



2020年 ユーザーワークショップ

MatchMaker

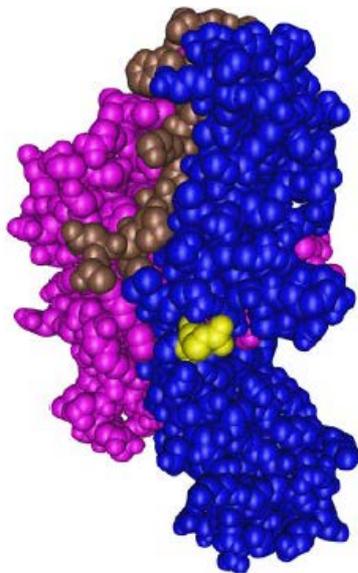
株式会社ベリタス

2020年11月25日

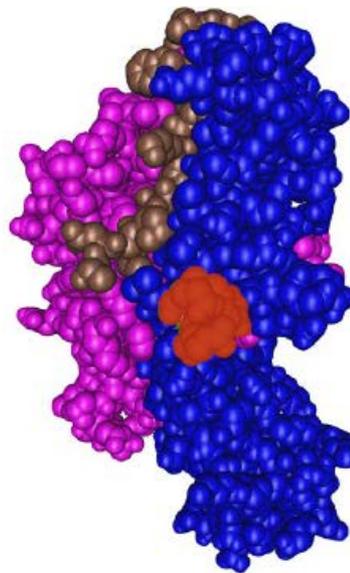
2020年11月28日

EpitopeとEplet

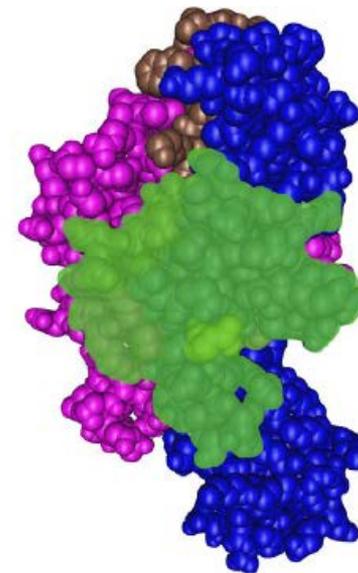
- Epitope (エピトープ)
 - Functional Epitope (機能的エピトープ)、Structural Epitope (構造エピトープ)
 - Functional Epitope \doteq Eplet



Polymorphic
amino acid



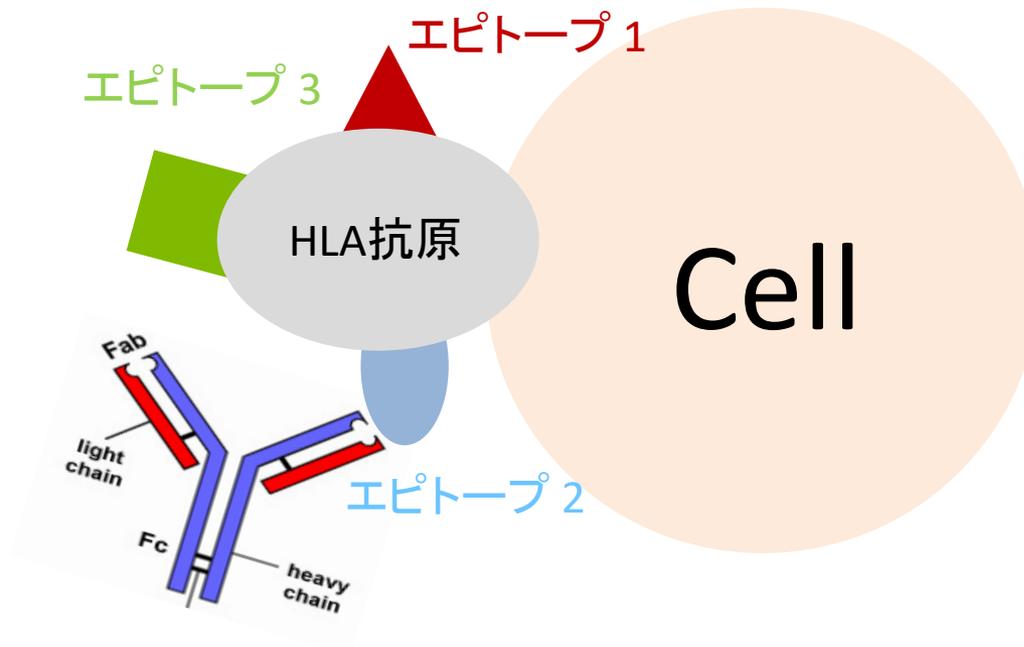
Eplet
3Å radius



Epitope
15Å radius

生体内におけるエピトープと抗HLA抗体

- 抗HLA抗体はHLA抗原の特異的なエピトープに反応（結合）
- HLA抗原に特異的に結合するのではなく、エピトープに特異的に結合する



MatchMakerとは

- Duquesnoyが作成したフリーソフト
 - 下記リンクよりダウンロード可能
<http://www.epitopes.net/index.html>
- HLA Fusion MatchMakerでは2つの解析が可能
 - Epitope Matching
PatientとDonorのタイピング結果を入力することMismatchの数を表示
 - Epitope Analysis
LABScreen Single Antigenデータをもとにエピトープ解析
- エピトープ解析を行うためには、ドナー、レシピエント共に4桁のタイピング情報が必要



MatchMakerのデータベース

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Class I												
2													
3	Class	Epitope Name	Sero Group	AA Position	Polymorphic Residues	Exposed	Antibody Reactivity	Frequency	Struct Epitope	Alleles			
4	I	1C		1	1C	Yes				C*01:02	C*02:02	C*02:10	C*05:01
5	I	16S		16	16S	Yes				C*02:02	C*02:10	C*04:03	C*02:03
6	I	17RS		14,17	R,S	Yes				A*30:01	A*30:02	A*01:02	A*01:20
7	I	17WR		14-17	14W17R(49E)	Yes				C*04:01	A*02:109	B*39:41	C*04:04
8	I	41T		41	41T	Yes	Confirmed			B*13:01	B*13:02	B*40:01	B*40:02
9	I	43RRM		43-44-45	43R44R45M	Yes				A*02:02	A*02:05	A*02:08	A*02:115
10	I	44KM ₃	44,45	(149,150,151,152)	(1 ¹ K,M (A,V,H,A) (V)	Yes	Confirmed			A*01:01	A*36:01	A*01:02	A*01:03
11	I	44RM		44-45	44R45M	Yes				A*02:01	A*02:02	A*02:03	A*02:05
12	I	44RMA		44-45-46	44R45M46A	Yes	Confirmed			B*13:01	B*13:02	B*15:01	B*15:02
13	I	44RME		44-45-46	44R45M46E(67V)	Yes				A*02:01	A*02:02	A*02:03	A*02:05
14	I	44RT		44,45,46	R,T,E	Yes	Provisional			B*18:01	B*35:01	B*35:08	B*37:01
15	I	44RT+69TNT		44-45-46 + 69-70-71	44R45T46E + 69T70N71T	Yes	Provisional			R*18:01	R*18:02	R*18:03	R*18:04

