IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

MHC-I Binding Predictions

tools.iedb.org

Presented by:
Raphael Trevizani

Outline

- MHC class I binding prediction
- MHC class II binding prediction
- TepiTool
- Datasets availability
- Benchmarking of class I tools
- Contributing tools

- How the tool works
- Recommendations
- Interpreting results
- Exercises

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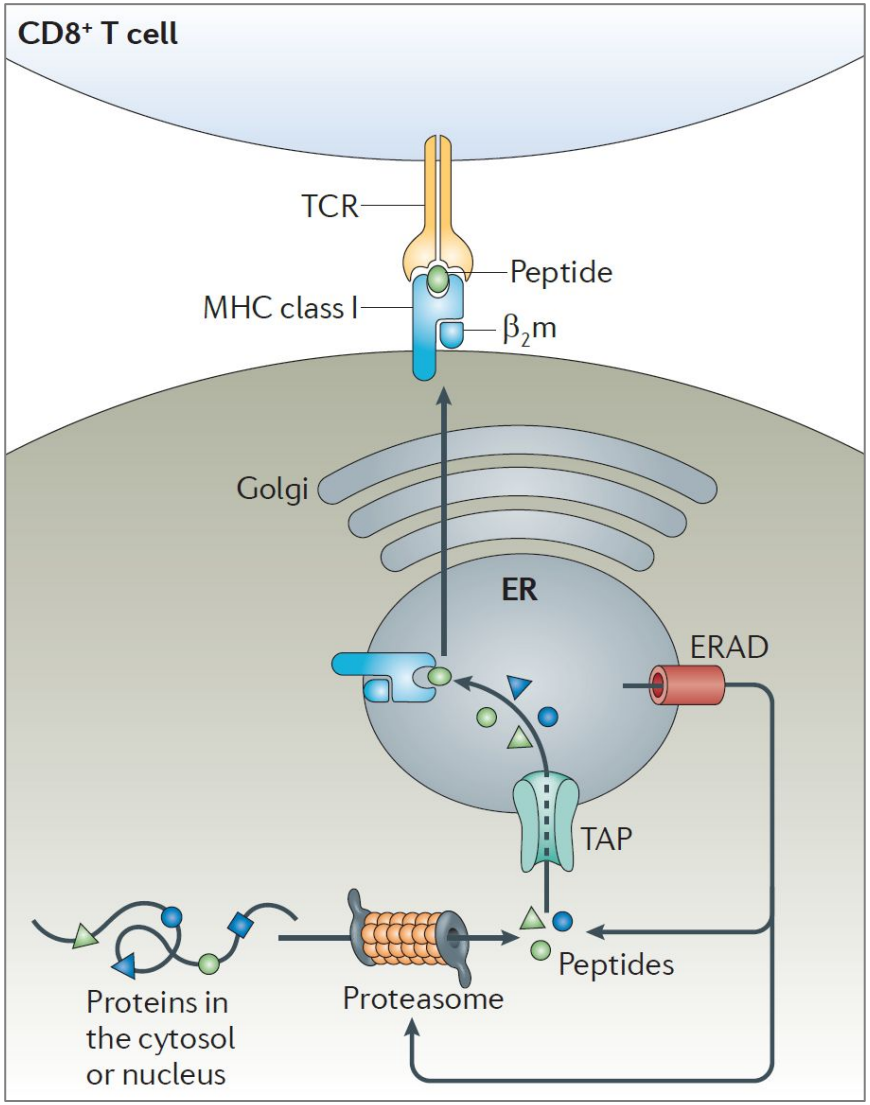

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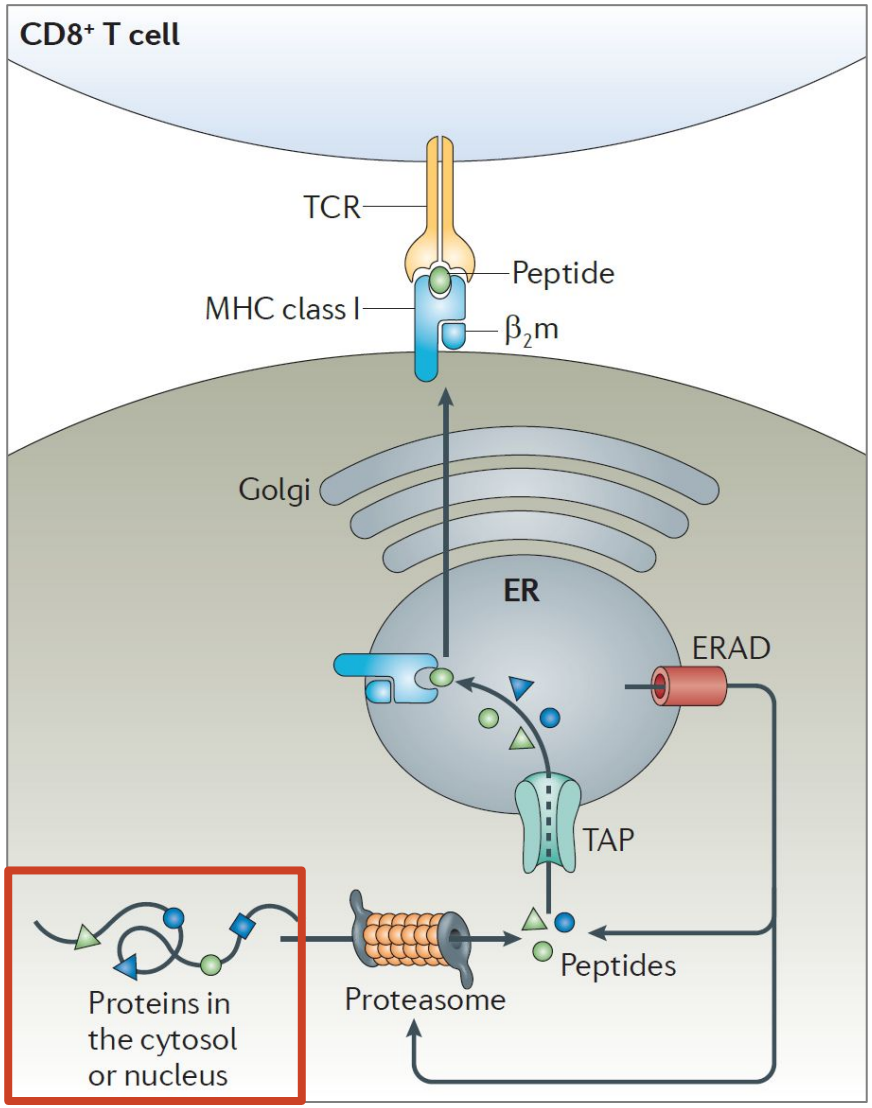

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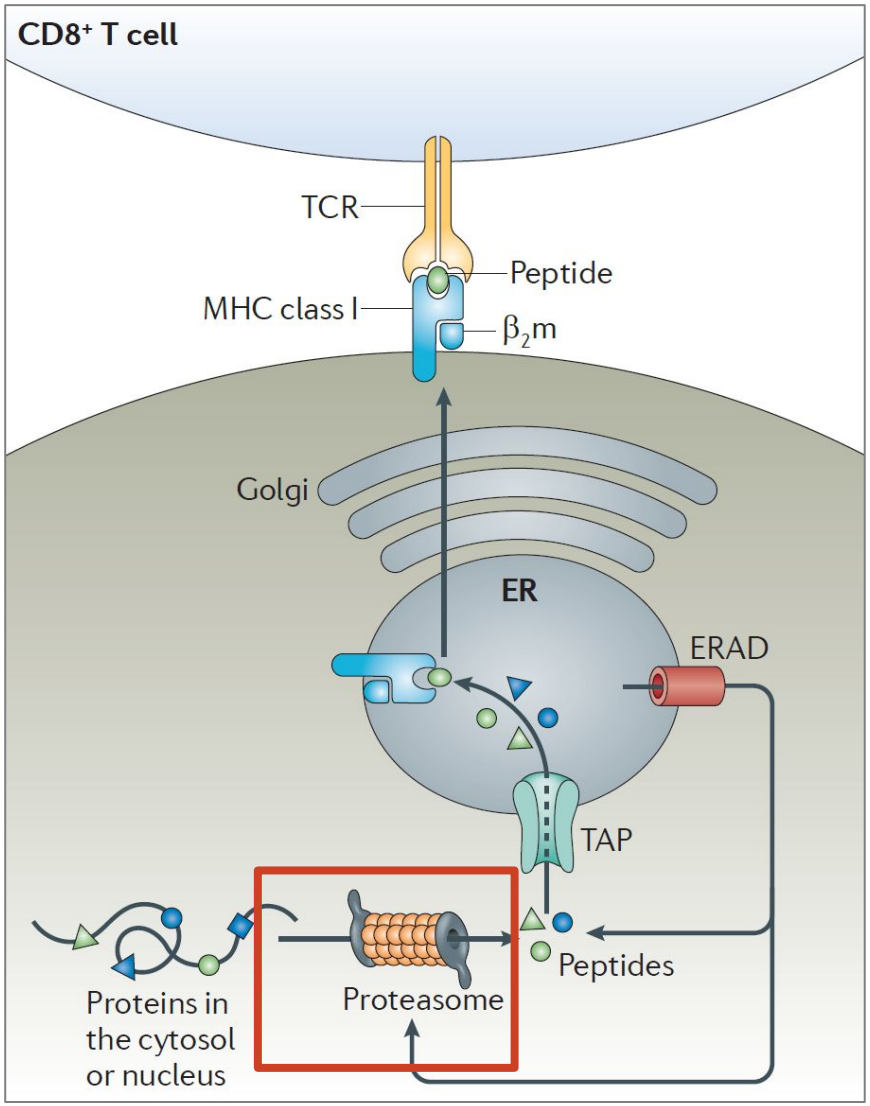

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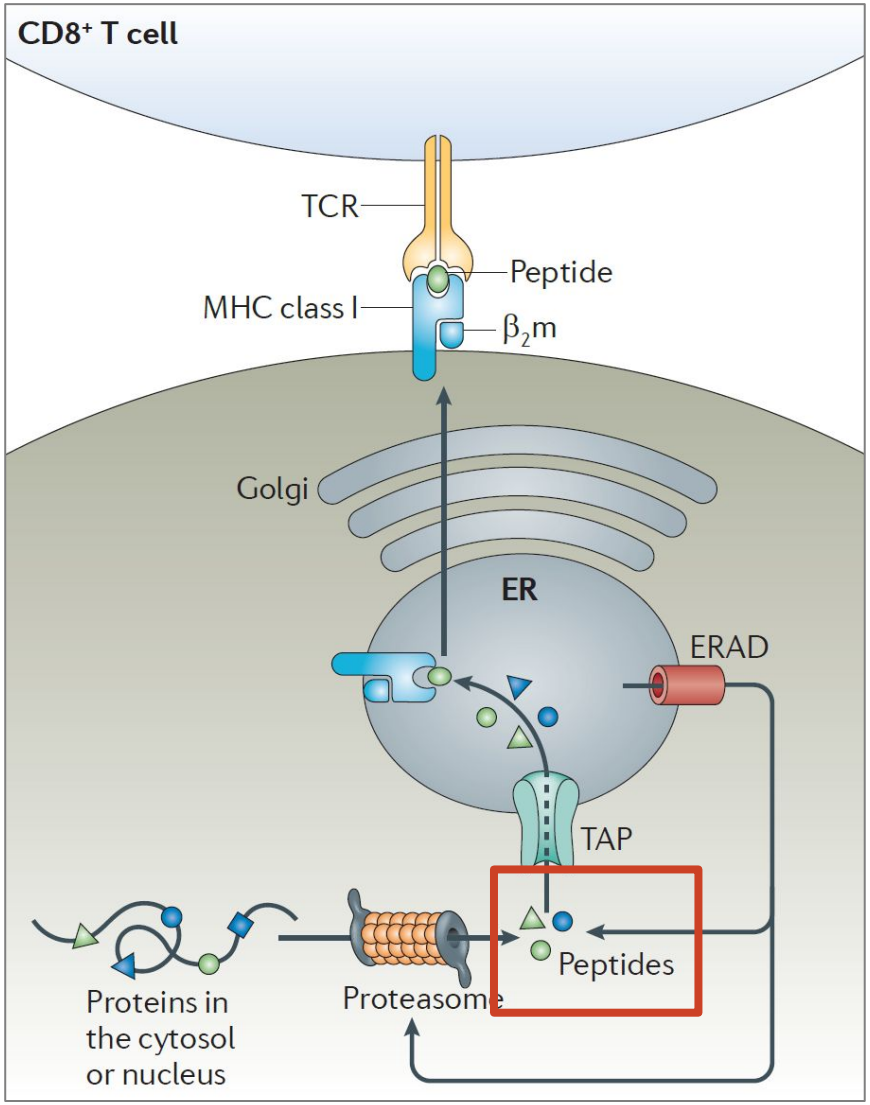

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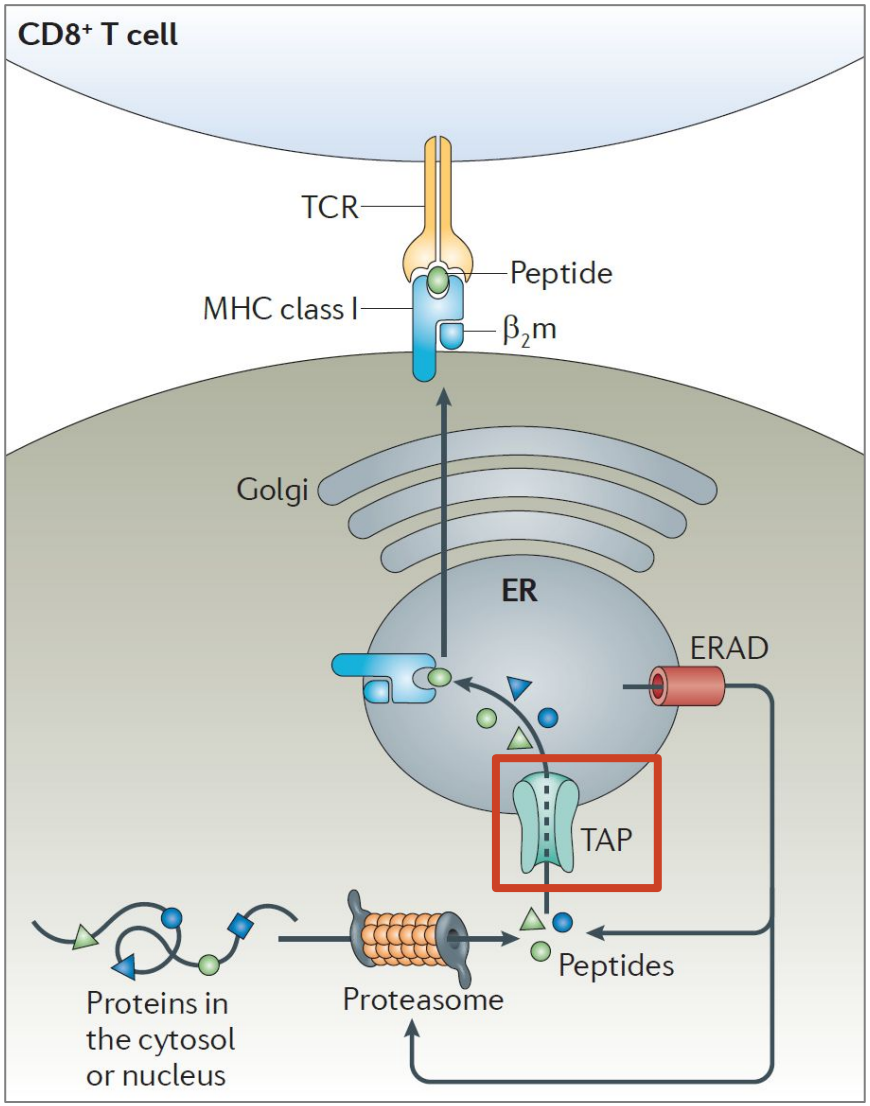

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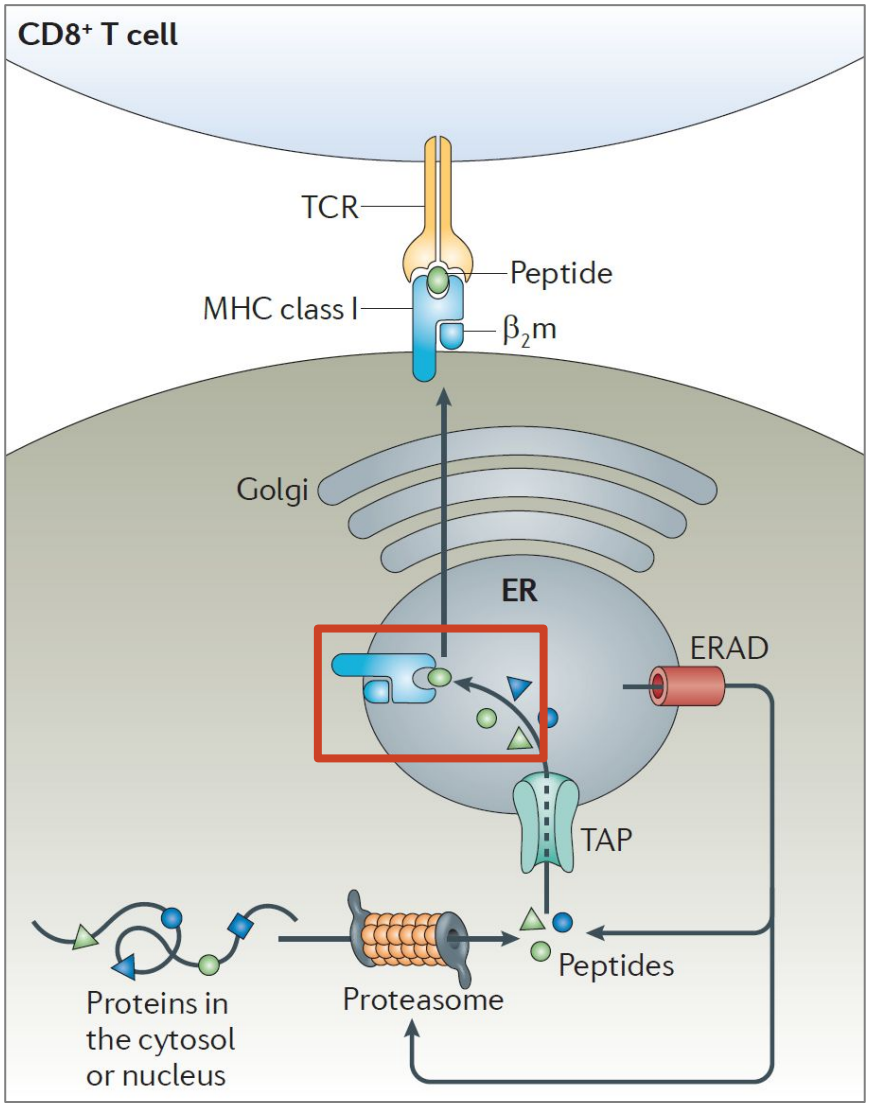

