

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

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



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



Antigens generated within the cell

- Viral particles
- Self proteins
- DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"



- Antigens generated within the cell
 - Viral particles
 - Self proteins
 - DRiPs (Defective Ribosomal Particles)
- Different factors influence peptide being "epitope"

- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only α chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only $\pmb{\alpha}$ chain impacts binding



- Expressed by almost all nucleated cells
- Presents antigen to CD8+ T cells (Cytotoxic T cells)
- One MHC encoded polymorphic chain (α) (2nd chain – β2-microglobulin)
- The binding groove is closed at both ends and can accommodate peptides of 8-15 AA
- Only α chain impacts binding



- 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	
FTSFFYRY	1285.0	
KSVFNSLY	1466.0	
RDWAHNSL	1804.6	
FSSCPVAY	1939.4	
RNWAHSSL	2201.7	
LSCAASGF	2830.1	
LASIDLKY	3464.0	

Machine learning algorithms



- 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	
FTSFFYRY	1285.0	
KSVFNSLY	1466.0	
RDWAHNSL	1804.6	
FSSCPVAY	1939.4	
RNWAHSSL	2201.7	
LSCAASGF	2830.1	
LASIDLKY	3464.0	

Machine learning algorithms



- 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	
FTSFFYRY	1285.0	
KSVFNSLY	1466.0	
RDWAHNSL	1804.6	
FSSCPVAY	1939.4	
RNWAHSSL	2201.7	
LSCAASGF	2830.1	
LASIDLKY	3464.0	

Machine learning algorithms



- 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
FTSFFYRY	1285.0
KSVFNSLY	1466.0
RDWAHNSL	1804.6
FSSCPVAY	1939.4
RNWAHSSL	2201.7
LSCAASGF	2830.1
LASIDLKY	3464.0

Machine learning algorithms



- 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	
FTSFFYRY	1285.0	
KSVFNSLY	1466.0	
RDWAHNSL	1804.6	
FSSCPVAY	1939.4	
RNWAHSSL	2201.7	
LSCAASGF	2830.1	
LASIDLKY	3464.0	

Machine learning algorithms



- 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

Ρ	Peptide binding data HLA-A*01:01		
	Peptide	IC ₅₀ (nM)	
	ASFCGSPY	51.4	
	LTDFGLSK	739.3	
	FTSFFYRY	1285.0	
	KSVFNSLY	1466.0	
	RDWAHNSL	1804.6	
	FSSCPVAY	1939.4	
	RNWAHSSL	2201.7	
	LSCAASGF	2830.1	
	LASIDLKY	3464.0	





- 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	
	FTSFFYRY	1285.0	
	KSVFNSLY	1466.0	
	RDWAHNSL	1804.6	
	FSSCPVAY	1939.4	
	RNWAHSSL	2201.7	
	LSCAASGF	2830.1	
	LASIDLKY	3464.0	

Machine learning algorithms



- 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	IC ₅₀ (nM)	
ASFCGSPY	51.4	
LTDFGLSK	739.3	
FTSFFYRY	1285.0	
KSVFNSLY	1466.0	
RDWAHNSL	1804.6	
FSSCPVAY	1939.4	
RNWAHSSL	2201.7	
LSCAASGF	2830.1	
LASIDLKY	3464.0	

Machine learning algorithms



- 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	IC ₅₀ (nM)	
ASFCGSPY	51.4	
LTDFGLSK	739.3	
FTSFFYRY	1285.0	
KSVFNSLY	1466.0	
RDWAHNSL	1804.6	
FSSCPVAY	1939.4	
RNWAHSSL	2201.7	
LSCAASGF	2830.1	
LASIDLKY	3464.0	

Machine learning algorithms



- 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





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)
2022NetMHCstabpan - 1.0	Rasmussen et al., 2016	0.980 AUC (average)


IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Home

Specialized Searches

Analysis Resource



23,297

References



IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Home

Specialized Searches

Analysis Resource

The IEDB has just launched its updated 3D viewers! Learn more via our help article here. START YOUR SEARCH HERE Welcome Epitope Analysis Resource The Immune Epitope Database (IEDB) is Epitope (?) Assay (?) T Cell Epitope Prediction (?) a freely available resource funded by NIAID. It catalogs experimental data on antibody Scan an antigen sequence for amino acid and T cell epitopes studied in humans, non-Any V T Cell human primates, and other animal species O Linear peptide B Cell MHC I Bindina in the context of infectious disease, allergy, MHC Ligand Exact ~ Ex: SIINFEKL autoimmunity and transplantation. The IEDB MHC II Binding also hosts tools to assist in the prediction Discontinuous Find Ex: neutralization and analysis of epitopes. MHC | Processing (Proteasome, TAP) O Non-peptidic Outcome: Positive Negative MHC I Immunogenicity Learn More Epitope Source (?) MHC Restriction (?) B Cell Epitope Prediction (?) **Upcoming Events & News** Organism Predict linear B cell epitopes using: Any AAI Exhibitor Booth May 6-10 Class I Ex: influenza, peanut Find Antigen Sequence Properties FOCiS Exhibitor Booth June 21-24 O Class II Virtual User Workshop Oct 26-28 Antigen Predict discontinuous B cell epitopes using * register here Non-classical antigen structure via: Ex: core, capsid, myos E Find Discotope Ex: HLA-A*02:01 Find IEDB SARS-CoV-2 Epitope Analysis Videos ElliPro Host (?) Disease (?) **Summary Metrics Epitope Analysis Tools** (?) Any Any Analyze epitope sets of: **Peptidic Epitopes** 1,539,170 O Human Infectious Non-Peptidic Epitopes 3.146 Population Coverage O Mouse Allergic 443,509 T Cell Assays **Conservation Across Antigens** O Non-human primate Autoimmune **B** Cell Assays 1,332,364 **Clusters with Similar Sequences** Ex: dog, camel Find Find ()Ex: asthma MHC Ligand Assays 4,631,827 **Epitope Source Organisms** 4,234 Reset **Restricting MHC Alleles** Search 970