- Duquesnoyのデータベースを参照にOne Lambdaが作成したエピトープ情報

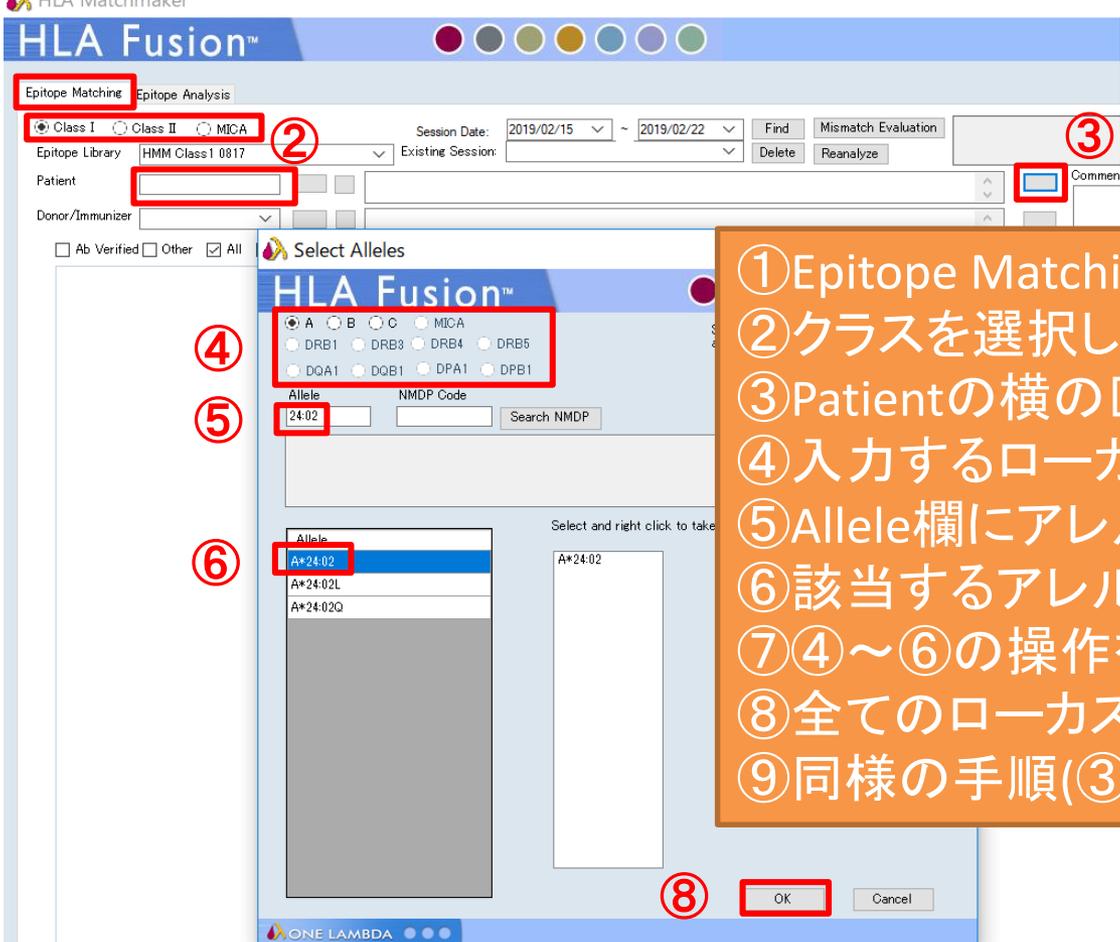
- Confirmed: 実験で証明されている
- Provisional: 理論的に存在が予測されるが実験では証明されていない
- Blank: unknown

初回の使用時にデータベースのインポート及び解析のための設定が必要

Epitope Matching

タイピング情報の入力

手入力する場合

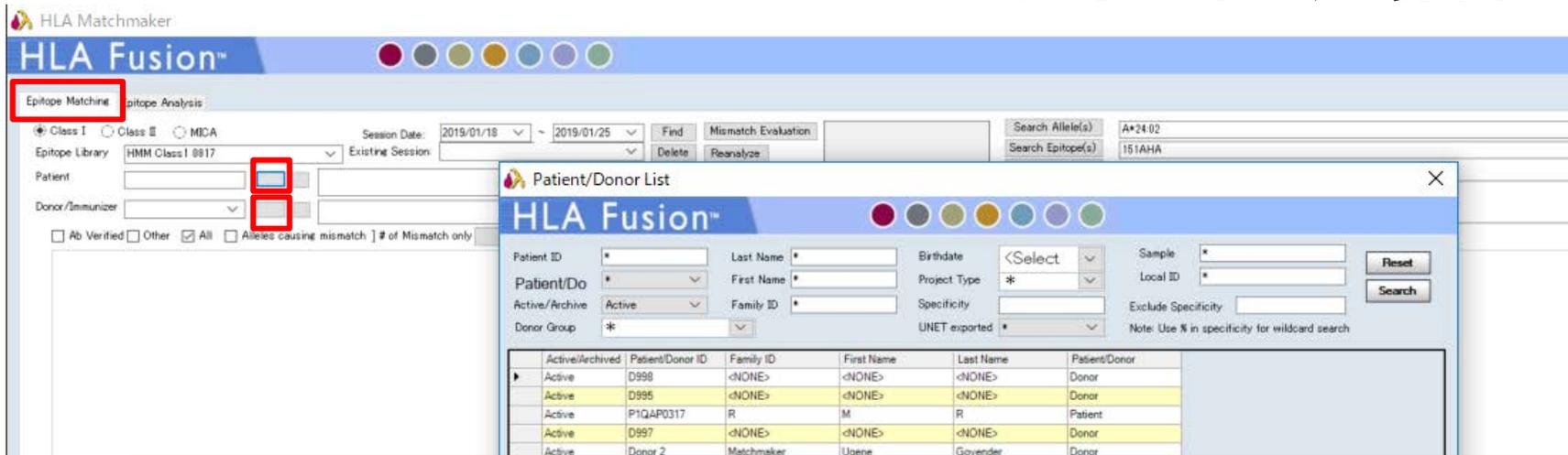


The screenshot shows the HLA Fusion software interface. The 'Epitope Matching' tab is active. The 'Class I' radio button is selected. The 'Patient' field is empty. The 'Select Alleles' dialog box is open, showing the 'A' locus selected. The 'Allele' field contains 'A*24:02'. The 'OK' button is highlighted.

- ① Epitope Matchingタブを開く
- ② クラスを選択し、Patient名を入力
- ③ Patientの横の□(Select alleles)をクリック
- ④ 入力するローカスを選択
- ⑤ Allele欄にアレルを入力
- ⑥ 該当するアレルをダブルクリック
- ⑦ ④～⑥の操作を繰り返す
- ⑧ 全てのローカスの入力が終了後OKをクリック
- ⑨ 同様の手順(③～⑧)でDonor情報も入力

タイピング情報の入力

HLA Fusionのデータベースより呼び出す場合



The screenshot shows the HLA Fusion software interface. The 'Epitope Matching' tab is selected. In the 'Patient' field, a small square button is highlighted with a red box. A 'Patient/Donor List' dialog box is open, displaying a table of patient and donor information.

Active/Archived	Patient/Donor ID	Family ID	First Name	Last Name	Patient/Donor
Active	D998	<NONE>	<NONE>	<NONE>	Donor
Active	D995	<NONE>	<NONE>	<NONE>	Donor
Active	PIQAP0317	R	M	R	Patient
Active	D997	<NONE>	<NONE>	<NONE>	Donor
Active	Donor 2	Matchmaker	Ugene	Govender	Donor

MatchMakerを開き、Epitope Matchingタブを開く

Patientの横の□(Select a patient from database)をクリック

登録されている情報が一覧で表示されるので、該当する情報を選択しダブルクリックする

Donor情報の入力も同様

インポートするcsvファイル内でPatientとDonor情報を紐づけて入力しておくことで、Patientを選択することで自動でDonor情報も入ります

ミスマッチ数の解析

- Patient及びDonorのタイピング結果を入力後、Calculateをクリック→結果が表示される

Epitope Matching Epitope Analysis

Class I Class II MICA
 Session Date: 2020/11/02 ~ 2020/11/09
 Find Mismatch Evaluation
 Epitope Library: HMM Class1 0817 Existing Session:
 Delete Reanalyze

Patient: Patient 64 A*02:06 A*33:03 B*15:01 B*44:03 C*07:02 C*14:03

Donor/Immunizer: Donor64 A*11:01 A*33:03 B*44:03 B*67:01 C*07:02 C*14:03

Ab Verified Other All
 Alleles causing mismatch
 Replace NMDP code **Calculate** Save Options
[iOn3D](#) [La](#)

表示するEpitopeの種類を選択可能

Patient	Donor	B # Mismatch All	C Mismatch All	C # Mismatch All	ClassI Uniq# Mismatch All	ClassI # Mismatch All
Patient 64 A*02:06, A*33:03, B*15:01, B*44:03, C*07:02, C*14:03	Donor64 A*11:01, A*33:03, B*44:03, B*67:01, C*07:02, C*14:03	18	16	0	33	34
Alleles contributing to the mismatch:		Alleles contributing to the mismatch:				
A*11:01 (62QE, 62QE+56G, 63EN, 63ERN, 66NAQ, 69AQT, 71QS, 79GT+90D, 97I, 113YR, 144KR, 144KR+151H, 151AHA, 152HA, 156QA, 163R, 163RW, 275EL)		B*67:01 (45EE, 62RNQ, 65QIA, 65QIA+76ESN, 66TY, 69AA, 69AA+65QI, 69AA+76E, 69AQT, 69ATS, 70IAQ, 73TDE, 113HN, 116F, 131S+163T, 158T)				