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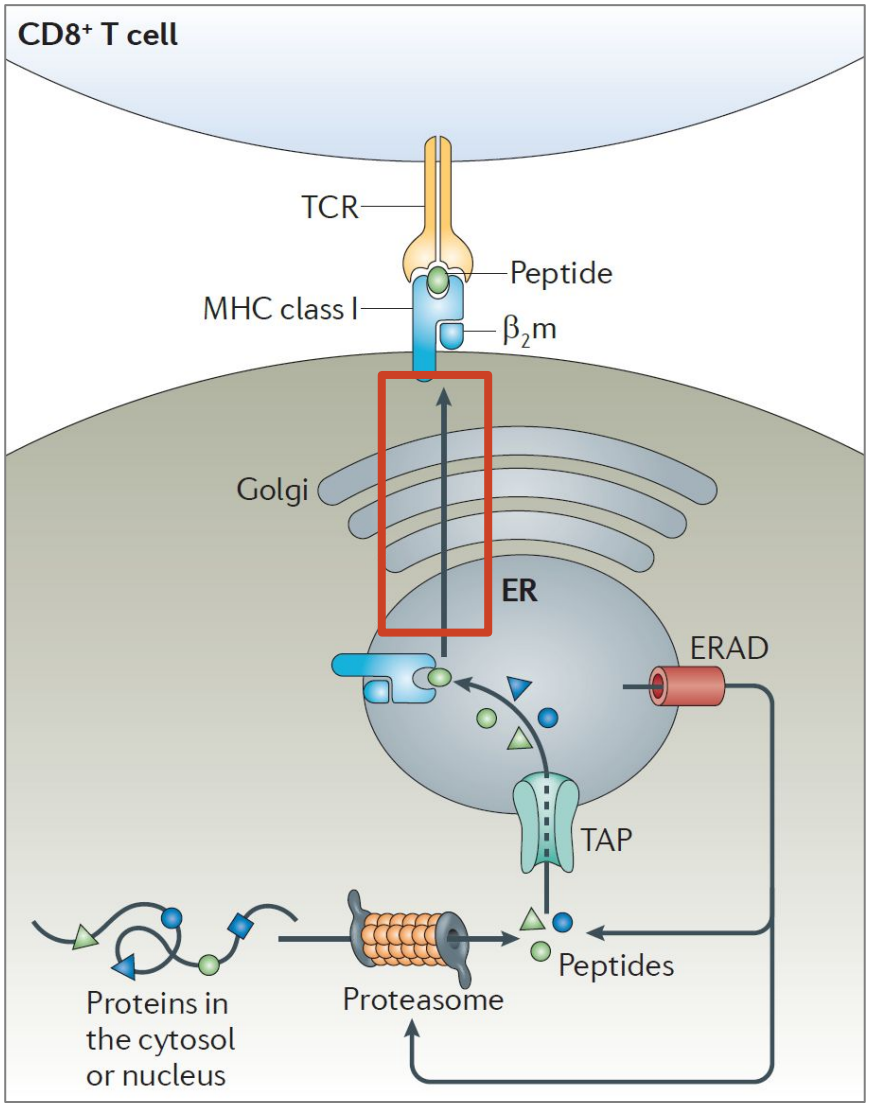

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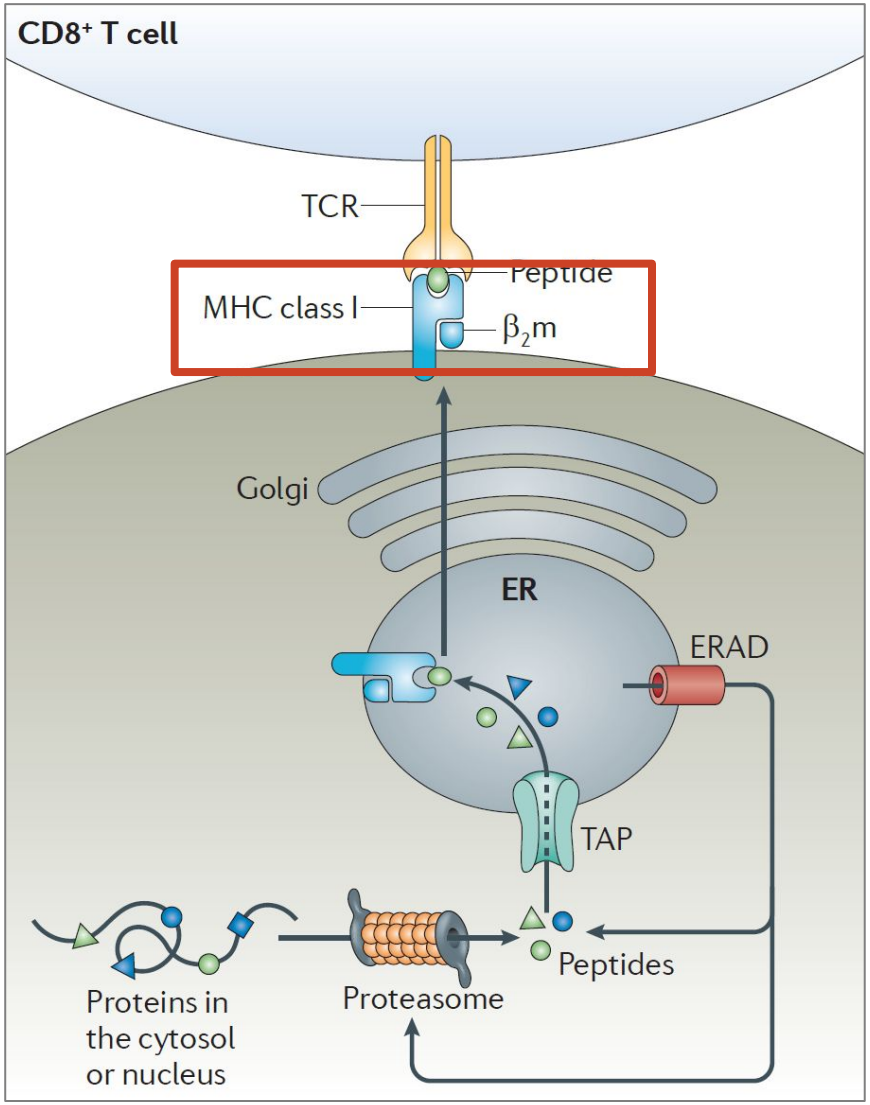

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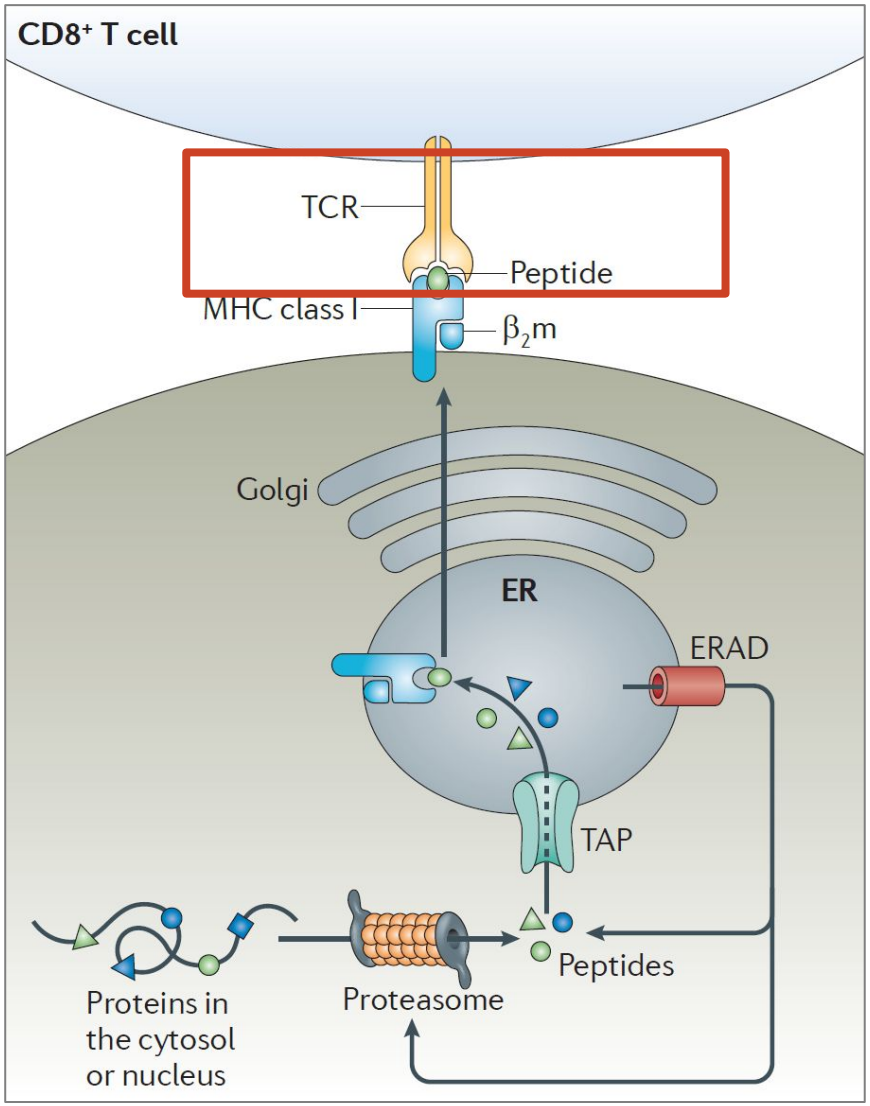

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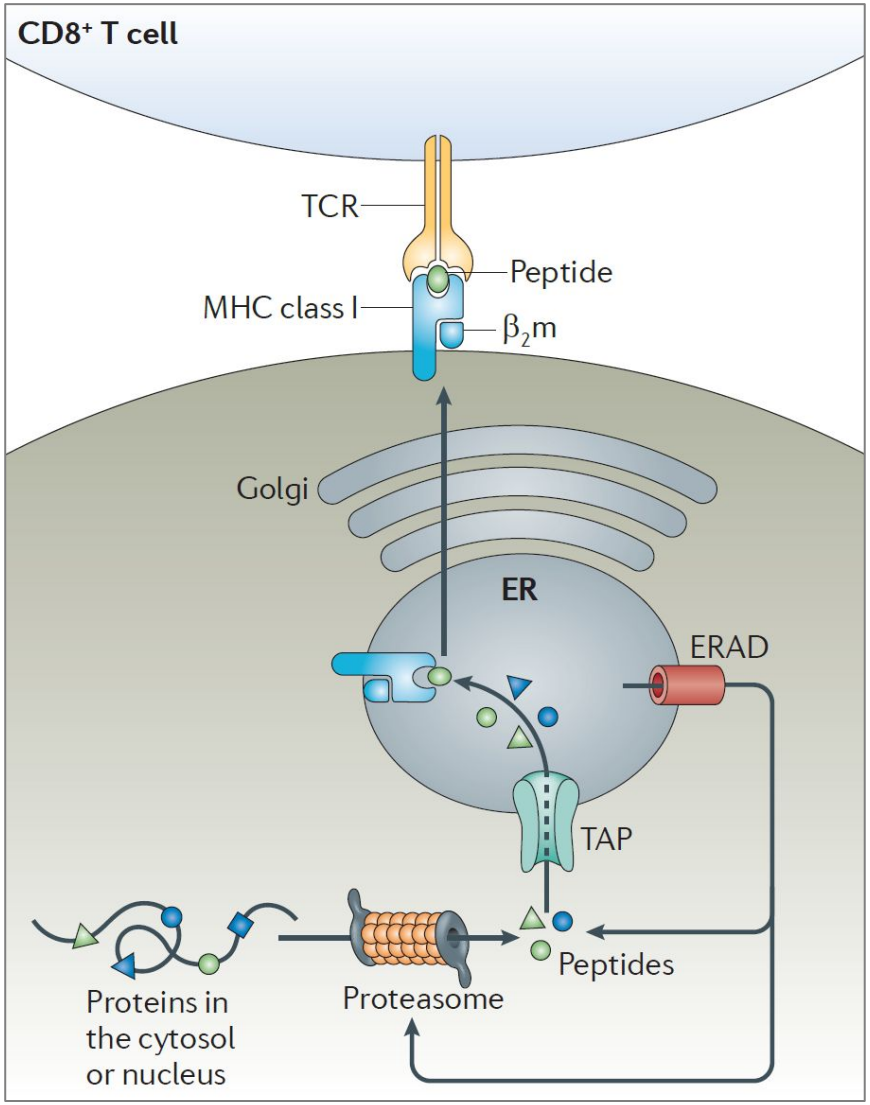

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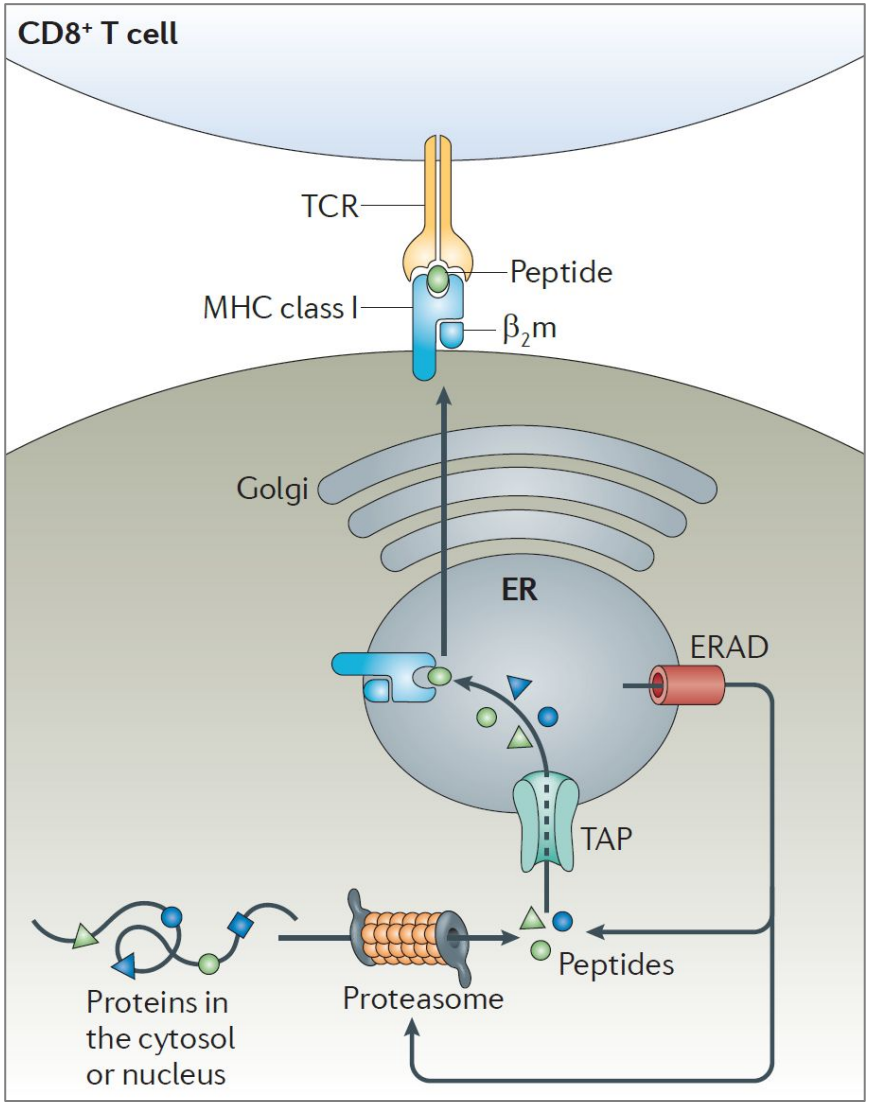

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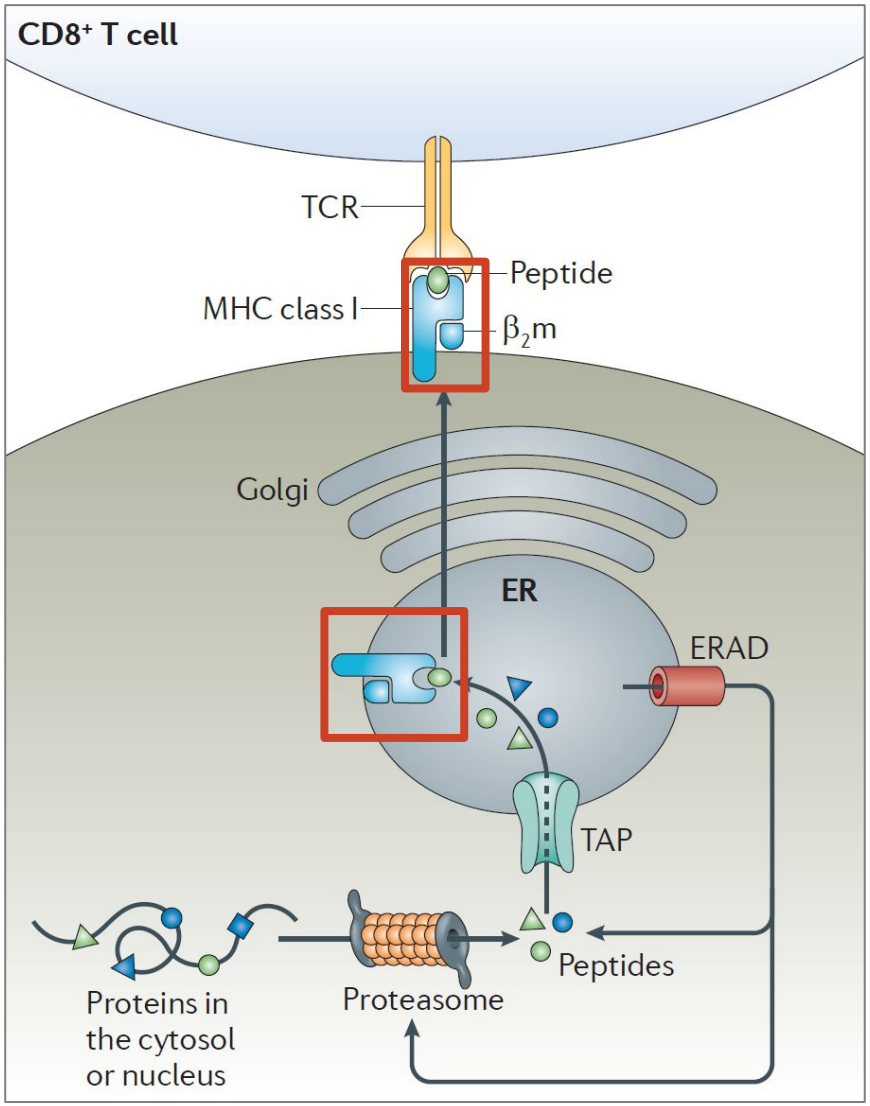

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Class I MHC molecule

- Expressed by almost all nucleated cells
- Presents antigen to **CD8+ T cells** (Cytotoxic T cells)
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- The binding groove is **closed** at both ends and can accommodate peptides of **8-15 AA**
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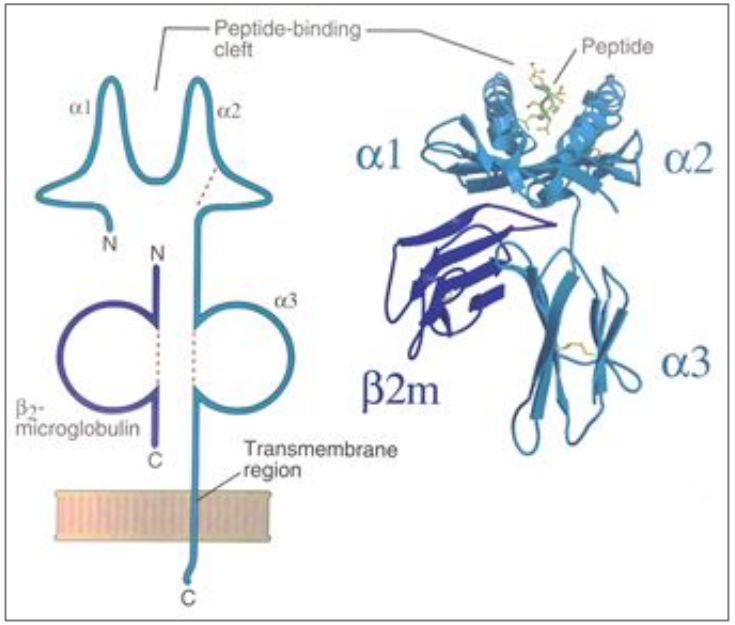