23,297

References

Home Help Example Reference	Download Contact										
WARDER OF THE											
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.											
Or select file containing sequence(s)	Choose File No file chosen										
	Choose a Prediction Method										
Prediction Method (?) Show all the method versions:	IEDB recommended 2020.09 (NetMHCpan EL 4.1) V Help on prediction method selections										
	Specify what to make binding predictions for										
MHC source species	human 🗸										
Show only frequently occuring alleles: Select MHC allele(s) Select HLA allele reference set: (Specify MHC allele sequence)	Allele Length HLA-A*01:01 9 0 HLA-B*07:02 10 0 V Upload allele file ?										
	Specify Output										
Sort peptides by	Predicted IC50 V										
Show	All predictions										
Output format	XHTML table 🗸										
Email address (optional)											
	Submit Reset										

tools.iedb.org/mhci/

Home Help Example Reference	Download Contact										
	11										
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.											
Or select file containing sequence(s)	Choose File No file chosen										
	Choose a Prediction Method										
Prediction Method ③ Show all the method versions:	IEDB recommended 2020.09 (NetMHCpan EL 4.1) Help on prediction method selections										
	Specify what to make binding predictions for										
MHC source species	human 🗸										
Show only frequently occuring alleles: Select MHC allele(s) Select HLA allele reference set: (Specify MHC allele sequence)	Allele Length HLA-A*01:01 9 ○ HLA-B*07:02 10 ○ ✓ ✓ Upload allele file ?										
	Specify Output										
Sort peptides by	Predicted IC50										
Show	All predictions										
Output format	XHTML table 🗸										
Email address (optional)											
	Submit Reset										

tools.iedb.org/mhci/

Home Help Example Reference Download Contact **MHC-I Binding Predictions** Prediction Method Version v2.24 [Older versions] Specify Sequence(s) >LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA Enter protein sequence(s) in FASTA format QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE or as whitespace-separated sequences. NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISD LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKROGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR Or select file containing sequence(s) Choose File No file chosen **Choose a Prediction Method** Prediction Method 🕐 IEDB recommended 2020.09 (NetMHCpan EL 4.1) V Help on prediction method selections Show all the method versions: Specify what to make binding predictions for MHC source species human × Allele Length Show only frequently occuring alleles: 🗹 🕐 Select MHC allele(s) HLA-A*01:01 9 0 0 HI A-B*07.02 10 Select HLA allele reference set: (Specify MHC allele sequence) Upload allele file (?) × Specify Output Sort peptides by Predicted IC50 v Show All predictions × Output format XHTML table V (?) Email address (optional)

tools.iedb.org/mhci/

Submit Reset

Home	Help	Example	Reference	Download	Contact														t.	പ	s.i	edł	o.or	σ/m	hci	1
мнс	-I Bi	nding	Predict	tions																	5.11			5/11		-
Predictio	on Metho	d Version	TTOUTO	v2.24 [Older ve	ersions]																					
					Specify S	eque	nce	e(s)																		
Enter pr or as wh	otein seq itespace	uence(s) in F separated se	ASTA format equences.	>LCMV Armst MGQIVTMFEA YGLKGPDIYKG SHNFCNLTSAF QSAQSQCRTF NHCTYAGPFG LKCFGNTAVAH LLMRNHLRDL DNMITEMLRK HRLTNKGICSC	rong, Protein LPHIIDEVIN VYQFKSVEFU NKKTFDHTL RGRVLDMFF MSRILLSQEK CNVNHDAEI MGVPYCNYS DYIKRQGSTI GAFKVPGVK	GP VIIVL MSH MSIVS TAFG TKFFT CDM KFWY PLALW	.IVITO LNLT SSLH GKYM TRRL ILRLI YLEH ADLL KRR	TGIKAY LTMPN HLSIR(YMRS) LAGTI LIDYN HAKT(LIMFS	AVYNFA 'NACSA RGNSN' SGWGV TFTWTI VKAALS TGETSV 'STSAYL'	ATCGIFAI ANNSHH YKAVSC' MTGSDG LSDSSG' SKFKEDV /PKCWL\ VSIFLHL	LISFLLLA IYISMGT DFNNG GKTTWC VENPGG /ESALHL VTNGSY VKIPTHI	AGRS SGLI SQTS SYCLT FKTT LNET RHIK	SCGM ELTFTNI YNLTFSE 'SYQYLII' TKWMII TVNSLIS THFSDQ (GGSCPH	DSII DA IQNRTW LAAE SDQ QIEQEA KP	VE		1	N								
Or selec	t file cont	aining seque	nce(s)	Choose File	No file o	hose	en																			
				Ch	oose a Pre	dictio	on M	Meth	hod												_					
Prediction Show all	on Metho I the meth	d 🕐 nod versions:		IEDB recom	mended 2 nended 2(020.0 20.0) 90 (1) 90	(Net Net)	tMHC MHCp	pan El	L 4.1) 4.1)	~ ±	<u>Help or</u>	n predi	ction m	ethod	selection	ns				Ρ	red	ictio	n	
MHC so Show on Select N Select H (Specify) Sort pep	urce spec ly frequer IHC allele <u>ILA allele</u> <u>MHC alle</u>	cies ntly occuring a e(s) reference se ele sequence	lleles: ☑ ? t: □ ? }	Consensus NetMHCpan IEDB recom NetMHCpan ANN 4.0 SMMPMBEC SMM CombLib_Si PickPocket netMHCcons netMHCstab	BA 4.1 mended 20 BA 4.0 c dney2008 pan	20.0	14 (N	(NetN	МНСр	oan EL	4.0)										L		met	thoc		
Show	,			All prodiction														-								
Output f	ormat			XHTML table	•		-																			
Email ad	Idress (oj	ptional)					0	?																		
															Su	bmit	Rese	t								