Alleles causing mismatch

Epitope Matching Epitope Analysis

Class I Class II MICA Session Date: 4/11/2019 ~ 4/18/2019 Find Mismatch Evaluation Search Allele(s) A*02:01
 Epitope Library HMM Class I 0817 Existing Session: Delete Reanalyze Search Epitope(s) 9F
 Patient Patient 1 A*03:01,A*31:01,B*07:02,B*40:01,C*03:04,C*07:02 Comment: List All Epitopes
 Donor/Immunizer Donor 3 A*29:02,A*32:01,B*14:02,C*03:04,C*07:02

Ab Verified Other Alleles causing mismatch # of Mismatch Calculate Replace all Import Export Save iCn3D Latest Version Session Name: MM_Match_20190418101649

Patient	Donor	A PatientEp AbVerified	A DonorEp AbVerified	A Mismatch AbVerified	# Mis Abv	B # Mismatch AbVerified	C PatientEp AbVerified	C DonorEp AbVerified	C Mismatch AbVerified	C # Mismatch AbVerified	ClassI # Mismatch AbVerified
Patient 1 A*03:01, A*31:01, B*07:02, B*40:01, C*03:04, C*07:02	Donor 1 A*34:02, A*66:01, B*13:02, B*51:01, C*06:02, C*16:01	56R, 62QE+56G, 66NV, 79GT, 138ML, 138MI+79GT, 144K, 144KR, 150AAH, 161D, 253Q	62RR, 66NV, 79GT, 79GT+90D, 90D, 138ML, 138MI+79GT, 145RT, 149TAH, 163R, 163RW, 253Q	62RR, 79GT+90D, 145RT, 149TAH, 163R, 163RW	6	16	21H, 65QKR+76VS, 76VRN, 80N, 90D, 163LW, 173K, 193PL3, 193PV, 219W, 253Q, 267QE	65QKR+76VS, 73AN, 76VRN, 80K, 80K+14R, 80N, 90D, 193PV	73AN, 80K, 80K+14R	3	25

拡大図

Alleles contributing to the mismatch:

A*34:02 (62RR, 79GT+90D, 145RT, 149TAH)
 A*66:01 (62RR, 79GT+90D, 145RT, 149TAH, 163R, 163RW)

Alleles causing mismatch:
 Mismatch Epitopeに起因するアレルが表示される

Search Epitope(s)

Epitope Matching Epitope Analysis

Class I Class II MICA

Session Date: 4/11/2019 ~ 4/18/2019

Epitope Library: HMM Class1 0817 Existing Session:

Patient: Patient 1

Donor/Immunizer: Donor 1

Ab Verified Other All Alleles causing mismatch | # of Mismatch only

Buttons: Replace NMDP code, Calculate, **Replace all**, Import, Export, Save, iCn3D, Latest Version

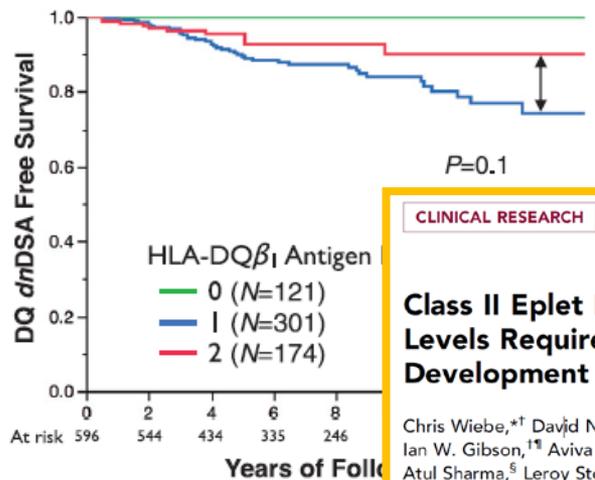
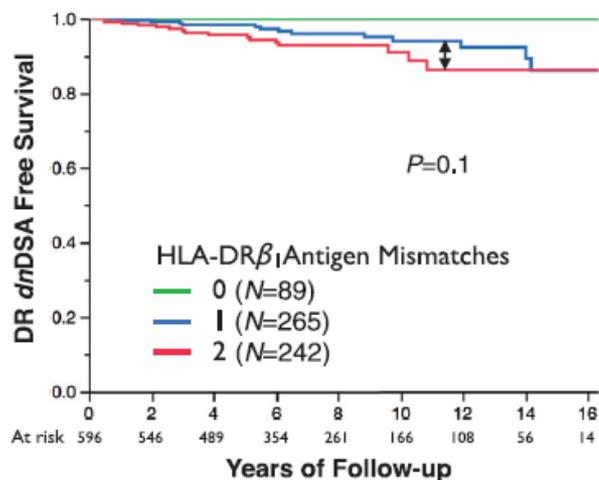
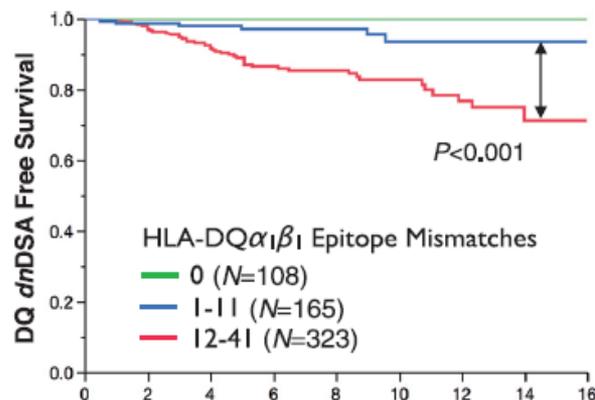
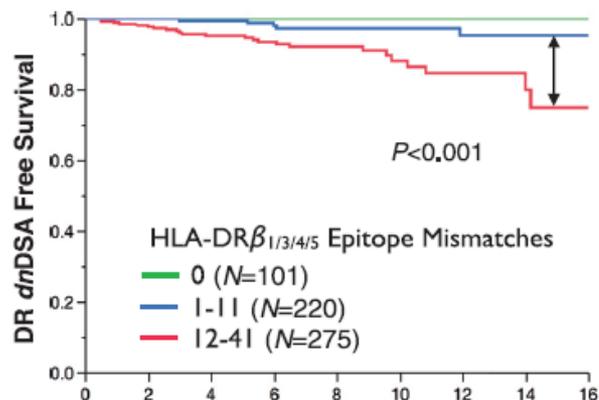
Search Allele(s): A*02:01
Search Epitope(s): 9F
List All Epitopes

Epitope	Exposed	Antibody Reactivity	Antibody Verified EP	Allele
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*03:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*32:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*36:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*74:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*80:01
9F	<input type="checkbox"/>		<input type="checkbox"/>	C*01:02
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:03
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:06
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:07
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:08
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:09
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:10
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:12
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:13
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:14
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:17
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:33
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*01:35
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:04
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:07
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:09
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:102
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:103
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:104
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:105
9F	<input type="checkbox"/>		<input type="checkbox"/>	A*02:106

