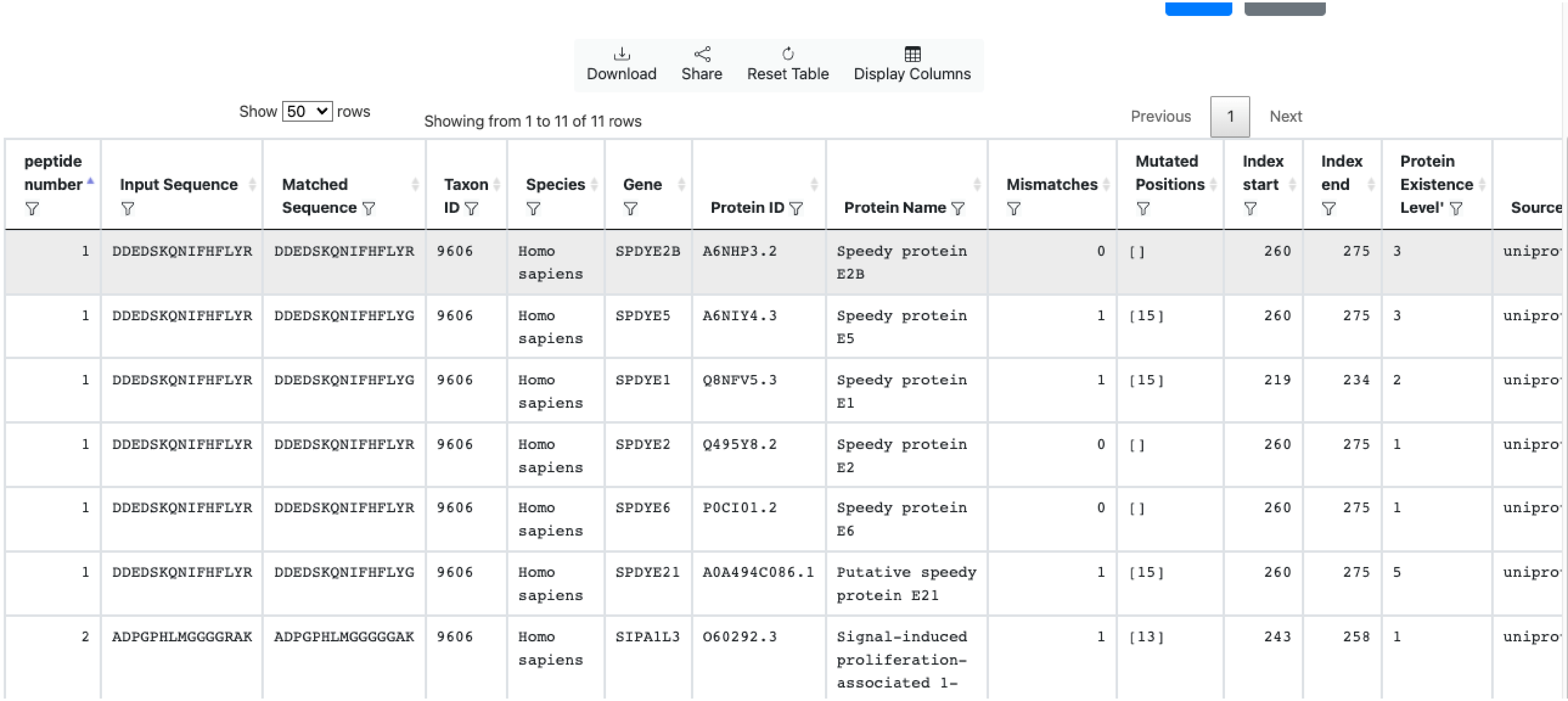
Number of mismatches: 0 [✓ 1] 2 3 4 5

Select a proteome: Human

Include all matches or one match per peptide:
○ One match per peptide
● All matches