Help Example Reference Download Contact Home **MHC-I Binding Predictions** Prediction Method Version v2.24 [Older versions] Specify Sequence(s) >LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE Enter protein sequence(s) in FASTA format or as whitespace-separated sequences. NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR Or select file containing sequence(s) Choose File No file chosen Choose a Prediction Method Prediction Method ? IEDB recommended 2020.09 (NetMHCpan EL 4.1) v Help on prediction method selections Show all the method versions: Specify what to make binding predictions for MHC source species human chimpanzee Show only frequently occuring alleles: 🔽 📀 COW Length Select MHC allele(s) gorilla Upload allele file ? V Select HLA allele reference set: human (Specify MHC allele sequence) macaque mouse **Specify Output** pig Sort peptides by dog × horse Show All predictions × Output format XHTML table ✓ (?) Email address (optional) Submit Reset

tools.iedb.org/mhci/

Choose species

2022 IEDB User Workshop

Example Reference Download Contact Home Help **MHC-I Binding Predictions** Prediction Method Version v2.24 [Older versions] Specify Sequence(s) >LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA Enter protein sequence(s) in FASTA format QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE or as whitespace-separated sequences. NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKROGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR Or select file containing sequence(s) Choose File No file chosen **Choose a Prediction Method** Prediction Method 3 IEDB recommended 2020.09 (NetMHCpan EL 4.1) V Help on prediction method selections Show all the method versions: Specify what to make binding predictions for MHC source species human × Allele Length Show only frequently occuring alleles 🔽 HLA-A*01:01 9 0 Select MHC allele(s) 0 HLA-B*07:02 10 Select HLA allele reference set: 🦳 🕐 (Specify MHC allele sequence) V Upload allele file ? × **Specify Output** Sort peptides by Predicted IC50 v Show All predictions × Output format XHTML table ➤ Email address (optional) (?) Submit Reset

tools.iedb.org/mhci/



Home Help Example Reference	Download Contact	tools.jedb.org/mhci/
MHC-I Binding Predic	tions	
Prediction Method Version	v2.24 [Older versions]	
(0	Specify Sequence(s)	
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.	>LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQVILQNRTWE NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE	
Г	LKCFGN I AVARCN VNHDAEFCDMILRLIDTNKAALSKFREDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR	Complete set
Or select file containing sequence(s)	Choose File No file chosen	
	Choose a Prediction Method	Poforonco alloloc
Prediction Method (?) Show all the method versions:	IEDB recommended 2020.09 (NetMHCpan EL 4.1) ➤ Help on prediction method selections	Reference alleles
	Specify what to make binding predictions for	
MHC source species	human 🗸	
Show only frequent, occuring alleles ? Select MHC allele(3) Select HLA allele reference set: ? (Specify MHC allele sequence)	Allele Length HLA-A*01:01 9 ○ HLA-B*07:02 10 ○ ✓ Upload allele file ?	
	Specify Output	
Sort peptides by	Predicted IC50 V	
Show	All predictions	
Output format	XHTML table 🗸	
Email address (optional)		
	Submit Reset	

Allele selection – Reference set for global coverage

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

http://iedb.zendesk.com/ent
ries/25054538-HLA-allele-fre
<u>quencies</u>

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		

2022 IEDB User Workshop

Home Help Example Reference	Download Contact	tools.jedb.org/mhci/
MHC-I Binding Predic	tions	
Prediction Method Version	v2.24 [Older versions]	
(0	Specify Sequence(s)	
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.	>LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQVILQNRTWE NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE	
Г	LKCFGN IAVARCNVNHDAEFCDMILRLIDTNKAALSKFKEDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR	Complete set
Or select file containing sequence(s)	Choose File No file chosen	
	Choose a Prediction Method	Poforonco alloloc
Prediction Method (?) Show all the method versions:	IEDB recommended 2020.09 (NetMHCpan EL 4.1) ➤ Help on prediction method selections	Reference alleles
	Specify what to make binding predictions for	
MHC source species	human 🗸	
Show only frequent, occuring alleles ? Select MHC allele(3) Select HLA allele reference set: ? (Specify MHC allele sequence)	Allele Length HLA-A*01:01 9 ○ HLA-B*07:02 10 ○ ✓ Upload allele file ?	
	Specify Output	
Sort peptides by	Predicted IC50 V	
Show	All predictions	
Output format	XHTML table 🗸	
Email address (optional)		
	Submit Reset	