表示を戻すときはReplace allをクリック

**Search Epitope(s): 全てのエピトープを対象にした検索結果を表示
入力しているタイピング結果に関するエピトープのみの
表示ではありません**

論文の紹介



CLINICAL RESEARCH www.jasn.org

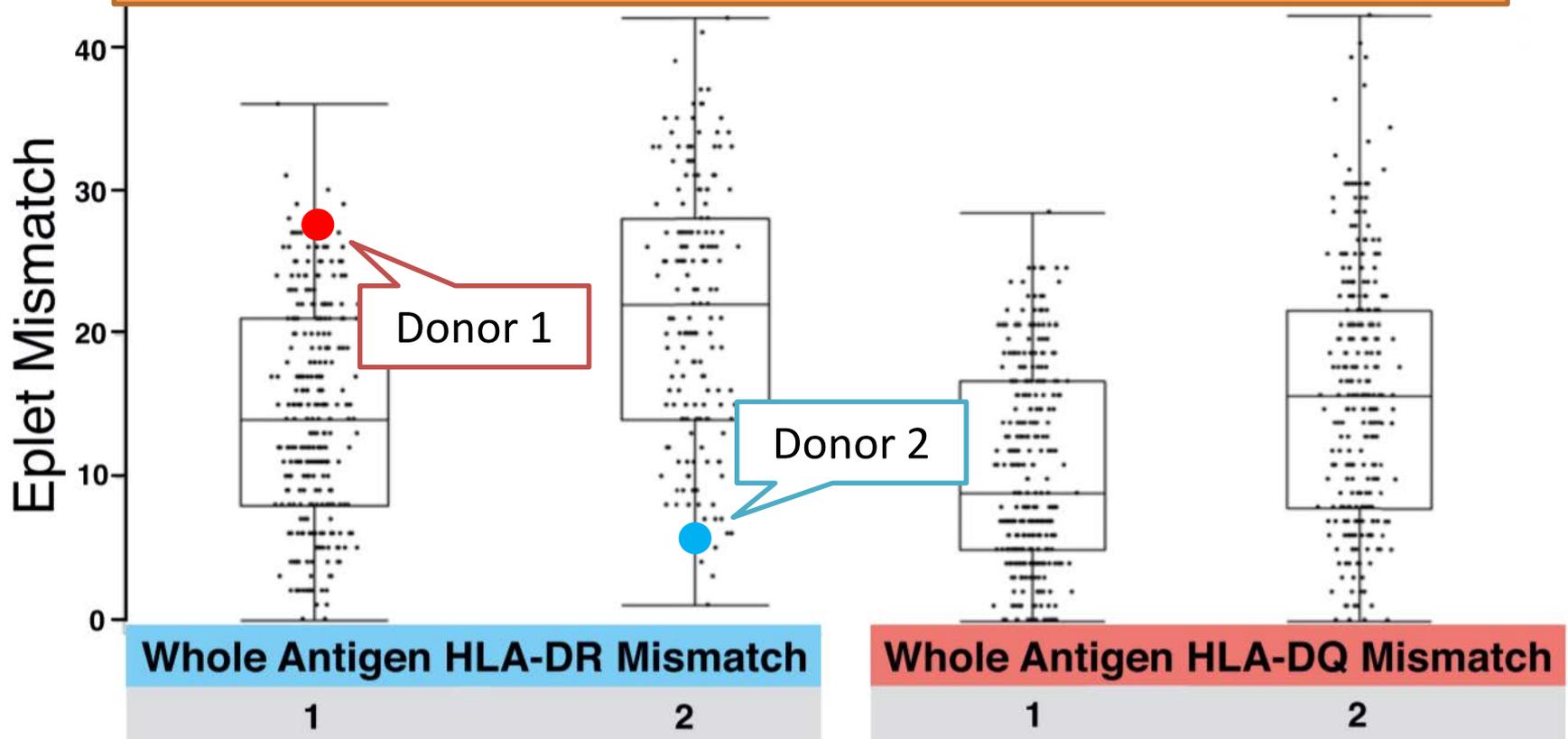
Class II Eplet Mismatch Modulates Tacrolimus Trough Levels Required to Prevent Donor-Specific Antibody Development

Chris Wiebe,^{*†} David N. Rush,^{*} Thomas E. Nevins,[‡] Patricia E. Birk,[§] Tom Blydt-Hansen,^{||} Ian W. Gibson,^{1§} Aviva Goldberg,[§] Julie Ho,^{***} Martin Karpinski,^{*} Denise Pochinco,[†] Atul Sharma,[§] Leroy Storsley,^{*} Arthur J. Matas,^{††} and Peter W. Nickerson^{*†**}

Departments of ^{*}Medicine, [§]Pediatrics and Child Health, [‡]Pathology, and ^{**}Immunology, University of Manitoba, Winnipeg, Manitoba, Canada; ¹Diagnostic Services of Manitoba, Winnipeg, Manitoba, Canada; Departments of [†]Pediatrics and ^{††}Surgery, University of Minnesota, Minneapolis, Minnesota; and ^{||}Department of Pediatrics, University of British Columbia, Vancouver, British Columbia, Canada

アレルミスマッチとエピトープミスマッチ

アレルのミスマッチ数とエピトープのミスマッチ数は相関しない
 Donor1はアレルミスマッチは1だが、エピトープミスマッチは約30
 Donor2はアレルミスマッチは2だが、エピトープミスマッチは10以下
 どちらがDonorとして適しているのか?という研究が進んでいる



Epitope Analysis

タイピング情報の入力

手入力する場合

① Epitope Analysisタブを開く

② Patientの横の□(Select alleles)をクリック

③ 入力するローカスを選択

④ Allele欄にアレルを入力

⑤ 該当するアレルをダブルクリック

⑥ ④～⑥の操作を繰り返す

⑦ 全てのローカスの入力が終了後OKをクリック

⑧ 同様の手順(②～⑦)でDonor情報も入力

Donor情報の入力
はここをクリック

Select Alleles

HI A Fusion™

A B C MICA
DRB1 DRB3 DRB4 DRB5
DOA1 DOB1 DPA1 DPB1

24

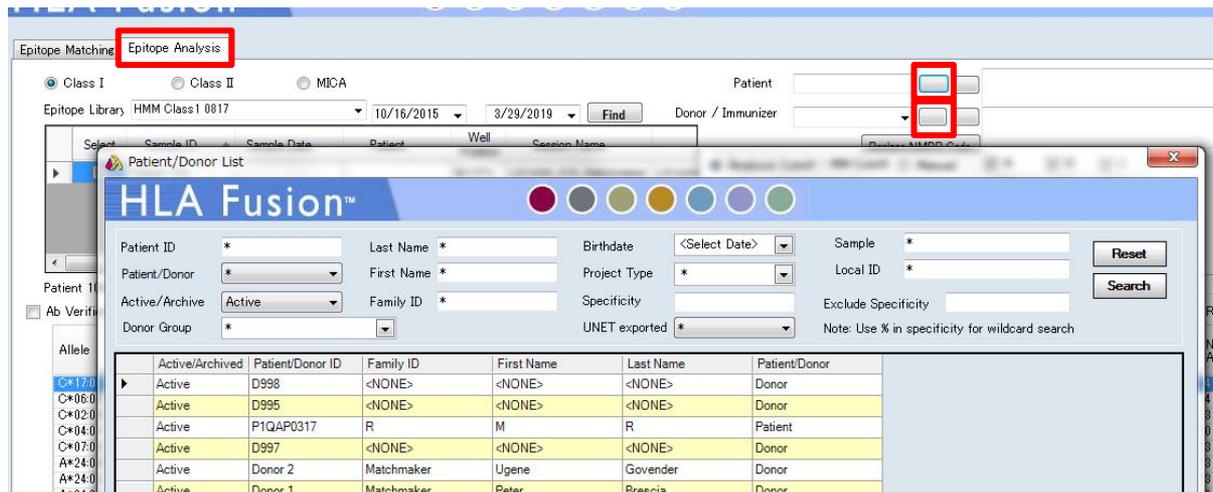
A*24:02

OK Cancel

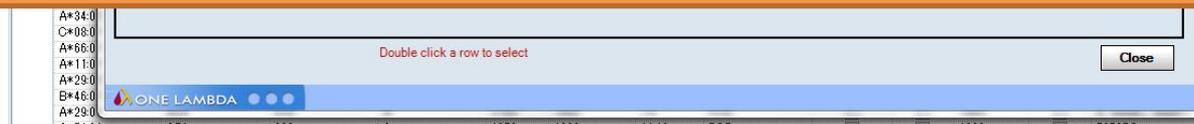
Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	All
Cw12	091	C	262	120	11.69						25, 32, 205
B53, Bw4	068	B	223	116	12.65						7, 22, 23, 24
Cw7	089	C	277	97	10						25, 32, 37, 3
A1	003	A	100	0	3.32						1, 1E, 12, 13
A2	004	A	23	0	1.89						2, 13, 17, 17
A2	005	A	22	0	1.67						2, 13, 17, 17

タイピング情報の入力

HLA Fusionのデータベースより呼び出す場合



MatchMakerを開き、Epitope Analysisタブを開く
Patientの横の□(Select a patient)をクリック
登録されている情報が一覧で表示されるので、該当する情報を選択しダブルクリックする
Donor情報の入力も同様。