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Cellular & Molecular Immunology, 5th Ed by Abbas and Lichtman

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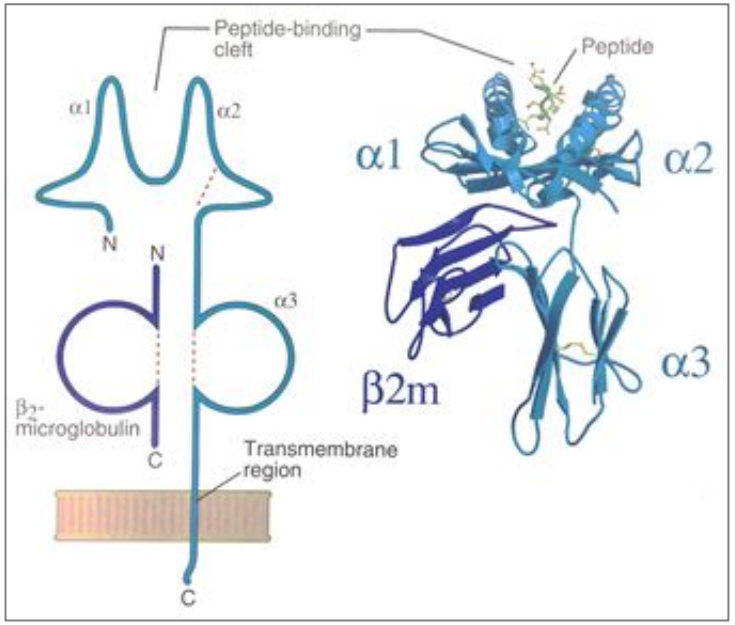

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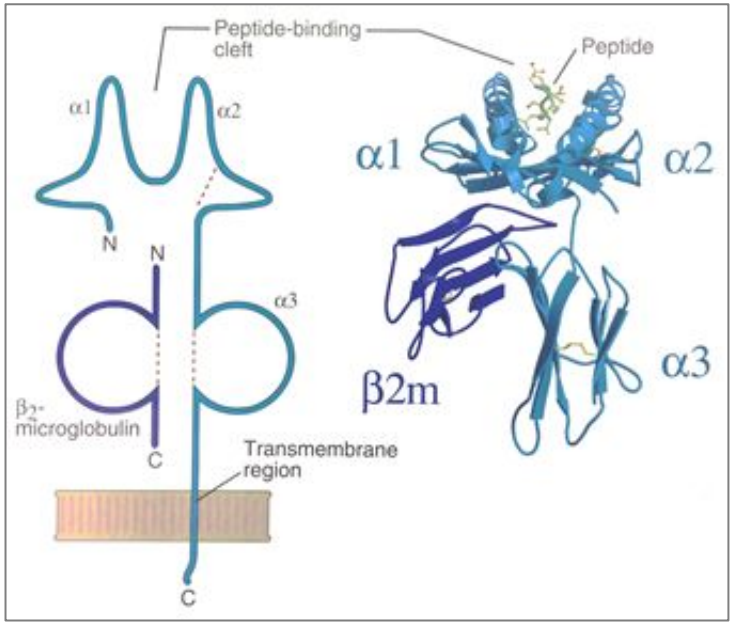

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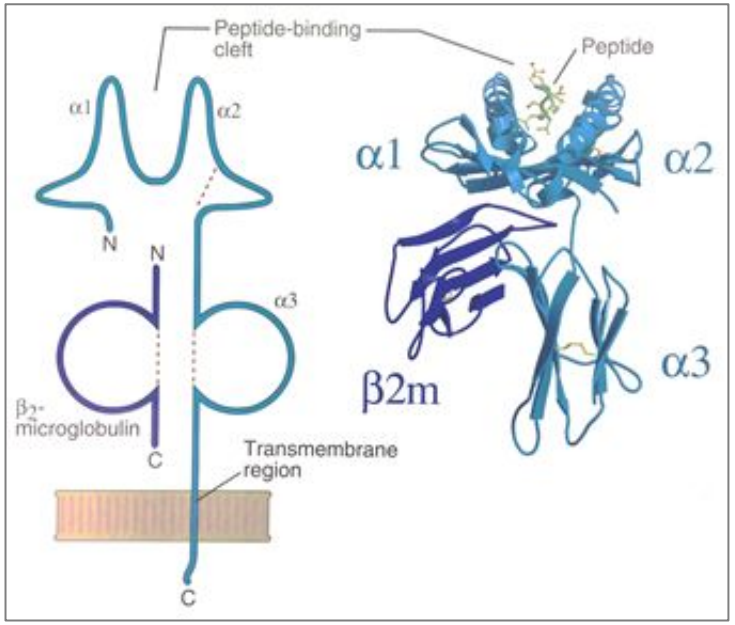

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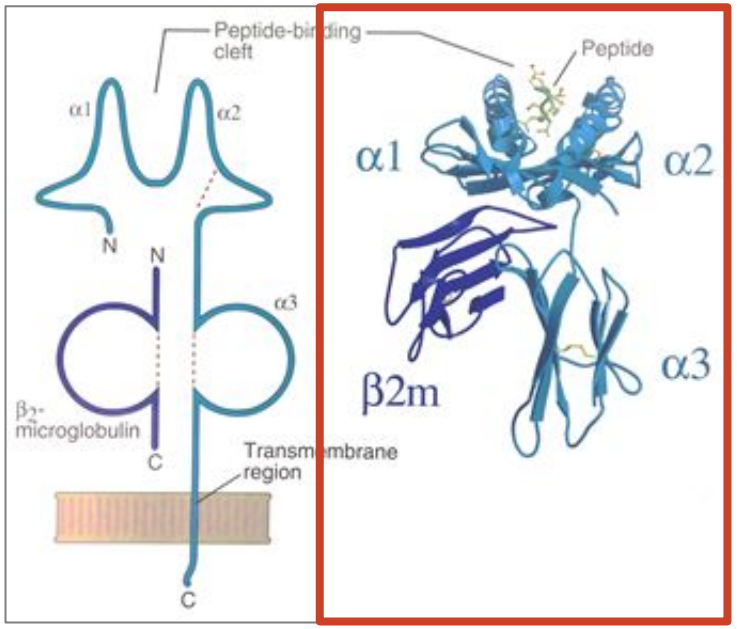

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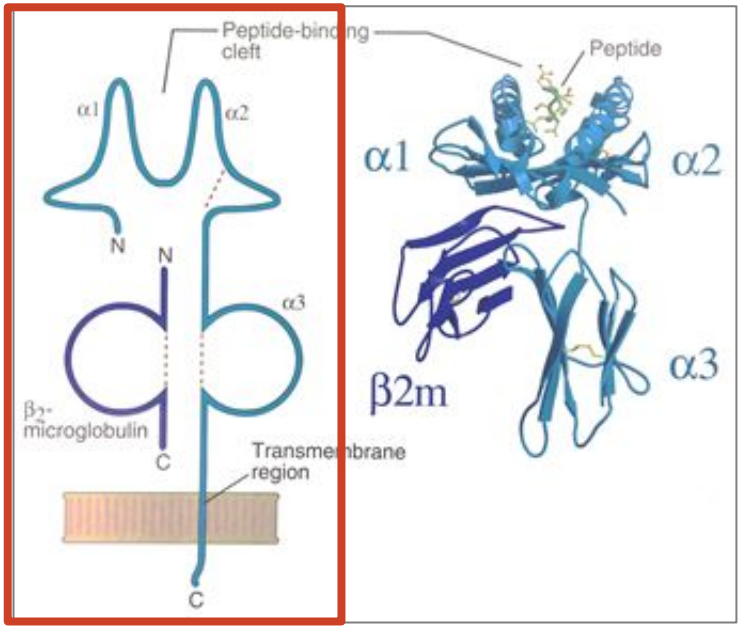

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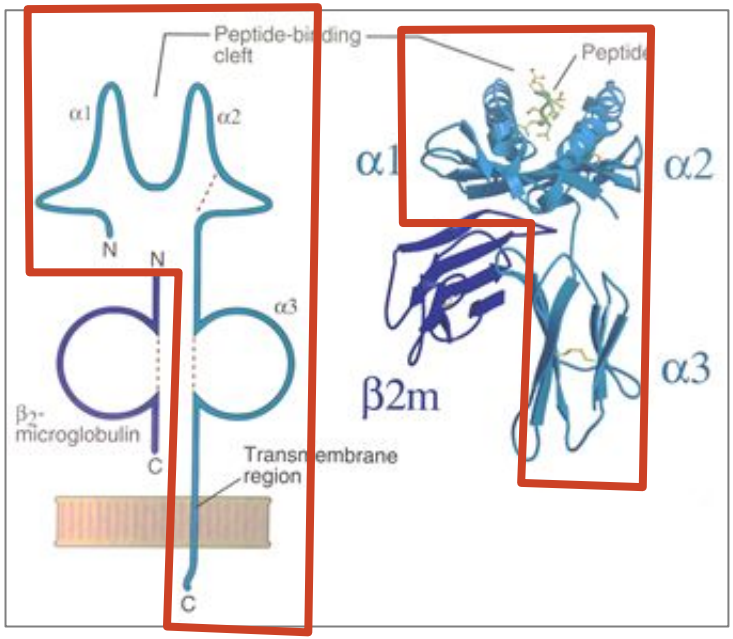

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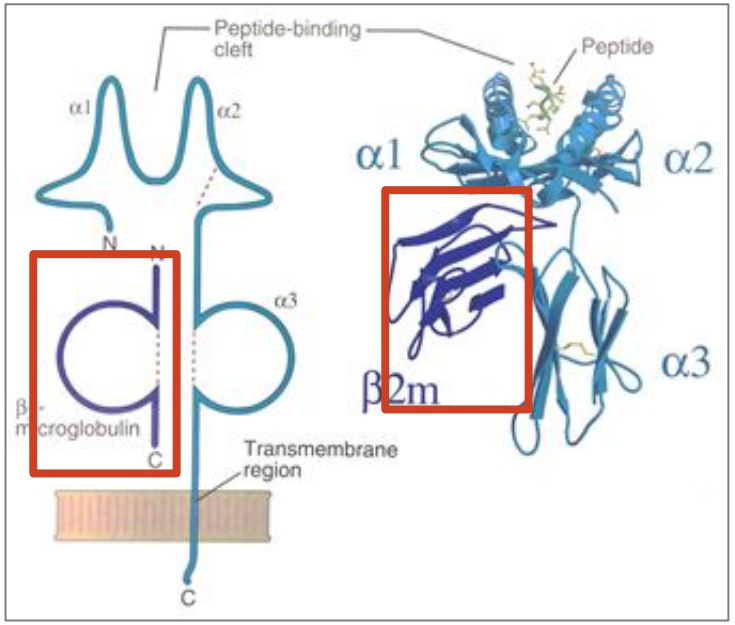

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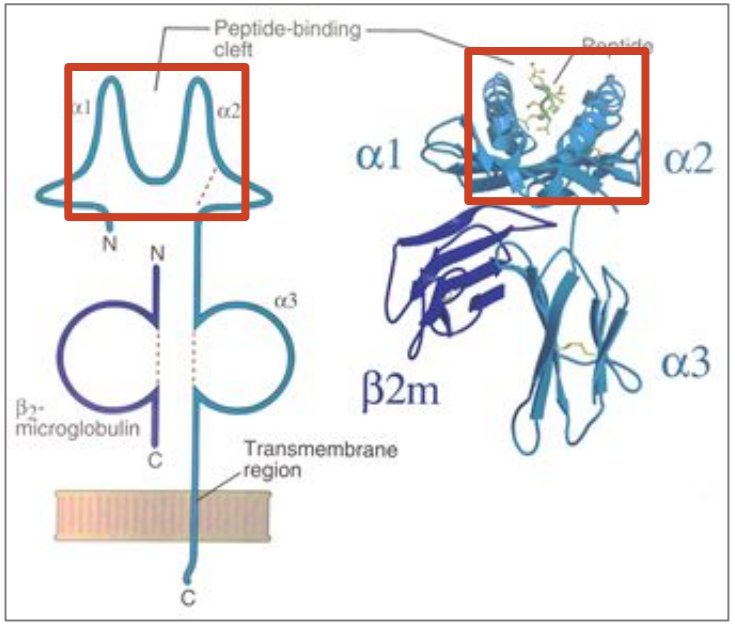

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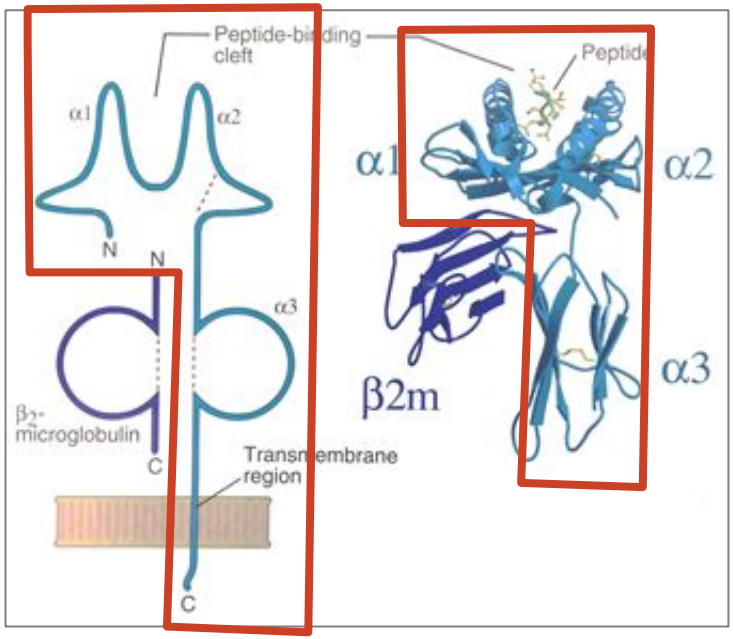

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MHC binding predictions

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

Peptide binding data HLA-A*01:01

Peptide	IC_{50} (nM)
ASFCGSPY	51.4
LTDFGLSK	739.3
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KSVFNSLY	1466.0
RDWAHNSL	1804.6
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Machine learning algorithms

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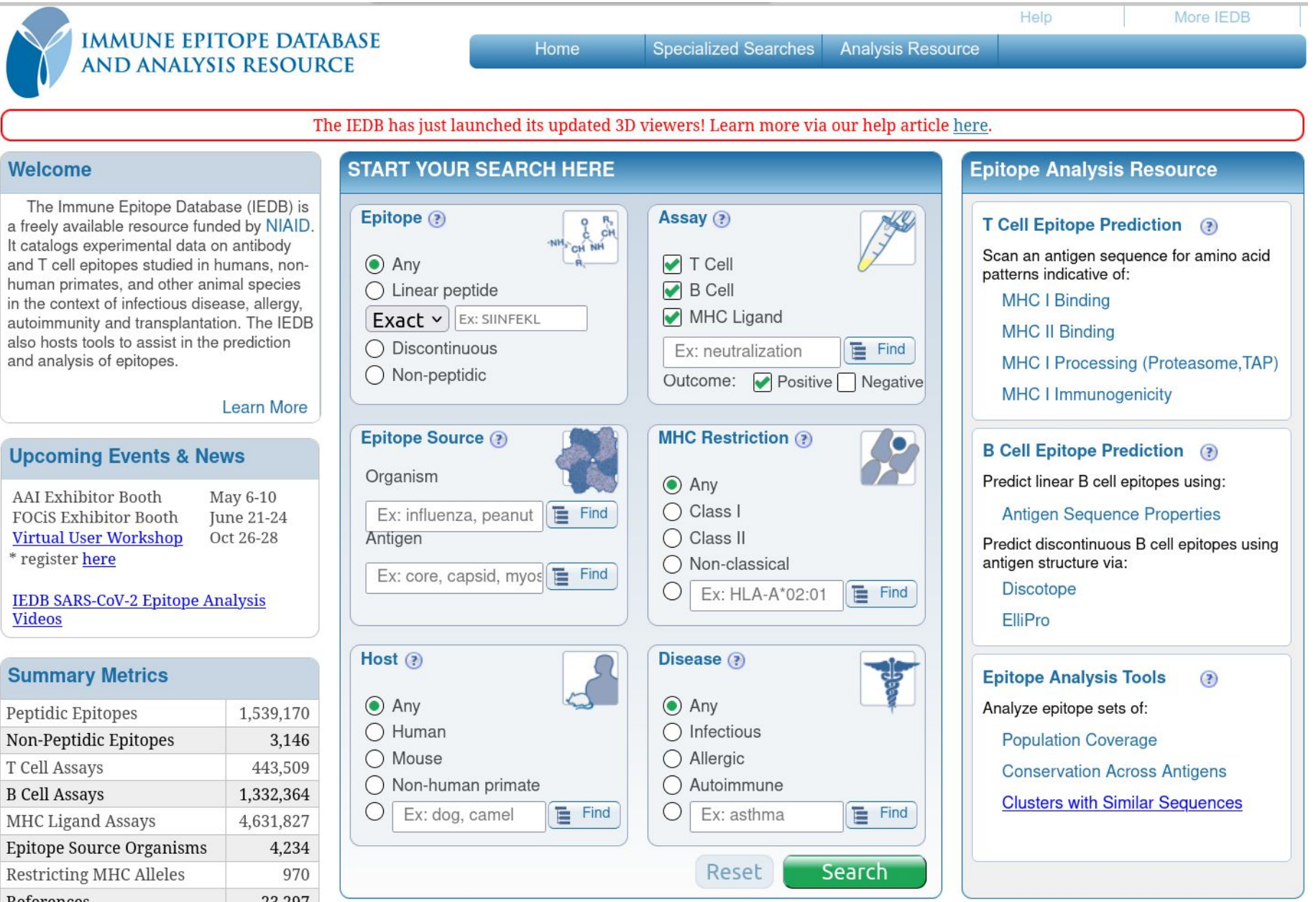
MHC class I binding prediction methods available