Home Help Example Reference	Download Contact	tools jedh org/mhci/
MHC-I Binding Predic	tions	
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 MGQIVTMFEALPHIIDEVINIVIIVIUIVTGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ	
	DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR	Complete set
Or select file containing sequence(s)	Choose File No file chosen	
	Choose a Prediction Method	Reference alleles
Prediction Method (2) Show all the method versions:	IEDB recommended 2020.09 (NetMHCpan EL 4.1) Help on prediction method selections	
	Specify what to make binding predictions for	
MHC source species	human 🗸	
Show only frequent, occuring alleles ? Select MHC allele (S. <u>Select HLA allele reference set</u> ? (<u>Specify MHC allele sequence</u>)	Allele Length HLA-A*01:01 9 HLA-B*07:02 10 ✔ Upload allele file	Specify allele(s) & peptide length (select or upload)
	Specify Output	
Sort peptides by	Predicted IC50 V	
Show	All predictions	
Output format	XHTML table 🗸	
Email address (optional)		
	Submit Reset	

Example Reference Download Contact Home Help **MHC-I Binding Predictions** Prediction Method Version v2.24 [Older versions] Specify Sequence(s) >LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE Enter protein sequence(s) in FASTA format or as whitespace-separated sequences. NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKROGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR Or select file containing sequence(s) Choose File No file chosen Choose a Prediction Method Prediction Method 🕐 IEDB recommended 2020.09 (NetMHCpan EL 4.1) V Help on prediction method selections Show all the method versions: Specify what to make binding predictions for MHC source species human × Allele Length Show only frequently occuring alleles: 🔽 🕐 HLA-A*01:01 9 0 Select MHC allele(s) 0 HLA-B*07:02 10 Select HLA allele reference set: (Specify MHC allele sequence) V Upload allele file ? × **Specify Output** Predicted IC50 Sort peptides by v Show All predictions × XHTML table ✓ Output format Email address (optional) bpeters@lji.org (?) Submit Reset

tools.iedb.org/mhci/



IEDB Analysis Resource		tools.iedb.org/mhci/
Home Help Example Reference Download Contact		
Induite Description Description Description Notice Description Contract MIGOVIDE Colspan="2">Contract Input Sequences # Name Sequence I LAW MGGIVTMFEALPHIDEVINIVILVITGIKAVYNFATCGIFALISFLLLAGRSCC Yamstrong, MIGGIVTMFEALPHIDEVINIVILVITGIKAVYNFATCGIFALISFLLLAGRSCC Protein GP MIGGIVTMFEALPHIDEVINIVILVITGIKAVYNFATCGIFALISFLLLAGRSCC Protein GP MIGGIVTMFEALPHIDEVINIVILVITGIKAVYNFATCGIFALISFLLLAGRSCC Protein GP MIGGIVTMFEALPHIDEVINIVILVITGIKAVYNFATCGIFALISFLLLAGRSCC RTKFFTRACGFTWRLASFFKREDVSEAL+IFKTTVNSLISDQLLANKINHLRDLMOST COLSPAN="2">COLSPAN="2" VARGALASKFKEDVSEAL+IFKTTVNSLISDQLLANKINHLRDLMOST COLSPAN="2" VARGALASKFKEDVSEAL+IFKTTVNSLISDQLLANKINHLRDLMOST MIGEOSTATUSIELINUNGGGCRAFTWGSVIT VARGALASKFKKSPUKGSQLHFKKTTVKSSQLEARKVDVKKSQLANKINGGGCARVPSVKV MIGEOSTATUSIELINGGGCARVPSVKV 2 LGMV Armstrong, Protein NP DUCARLSLOCYMAREQOSCARVPOVKVKSSLLINNOFG KGSGTPILNDVVGALTDLQUVGMRKPAGGSGCARVFVVKVKVKVKVKVKVKVKVKVKVKVKVKVKVKVKVKVK	SMYGLKGPDIYK NFCNLTSAFNKK RTFRGRVLDMF PFGMSRILLSDE QGNVNHDAEFC YCMYSKFWYL GGSTPLALMDLL TWIKRR ZMIRKEKRDDK MRSERPQASGV TMPSLTAAGMA USGYNFSLGAA YENLTKYCJSG	Input sequence
Download result Image: Control of the second seco	Icore Score Percentile Rank ▼ RTSIVGRAW 0.993694 0.01 LSKEVKSFQW 0.992161 0.01 GETSVPKCW 0.988359 0.01 TIDLTSEK 0.988559 0.01 GETSVPKCW 0.988201 0.01	Output
HLAB-958.01 2 319 327 9 RTSIVGRAM RTSIVGRAM HLAA-724.02 1 71 79 9 VVQFKSVEF VVQFKSVEF HLAA-724.02 1 1197 205 9 TAFGGKYMR TAFGGKYMR TAFGGKYMR HLAB-768.01 1 197 205 9 TAFGGKYMR TAFGGKYMR HLAB-715.01 2 271 279 9 SEDLLKAVL SEDLLKAVL HLAB-768.02 2 23 31 9 FTSDVKAAV FTSDVKAAV HLAA-768.02 2 23 31 9 FTSDVKAAV FTSDVKAAV HLAA-768.02 1 77 79 9 VVQFKSVEF VVQFKSVEF HLAA-768.02 1 17 25 9 EVINIVIIV EVINIVIIV HLA-715.01 2 15 23 9 AIRRELQSF AIRRELQSF HLA-4711.01 1 382 390 9 KTGETSVPK KTGETSVPK HLA-A*	I RTSIVGRAW 0.98299 0.01 VVQFKSVEF 0.980795 0.01 TAFGGKYMR 0.976891 0.01 SEDLLKAVL 0.974336 0.01 KQFKQDSKY 0.974222 0.01 FTSDVKAAV 0.958917 0.01 TTIDLTSEK 0.98473 0.01 EVINIVIV 0.947546 0.01 EVINIVIV 0.94421 0.01 ALRERLQSF 0.94328 0.01 KTGETSVPK 0.93577 0.01 STSKKNVLK 0.935352 0.01 HCKDENFYL 0.93742 0.01	percentile rank)
HLA-A'30102 2 414 422 9 KQFKQDSKY KQFKQDSKY HLA-A'32:01 2 8 16 9 KSFQWTQAL KSFQWTQAL HLA-A'30:02 1 233 241 9 RTWENHCTY RTWENHCTY HLA-A'30:02 1 233 241 9 RTWENHCTY RTWENHCTY HLA-B'30:01 2 333 351 9 RTWENHCTY RTWENHCTY HLA-B'80:01 2 46 55 10 EVSNVQRIMR EVSNVQIMR HLA-B'40:01 2 512 520 9 KEITPHCAL KEITPHCAL	KUFKUDSKY V080268 0.01 KSEQWTQAL 0.87178 0.01 RTWENHCTY 0.885525 0.01 RTWENHCTY 0.840246 0.01 SPRPAPGAA 0.967013 0.02 EVSNVQRIMR 0.966314 0.02 KEITPHCAL 0.99127 0.02	