解析結果

3105 / 200908_LS1A04011_NC029-1New_20200908_141854

Read LABScreen Analysis

Ab Verified Other All # of Eplets Only Cn3D Latest Version Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	All	N. All	Imm All	N. Imm All	TP All	N. TP All
A*25.01	A25	013	A	20207	20136	455.04	POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input type="checkbox"/>	62RNR, 63NN, 145RT	3	62RNR, 63NN,...	3		0
A*66.01	A66	027	A	19106	18741	157.68	POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input checked="" type="checkbox"/>	62RNR, 63NN, 145RT	3	62RNR, 63NN,...	3		0
A*26.01	A26	014	A	18785	18651	308.04	POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input checked="" type="checkbox"/>	62RNR, 63NN, 73TDA, 7... 5	5	62RNR, 63NN,...	5		0

All positive epitopes (all locu 18) 20/24 Positive Alleles

Epitope	# Alleles	Locus	Donor Allele Not in Panel
<input type="checkbox"/> 62RNR	11	A	

Reset Export Sequence Find Row Count: 99

Rxn	Missing EP Def	Cutoff	Self	Imm	All	N. All	Imm All	N. Imm All	TP All	N. TP All
POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input type="checkbox"/>	62RNR, 63NN, 145RT	3	62RNR, 63NN,...	3		0
POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input checked="" type="checkbox"/>	62RNR, 63NN, 145RT	3	62RNR, 63NN,...	3		0
POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input checked="" type="checkbox"/>	62RNR, 63NN, 73TDA, 7... 5	5	62RNR, 63NN,...	5		0
POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input type="checkbox"/>	62LQ, 73TDA, 76ANT, 1... 4	4	73TDA, 76ANT,...	3	62LQ	1
POS	<input type="checkbox"/>	1789	<input type="checkbox"/>	<input type="checkbox"/>	62RNR, 63NN, 145RT	3	62RNR, 63NN,...	3		0

Rxn	各ビーズの陽性/陰性の結果
Self	Patientのアレルにチェックが入る(タイピング結果を入力している場合)
Imm	Donorのアレルにチェックが入る(タイピング結果を入力している場合)
All	陽性と判定されたエピトープ
N. All	陽性と判定されたエピトープの数
Imm All	ドナー由来と考えられエピトープ
N. Imm All	ドナー由来と考えられエピトープの数
TP All	Third Party由来と考えられエピトープ(ドナー以外に由来する)
N. TP All	Third Party由来と考えられエピトープの数(ドナー以外に由来する)

解析結果-2

Epitope Matching Epitope Analysis

Class I Class II MICA Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 Not in panel

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select Sample ID Sample Date Patient Well Position Session Name

<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 337 216 124 131

m+3SD 2128 1925 1742 1096

Positiveと判定されたEpitopeが全て表示

Ab Verified Other All # of Epitopes Only Rxn Table Can3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
B*13:02	B13.Bw4	036	B	23747	23569	107.11	POS		2305		<input checked="" type="checkbox"/>	144QL	1	144QL	1	
B*13:01	B13.Bw4	037	B	22791	22565	70.81	POS		2305		<input type="checkbox"/>	144QL	1	144QL	1	
A*02:06	A2	006	A	18955	16745	50.24	POS		2305		<input type="checkbox"/>	430+62GER, 6...	6		0	430+62GER, 6...
A*02:01	A2	004	A	15536	16335	54.79	POS		2305		<input type="checkbox"/>	430+62GER, 6...	6		0	430+62GER, 6...
A*02:03	A2	005	A	15562	15372	59.03	POS		2305		<input type="checkbox"/>	430+62GER, 6...	5		0	430+62GER, 6...
A*8:02	A68	030	A	15154	14953	49.72	POS		2305		<input type="checkbox"/>	127K, 144TKH, 14...	3		0	127K, 144TKH, 14...
A*69:01	A69	031	A	15105	14908	50.55	POS		2305		<input type="checkbox"/>	107W, 127K, 14...	4		0	107W, 127K, 14...
A*68:01	A68	029	A	15035	14757	25.78	POS		2305		<input type="checkbox"/>	127K, 144TKH, 14...	3		0	127K, 144TKH, 14...
A*24:03	A24	012	A	8964	8751	25.74	POS		2305		<input type="checkbox"/>	65GK, 127K, 14...	3		0	65GK, 127K, 14...
A*24:02	A24	011	A	8645	8426	23.33	POS		2305		<input type="checkbox"/>	65GK, 127K, 14...	3		0	65GK, 127K, 14...
A*23:01	A23	010	A	8287	8049	18.07	POS		2305		<input type="checkbox"/>	65GK, 127K, 14...	2		0	65GK, 127K, 14...
A*66:02	A66	028	A	5848	5624	15.2	POS		2305		<input type="checkbox"/>	65GK, 127K, 14...	2		0	65GK, 127K, 14...
A*66:01	A66	027	A	5322	5122	17.75	POS		2305		<input checked="" type="checkbox"/>			0		
B*15:12	B76.Bw6	043	B	2520	2305	7.13	POS		2305		<input type="checkbox"/>			0		
B*58:01	B58.Bw4	074	B	1953	1730	5.11	NEG		2305		<input type="checkbox"/>			0		
B*57:01	B57.Bw4	072	B	1876	1674	6.11	NEG		2305		<input type="checkbox"/>			0		
B*73:01	B73.Bw6	077	B	1789	1608	7.71	NEG		2305		<input type="checkbox"/>			0		
B*27:03	B27.Bw6	048	B	1792	1590	5.23	NEG		2305		<input type="checkbox"/>			0		
B*27:05	B27.Bw4	047	B	1720	1523	5.91	NEG		2305		<input type="checkbox"/>			0		
B*56:01	B56.Bw6	071	B	1711	1523	6.74	NEG		2305		<input type="checkbox"/>			0		

All positive epitopes (all locu 9): 11/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/>	127K	9 A	127K
<input type="checkbox"/>	144TKH	6 A	142T143T144K145H
<input type="checkbox"/>	145KHA	5 A	144K145H149A
<input type="checkbox"/>	107W	4 A	107W
<input type="checkbox"/>	430+62GER	3 A	430 + 62G6E65R
<input type="checkbox"/>	62GK2	3 A	62G6E65R66K (73T74H7...
<input type="checkbox"/>	65GK	3 A	E.E.G.K.A
<input type="checkbox"/>	144KR+127K	2 A	142I143T144K145R + 127K
<input type="checkbox"/>	144QL	2 B	144Q145L149A

Epitope Matching Epitope Analysis

Class I Class II MICA Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02 Not in panel

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Select Sample ID Sample Date Patient Well Position Session Name

<input checked="" type="checkbox"/>	112			3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112			32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 337 216 124 131

m+3SD 2128 1925 1742 1096

チェックを入れたEpitopeのみ表示

Ab Verified Other All # of Epitopes Only Rxn Table Can3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 3

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
A*02:06	A2	006	A	18955	16745	50.24	POS		2305		<input type="checkbox"/>	430+62GER, 6...	6		0	430+62GER, 6...
A*02:01	A2	004	A	15536	16335	54.79	POS		2305		<input type="checkbox"/>	430+62GER, 6...	6		0	430+62GER, 6...
A*02:03	A2	005	A	15562	15372	59.03	POS		2305		<input type="checkbox"/>	430+62GER, 6...	5		0	430+62GER, 6...