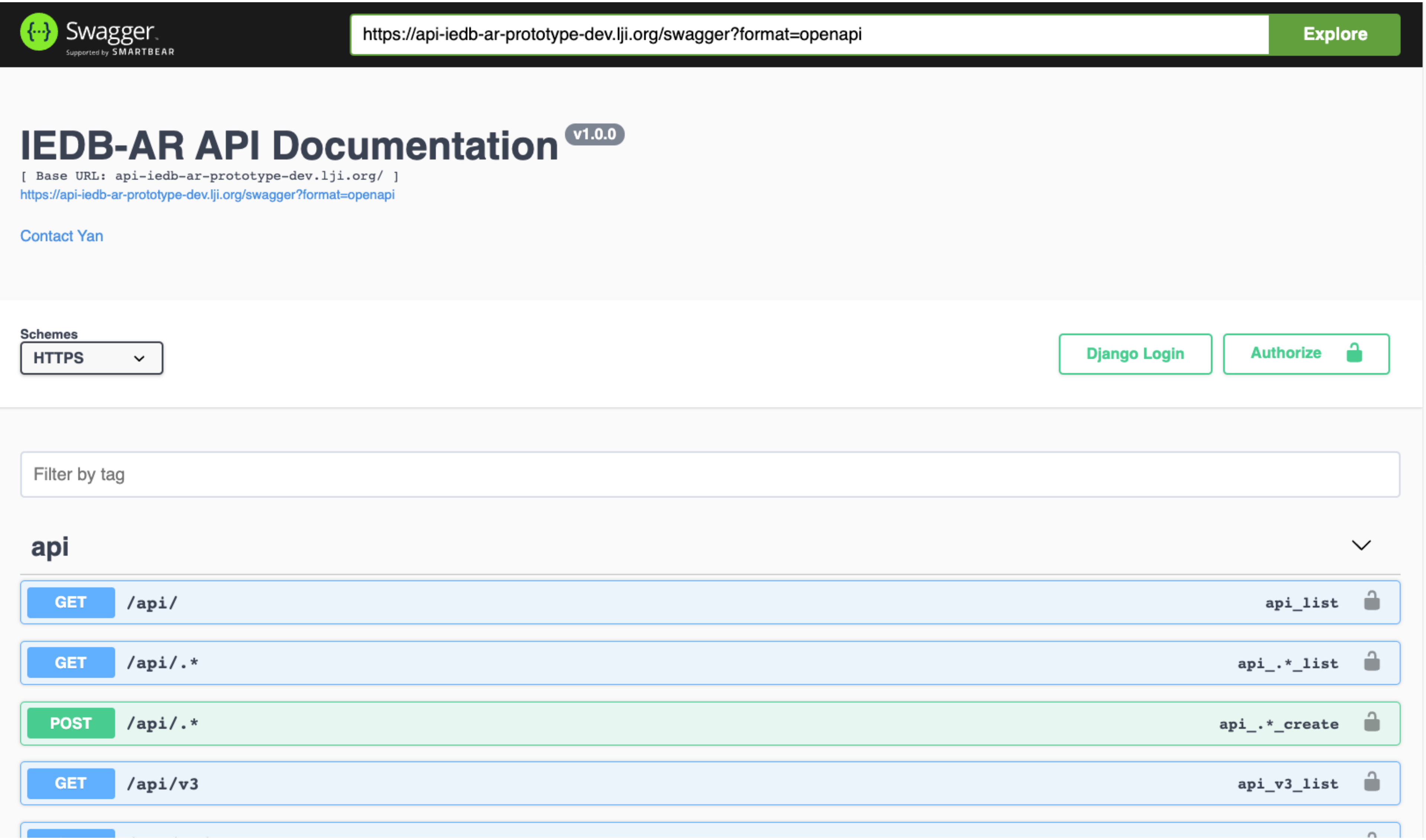
☐ Notify me when prediction is complete

Results will load once step is run



Showing from 1 to 11 of 11 rows

peptide number	Input Sequence	Matched Sequence	Taxon ID	Species	Gene	Protein ID	Protein Name	Mismatches	Mutated Positions	Index start	Index end	Protein Existence Level'	Source
1	DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYR	9606	Homo sapiens	SPDYE2B	A6NHP3.2	Speedy protein E2B	0	[]	260	275	3	unipro
1	DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYG	9606	Homo sapiens	SPDYE5	A6NIY4.3	Speedy protein E5	1	[15]	260	275	3	unipro
1	DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYG	9606	Homo sapiens	SPDYE1	Q8NFV5.3	Speedy protein E1	1	[15]	219	234	2	unipro
1	DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYR	9606	Homo sapiens	SPDYE2	Q495Y8.2	Speedy protein E2	0	[]	260	275	1	unipro
1	DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYR	9606	Homo sapiens	SPDYE6	P0CI01.2	Speedy protein E6	0	[]	260	275	1	unipro
1	DDEDSKQNIFHFLYR	DDEDSKQNIFHFLYG	9606	Homo sapiens	SPDYE21	A0A494C086.1	Putative speedy protein E21	1	[15]	260	275	5	unipro
2	ADPGPHLMGGGGRAK	ADPGPHLMGGGGGAK	9606	Homo sapiens	SIPA1L3	O60292.3	Signal-induced proliferation-associated 1-	1	[13]	243	258	1	unipro