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	1 <mark>97</mark>	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
	100 ¹⁰	-3222	100000					122121000000000	2012 2 4 50

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	1 <mark>97</mark>	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
	- 10 ^{- 1}		- 200230					12212002012020	2019 2 4 30

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	1 <mark>97</mark>	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
	100 M	-3323	1.2000.00	2				12000	2012 1 2 2 2

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	1 <mark>9</mark> 7	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
	- 53	5.5.5.5 G	1000430	12				010512002012000	1011112

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	1 <mark>97</mark>	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
	- 10 ^{- 1}	-3333	1.222243					120200000000000	1011111111

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	0.94442 <mark>1</mark>	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
Tensoral Distriction	5.0	1050002							2013/29.00

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	1 <mark>9</mark> 7	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
Sector Distriction	5.0	105020	1.100000					Charles and the second second	000000000

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	1 <mark>97</mark>	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	.0.047EAE	0.01	L
HLA-A*68:02	1	17	25	9	EVINIVIIV	EVINIVIIV	EVINIVII A	percer	ntile rank for	а
HLA-B*15:01	2	15	23	9	ALRRELQSF	ALRRELQSF	ALRRELQS P	eptide	is the percen	tag
HLA-A*11:01	1	382	390	9	KTGETSVPK	KTGETSVPK	KTGETSVP O	f rando	mly sampled	
HLA-A*11:01	2	82	90	9	STSKKNVLK	STSKKNVLK	STSKKNVL D	eptides	s scoring bett	er
HLA-B*08:01	2	217	225	9	RLKDKHPVL	RLKDKHPVL	RLKDKHPV t	han the	peptide.	
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	
	1 Q 1									f

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	1 <mark>97</mark>	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
	- 163 ^{- 77}	1882	1 100000					(1993) 100 CONTRACTOR	2019 22 20

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

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

• 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

²⁰²² IEDB User Workshop

• 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

²⁰²² IEDB User Workshop

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

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

allele	seq_num	start	end	length	peptide	core	icore	score	rank
HLA-B*57:01	2	2 319	327	, 9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.993694	0.01
HLA-B*57:01	2	2 3	3 12	2 10	LSKEVKSFQW	LSKEVSFQW	LSKEVKSFQW	0.992161	0.01
HLA-B*44:03	1	1 384	392	9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.98935	0.01
HLA-A*68:01	2	2 330	338	\$ 9	TTIDLTSEK	TTIDLTSEK	TTIDLTSEK	0.988559	0.01
HLA-B*44:02	1	L 384	392	2 9	GETSVPKCW	GETSVPKCW	GETSVPKCW	0.988201	0.01
HLA-B*58:01	2	2 319	327	9	RTSIVGRAW	RTSIVGRAW	RTSIVGRAW	0.98239	0.01
HLA-A*24:02	1	L 71	L 79	, 9	VYQFKSVEF	VYQFKSVEF	VYQFKSVEF	0.980795	0.01
HLA-A*68:01	1	1 197	/ 205	; <u>9</u>	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01