All positive epitopes (all locu 9): 3/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/>	127K	9 A	127K
<input type="checkbox"/>	144TKH	6 A	142T143T144K145H
<input type="checkbox"/>	145KHA	5 A	144K145H149A
<input type="checkbox"/>	107W	4 A	107W
<input checked="" type="checkbox"/>	430+62GER	3 A	430 + 62G6E65R
<input type="checkbox"/>	62GK2	3 A	62G6E65R66K (73T74H7...
<input type="checkbox"/>	65GK	3 A	E.E.G.K.A
<input type="checkbox"/>	144KR+127K	2 A	142I143T144K145R + 127K
<input type="checkbox"/>	144QL	2 B	144Q145L149A

画面の表示

HLA Fusion™

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class I 0817 4/ 3/2019 4/17/2019 Find Donor / Immunizer Donor 1

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout

Ab Verified Other All # of Epitopes Only Rxn Table iCn3D Latest Version

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff
A*02:01	A2	006	A	16955	16745	50.24	POS		2305
A*02:03	A2	005	A	15562	15372	59.03	POS		2305
A*68:02	A68	030	A	15154	14953	49.72	POS		2305
A*69:01	A69	031	A	15105	14906	50.55	POS		2305
A*68:01	A68	029	A	15035	14757	25.78	POS		2305
A*24:03	A24	012	A	8964	8751	25.74	POS		2305
A*24:02	A24	011	A	8645	8426	23.33	POS		2305
A*23:01	A23	010	A	8287	8043	18.07	POS		2305

Find Allele Find Epitope Find Pos Epitope Find Cutoff 127K

Show Self Show Imm Show POS Reset Export

All positive epitopes (all loci): 9/14 Positive Alleles Cover

Epitope	#	Locus	Residue
<input checked="" type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input checked="" type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 49Q+62GER	3	A	49Q + 62G63E65R
<input type="checkbox"/> 62GK2	3	A	62G63E65R66K (73T74H)
<input type="checkbox"/> 65GK	3	A	E.E.G.K.A
<input type="checkbox"/> 144KR+127K	2	A	142I143T144K145R + 127
<input type="checkbox"/> 144QL	2	B	144Q145L149A

127K

Row Count: 9

1C(10) 1C(19) 1C

Statistics

002) 19961.45

001) 161.72

C:123.432

14

OLI Current

490.94 490.94

613.87 613.87

2305.94 2305.94

5122.95 5122.95

Antigen

User Cutoff Locus Cutoff

検索結果は解析画面に反映されます

カットオフ値 -Analysis Cutoff

The screenshot displays the HLA Fusion software interface. On the left, a bar chart shows the distribution of scores for various HLA alleles. The main window shows the 'HLA Fusion' analysis results for 'Patient 104'. A table lists the results for various HLA alleles, with a 'Cutoff' column highlighted in red. The cutoff value is 1863.94. A text box in the center of the screenshot reads: 'HLA Fusionの解析画面で使用したカットオフ値を使用' (Use the cutoff value used in the HLA Fusion analysis screen).

Allele	Score	Pos	Self	Imm	All
C*17:01	1863.94	POS	1863		244, 5036C
C*06:02	11962	POS	1863		244, 5037C
C*02:02	11163	POS	1863		244, 5038C
C*04:01	10896	POS	1863		
C*07:02	10729	POS	1863		
A*24:03	10576	POS	1863		203, 407, 5
A*24:02	10453	POS	1863		203, 203PC
A*34:01	10225	POS	1863		5008C, 508
C*05:01	10196	POS	1863		40, 244
A*66:02	10171	POS	1863		5049PC, 50
C*18:02	9988	POS	1863		244, 5037C
C*12:03	8023	POS	1863		
B*08:01	7795	POS	1863		11, 5027C
A*68:01	7349	POS	1863		
A*68:02	6299	POS	1863		
A*43:01	6210	POS	1863		5, 5005C
C*01:02	6106	POS	1863		5032C
A*03:01	5715	POS	1863		
A*33:03	5320	POS	1863		
C*16:01	5290	POS	1863		5035C, 507
C*14:02	5109	POS	1863		
A*32:01	4931	POS	1863		
C*15:02	4598	POS	1863		244, 5034C
A*69:01	4519	POS	1863		5067E
A*33:01	3996	POS	1863		
C*03:04	3142	POS	1863		
C*03:02	3040	POS	1863		
C*03:03	2656	POS	1863		5080E
A*26:01	2420	POS	1863		5062E
A*34:02	2351	POS	1863		5009C

Statistics:
PC: (002) 6374.99
NC: (001) 47.23
PC/NC: 134.978
%SA: 38
Cutoff OLI Currens
X2 129.75 129.75
X6 1863.94 1863.94
X8 3896.52 3896.52
ResultType: Default
Excluded Antigen
Formula: Baseline
User Cutoff Locus Cutoff
Comments (System):
Unacceptable Antigen

カットオフ値 -Manual cutoff

Epitope Matching Epitope Analysis

Class I Class II MICA

Epitope Library HMM Class1 0817 4/ 3/2019 4/17/2019 Find

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*51:01 C*06:02 C*16:01

Analysis Cutoff Manual A B C

Data Type Baseline Cutoff 1500 2000 500

Mean of Self (m) 3542 3374 316 6936

SD 3784 2341 106 3794

m+3SD 14744 10397 634 18318

Find Allele Find Epitope Find Pos Epitope Find Cutoff

Ab Verified Other All # of Epitopes Only Rxn Table iCr3D Latest Version Show Self Show Imm Show POS Reset Export Row Count: 99

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
C*08:01	Cw8	090	C	2522	2351	8.8										
A*66:01							POS		1500		<input checked="" type="checkbox"/>	177KT	1		0	177KT
A*11:01							POS		1500			151AHA	1		0	151AHA
A*29:02							POS		1500			62LQ	1		0	62LQ
B*46:01							POS		2000				0		0	
A*29:01							POS		1500			62LQ	1		0	62LQ
A*74:01							POS		1500				0		0	
A*11:02							POS		1500			151AHA	1		0	151AHA
B*51:02							NEG		2000				0		0	
B*51:01							NEG		2000		<input checked="" type="checkbox"/>		0		0	
A*02:03	A2	005	A	1467	1345	7.63	NEG		1500				0		0	
B*53:01	B53,Bw4	068	B	1397	1246	5.63	NEG		2000				0		0	
B*35:01	B35,Bw6	049	B	1279	1185	9.34	NEG		2000				0		0	
B*15:16	B63,Bw4	046	B	1416	1139	2.88	NEG		2000				0		0	
A*25:01	A25	013	A	1217	1118	8.29	NEG		1500				0		0	
A*02:01	A2	004	A	1216	1102	6.96	NEG		1500				0		0	
A*31:01	A31	020	A	1211	1033	4.04	NEG		1500		<input checked="" type="checkbox"/>		0		0	
A*80:01	A80	033	A	1182	1000	3.85	NEG		1500				0		0	
A*30:01	A30	018	A	1115	975	4.9	NEG		1500				0		0	
A*02:06	A2	006	A	1081	958	5.58	NEG		1500				0		0	
A*30:02	A30	019	A	1004	874	4.88	NEG		1500				0		0	
B*78:01	B78,Bw6	078	B	887	766	4.67	NEG		2000				0		0	
B*54:01	B54,Bw6	069	B	893	703	2.75	NEG		2000				0		0	
B*15:02	B75,Bw6	041	B	683	563	3.64	NEG		2000				0		0	
A*23:01	A23	010	A	656	548	3.99	NEG		1500				0		0	
B*39:01	B39,Bw6	052	B	614	525	4.8	NEG		2000				0		0	
B*38:01	B38,Bw4	051	B	572	485	4.6	NEG		2000				0		0	
B*15:10	B71,Bw6	043	B	543	437	3.37	NEG		2000				0		0	
B*15:11	B75,Bw6	098	B	566	430	2.59	NEG		2000				0		0	
B*07:02	B7,Bw6	034	B	600	423	2.01	NEG		2000		<input checked="" type="checkbox"/>		0		0	
B*81:01	B81,Bw6	079	B	541	412	2.64	NEG		2000				0		0	
B*15:13	B77,Bw4	045	B	430	339	3.27	NEG		2000				0		0	
B*49:01	B49,Bw4	060	B	344	269	3.39	NEG		2000				0		0	
B*40:02	B61,Bw6	054	B	390	253	1.77	NEG		2000				0		0	
B*18:01	B18,Bw6	047	B	375	250	1.89	NEG		2000				0		0	
B*27:08	B27,Bw6	048	B	346	248	2.37	NEG		2000				0		0	
B*50:01	B50,Bw6	064	B	339	229	2.01	NEG		2000				0		0	
B*40:01	B60,Bw6	050	B	240	210	1.57	NEG		2000				0		0	