Method	Reference	Performance Reported
NetMHCpan EL - 4.1	Reynisson et al., 2020	0.978 AUC (evaluated on EL data)
NetMHCpan EL - 4.0	Paul et al., 2020	0.977 AUC (average)
NetMHCpan BA - 4.1	Reynisson et al., 2020	0.893 AUC (evaluated on BA data)
NetMHCpan BA - 4.0	Paul et al., 2020	0.975 AUC (average)
Consensus	Moutaftsi et al., 2006	
ANN (NetMHC - 4.0)	Andreatta & Nielsen, 2016	0.887 AUC (average)
SMM with Peptide:MHC Binding Energy Covariance matrix (SMMPMBEC)	Kim et al., 2009	0.894 AUC (average)
Stabilized matrix method (SMM)	Peters & Sette, 2005	0.887 AUC (average) (Kim et. al., 2009)
Combinatorial library (CombLib)	Sidney et al., 2008	0.909 AUC (HLA-A*0201)
PickPocket - 1.1	Zhang et al., 2009	0.895 AUC (average)
NetMHCcons - 1.1	Karosiene et al., 2012	0.729 PCC (average)
NetMHCstabpan - 1.0	Rasmussen et al., 2016	0.980 AUC (average)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The IEDB has just launched its updated 3D viewers! Learn more via our help article here.
Welcome
The Immune Epitope Database (IEDB) is a freely available resource funded by NIAID. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of infectious disease, allergy, autoimmunity and transplantation. The IEDB also hosts tools to assist in the prediction and analysis of epitopes.
Learn More
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FOCiS Exhibitor Booth June 21-24
Virtual User Workshop Oct 26-28
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IEDB SARS-CoV-2 Epitope Analysis Videos
Summary Metrics
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Non-Peptidic Epitopes 3,146
T Cell Assays 443,509
B Cell Assays 1,332,364
MHC Ligand Assays 4,631,827
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Restricting MHC Alleles 970
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Exact
Ex: SIINFEKL
Discontinuous
Non-peptidic
Assay
T Cell
B Cell
MHC Ligand
Ex: neutralization
Find
Outcome: Positive Negative
Epitope Source
Organism
Ex: influenza, peanut
Find
Antigen
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Find
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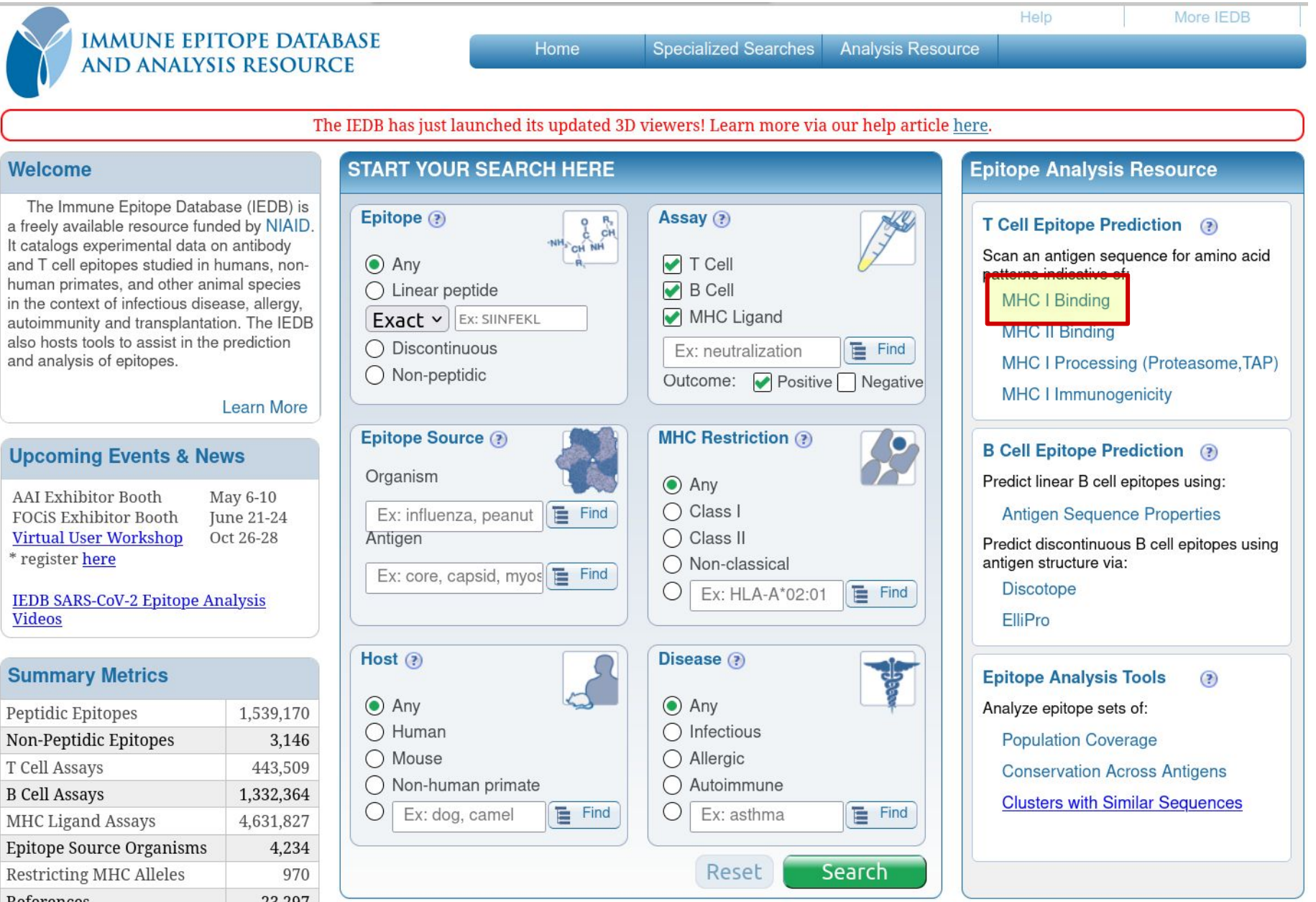
Class I
Class II
Non-classical
Ex: HLA-A*02:01
Find
Host
Any
Human
Mouse
Non-human primate
Ex: dog, camel
Find
Disease
Any
Infectious
Allergic
Autoimmune
Ex: asthma
Find
Reset
Search
Epitope Analysis Resource
T Cell Epitope Prediction
Scan an antigen sequence for amino acid patterns indicative of:
MHC I Binding
MHC II Binding
MHC I Processing (Proteasome,TAP)
MHC I Immunogenicity
B Cell Epitope Prediction
Predict linear B cell epitopes using:
Antigen Sequence Properties
Predict discontinuous B cell epitopes using antigen structure via:
Discotope
ElliPro
Epitope Analysis Tools
Analyze epitope sets of:
Population Coverage
Conservation Across Antigens
Clusters with Similar Sequences


IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE
Help
More IEDB
Home
Specialized Searches
Analysis Resource
The IEDB has just launched its updated 3D viewers! Learn more via our help article here.
Welcome
The Immune Epitope Database (IEDB) is a freely available resource funded by NIAID. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of infectious disease, allergy, autoimmunity and transplantation. The IEDB also hosts tools to assist in the prediction and analysis of epitopes.
Learn More
Upcoming Events & News
AAI Exhibitor Booth May 6-10
FOCiS Exhibitor Booth June 21-24
Virtual User Workshop Oct 26-28
* register here
IEDB SARS-CoV-2 Epitope Analysis Videos
Summary Metrics
Peptidic Epitopes 1,539,170
Non-Peptidic Epitopes 3,146
T Cell Assays 443,509
B Cell Assays 1,332,364
MHC Ligand Assays 4,631,827
Epitope Source Organisms 4,234
Restricting MHC Alleles 970
References 23,297
START YOUR SEARCH HERE
Epitope
Any
Linear peptide
Exact
Ex: SIINFEKL
Discontinuous
Non-peptidic
Assay
T Cell
B Cell
MHC Ligand
Ex: neutralization
Find
Outcome: Positive Negative
Epitope Source
Organism
Ex: influenza, peanut
Find
Antigen
Ex: core, capsid, myos
Find
MHC Restriction
Any
Class I
Class II
Non-classical
Ex: HLA-A*02:01
Find
Host
Any
Human
Mouse
Non-human primate
Ex: dog, camel
Find
Disease
Any
Infectious
Allergic
Autoimmune
Ex: asthma
Find
Reset
Search
Epitope Analysis Resource
T Cell Epitope Prediction
Scan an antigen sequence for amino acid patterns indicative of:
MHC I Binding
MHC II Binding
MHC I Processing (Proteasome,TAP)
MHC I Immunogenicity
B Cell Epitope Prediction
Predict linear B cell epitopes using:
Antigen Sequence Properties
Predict discontinuous B cell epitopes using antigen structure via:
Discotope
ElliPro
Epitope Analysis Tools
Analyze epitope sets of:
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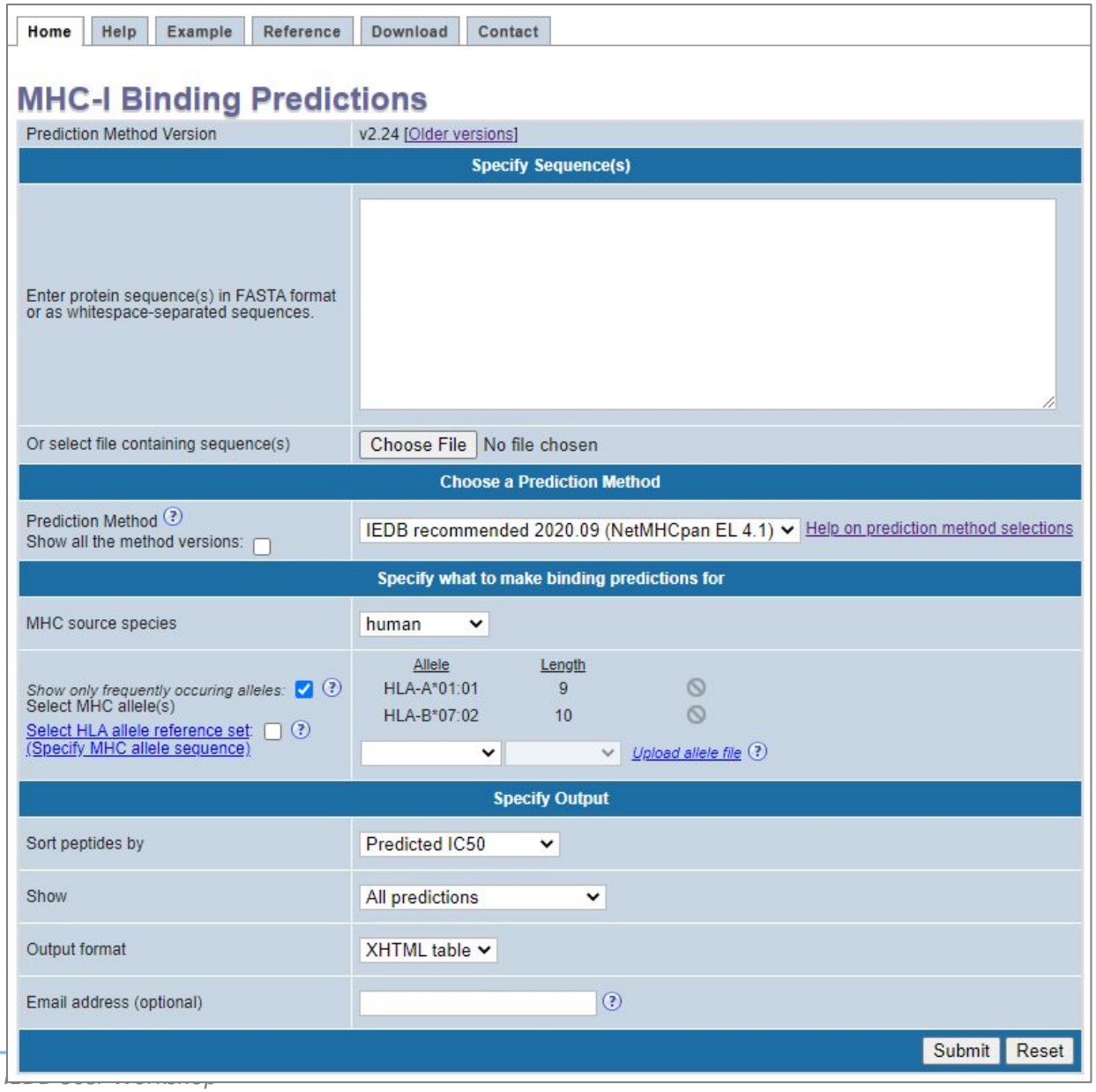
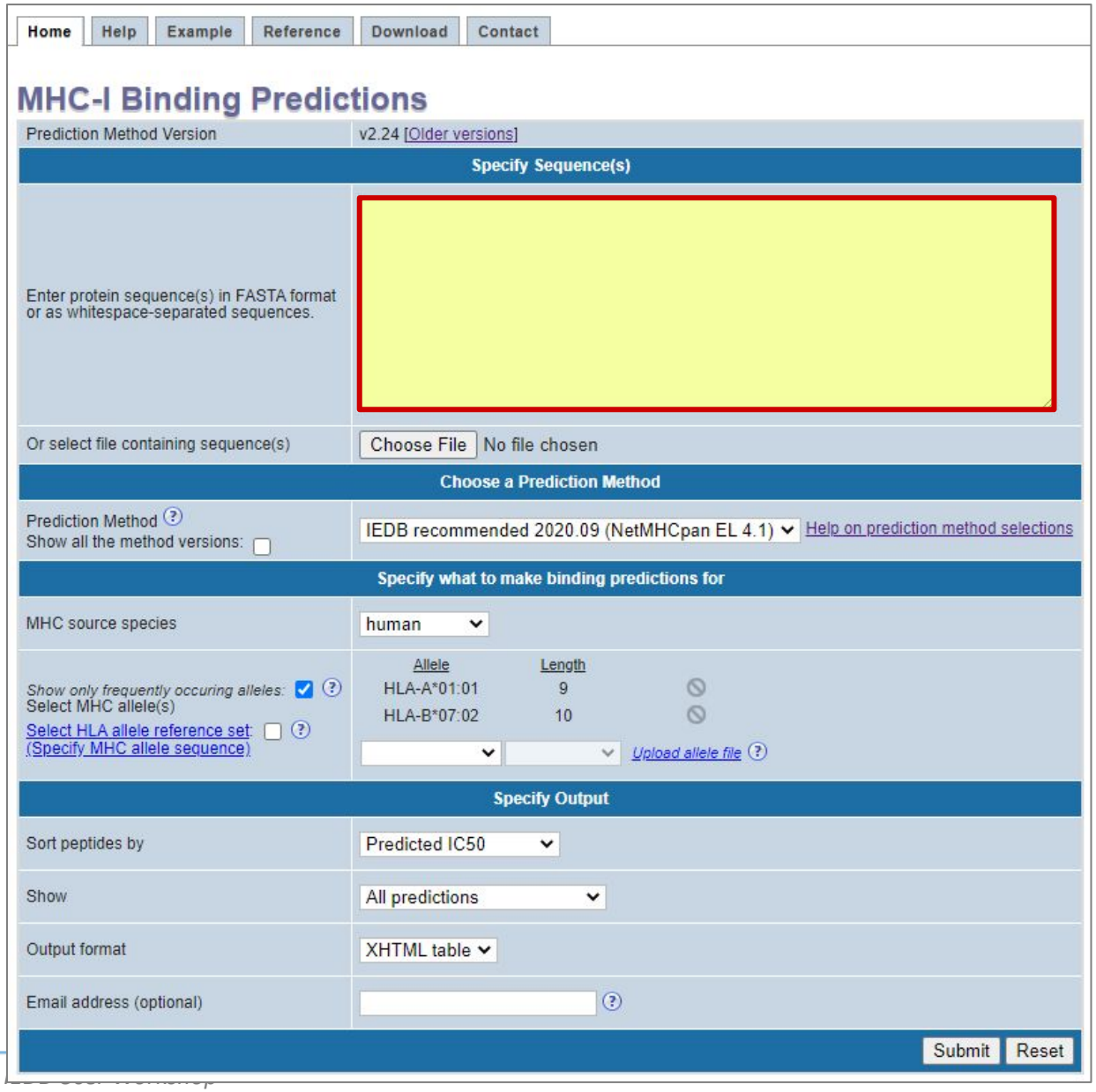
Conservation Across Antigens
Clusters with Similar Sequences