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-A*68:01	1	107	205	0	TAECCKYMP	TAECCKYMD	TAECCKYMP	0.074401	0.01
		177	203	,		TAPOGRTMIK	TAPGGRIMR	0.976691	
		177	205	,		TAPGGRTMR	TAPGGRIMR	0.976691	
LA-B*15:01	1	389	398	10	PKCWLVTNGS	KCWLVTNGS	KCWLVTNGS	0.976691	0 10
LA-B*15:01 LA-B*15:01	1	389 314	398 323	10 10	PKCWLVTNGS	KCWLVTNGS EFCDMLRLI	KCWLVTNGS EFCDMLRLI	0.978891	0 10
LA-B*15:01 LA-B*15:01 LA-B*15:01	1	389 314 155	398 323 164	10 10 10	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN	KCWLVTNGS EFCDMLRLI YAVSCDFNN	KCWLVTNGS EFCDMLRLI YKAVSCDFNN	0.978891	0 10 0 10 0 10
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01	1	389 314 155 389	398 323 164 397	10 10 10 9	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG	0.978891	0 10 0 10 0 10 0 10
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01	1 1 1 1 1 1	389 314 155 389 89	398 323 164 397 97	10 10 10 9 9	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG PNACSANNS	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG PNACSANNS	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG PNACSANNS		0 10 0 10 0 10 0 10 0 10
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01	1 1 1 1 1 1 1	389 314 155 389 89 12	398 323 164 397 97 20	10 10 10 9 9 9	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN		0 10 0 10 0 10 0 10 0 10 0 10 0 10
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01	1 1 1 1 1 1 1 1 1	389 314 155 389 89 12 389	398 323 164 397 97 20 398	10 10 10 9 9 9 10	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN PKCWLVTNGS	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN PKWLVTNGS	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN PKCWLVTNGS		0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10

la ca	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-A*68:01	1	197	205	9	TAFGGKYMR	TAFGGKYMR	TAFGGKYMR	0.976691	0.01
LA D*15.01	1	200	202	10	DICOMINATION		KOMUNTNICS		0 10
LA-B*15:01	1	389	398 323	10	PKCWLVTNGS	KCWLVTNGS	KCWLVTNGS		0 100
LA-B*15:01 LA-B*15:01	1	389 314 155	398 323 164	10 10	PKCWLVTNGS EFCDMLRLID YKAVSCDENN	KCWLVTNGS EFCDMLRLI YAVSCDENN	KCWLVTNGS EFCDMLRLI YKAVSCDENN		0 100 0 100
LA-B*15:01 LA-B*15:01 LA-B*15:01	1 1 1	389 314 155 389	398 323 164 397	10 10 10 9	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG		0 100 0 100 0 100 0 100
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01	1 1 1 1 1	389 314 155 389 89	398 323 164 397 97	10 10 10 9 9	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG PNACSANNS	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG PNACSANNS	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG PNACSANNS		0 100 0 100 0 100 0 100 0 100
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01	1 1 1 1 1 1	389 314 155 389 89 12	398 323 164 397 97 20	10 10 10 9 9	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN		0 100 0 100 0 100 0 100 0 100 0 100
LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*15:01 LA-B*07:02	1 1 1 1 1 1 1 1	389 314 155 389 89 12 389	398 323 164 397 97 20 398	10 10 10 9 9 9 10	PKCWLVTNGS EFCDMLRLID YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN PKCWLVTNGS	KCWLVTNGS EFCDMLRLI YAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN PKWLVTNGS	KCWLVTNGS EFCDMLRLI YKAVSCDFNN PKCWLVTNG PNACSANNS PHIIDEVIN PKCWLVTNGS		0 100 0 100 0 100 0 100 0 100 0 100 0 100

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-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
HLA-A*03:01	1	439	447	9	LLMFSTSAY	LLMFSTSAY	LLMFSTSAY	0.179096	1
HLA-A*11:01	2	101	110	10	SLAADLEKLK	SLADLEKLK	SLAADLEKLK	0.168581	1
HLA-A*02:03	2	30	38	9	AVIKDATNL	AVIKDATNL	AVIKDATNL	0.157418	1
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
HLA-B*07:02	2	12	20	9	WTQALRREL	WTQALRREL	WTQALRREL	0.1172	1
ILA-B*15:01	1	155	164	10	YKAVSCDFNN	YAVSCDFNN	YKAVSCDFNN		0 10
LA-B*15:01	1	389	397	9	PKCWLVTNG	PKCWLVTNG	PKCWLVTNG		0 10
LA-B*15:01	1	89	97	9	PNACSANNS	PNACSANNS	PNACSANNS		0 10
ILA-B*15:01	1	12	20	9	PHIIDEVIN	PHIIDEVIN	PHIIDEVIN		0 10
LA-B*07:02	1	389	398	10	PKCWLVTNGS	PKWLVTNGS	PKCWLVTNGS		0 10
ILA-B*07:02	1	299	308	10	FGNTAVAKCN	FGNTAVAKN	FGNTAVAKCN		0 10

• 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

²⁰²² IEDB User Workshop

• 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

²⁰²² IEDB User Workshop
• 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

²⁰²² IEDB User Workshop

- 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

²⁰²² IEDB User Workshop

Home Help Example Reference Download

Contact

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 NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGVCLTKWMILAAE LKCFGMTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ 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)					
MHC source species	Consensus NetMHCpan BA 4.1					
Show only frequently occuring alleles: (3)	ANN 4.0 SMMPMBEC					
Select Millo allele(3)	SMM					
	CombLib_Sidney2008					
	PickPocket					
Sort peptides by	netMHCcons					
Output format	netMHCstabpan					
Email address (optional)						
	Submit Reset					

Home Help Example Reference Download

Contact

Prediction Method Version	v2.24 [Older versions]				
	Specify Sequence(s)				
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.	<pre>>LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR</pre>				
	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				
	IEDB recommended 2020.09 (NetMHCpan EL 4.1)				
MHC source species	Consensus NetMHCpan BA 4.1				
Show only frequently occuring alleles: 💟 (3) Select MHC allele(s)	ANN 4.0 SMMPMBEC				
	SMM				
	CombLib_Sidney2008				
Sort poptidos by	PickPocket				
Solit peptides by	netMHCcons				
Output format	netMHCstabpan				
Email address (optional)	•				
	Submit Reset				





Grouped final





OXFORD

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.