MatchMaker上で手動で
カットオフ値の変更が可能

検索機能

Patient Donor269 A*11:01 A*30:02 B*15:11 B*40:06

Donor / Immunizer Donor98 A*66:01 A*26:01 B*35:01 B*35:01 C*03:03 C*03:01

Replace NMDP Code

Analysis Cutoff
 MM Cutoff
 Manual
 A
 B
 C

Data Type	Baseline	Cutoff	1789	1789	1789
Mean of Self (m)	2322		4440	203	
SD	2141		439	51	
m+3SD	8744		5757	356	

空欄に検索対象を入力し
Find XXXをクリック

Reset Export Sequence **Find** Row Count: 99

Rxn	Missing EP Def	Self	Cutoff	Find Eplet	N. All	Imm All	N. Imm All	TP All
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789	Find Eplet				
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789	Find Positive Eplet				
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789	Find Allele	3	62RNR, 63NN,...	3	
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789	Find Cutoff for Eplet	3	62RNR, 63NN,...	3	
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		5	62RNR, 63NN,...	5	
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		4	73TDA, 76ANT,...	3	62L
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		3	62RNR, 63NN,...	3	
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		3	62RNR, 66RKQ,...	2	66F
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		3	62RNR, 63NN,...	3	
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		0		0	
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		5	9T, 62LQ, 73T,...	2	9T,
POS	<input type="checkbox"/>	<input type="checkbox"/>	1789		4	73TDA, 76ANT,...	3	6T

Rxn Table-1



Epitope Matching Epitope Analysis

Class I Class II MICA

Patient Patient 1 A*03:01 A*31:01 B*07:02 B*40:01 C*03:04 C*07:02

Epitope Library HMM Class I 0817 2/17/2017 4/10/2019 Find Donor / Immunizer Donor 1 A*34:02 A*66:01 B*13:02 B*61:01 C*06:02 C*16:01

Select	Sample ID	Sample Date	Patient	Well Position	Session Name
<input type="checkbox"/>	112	Jan 15, 2019	112	32 (H4)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	112	Jan 15, 2019	112	3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input checked="" type="checkbox"/>	112	Jan 15, 2019	112	3 (C1)	05-25-17 SAC1_lot 7 Bordeaux P1
<input type="checkbox"/>	171	Mar 05, 2019	112	78 (F10)	05-25-17 SAC1_lot 7 Bordeaux P1

Analysis Cutoff 1 MM Cutoff Manual A B C

Data Type Baseline Cutoff 2305 2305 2305

Mean of Self (m) 1116 1277 1370 703

SD 937 216 124 131

m*3SD 2128 1925 1742 1096

3105 / trr200908_LS1A04011_NC023-1New_20200908_141854

Read IARScreen Analysis

Ab Verified Other All # of Epitopes Only Latest Version Rxn Table

Reset Export Sequence Find Row Count: 99

Allele	Sero	Bead ID	Loc	Raw	Baseli	Ratio	Rxn	Miss EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Ve	Imm Ab Verit	N. Im Ab Ver	TP Ab Verified	N. TP Ab Verit
B*13:02	B13.Bw4	036	B	23747	23569	107.11	POS		2305			<input checked="" type="checkbox"/>	144QL	1	144QL	1	0
B*13:01	B13.Bw4	097	B	22791	22585	70.81	POS		2305			<input type="checkbox"/>	144QL	1	144QL	1	0
A*02:06	A2	006	A	16955	16745	50.24	POS		2305			<input type="checkbox"/>	430+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6	0	430+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6
A*02:01	A2	004	A	16936	16835	54.79	POS		2305			<input type="checkbox"/>	430+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6	0	430+62GER, 62GK2, 107W, 127K, 144TKH, 145KHA	6
A*02:03	A2	005	A	15562	15372	59.03	POS		2305			<input type="checkbox"/>	430+62GER, 62GK2, 107W, 127K, 144TKH	5	0	430+62GER, 62GK2, 107W, 127K, 144TKH	5
A*68:02	A68	030	A	15154	14953	49.72	POS		2305			<input type="checkbox"/>	127K, 144TKH, 145KHA	3	0	127K, 144TKH, 145KHA	3
A*69:01	A69	031	A	15105	14905	50.55	POS		2305			<input type="checkbox"/>	107W, 127K, 144TKH, 145KHA	4	0	107W, 127K, 144TKH, 145KHA	4
A*68:01	A68	029	A	15035	14757	25.79	POS		2305			<input type="checkbox"/>	127K, 144TKH, 145KHA	3	0	127K, 144TKH, 145KHA	3
A*24:03	A24	012	A	8984	8751	25.74	POS		2305			<input type="checkbox"/>	65GK, 127K, 144KR+127K	3	0	65GK, 127K, 144KR+127K	3
A*24:02	A24	011	A	8645	8426	23.33	POS		2305			<input type="checkbox"/>	65GK, 127K, 144KR+127K	3	0	65GK, 127K, 144KR+127K	3
A*23:01	A23	010	A	8287	8043	18.07	POS		2305			<input type="checkbox"/>	65GK, 127K	2	0	65GK, 127K	2
A*66:02	A66	028	A	5848	5624	15.2	POS		2305			<input type="checkbox"/>		0	0		0
A*66:01	A66	027	A	5322	5122	17.75	POS		2305			<input checked="" type="checkbox"/>		0	0		0
B*15:12	B76.Bw6	043	B	2520	2305	7.13	POS		2305			<input type="checkbox"/>		0	0		0
B*58:01	B58.Bw4	074	B	1953	1730	5.11	NEG		2305			<input type="checkbox"/>		0	0		0
B*57:01	B57.Bw4	072	B	1876	1674	6.11	NEG		2305			<input type="checkbox"/>		0	0		0
B*73:01	B73.Bw6	077	B	1789	1608	7.71	NEG		2305			<input type="checkbox"/>		0	0		0

All positive epitopes (all locu): 11/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 430+62GER	3	A	430+ 62G68E65R
<input type="checkbox"/> 62GK2	3	A	62G68E65R66K (73T74H7...
<input type="checkbox"/> 65GK	3	A	E.E.G.K.A
<input type="checkbox"/> 144KR+127K	2	A	142I143T144K145R + 127K
<input type="checkbox"/> 144QL	2	B	144Q145L149A

Allele	Panel	Pos	MFI	127K	144TK	145KH	107W	430+6	62GK2	65GK	144KR	144QL	62EE 75% 3/4	82LR+ 75% 3/4	80I+90 75% 3/4	82LR+ 60% 3/5	82LR+ 60% 3/5	166DG 60% 3/5	82LR+ 60% 3/5	62GE 50% 3/6	62RR 41% 5/12	149TA 37% 3/8	80TLR 28% 2/7	145RT 28% 2/7	44RM 27% 3/11	82LR+ 22% 2/9	82LR 20% 5/24	163LS 20% 1/5	80I 17% 3/17	
B*13:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	23569																											
B*13:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	22585																											
A*02:06	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	16745	+	+	+	+	+	+																					
A*02:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	16835	+	+	+	+	+	+																					
A*02:03	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	15372	+	+	+	+	+	+																					
A*68:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14953	+	+	+	+	+	+																					
A*69:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14905	+	+	+	+	+	+																					
A*68:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14757	+	+	+	+	+	+																					
A*24:03	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8751	+	+	+	+	+	+																					
A*24:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8426	+	+	+	+	+	+																					
A*23:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8043	+	+	+	+	+	+																					
A*66:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	5624																											
A*66:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	5122																											
B*15:12	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	2305																											
B*58:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	1730																											
B*57:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	1674																											

Rxn Table-2

Allele	Panel	Pos	MFI	127K	144TK	145KH	107W	43Q+6	62GK2	65GK	144KR	144QL	62EE 75% 3/4	82LR+ 75% 3/4	80I+90 75% 3/4	82LF 60% 3/5
A*02:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	16335	+	+	+	+	+	+							
A*02:03	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	15372	+	+		+	+	+							
A*68:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14953	+	+	+										
A*69:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14906	+	+	+	+									
A*68:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	14757	+	+	+										
A*24:03	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8751	+									/	/	/	/
A*24:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8426	+									/	/	/	/
A*23:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	8043	+									/	/	/	/
A*66:02	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	5624													
A*66:01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	5122													
B*15:12	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	2305													
B*58:01	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1730													

ダブルクリックすると、
検索結果が表示される

112 / 05-25-17 SAC1_lot 7 Bordeaux P1_adsorbout_1

Read LABScreen Analysis Find Allele Find Epitope Find Pos Epitope Find Cutoff **62EE**