MHC-I binding prediction - example



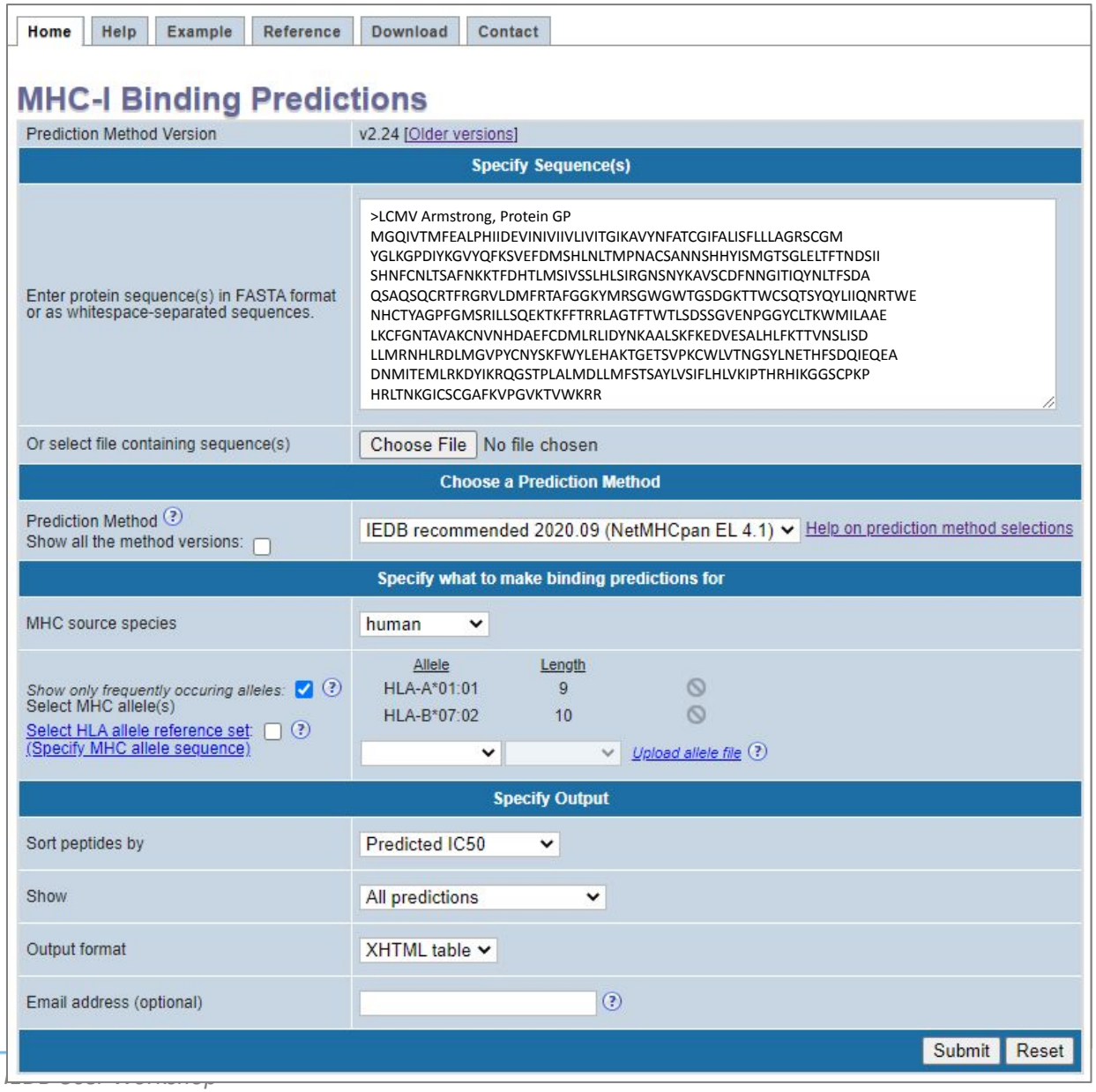
tools.iedb.org/mhci/

MHC-I binding prediction - example



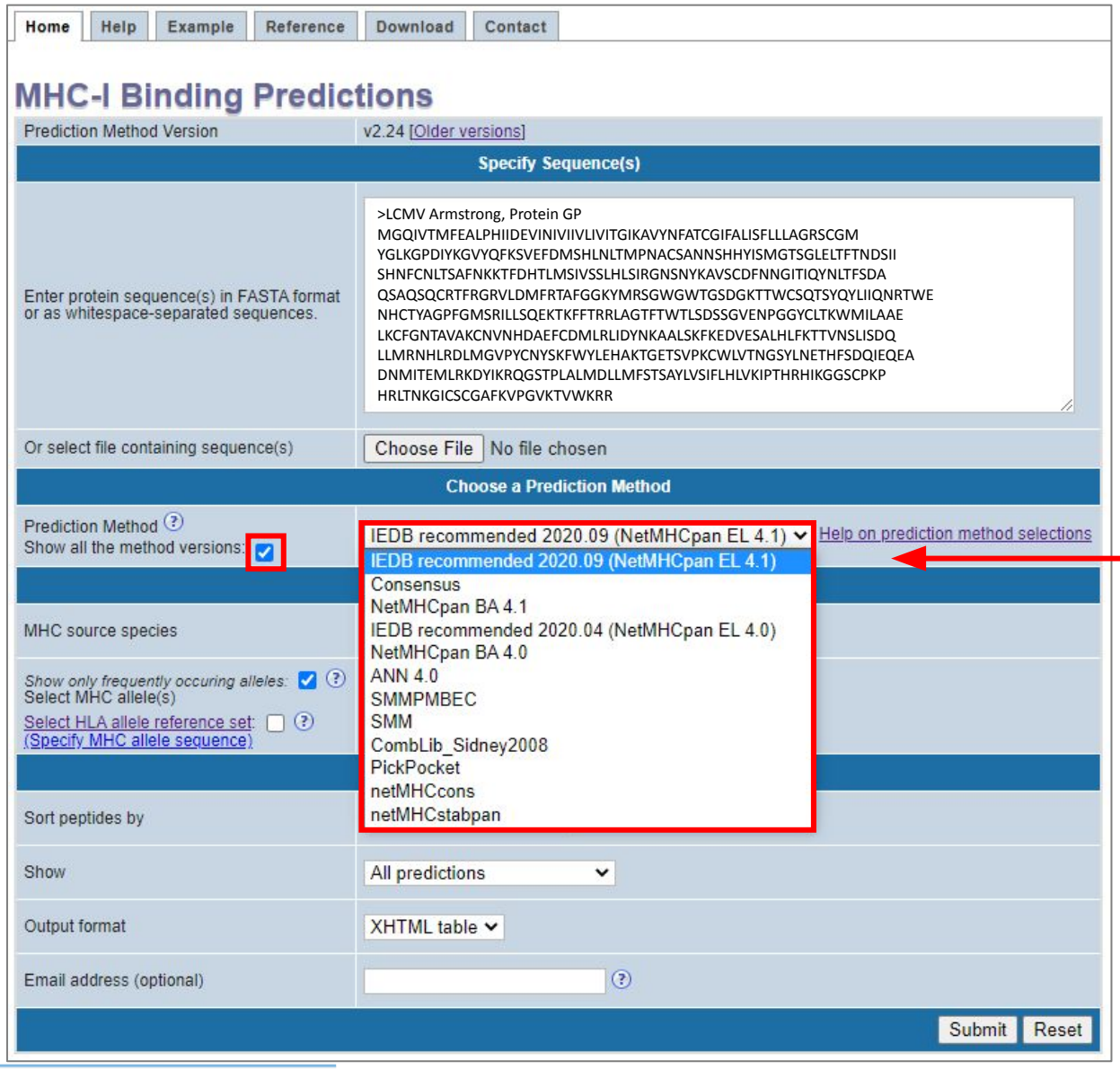
tools.iedb.org/mhci/

MHC-I binding prediction - example



tools.iedb.org/mhci/

MHC-I binding prediction - example



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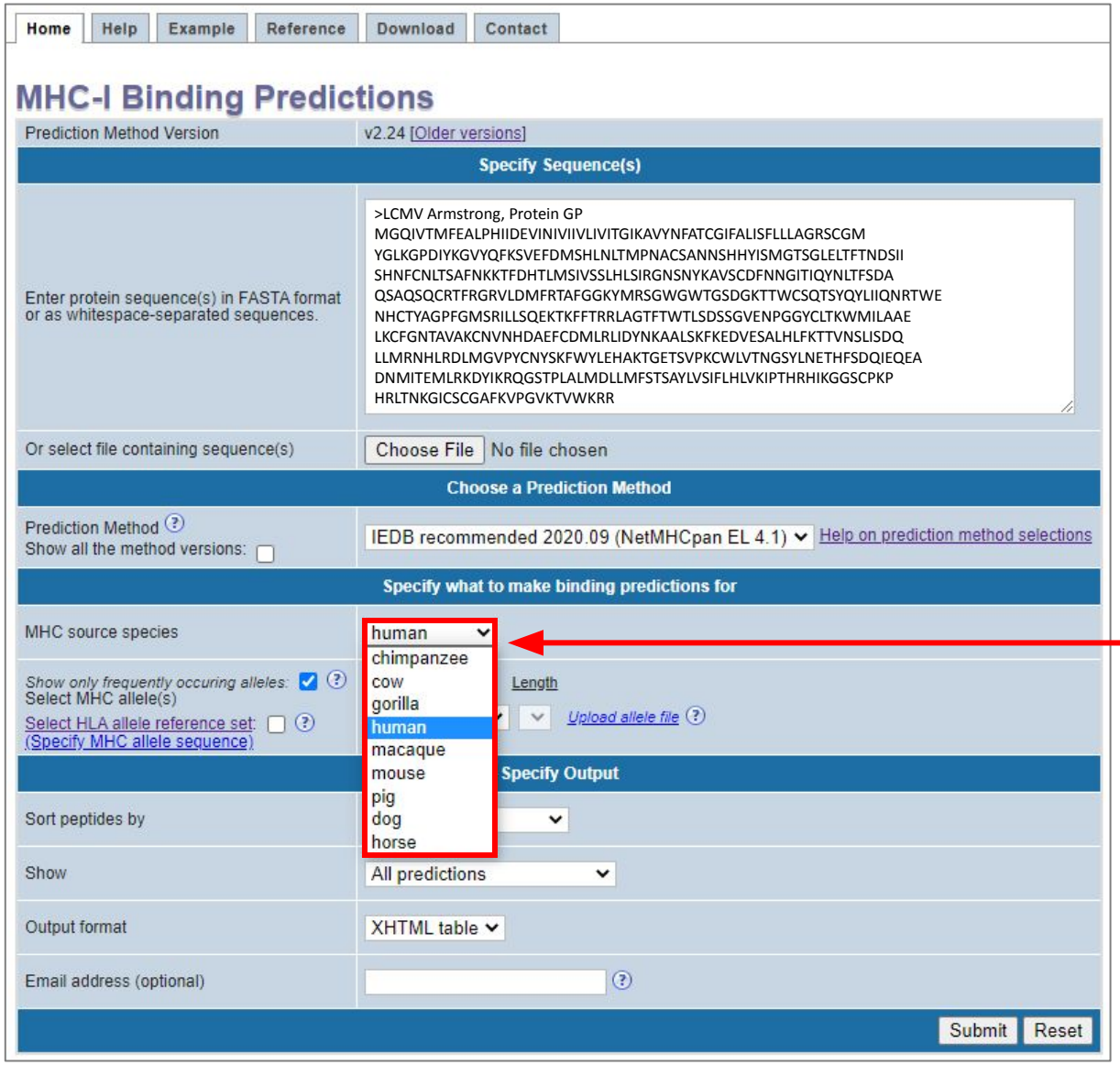
Prediction method

MHC-I binding prediction – example



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Choose species

MHC-I binding prediction – example

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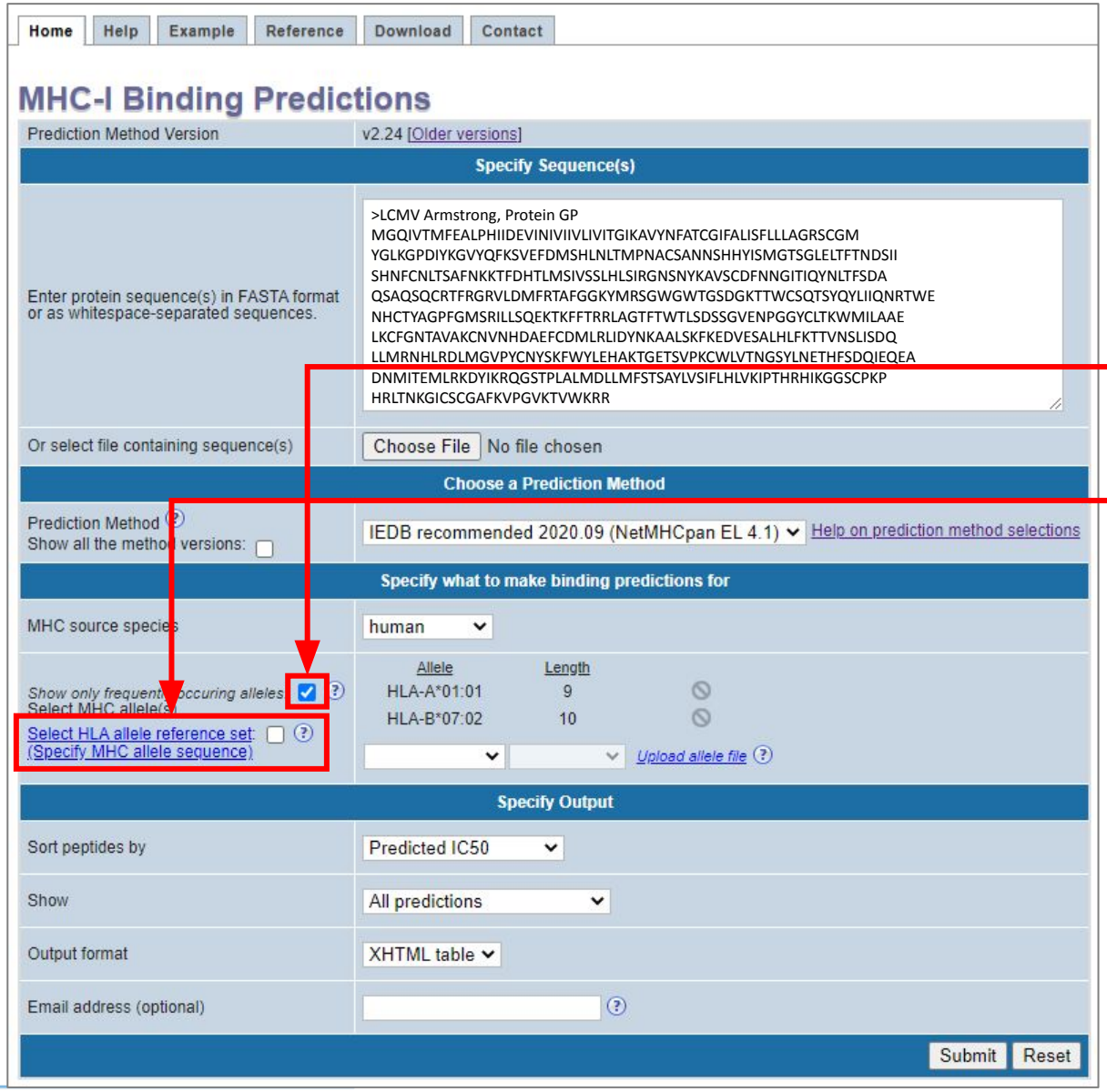
Complete set

MHC-I binding prediction – example



tools.iedb.org/mhci/

Complete set

Reference alleles

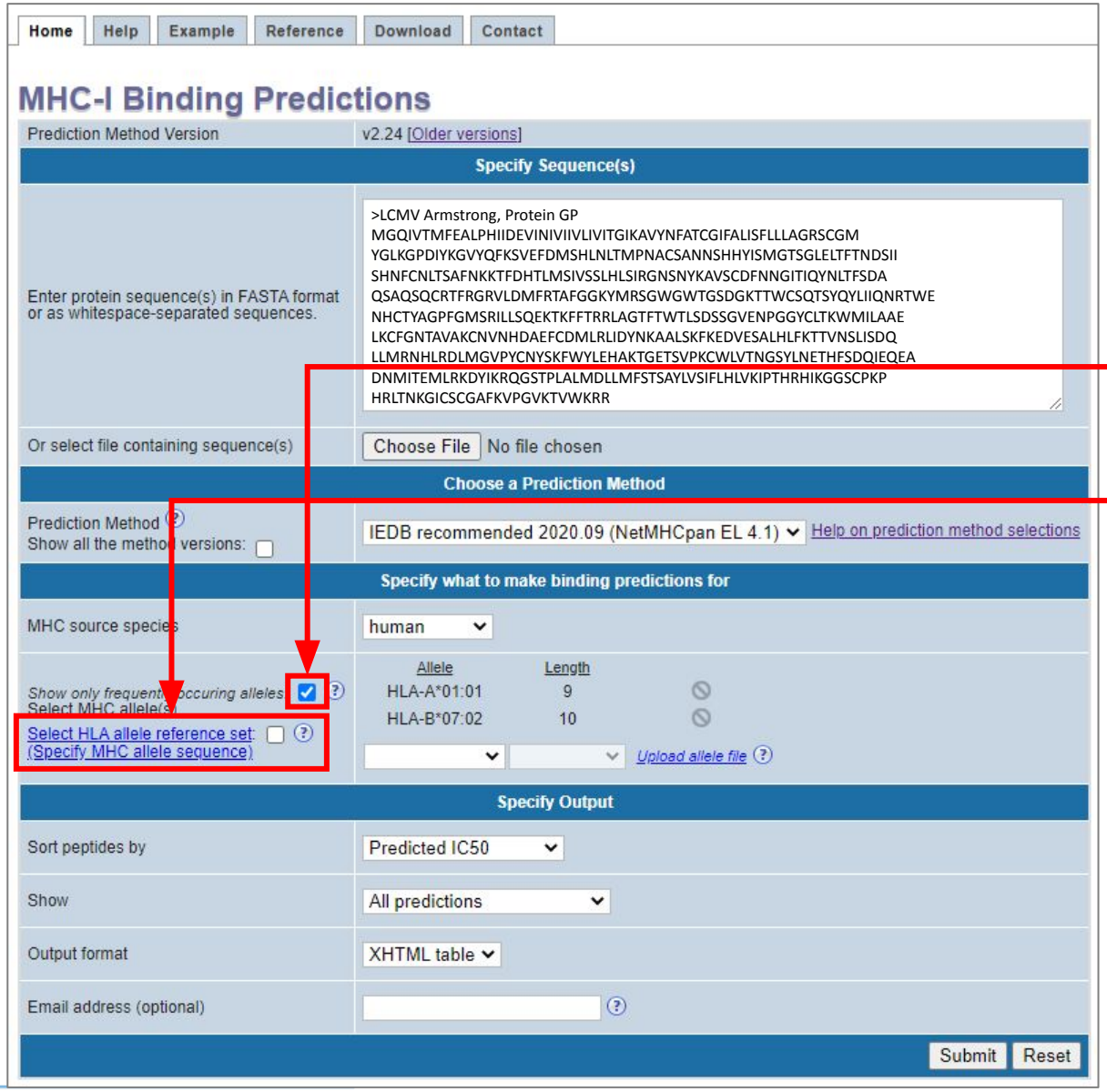
Allele selection – Reference set for global coverage

