

1/45

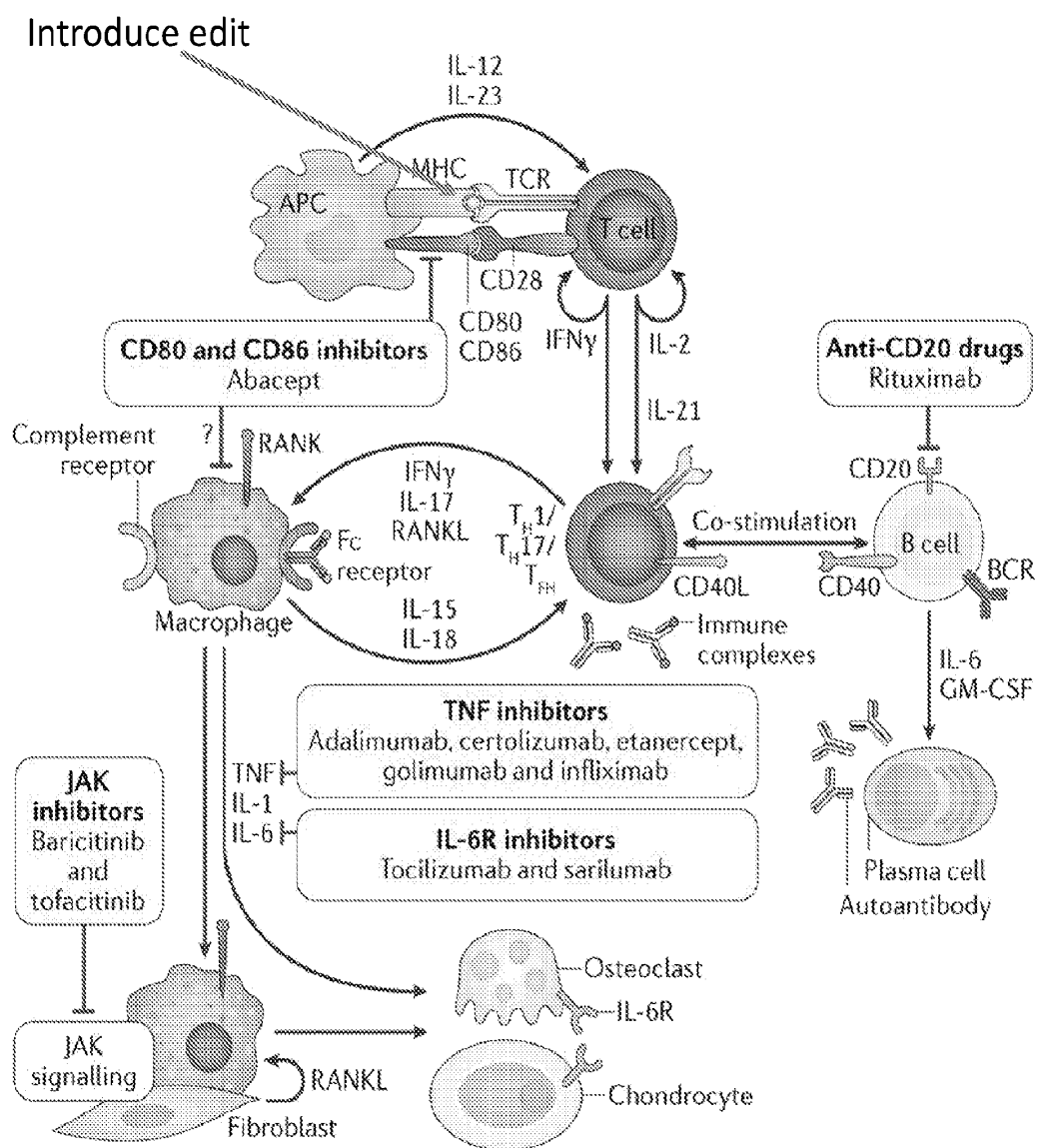


Fig. 1

SUBSTITUTE SHEET (RULE 26)