Ab Verified Other All # of Epitopes Only Rxn Table [iCn3D](#) Latest Version

Show Self Show Imm Show POS Reset Export

Allele	Sero	Bead ID	Loc	Raw	Baseli	Ratio	Rxn	Miss EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Ve	Imm Ab Verif	N. Im Ab Ver
A*24:03	A24	012	A	8964	8751	25.74	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K, 144KR+127K	3		0
A*24:02	A24	011	A	8645	8426	23.33	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K, 144KR+127K	3		0
A*23:01	A23	010	A	8287	8043	18.07	POS		2305	<input type="checkbox"/>	<input type="checkbox"/>	65GK, 127K	2		0
A*80:01	A80	033	A	1045	801	2.28	NEG		2305	<input type="checkbox"/>	<input type="checkbox"/>		0		0

Rxn Table

- +: Positive判定のアレルのみに含まれるEpitope (陽性と判定されたEpitopeのみが対象)
- /: Negative判定のアレルにも含まれるEpitope
- Positive判定のアレルにのみ「/」が表示される
- 例) 計4アレルのうち3アレルがPositive

All positive epitopes (all locu9: 11/14 Positive Alleles Covered.

Epitope	#	Locus	Residue
<input type="checkbox"/> 127K	9	A	127K
<input type="checkbox"/> 144TKH	6	A	142T143T144K145H
<input type="checkbox"/> 145KHA	5	A	144K145H149A
<input type="checkbox"/> 107W	4	A	107W
<input type="checkbox"/> 43Q+62GER	3	A	43Q + 62G63E65R
<input type="checkbox"/> 62GK2	3	A	62G63E65R66K (73T74H7...
<input type="checkbox"/> 65GK	3	A	E,E,G,K,A
<input type="checkbox"/> 144KR+127K	2	A	142I143T144K145R + 127K
<input type="checkbox"/> 144QL	2	B	144Q145L149A

Single&Supplement Combine data

Read LABScreen Analysis
 解析画面でSAとSupplementをcombineした状態でMatchMakerを立ち上げ、クリックするとCombineしたデータを表示

The screenshot displays the Epitope Analysis software interface. At the top, there are tabs for 'Epitope Matching' and 'Epitope Analysis'. Below these, there are radio buttons for 'Class I', 'Class II', and 'MICA'. A dropdown menu shows 'Epitope Library' set to 'HMM Class I 0817'. A table lists samples with columns for 'Select', 'Sample ID', 'Sample Date', 'Patient', 'Well Position', and 'Session Name'. The 'Read LABScreen Analysis' button is highlighted with a red box, and the 'Combined' option in the 'Latest Version' dropdown is also highlighted.

Allele	Sero	Bead ID	Locus	Raw	Baseline	Ratio	Rxn	Missing EP Def	Cutoff	Self	Imm	Ab Verified	N. Ab Verified	Imm Ab Verified	N. Imm Ab Verified	TP Ab Verified
B*44:02	B44,Bw4	057	B	8496	8334	23.45	POS		1878				0		0	
C*15:02	Cw15	093	C	4325	4163	11.95	POS		1878				0		0	
C*16:02	Cw16	1057	C	5952	2194	1.11	POS		1878				0		0	
B*13:01	B13,Bw4	097	B	2310	2175	8.11	POS		1878				0		0	
C*03:02	Cw10	083	C	2025	1878	6.32	POS		1878				0		0	
B*15:13	B77,Bw4	045	B	1174	1073	6.2	NEG		1878				0		0	
C*03:04	Cw10	085	C	1185	1007	2.92	NEG		1878				0		0	
B*15:02	B75,Bw6	041	B	859	730	3.19	NE									
B*44:03	B44,Bw4	058	B	462	324	1.59	NE									
C*17:01	Cw17	095	C	477	298	1.17	NE									
A*68:02	A68	030	A	493	269	0.92	NE									
A*31:01	A31	020	A	381	237	1.23	NE									
A*66:02	A66	028	A	344	207	1.18	NE									
B*67:01	B67,Bw6	076	B	395	196	1.13	NE									
A*30:02	A30	019	A	305	182	1.23	NE									
A*34:01	A34	023	A	300	158	0.99	NE									
B*07:14	B7,Bw6	1012	B	3978	157	0.46	NE									
B*53:01	B53,Bw4	068	B	284	145	0.96	NE									

The bottom right window shows a detailed analysis for B*44:02, including a bar chart of raw data, a sequence alignment view, and a table of epitope assignments. The 'Final Assignments' table is as follows:

Epitope	Score	Assignment
B*44:02	4.529,74	B*44:02
C*15:02	2.092,93	C*15:02
C*16:02	1.120,40	C*16:02
B*13:01	1.087,87	B*13:01

iCn3D表示機能

AlleleまたはSeroをクリックすると立体構造を確認することができます
インターネットに接続しているPCでのみ使用
できます

The screenshot shows the iCn3D software interface. At the top, there are tabs for 'Epitope Matching' and 'Epitope Analysis'. Below that, there are radio buttons for 'Class I', 'Class II', and 'MICA'. A table lists various alleles with columns for Allele, Ser, Bead ID, Locus, Raw, Baseline, and Ratio. A search panel on the right includes fields for 'Search Allele(s)', 'Search Epitope(s)', and 'List All Epitopes'. A dropdown menu labeled 'Latest Version' is highlighted with a red box.

The screenshot shows the iCn3D 3D structure viewer. The main window displays a 3D model of a protein structure, labeled 'PDB ID 5E01: Crystal Structure Of Hla-b0702-r19'. The structure is composed of blue and pink spheres. To the right, there is a 'Sequences and Annotations' panel with tabs for 'Summary' and 'Details'. The 'Details' tab is active, showing annotations for 'SE01_A' and 'SE01_B'. The 'SE01_A' section shows 'HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 ALPHA CHAIN (Gene: HLA-B)' with a domain 'MHC_I' and 'IgC_MH...'. The 'SE01_B' section shows 'BETA-2-MICROGLOBULIN (Gene: B2M)' with a domain 'IgC_beta2m'. The 'SE01_C' section shows 'B19 PEPTIDE'.

- Latest Version: 最新のwebsiteの閲覧
- Compatible Version: 機能が制限されたページの閲覧
- Safe Mode: 限られた機能のみでの閲覧

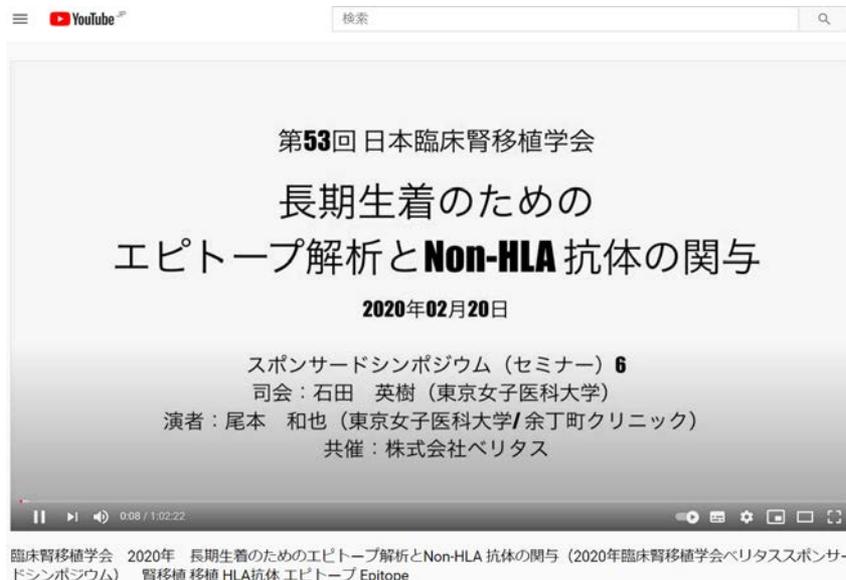
関連動画のご紹介

2020/06/11

腎移植におけるエピトープ解析の今（2020年2月 ベリタスプライベートセミナー）



https://www.veritastk.co.jp/products/reference_detail/hla200602.html



https://www.youtube.com/watch?v=uiJ5jPw_mTQ&t=6s