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

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

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

MHC-I binding prediction – example

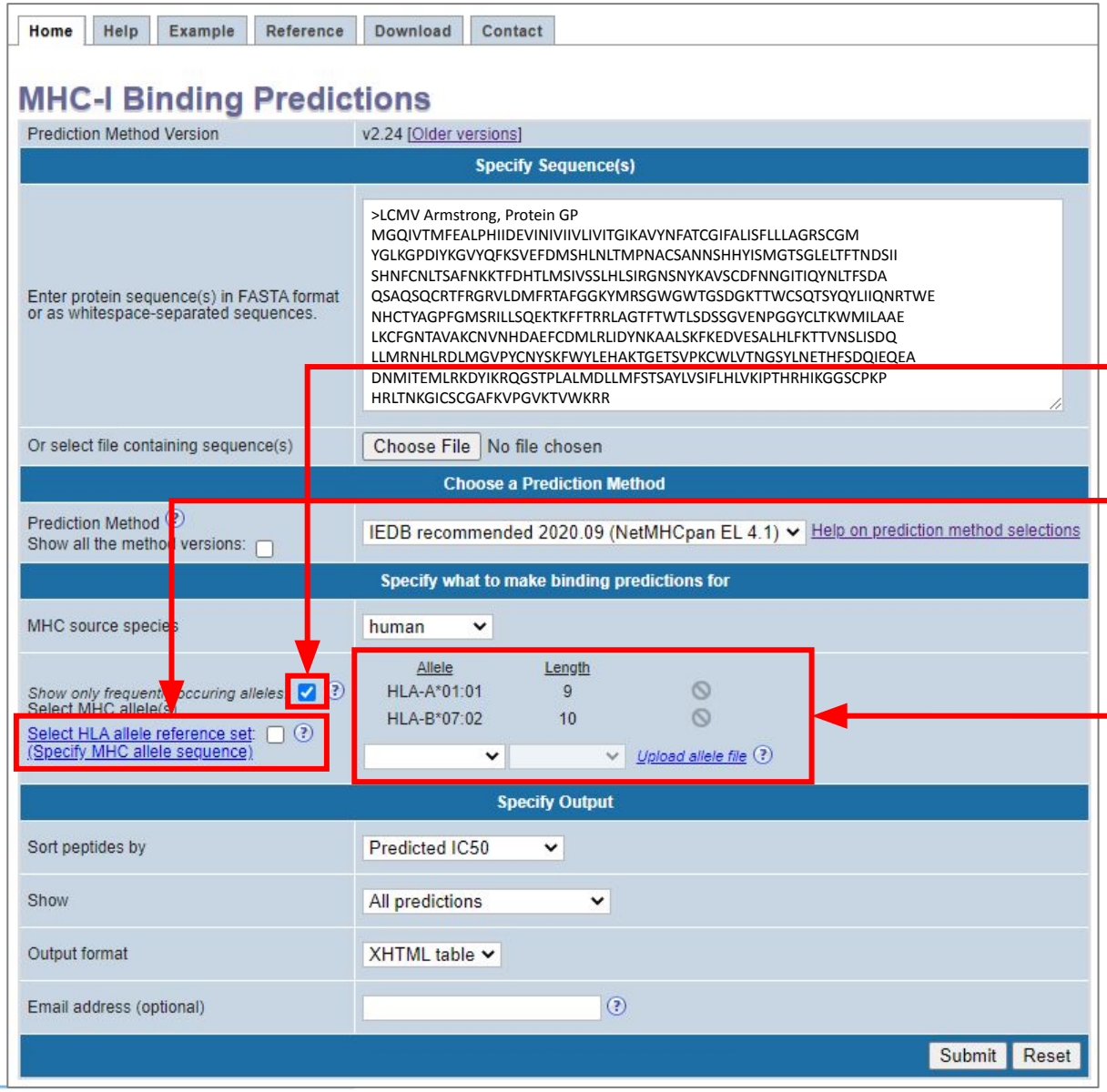


tools.iedb.org/mhci/

Complete set

Reference alleles

MHC-I binding prediction – example



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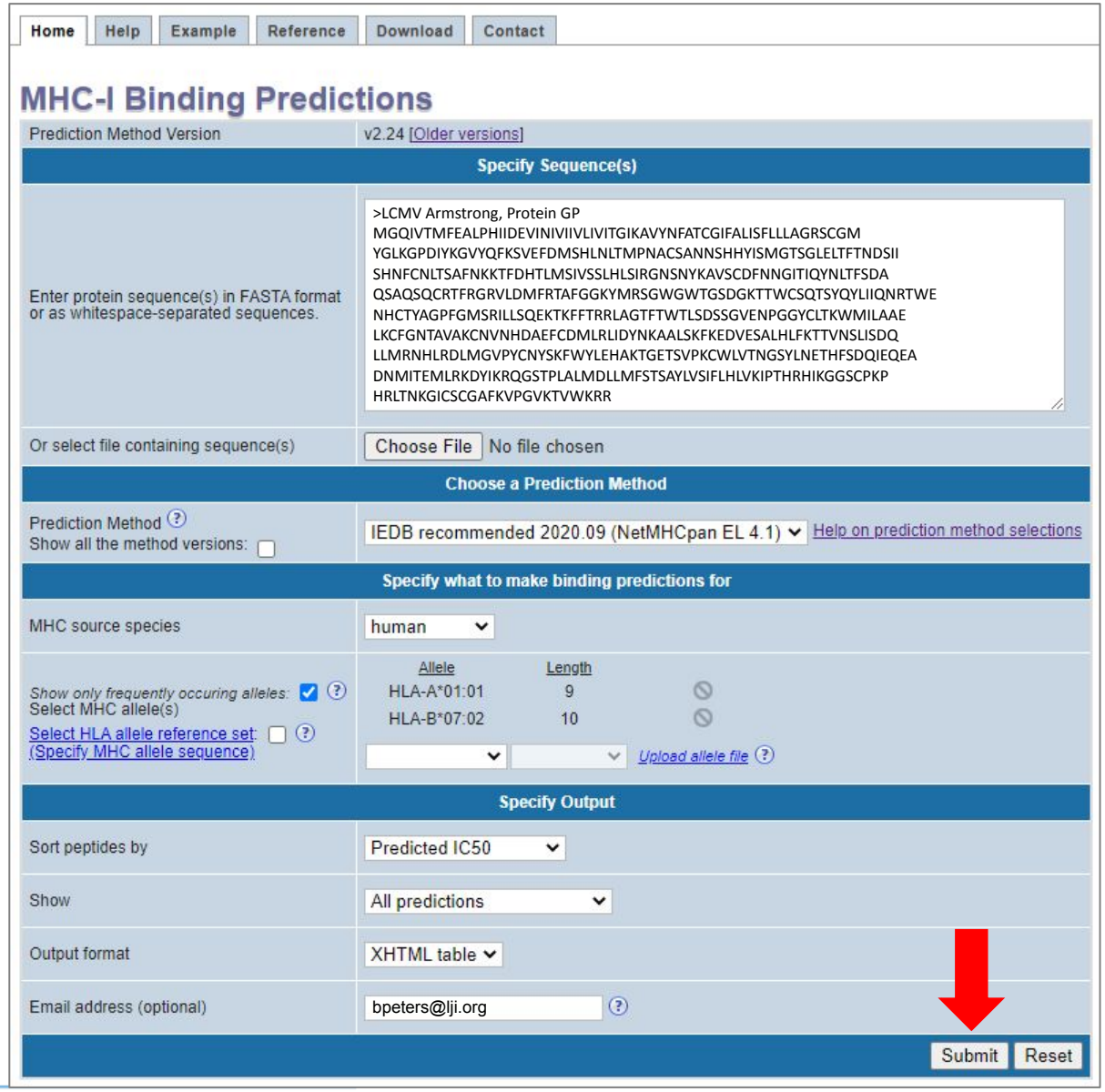
Complete set

Reference alleles

Specify allele(s) & peptide length
(select or upload)

MHC-I binding prediction – example



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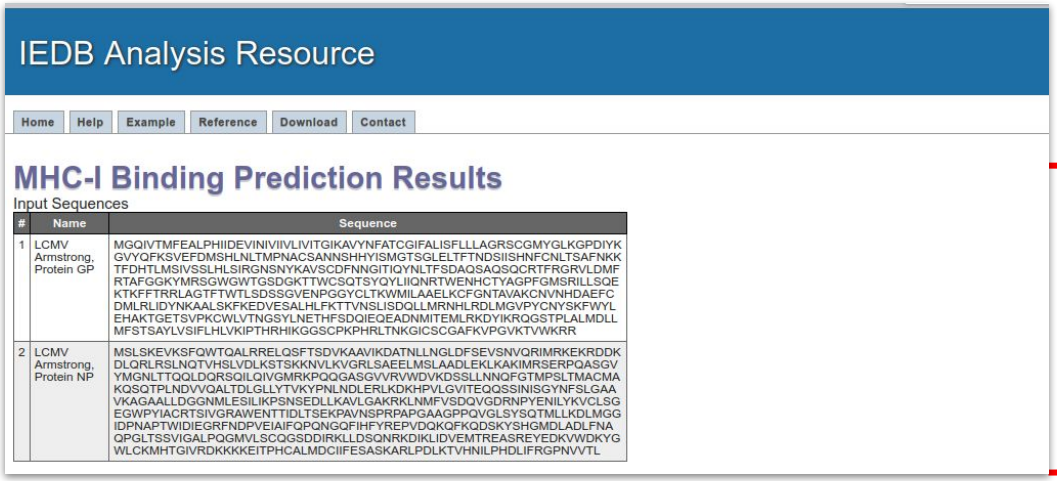
MHC-I binding prediction – example



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MHC-I Binding Prediction Results

Input Sequences

#	Name	Sequence
1	LCMV Armstrong, Protein GP	MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGMYGLKGPDIYK GVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSIISHNFCNLTSAFNKK TFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDAQSAQSQCRTFRGRVLDMF RTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWENHCTYAGPFGMSRILLSQE KTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFGNTAVAKCNVNHDAEFC DMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQLLMRNHLRDLMGVPYCNYSKFWYL EHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEMLRKDYIKRQGSTPLALMDLL MFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKPHRLTNKGICSCGAFKVPGVKTVWKRR
2	LCMV Armstrong, Protein NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATNLLNGLDFSEVSNVQRIMRKEKRDDK DLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMSLAADLEKLKAKIMRSERPQASGV YMGNLTTQQLDQRSQILQIVGMRKPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTMACMA KQSQTPLNDVVQALTDLGLLYTVKYPNLNDLERLKDKHPVLGVITEQQSSINISGYNFSLGAA VKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKRKLNMFVSDQVGDRNPYENILYKVCLSG EGWPYIACRTSIVGRAWENTTIDLTSEKPAVNSPRPAPGAAGPPQVGLSYSQTMLLKDLMGG IDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPVDQKQFKQDSKYSHGMDLADLFNA QPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRKDIKLIDVEMTREASREYEDKVWDKYG WLCKMHTGIVRDKKKKEITPHCALMDCIIFESASKARLPDLKTVHNILPHDLIFRGPNVVTL	

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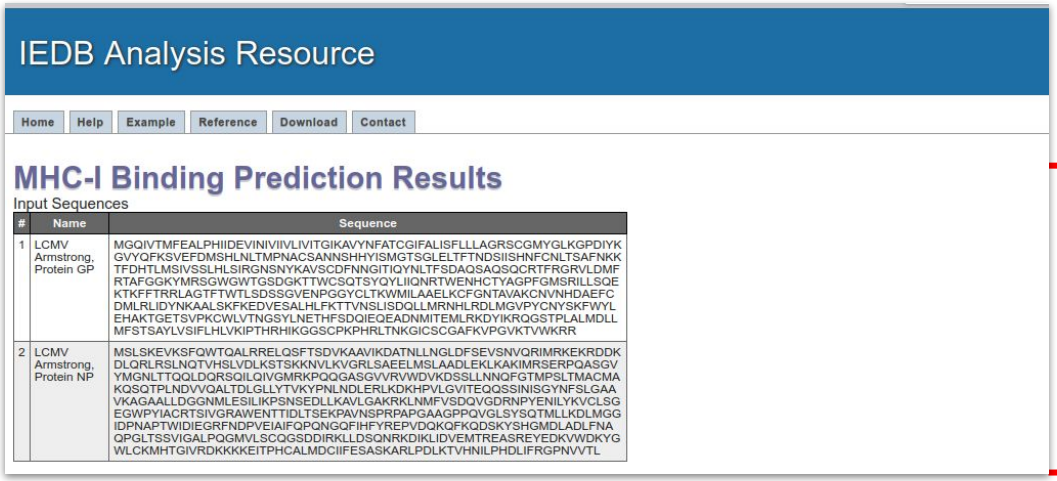
Input sequence

MHC-I binding prediction – example



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MHC-I Binding Prediction Results

Input Sequences

#	Name	Sequence
1	LCMV Armstrong, Protein GP	MGQIVTMFEALPHIIDEVINIVIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGMYGLKGPDIYK GVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSIISHNFCNLTSAFNKK TFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDAQSAQSQCRTFRGRVLDMF RTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWENHCTYAGPFGMSRILLSQE KTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFGNTAVAKCNVNHDAEFC DMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQLLMRNHLRDLMGVPYCNYSKFWYL EHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEMLRKDYIKRQGSTPLALMDLL MFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKPHRLTNKGICSCGAFKVPGVKTVWKRR
2	LCMV Armstrong, Protein NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATNLLNGLDFSEVSNVQRIMRKEKRDDK DLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMSLAADLEKLKAKIMRSERPQASGV YMGNLTTQQLDQRSQILQIVGMRKPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTMACMA KQSQTPLNDVVQALTDLGLLYTVKYPNLNDLERLKDKHPVLGVITEQQSSINISGYNFSLGAA VKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKRKLNMFVSDQVGDRNPYENILYKVCLSG EGWPYIACRTSIVGRAWENTTIDLTSEKPAVNSPRPAPGAAGPPQVGLSYSQTMLLKDLMGG IDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPVDQKQFKQDSKYSHGMDLADLFNA QPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRKDIKLIDVEMTREASREYEDKVWDKYG WLCKMHTGIVRDKKKKEITPHCALMDCIIFESASKARLPDLKTVHNILPHDLIFRGPNVVTL

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Input sequence

Download result

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Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01
HLA-A*32:01	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.840246	0.01
HLA-B*07:02	2	343	351	9	SPRPAPGAA	SPRPAPGAA	SPRPAPGAA	0.967013	0.02
HLA-A*68:01	2	46	55	10	EVSNVQRIMR	EVSNVQIMR	EVSNVQRIMR	0.966314	0.02
HLA-B*40:01	2	512	520	9	KEITPHCAL	KEITPHCAL	KEITPHCAL	0.96127	0.02

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

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Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Citations

Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Citations

Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Citations

Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Citations

Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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Citations

Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVE	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVII		
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQS		
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVP		
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVL		
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPV		
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

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

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Citations

Allele	#	Start	End	Length	Peptide	Core	Icore	Score	Percentile Rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVPK	0.93577	0.01
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVLK	0.935352	0.01
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPVL	0.923742	0.01
HLA-A*30:02	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.882628	0.01
HLA-A*32:01	2	8	16	9	KSFQWTQAL	KSFQWTQAL	KSFQWTQAL	0.87178	0.01
HLA-A*30:02	1	233	241	9	RTWENHCTY	RTWENHCTY	RTWENHCTY	0.855525	0.01

Downloaded prediction results

allele	seq_num	start	end	length	peptide	core	icore	score	rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-B*57:01	2	152	160	9	GASGVVRVW	GASGVVRVW	GASGVVRVW	0.979299	0.03
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-B*07:02	2	343	351	9	SPRPAPGAA	SPRPAPGAA	SPRPAPGAA	0.967013	0.02
HLA-A*68:01	2	46	55	10	EVSNVQRIMR	EVSNVQIMR	EVSNVQRIMR	0.966314	0.02
HLA-B*07:02	2	118	126	9	RPQASGVYM	RPQASGVYM	RPQASGVYM	0.96239	0.03
HLA-B*40:01	2	512	520	9	KEITPHCAL	KEITPHCAL	KEITPHCAL	0.96127	0.02
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-B*58:01	2	152	160	9	GASGVVRVW	GASGVVRVW	GASGVVRVW	0.95723	0.03
HLA-A*02:03	2	69	77	9	SLNQTVHSL	SLNQTVHSL	SLNQTVHSL	0.955613	0.02
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-B*57:01	1	166	174	9	ITIQYNLTF	ITIQYNLTF	ITIQYNLTF	0.942594	0.07
HLA-A*02:01	1	6	14	9	TMFEALPHI	TMFEALPHI	TMFEALPHI	0.942547	0.03
HLA-A*03:01	2	462	470	9	KLLDSQNRK	KLLDSQNRK	KLLDSQNRK	0.940919	0.02
HLA-B*57:01	2	151	160	10	QGASGVVRVW	QASGVVRVW	QGASGVVRVW	0.940695	0.07

Selection of “binders”

allele	seq_num	start	end	length	peptide	core	icore	score	rank
HLA-B*57:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-B*57:01	2	152	160	9	GASGVVRVW	GASGVVRVW	GASGVVRVW	0.979299	0.03
HLA-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
HLA-B*40:01	2	271	279	9	SEDLLKAVL	SEDLLKAVL	SEDLLKAVL	0.974336	0.01
HLA-B*15:01	2	414	422	9	KQFKQDSKY	KQFKQDSKY	KQFKQDSKY	0.974222	0.01
HLA-B*07:02	2	343	351	9	SPRPAPGAA	SPRPAPGAA	SPRPAPGAA	0.967013	0.02
HLA-A*68:01	2	46	55	10	EVSNVQRIMR	EVSNVQIMR	EVSNVQRIMR	0.966314	0.02
HLA-B*07:02	2	118	126	9	RPQASGVYM	RPQASGVYM	RPQASGVYM	0.96239	0.03
HLA-B*40:01	2	512	520	9	KEITPHCAL	KEITPHCAL	KEITPHCAL	0.96127	0.02
HLA-A*68:02	2	23	31	9	FTSDVKAAV	FTSDVKAAV	FTSDVKAAV	0.958917	0.01
HLA-A*11:01	2	330	338	9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.958437	0.01
HLA-B*58:01	2	152	160	9	GASGVVRVW	GASGVVRVW	GASGVVRVW	0.95723	0.03
HLA-A*02:03	2	69	77	9	SLNQTVHSL	SLNQTVHSL	SLNQTVHSL	0.955613	0.02
HLA-A*23:01	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.947546	0.01
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVIIV	0.944421	0.01
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQSF	0.94328	0.01
HLA-B*57:01	1	166	174	9	ITIQYNLTF	ITIQYNLTF	ITIQYNLTF	0.942594	0.07
HLA-A*02:01	1	6	14	9	TMFEALPHI	TMFEALPHI	TMFEALPHI	0.942547	0.03
HLA-A*03:01	2	462	470	9	KLLDSQNRK	KLLDSQNRK	KLLDSQNRK	0.940919	0.02
HLA-B*57:01	2	151	160	10	QGASGVVRVW	QASGVVRVW	QGASGVVRVW	0.940695	0.07

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- Pick peptides **below percentile rank 1.0**

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HLA-B*57:01	2	3	12	10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
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HLA-B*58:01	2	319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	71	79	9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
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HLA-B*15:01	1	314	323	10	EFCDMLRLID	EFCDMLRLI	EFCDMLRLI	0	100
HLA-B*15:01	1	155	164	10	YKAVSCDFNN	YAVSCDFNN	YKAVSCDFNN	0	100
HLA-B*15:01	1	389	397	9	PKCWLVTNG	PKCWLVTNG	PKCWLVTNG	0	100
HLA-B*15:01	1	89	97	9	PNACSANNS	PNACSANNS	PNACSANNS	0	100
HLA-B*15:01	1	12	20	9	PHIIDEVIN	PHIIDEVIN	PHIIDEVIN	0	100
HLA-B*07:02	1	389	398	10	PKCWLVTNGS	PKWLVTNGS	PKCWLVTNGS	0	100
HLA-B*07:02	1	299	308	10	FGNTAVAKCN	FGNTAVAKN	FGNTAVAKCN	0	100