2/45

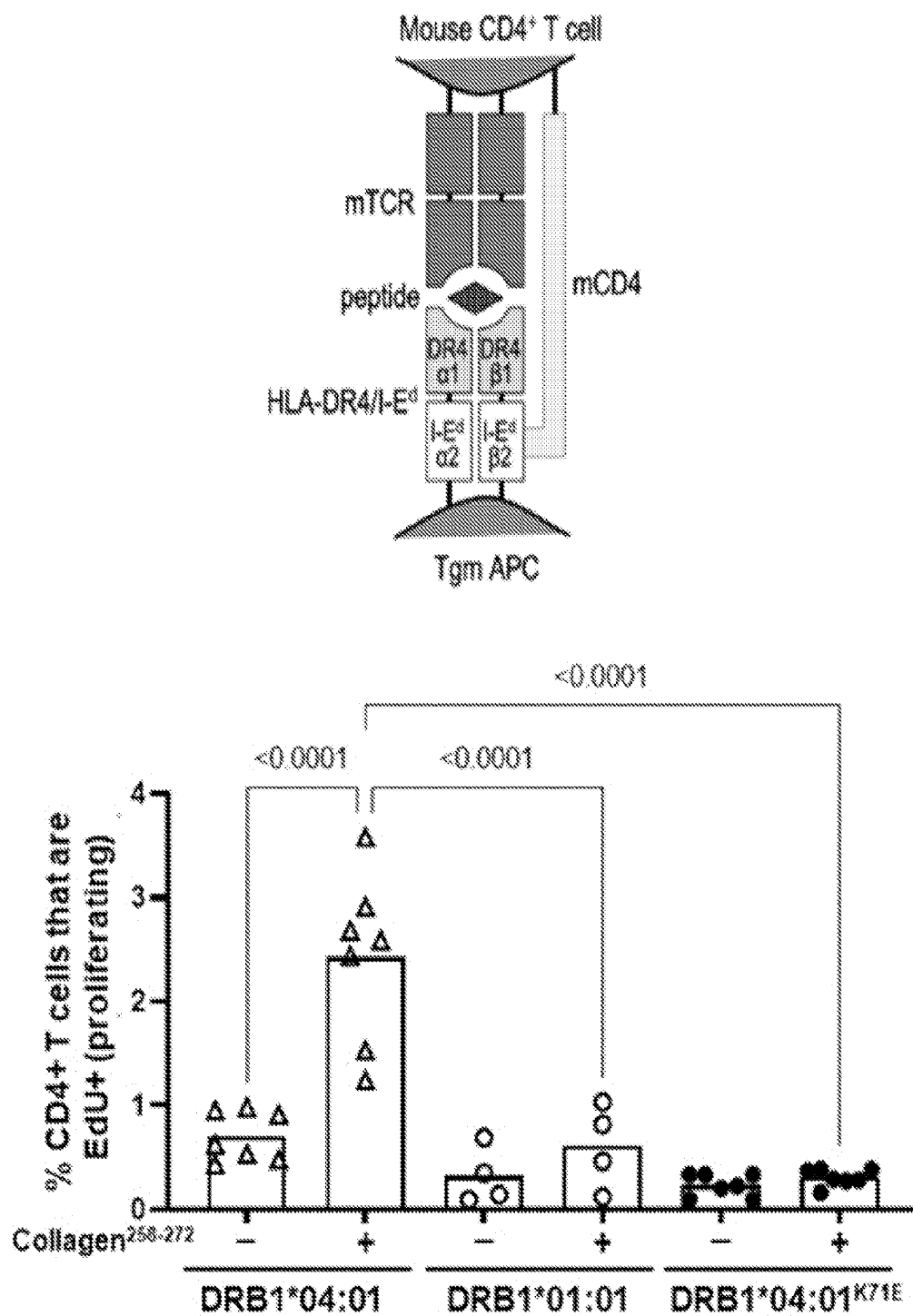


Fig. 2

SUBSTITUTE SHEET (RULE 26)