Home Help Example Reference Download

Contact

Prediction Method Version	v2.24 [Older versions]				
	Specify Sequence(s)				
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.	<pre>>LCMV Armstrong, Protein GP MGQIVTMFEALPHIIDEVINIVIIVLIVITGIKAVYNFATCGIFALISFLLLAGRSCGM YGLKGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGTSGLELTFTNDSII SHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNYKAVSCDFNNGITIQYNLTFSDA QSAQSQCRTFRGRVLDMFRTAFGGKYMRSGWGWTGSDGKTTWCSQTSYQYLIIQNRTWE NHCTYAGPFGMSRILLSQEKTKFFTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAE LKCFGNTAVAKCNVNHDAEFCDMLRLIDYNKAALSKFKEDVESALHLFKTTVNSLISDQ LLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEA DNMITEMLRKDYIKRQGSTPLALMDLLMFSTSAYLVSIFLHLVKIPTHRHIKGGSCPKP HRLTNKGICSCGAFKVPGVKTVWKRR</pre>				
	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				
	IEDB recommended 2020.09 (NetMHCpan EL 4.1)				
MHC source species	Consensus NetMHCpan BA 4.1				
Show only frequently occuring alleles: ③ Select MHC allele(s)	ANN 4.0 SMMPMBEC				
	SMM				
	CombLib_Sidney2008				
Sort poptidos by	PickPocket				
Solit peptides by	netMHCcons				
Output format	netMHCstabpan				
Email address (optional)	•				
	Submit Reset				

н	ome Hel	Example Reference Download Contact
N	HC-	Binding Production Posults
In	out Seque	ices
#	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

Н	ome Help	Example Reference Download Contact
N	IHC-I	Binding Prediction Results
In	out Sequen	ces
#	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

Home He	elp	Exampl	e Re	eference	Download	Contact	
MHC	-	Bind	din	g Pr	edic	IC50 (pM)	ts
input Sequ	ence	es	_	_		10.50 (1111)	
# Name 1 LCMV Armstrong	ŋ,	MGQIVTI GVYQFK			VIIVLIVIT MPNACSA	4.75	LAGRSCGMYGLKGPDIYK TNDSIISHNFCNLTSAFNKK
Protein G	P	TFDHTLN RTAFGGI KTKFFTF	ISIVSSI KYMRS RLAGT	LHLSIRGN GWGWTG FTWTLSD	ISNYKAVS SDGKTTV SSGVENI	8.90	2SAQSQCRTFRGRVLDMF HCTYAGPFGMSRILLSQE GNTAVAKCNVNHDAEFC
		EHAKTGI MFSTSA	ETSVPH LVSIFL	CWLVTN HLVKIPTH	GSYLNET IRHIKGGS	9.29	RDLMGVPYCNYSKFWYL RKDYIKRQGSTPLALMDLL KVPGVKTVWKRR
Prediction	meth	nod: net	mhccc	ons 1.1	Low Sco	10.18	
Citations	uru					11.11	
Allele 🌻	# \$	Start 🔷	End 🛊	Length ≑	Peptide	15.06	le Rank 🗢
HLA-A*02:01	1	6	14	9	TMFEAL	15.90	0.1
HLA-A*02:01	1	440	448	9	LMFSTS	15.96	.31
HLA-A*02:01	1	447	455	9	YLVSIF	10.00	.32
HLA-A*02:01	1	435	443	9	ALMDLL	39.38	.39
HLA-A*02:01	1	137	145	9	TLMSIV		.42
HLA-A*02:01	1	10	18	9	ALPHII	42.94	0.6
HLA-A*02:01	1	45	53	9	ALISFL		0.6
HLA-A*02:01	1	14	22	9	IIDEVI	65.49	1.3
HLA-A*02:01	1	42	50	9	GIFALI	76 20	1.4
HLA-A*02:01	1	38	46	9	FATCGI	10.20	1.7
HLA-A*02:01	1	448	456	9	LVSIFL	99.33	1.9
HLA-A*02:01	1	436	444	9	LMDLLM	00.00	2.2
HLA-A*02:01	1	13	21	9	HIIDEV	120.03	2.4

2022 IEDB User Workshop

• 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

²⁰²² IEDB User Workshop

- 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 nivi 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