https://api-iedb-ar-prototype-dev.lji.org/swagger?format=openapi

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

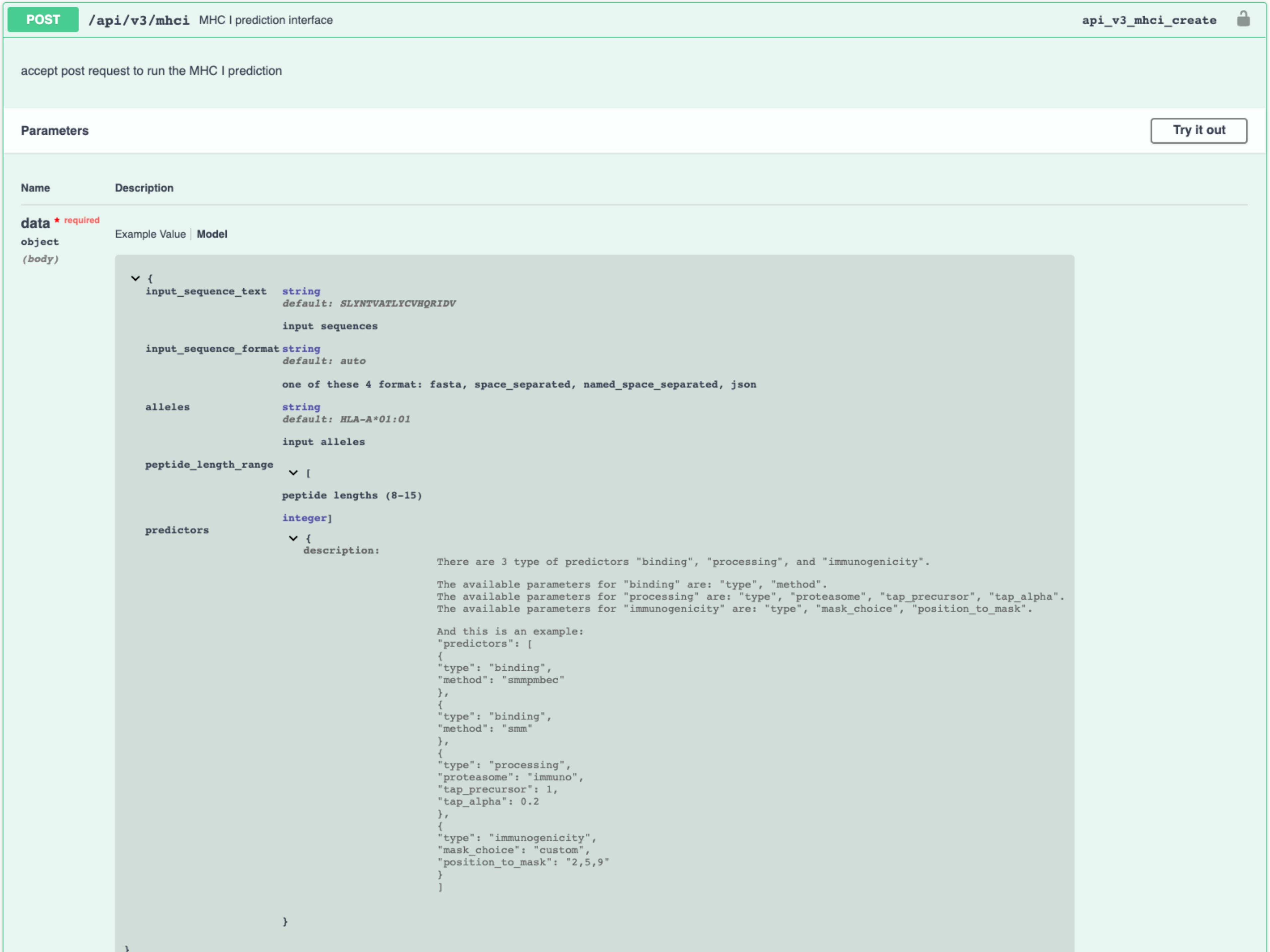
Schemes: HTTPS

GET `/api/` `api_list`

GET `/api/.*` `api_.*_list`

POST `/api/.*` `api_.*_create`

GET `/api/v3` `api_v3_list`



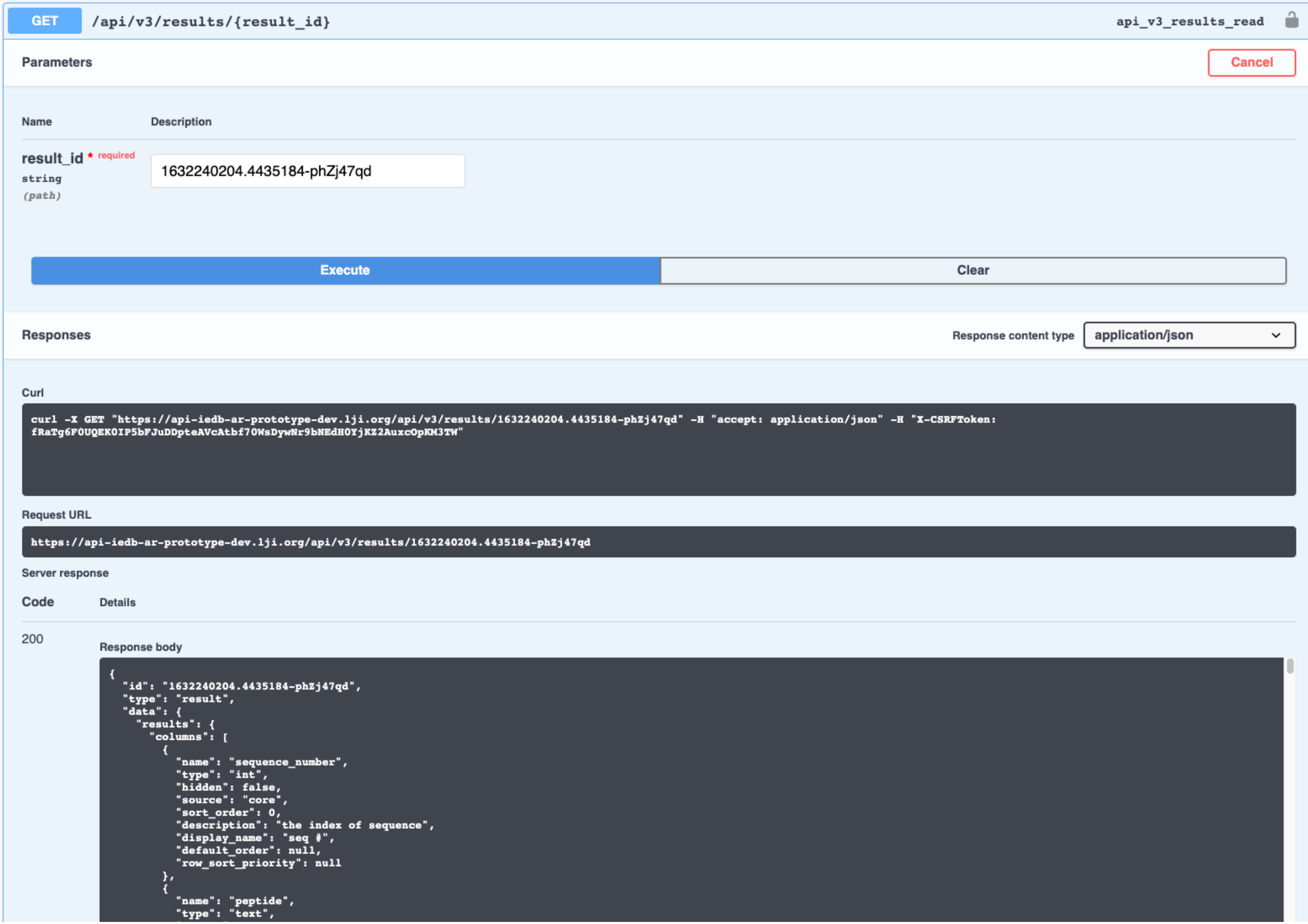
`/api/v3/mhci` MHC I prediction interface `api_v3_mhci_create`

accept post request to run the MHC I prediction

Parameters

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   [

                       peptide lengths (8-15)

                       integer]
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"
                                   }
                                   ]


                       }
}
```



result_id * required
string
(path)

1632240204.4435184-phZj47qd

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: fRaTg6F0UQEK0IP5bFJuDDpteAVcAtbf70WsDywNr9bNEdH0YjKZ2AuxcOpKM3TW"
```

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",
```