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HLA-B*15:01	1	389	397	9	PKCWLVTNG	PKCWLVTNG	PKCWLVTNG	0	100
HLA-B*15:01	1	89	97	9	PNACSANNS	PNACSANNS	PNACSANNS	0	100
HLA-B*15:01	1	12	20	9	PHIIDEVIN	PHIIDEVIN	PHIIDEVIN	0	100
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HLA-A*01:01	2	486	495	10	EYEDKVWDKY	EYDKVWDKY	EYEDKVWDKY	0.092657	0.99
HLA-A*23:01	1	35	43	9	VYNFATCGI	VYNFATCGI	VYNFATCGI	0.074508	0.99
HLA-A*26:01	2	30	38	9	AVIKDATNL	AVIKDATNL	AVIKDATNL	0.065855	0.99
HLA-A*26:01	2	117	125	9	ERPQASGVY	ERPQASGVY	ERPQASGVY	0.064905	0.99
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HLA-B*51:01	1	139	147	9	MSIVSSLHL	MSIVSSLHL	MSIVSSLHL	0.138797	1
HLA-B*07:02	2	345	354	10	RPAPGAAGPP	RPAPGAAPP	RPAPGAAGPP	0.117258	1
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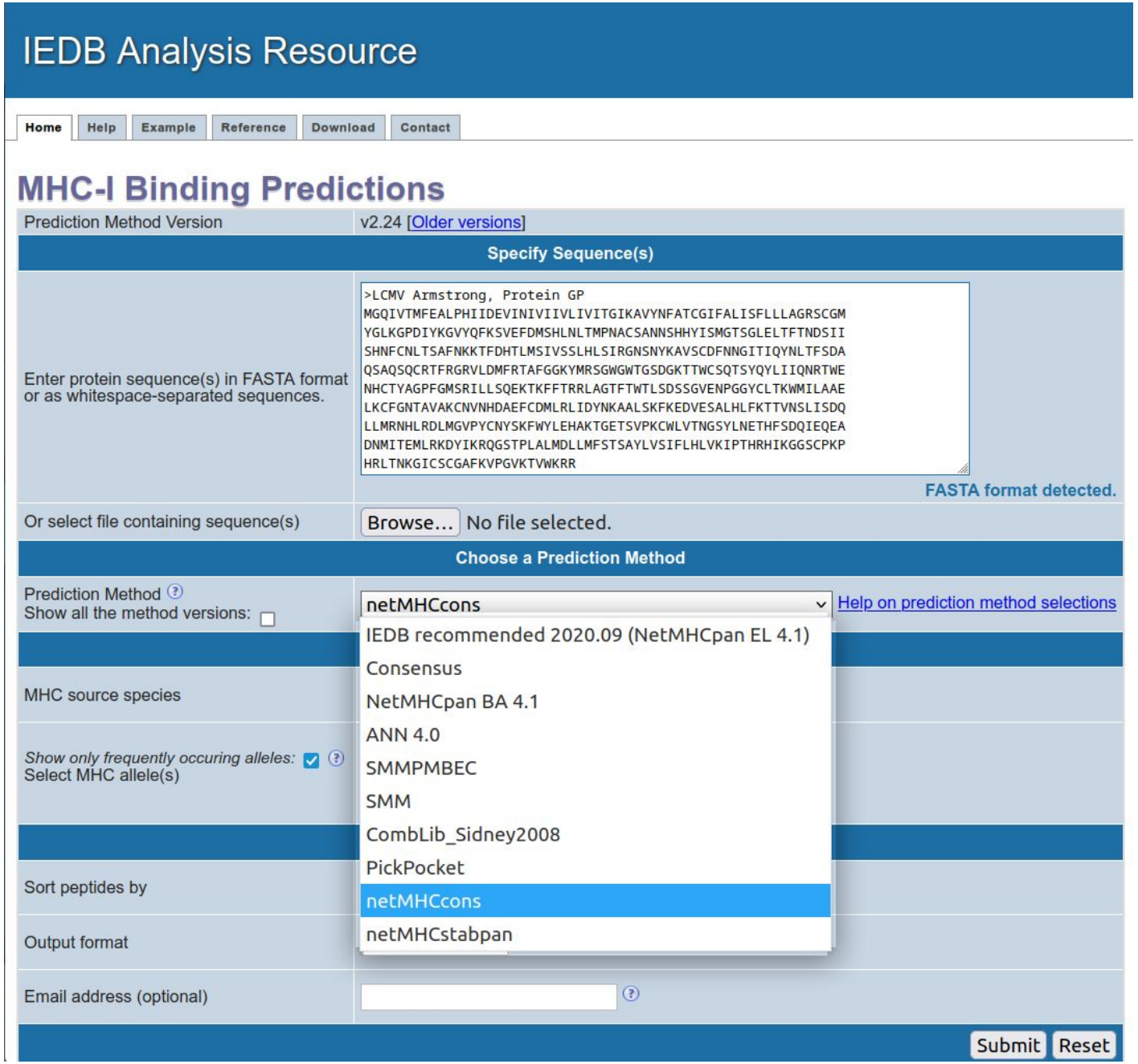
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MHC-I Binding Predictions
Prediction Method Version
v2.24 [Older versions]
Specify Sequence(s)
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.
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Or select file containing sequence(s)
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Show all the method versions:
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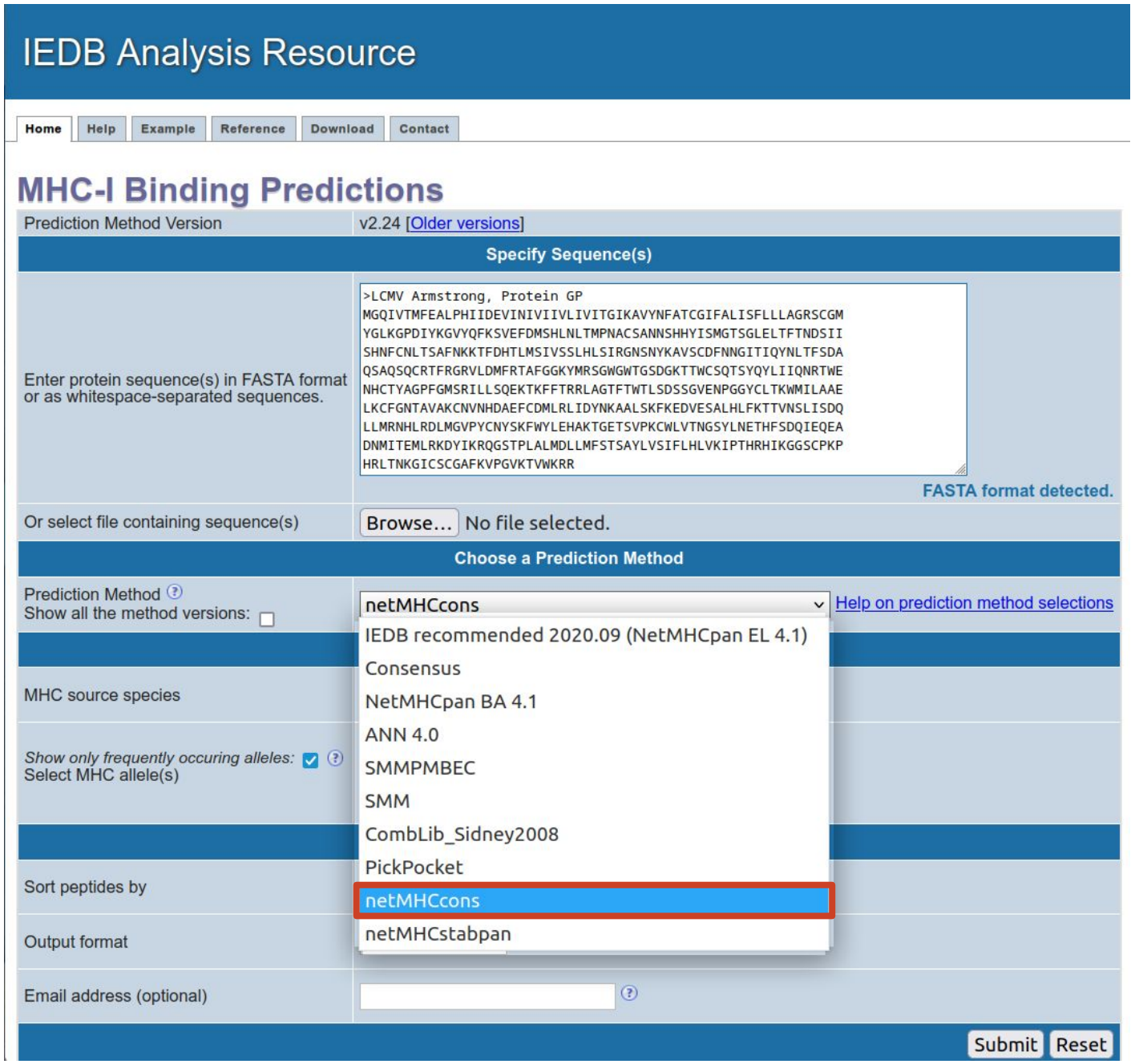
IEDB recommended 2020.09 (NetMHCpan EL 4.1)
Consensus
NetMHCpan BA 4.1
ANN 4.0
SMMPMBEC
SMM
CombLib_Sidney2008
PickPocket
netMHCcons
netMHCstabpan
MHC source species
Show only frequently occuring alleles:
Select MHC allele(s)
Sort peptides by
Output format
Email address (optional)
Submit
Reset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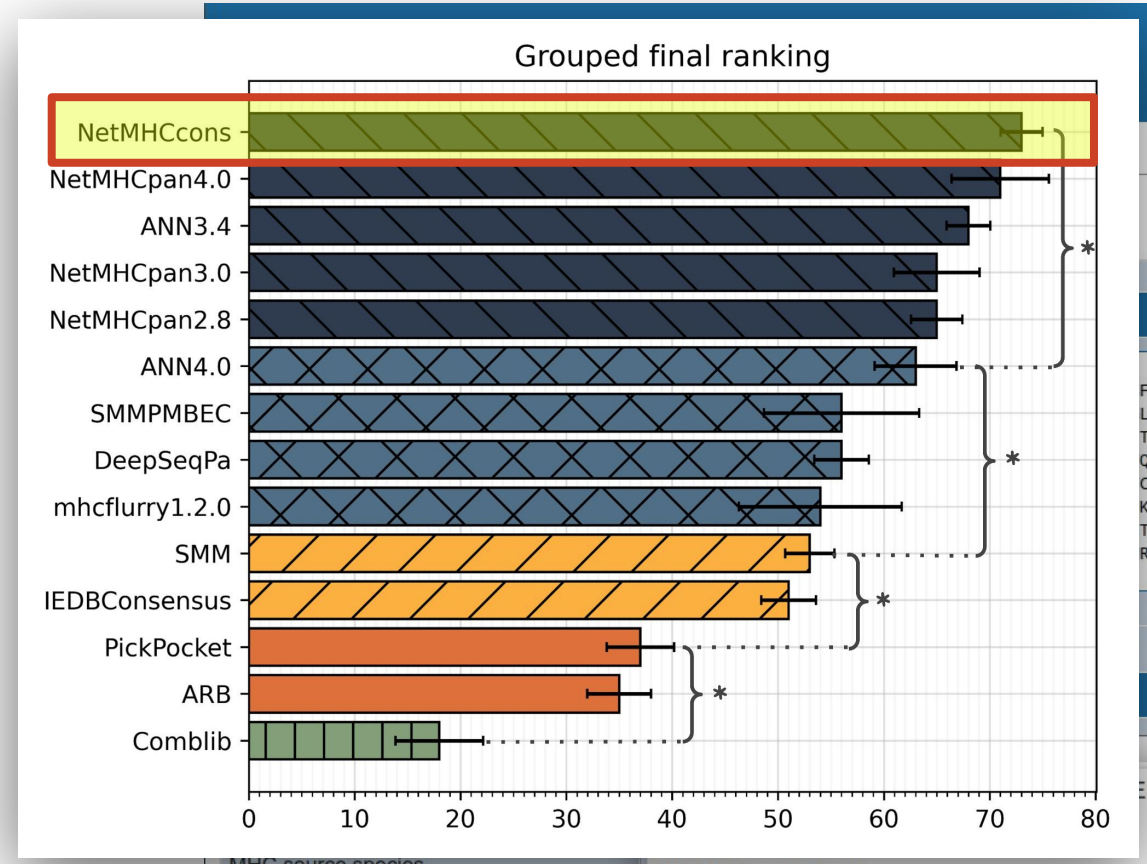
MHC-I Binding Predictions
Prediction Method Version
v2.24 [Older versions]
Specify Sequence(s)
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.
>LCMV Armstrong, Protein GP
MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM
YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII
SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE
NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE
LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
HRLTNKGICSCGAFKVPGVKTVWKRR
FASTA format detected.
Or select file containing sequence(s)
Browse...
No file selected.
Choose a Prediction Method
Prediction Method
Show all the method versions:
netMHCcons
Help on prediction method selections
IEDB recommended 2020.09 (NetMHCpan EL 4.1)
Consensus
NetMHCpan BA 4.1
ANN 4.0
SMMPMBEC
SMM
CombLib_Sidney2008
PickPocket
netMHCcons
netMHCstabpan
MHC source species
Show only frequently occuring alleles:
Select MHC allele(s)
Sort peptides by
Output format
Email address (optional)
Submit
Reset



FLLLAGRSCGM
LELTFTNDSII
TIQYNLTFSDA
QYLIIQNRTWE
CLTKWMILAAE
KTTVNSLISDQ
THFSDQIEQEA
RHIKGGSCPKP

FASTA format detected.

Help on prediction method selections

EL 4.1)

MHC source species

NetMHCpan BA 4.1
ANN 4.0
SMMPMBEC
SMM
CombLib_Sidney2008
PickPocket
netMHCcons
netMHCstabpan

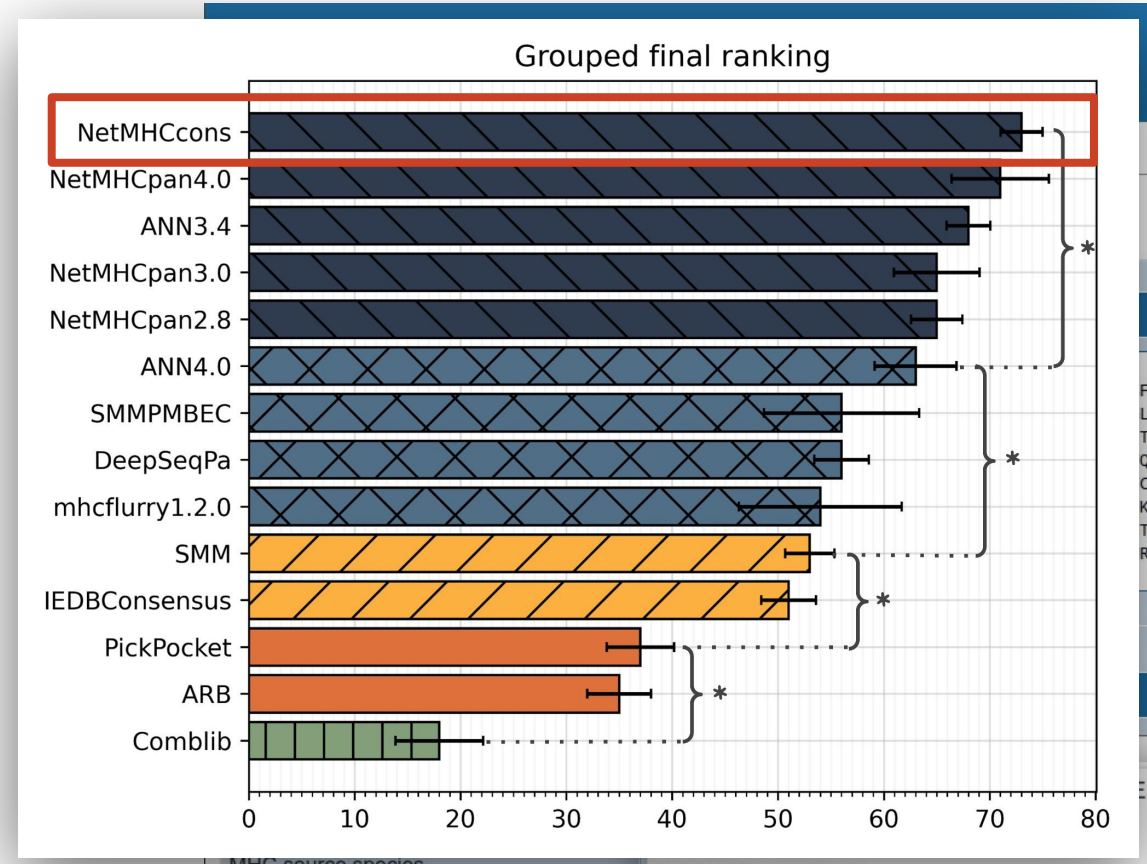
Show only frequently occuring alleles:
Select MHC allele(s)

Sort peptides by

Output format

Email address (optional)

Submit Reset



FLLLAGRSCGM
LELTFTNDSII
TIQYNLTFSDA
QYLIIQNRTWE
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Select MHC allele(s)

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Email address (optional)

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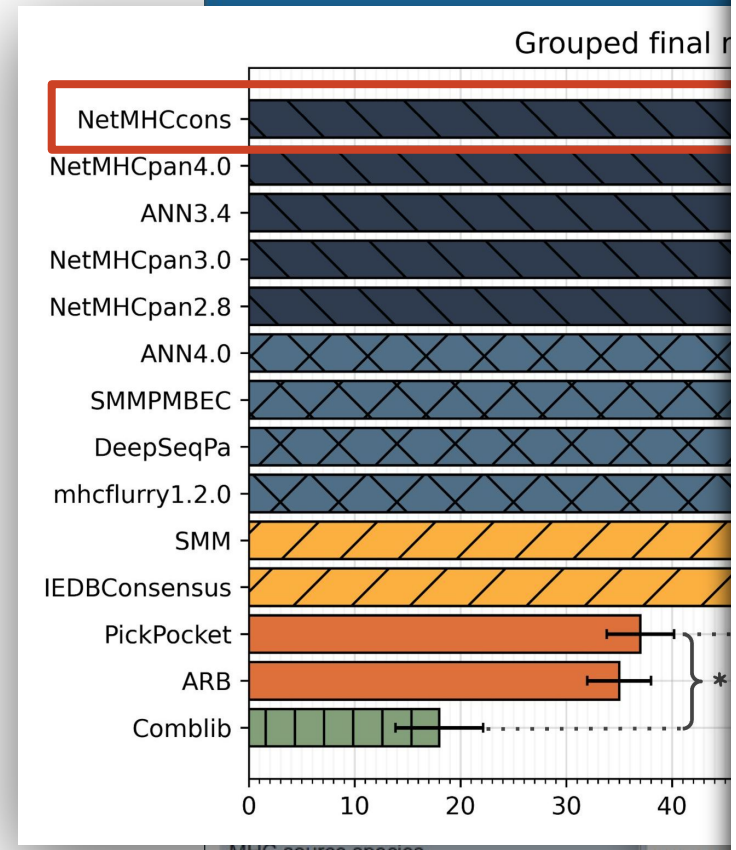
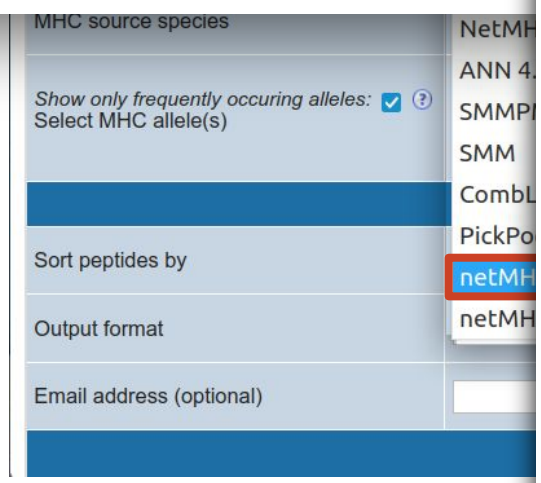




Briefings in Bioinformatics, 2022, 1–9
https://doi.org/10.1093/bib/bbac259
Problem Solving Protocol

A comprehensive analysis of the IEDB MHC class-I automated benchmark

Raphael Trevizani, Zhen Yan, Jason A. Greenbaum, Alessandro Sette, Morten Nielsen and Bjoern Peters *
*Corresponding author: bpeters@lji.org

Abstract

In 2014, the Immune Epitope Database automated benchmark was created to compare the performance of the MHC class I binding predictors. However, this is not a straightforward process due to the different and non-standardized outputs of the methods. Additionally, some methods are more restrictive regarding the HLA alleles and epitope sizes for which they predict binding affinities, while others are more comprehensive. To address how these problems impacted the ranking of the predictors, we developed an approach to assess the reliability of different metrics. We found that using percentile-ranked results improved the stability of the ranks and allowed the predictors to be reliably ranked despite not being evaluated on the same data. We also found that given the rate new data are incorporated into the benchmark, a new method must wait for at least 4 years to be ranked against the pre-existing methods. The best-performing tools with statistically indistinguishable scores in this benchmark were NetMHCcons, NetMHCpan4.0, ANN3.4, NetMHCpan3.0 and NetMHCpan2.8. The results of this study will be used to improve the evaluation and display of benchmark performance. We highly encourage anyone working on MHC binding predictions to participate in this benchmark to get an unbiased evaluation of their predictors.

Keywords: Epitope prediction, Benchmark, MHC-I, CD8+, IEDB tools

Introduction

T cell epitopes are molecules bound by MHC molecules that are recognized by T cell receptors that trigger an immune response. Most T cell epitopes are peptides, which are subdivided based on the type of MHC molecule. MHC class I molecules present peptides to CD8+ T cells, while MHC class II molecules present peptides to CD4+ T cells. This work focuses on peptides bound to MHC class I molecules, which play a critical role in the detection of intracellular infections and cancer [1].