²⁰²² IEDB User Workshop

- 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

²⁰²² IEDB User Workshop

- 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

²⁰²² IEDB User Workshop

• 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

• 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

Allele-specific thresholds

IEDB Analysis Resource

Prediction Method Version	v2.24 [Older versions]					
Specify Sequence(s)						
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences.						
Or select file containing sequence(s)	Browse No file selected.					
	Choose a Prediction Method					
Prediction Method ⑦ Show all the method versions:	IEDB recommended 2020.09 (NetMHCpan EL 4.1) V Help on prediction method selections					
	Specify what to make binding predictions for					
MHC source species	human ~					
Show only frequently occuring alleles: (?) Select MHC allele(s) Select HLA allele reference set: (?) (Specify MHC allele sequence)	Allele Length V Upload allele file ③					
	Specify Output					
Sort peptides by	Predicted Score (descend) v					
Output format	XHTML table ~					
Email address (optional)	•					
	Submit Reset					

411	Ilele-specific thresholds						
	I	EDB Analys	sis Resource				
	H	ome Help Example	Reference Download Contact				
	N	IHC-I Bindi	ng Predictions				
		Or select file containing sequence(s)	Browse No file selected.				
		Prediction Method ^③ Show all the method versions:	Choose a Prediction Method IEDB recommended 2020.09 (NetMHCpan EL 4.1) Help on prediction method selections				
			Specify what to make binding predictions for				
		MHC source species Show only frequently occuring alleles: () Select MHC allele(s) Select HLA allele reference set: () () Specify MHC allele sequence)	Allele Length ✓ ✓ Upload allele file				
			Specify Output				
		Sort peptides by	Predicted Score (descend) v				
		Output format	XHTML table v				
		Email address (optional)	•				
			Submit Reset				

Home Help

Example Reference

Download Contact

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.

Home Help Example Reference Download Contact

Prediction Method Version	2013-02-22 [Older versions]	1
	Specify Sequence(s)	
Enter protein sequence(s) in FASTA format or as whitespace-separated sequences. (Browse for sequences in NCBI)		2



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 s	sorted by popula	ation frequency	A	leles sorted by	name
Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)	Allele	Population frequency of allele	Allele speci affinit cutoff (IC50
A*0201	25.2	255	A*0101	16.2	100 C
A*2402	16.8	849	A*0201	25.2	
A*0101	16.2	884	A*0203	3.3	
A*0301	15.4	602	A*0206	4.9	
B*0702	13.3	687	A*0301	15.4	
A*1101	12.9	382	A*1101	12.9	
B*0801	11.5	663	A*2301	6.4	
B*4001	10.3	639	A*2402	16.8	
B*4402	9.2	904	A*2501	2.5	
B*4403	7.6	780	A*2601	4.7	
B*3501	6.5	348	A*2902	2.9	
A*2301	6.4	740	A*3001	5.1	
A*3201	5.7	131	A*3002	5	
B*5101	5.5	939	A*3101	4.7	
B*5301	5.4	538	A*3201	5.7	
B*1501	5.2	528	A*3301	3.2	
A*3001	5.1	109	A*6801	4.6	
A*3002	5	674	A*6802	3.3	

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

2022 IEDB User Workshop

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

representative of the nine major supertypes. The tables can also be downloaded as an RTF file (see attached file).



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,

Alleles sorted by population frequency		AI	Alleles sorted by name		
	Population frequency of lele	Allele specific affinity cutoff (IC50 nM)	Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
Allele	25.2	255	A*0101	16.2	88
A*0201	16.8	849	A*0201	25.2	25
410400	16.2	884	A*0203	3.3	9
A-2402	15.4	602	A*0206	4.9	e
A*0101	13.3	687	A*0301	15.4	60
A*0301	12.9	382	A*1101	12.9	38
710001	11.5	663	A*2301	6.4	74
B-0702	10.3	639	A*2402	16.8	84
A*1101	9.2	904	A*2501	2.5	79
B*0801	7.6	780	A*2601	4.7	81
00001	6.5	348	A*2902	2.9	64
B-4001	6.4	740	A*3001	5.1	10
7452012	5.7	131	A*3002	5	67
B*5101	5.5	939	A*3101	4.7	32
B*5301	5.4	538	A*3201	5.7	13
B*1501	5.2	528	A*3301	3.2	60
A*3001	5.1	109	A*6801	4.6	19
A*3002 5		674	A*6802	3.3	25

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			Alleles sorted by name			
Allele	Population frequency or allele	Allele specific affinity cutoff (IC50 nM)]	Allele	Population frequency of allele	Allele specific affinity cutoff (IC50 nM)
A*0201	25.	255		A*0101	16.2	884
A*2402	16.	849		A*0201	25.2	255
A*0101	16.	884	1	A*0203	3.3	92
A*0301	15.	603	•	A*0206	4.9	60
B*0702	13.	602	4	A*0301	15.4	602
A*1101	12.	687		A*1101	12.9	382
B*0801	11.	382		A*2301	6.4	740
B*4001	10.	663		A*2402	16.8	849
B*4402	9.	639		A*2501	2.5	795
B*4403	7.	904		A*2601	4.7	815
B*3501	6.5	340		A*2902	2.9	641
A*2301	6.4	740		A*3001	5.1	109
A*3201	5.7	131		A*3002	5	674
B*5101	5.5	939		A*3101	4.7	329
B*5301	5.4	538		A*3201	5.7	131
B*1501	5.2	528		A*3301	3.2	606
A*3001	5.1	109		A*6801	4.6	197
A*3002	5	674		A*6802	3.3	259

• 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

²⁰²² IEDB User Workshop

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

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

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.