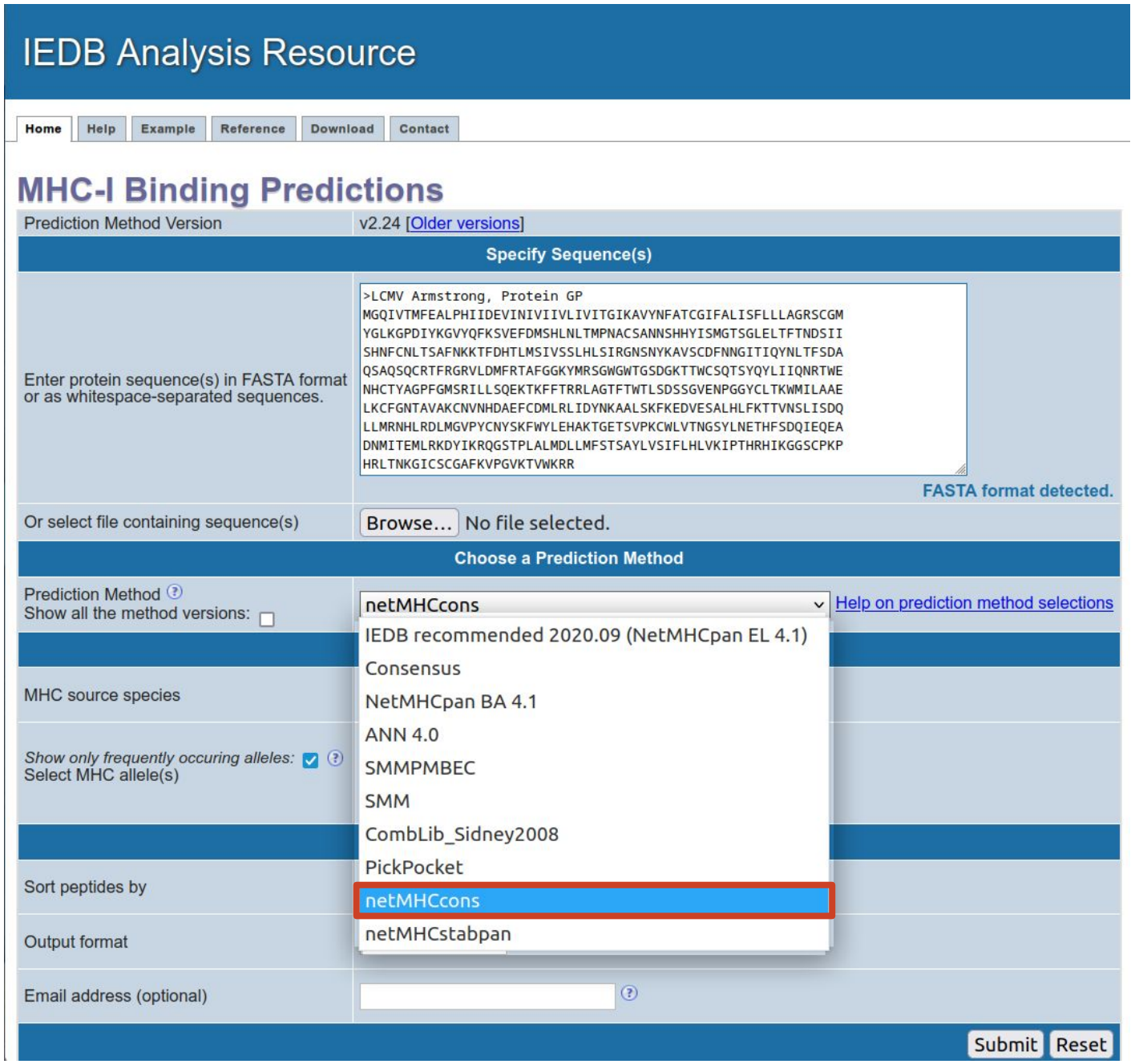
The many applications associated with epitope mapping lead to the development of a large number of computational methods to predict T cell epitopes from the amino acid sequence [2], mostly focusing on the prediction of peptide binding to MHC molecules [3]. However, the broad selection of prediction servers available makes it burdensome for users to choose the best server and for developers to demonstrate the superiority of their newly developed methods.

To address the need for a blind test of MHC-I binding predictors, an automated benchmark was established in 2014 that uses data curated by the Immune Epitope Database (IEDB) [4,http://tools.iedb.org/auto_bench/mhci/weekly]. This ensures that the data benchmarked will be 'new' to the participating tools, and provide a realistic assessment of the performance.

To optimally establish a benchmark encompasses several challenges. For instance, many methods restrict MHC-I alleles and peptide sizes by design [5–14], while others are more comprehensive [15–17], which impedes the use of the same datasets for all evaluations. This complication was addressed in the initial development of the benchmark but it was left unchecked on purpose for future assessment [4]. Other initially unforeseen obstacles emerged from the accumulation of data and the enrollment of new predictors.

In this paper, we address these concerns by simulating several hypothetical scenarios. We start by presenting

Raphael Trevizani is a research scientist at Fiocruz and a consultant for the La Jolla Institute for Immunology working on the development of tools for immunoinformatics.
Zhen Yan is a Bioinformatics Application Developer of Bioinformatics Core at La Jolla Institute for Immunology. He is involved in the development and implementation of Bioinformatics tools related to immunology.
Jason Greenbaum is Director of the Bioinformatics Core at La Jolla Institute for Immunology and is involved in the development and implementation of computational tools and pipelines related to immunology.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MHC-I Binding Predictions
Prediction Method Version
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Specify Sequence(s)
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SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA
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LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ
LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA
DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP
HRLTNKGICSCGAFKVPGVKTVWKRR
FASTA format detected.
Or select file containing sequence(s)
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No file selected.
Choose a Prediction Method
Prediction Method
Show all the method versions:
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netMHCcons
netMHCstabpan
MHC source species
Show only frequently occuring alleles:
Select MHC allele(s)
Sort peptides by
Output format
Email address (optional)
Submit
Reset

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MHC-I Binding Prediction Results

Input Sequences

#	Name	Sequence
1	LCMV Armstrong, Protein GP	MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGMYGLKGPDIYK GVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSIISHNFCNLTSAFNKK TFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDAQSAQSQCRTFRGRVLDMF RTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWENHCTYAGPFGMSRILLSQE KTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFGNTAVAKCNVNHDAEFC DMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQLLMRNHLRDLMGVPYCNYSKFWYL EHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEMLRKDYIKRQGSTPLALMDLL MFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKPHRLTNKGICSCGAFKVPGVKTVWKRR

Prediction method: netmhccons 1.1 | Low Score = good binder

Download result

Citations

Allele	#	Start	End	Length	Peptide	IC50 (nM)	Percentile Rank
HLA-A*02:01	1	6	14	9	TMFEALPHI	4.75	0.1
HLA-A*02:01	1	440	448	9	LMFSTSAYL	8.90	0.31
HLA-A*02:01	1	447	455	9	YLVSIFLHL	9.29	0.32
HLA-A*02:01	1	435	443	9	ALMDLLMFS	10.18	0.39
HLA-A*02:01	1	137	145	9	TLMSIVSSL	11.11	0.42
HLA-A*02:01	1	10	18	9	ALPHIIDEV	15.96	0.6
HLA-A*02:01	1	45	53	9	ALISFLLLA	15.96	0.6
HLA-A*02:01	1	14	22	9	IIDEVINIV	39.38	1.3
HLA-A*02:01	1	42	50	9	GIFALISFL	42.94	1.4
HLA-A*02:01	1	38	46	9	FATCGIFAL	65.49	1.7
HLA-A*02:01	1	448	456	9	LVSIFLHLV	76.20	1.9
HLA-A*02:01	1	436	444	9	LMDLLMFST	99.33	2.2
HLA-A*02:01	1	13	21	9	HIIDEVINI	120.03	2.4

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MHC-I Binding Prediction Results

Input Sequences

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1	LCMV Armstrong, Protein GP	MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGMYGLKGPDIYK GVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSIISHNFCNLTSAFNKK TFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDAQSAQSQCRTFRGRVLDMF RTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWENHCTYAGPFGMSRILLSQE KTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFGNTAVAKCNVNHDAEFC DMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQLLMRNHLRDLMGVPYCNYSKFWYL EHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEMLRKDYIKRQGSTPLALMDLL MFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKPHRLTNKGICSCGAFKVPGVKTVWKRR

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HLA-A*02:01	1	42	50	9	GIFALISFL	42.94	1.4
HLA-A*02:01	1	38	46	9	FATCGIFAL	65.49	1.7
HLA-A*02:01	1	448	456	9	LVSIFLHLV	76.20	1.9
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MHC-I Binding Predic ts

Input Sequences

#	Name		
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Prediction method: netmhccons 1.1 | Low Sco

Download result

Citations

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HLA-A*02:01	1	10	18	9	ALPHII	0.6
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IC50 (nM)
4.75
8.90
9.29
10.18
11.11
15.96
15.96
39.38
42.94
65.49
76.20
99.33
120.03

Selection of “binders”

- Pick peptides **below percentile rank 1.0**

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

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

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

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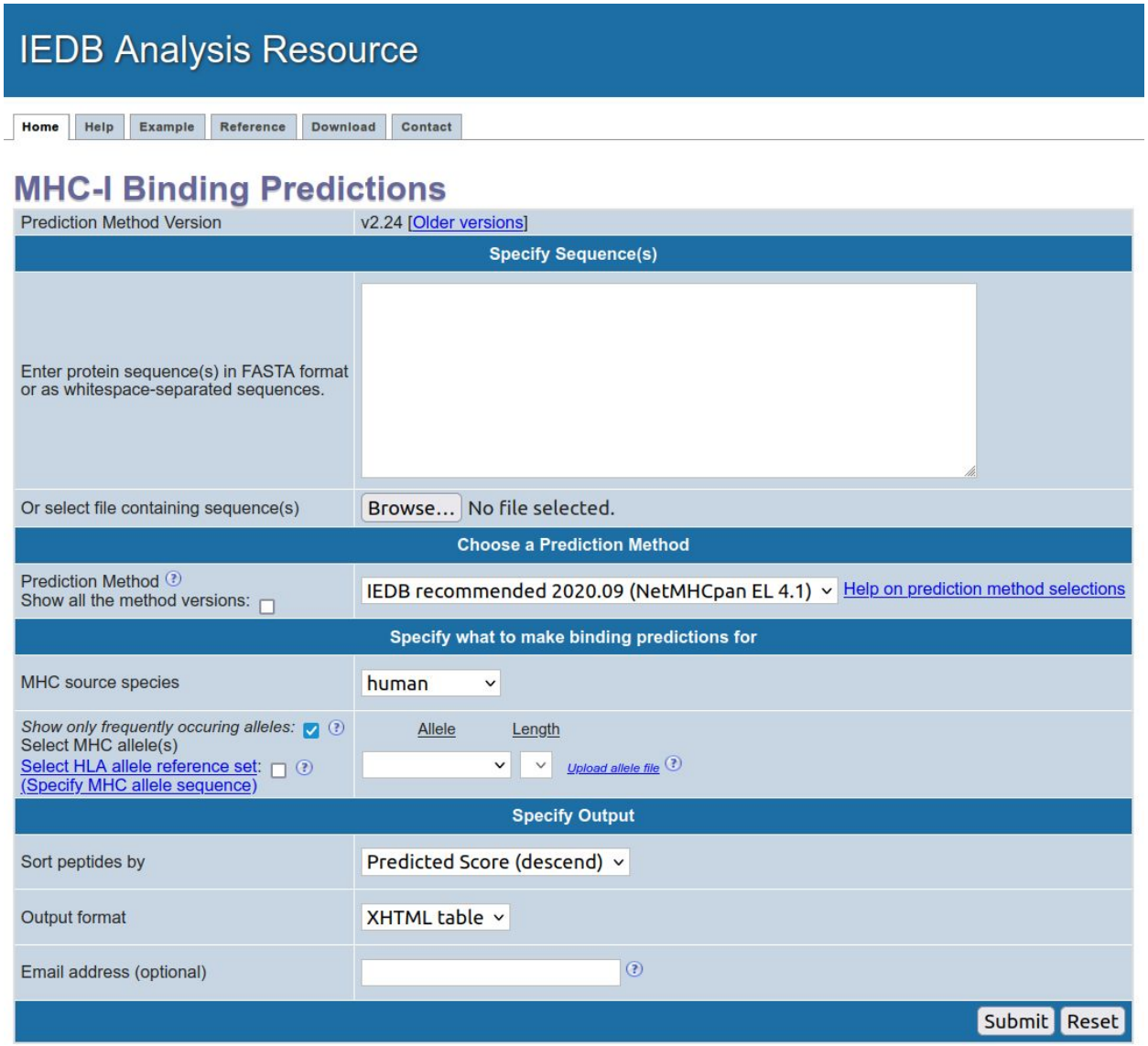
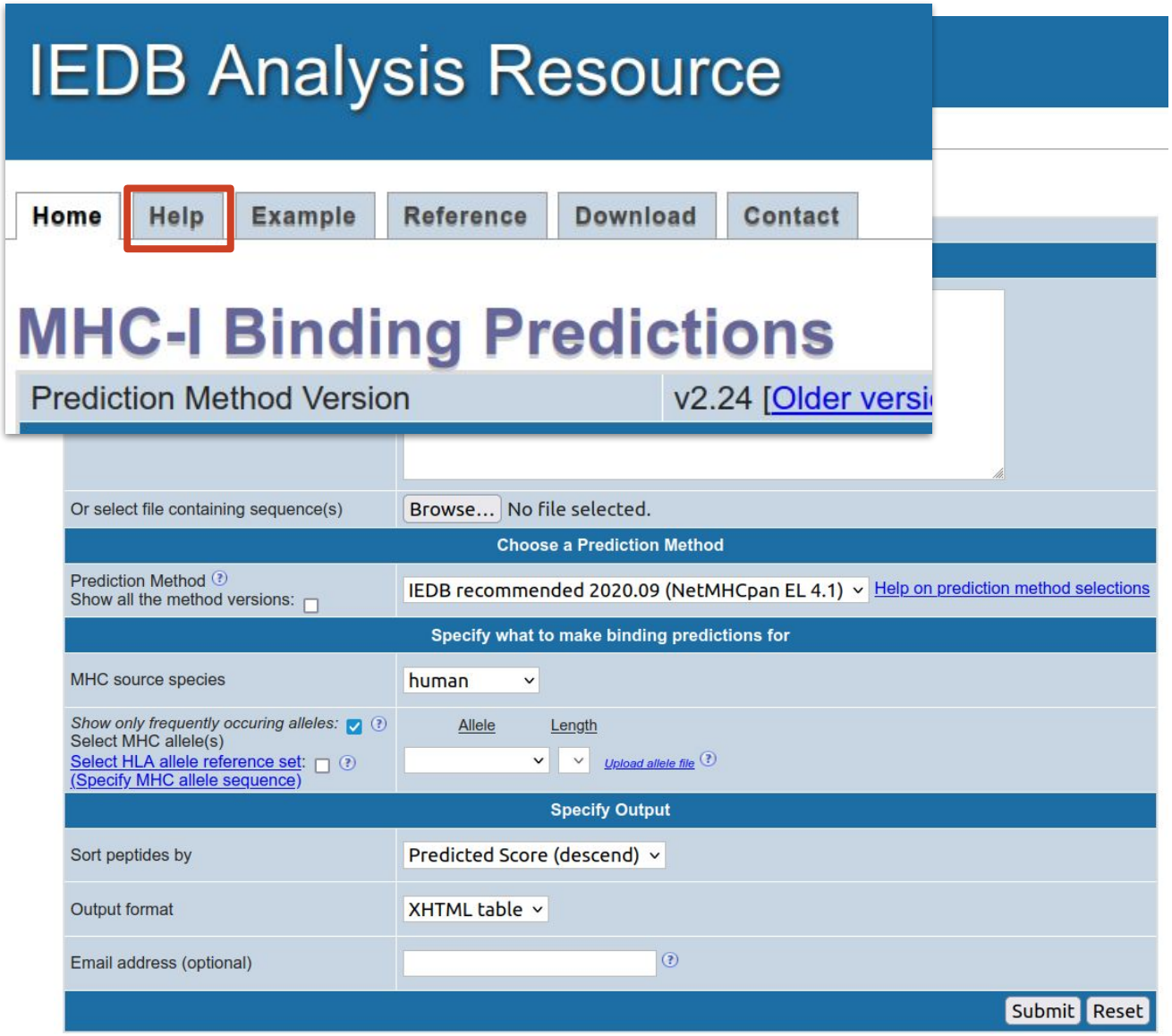
Allele-specific thresholds



Allele-specific thresholds



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MHC-I binding predictions - Tutorial

Guidelines for selecting thresholds (cut-offs) for MHC class I and II binding predictions can be found here.

How to obtain predictions

This website provides access to predictions of peptide binding to MHC class I molecules. The screenshot below illustrates the s
Each of the steps is described in more detail below.

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Selecting thresholds (cut-offs) for MHC class I and II binding predictions

Ward Fleri
posted this on May 21, 2013 04:33 PM

MHC class I

For MHC class I T cell epitope predictions, selection of predicted binders can be done based on the percentile rank or MHC binding affinity. The IEDB currently recommends making selections based on a percentile rank of <= 1% for each (MHC allele, length) combination to cover most of the immune responses.[1, 2] Alternatively, a binding affinity (IC50) threshold of 500 nM identifies peptide binders recognized by T cells and this threshold can be used to select peptides.[3] Recently, a paper from our group showed that absolute binding affinity threshold correlates better with immunogenicity and also that, for even better correlation, MHC-specific thresholds should be used.[4] The tables below show the allele-specific thresholds for the 38 most common HLA-A and HLA-B alleles, representative of the nine major supertypes. The tables can also be downloaded as an RTF file (see attached file).

Alleles sorted by population frequency		
Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
A*0201	25.2	255
A*2402	16.8	849
A*0101	16.2	884
A*0301	15.4	602
B*0702	13.3	687
A*1101	12.9	382
B*0801	11.5	663
B*4001	10.3	639
B*4402	9.2	904
B*4403	7.6	780
B*3501	6.5	348
A*2301	6.4	740
A*3201	5.7	131
B*5101	5.5	939
B*5301	5.4	538
B*1501	5.2	528
A*3001	5.1	109
A*3002	5	674

Alleles sorted by name		
Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
A*0101	16.2	884
A*0201	25.2	255
A*0203	3.3	92
A*0206	4.9	60
A*0301	15.4	602
A*1101	12.9	382
A*2301	6.4	740
A*2402	16.8	849
A*2501	2.5	795
A*2601	4.7	815
A*2902	2.9	641
A*3001	5.1	109
A*3002	5	674
A*3101	4.7	329
A*3201	5.7	131
A*3301	3.2	606
A*6801	4.6	197
A*6802	3.3	259

Selecting thresholds (cut-offs) for MHC class I and II binding predictions

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B*0702	13.3	687
A*1101	12.9	382
B*0801	11.5	663
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B*4402	9.2	904
B*4403	7.6	780
B*3501	6.5	348
A*2301	6.4	740
A*3201	5.7	131
B*5101	5.5	939
B*5301	5.4	538
B*1501	5.2	528
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Alleles sorted by name		
Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
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A*0203	3.3	92
A*0206	4.9	60
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A*2301	6.4	740
A*2402	16.8	849
A*2501	2.5	795
A*2601	4.7	815
A*2902	2.9	641
A*3001	5.1	109
A*3002	5	674
A*3101	4.7	329
A*3201	5.7	131
A*3301	3.2	606
A*6801	4.6	197
A*6802	3.3	259

Selecting thresholds (cut-offs) for MHC class I and II binding predictions

Ward Fleri
posted this on May 21, 2013 04:33 PM

MHC class I

For MHC class I T cell epitope predictions, selection of predicted binders can be done based on the percentile rank or MHC binding affinity. The IEDB currently recommends making selections based on a percentile rank of <= 1% for each (MHC allele, length) combination to cover most of the immune responses.[1, 2] Alternatively, a binding affinity (IC50) threshold of 500 nM identifies peptide binders recognized by T cells and this threshold can be used to select peptides.[3] Recently, a paper from our group showed that absolute binding affinity threshold correlates better with immunogenicity and also that, for even better correlation, MHC-specific thresholds should be used.[4] The tables below show the allele-specific thresholds for the 38 most common HLA-A and HLA-B alleles, representative of the nine major supertypes. The tables can also be downloaded as an RTF file (see attached file).

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Selection of “binders”

- Pick peptides **below percentile rank 1.0**

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

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

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

Recommendations

- All approaches (affinity and ranking) are reasonable, and have been applied in numerous studies

- Thresholds can be combined (peptides in top 1% and IC50 <500nM)

- Current studies suggest that allele specific thresholds can be derived

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Alternate approaches for selecting binders

- Change threshold values depending on your need
  - e.g. in case you have too few or too many predicted binders.

- Set a desired percentage within your peptide set (irrespective of IEDB percentile rank) in case you want to study a fixed number of best possible peptides.