3/45

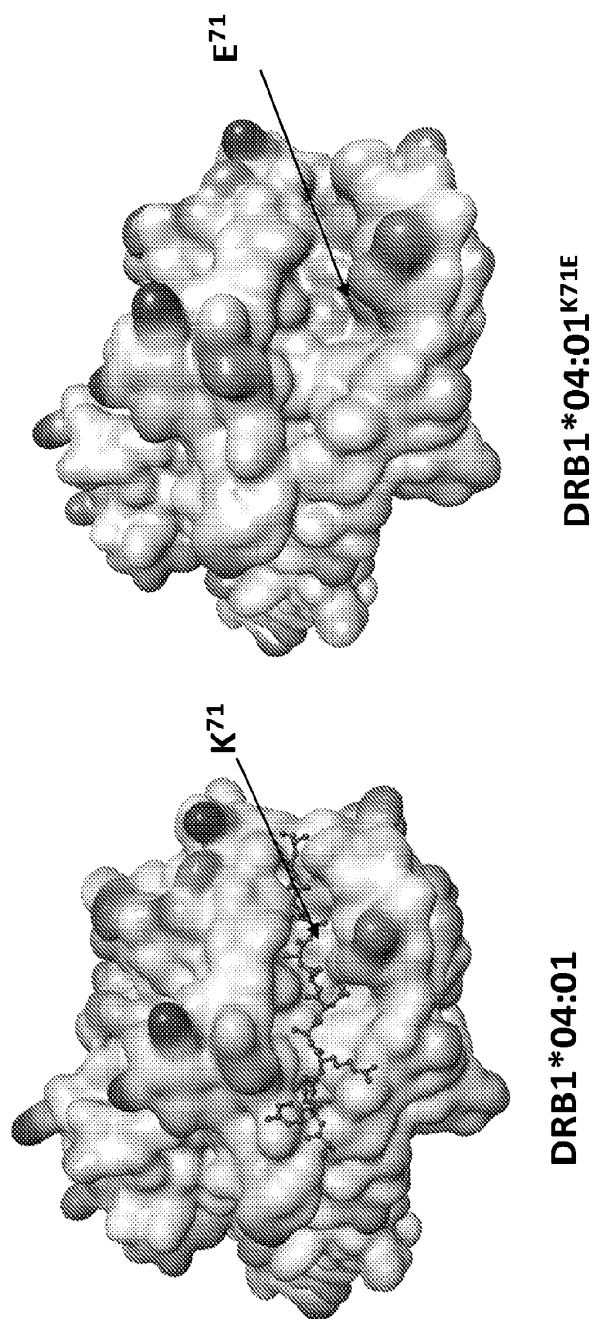


Fig.3A

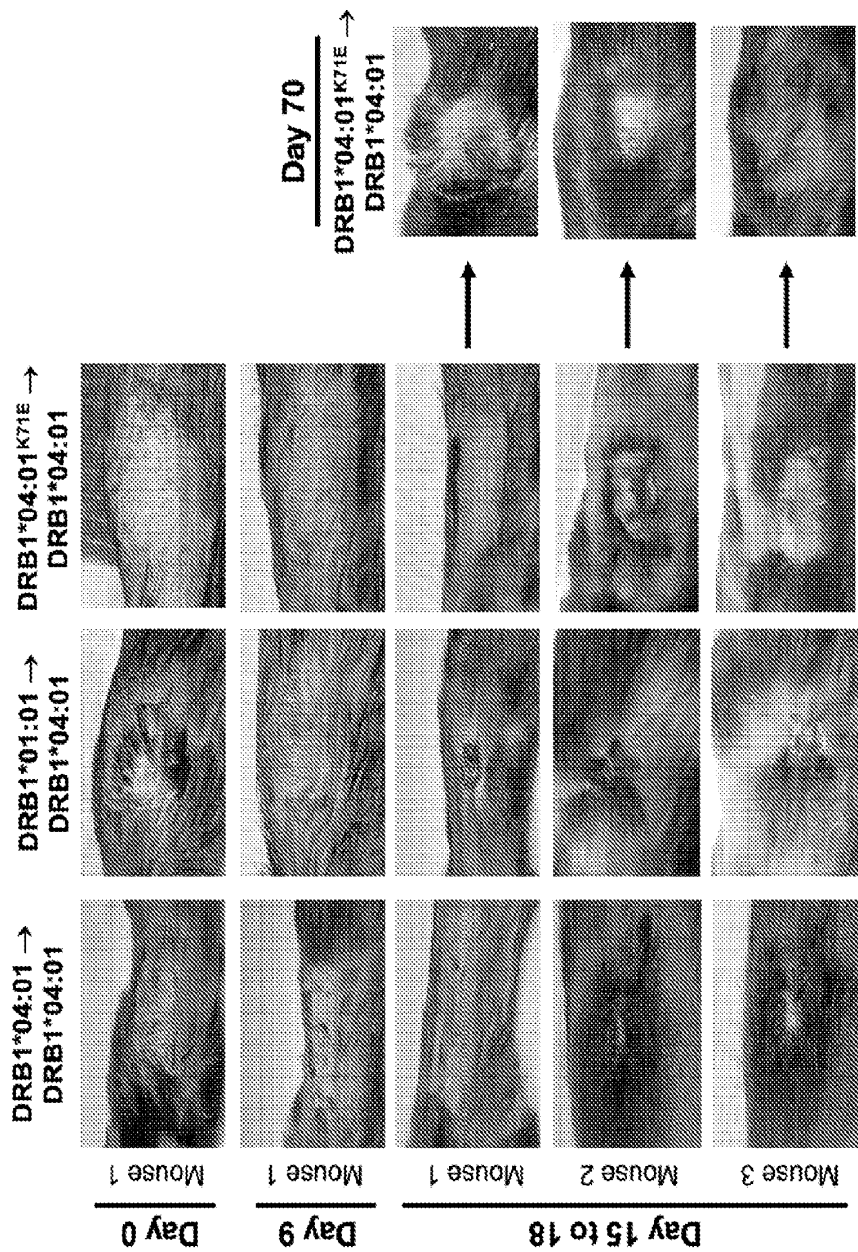


Fig.3B

DRB1*01:01, DRB1*11:01 and DRB1*15:01 Alignment

AA Pos.	10	20	30	40	50	60	70	80	90	100
DRB1*01:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*11:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*15:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*01:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*11:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*15:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*01:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*11:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*15:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*01:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*11:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*15:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*01:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*11:01:01:01	Q	U	I	N	E	R	L	A	R	C
DRB1*15:01:01:01	Q	U	I	N	E	R	L	A	R	C

Fig. 4

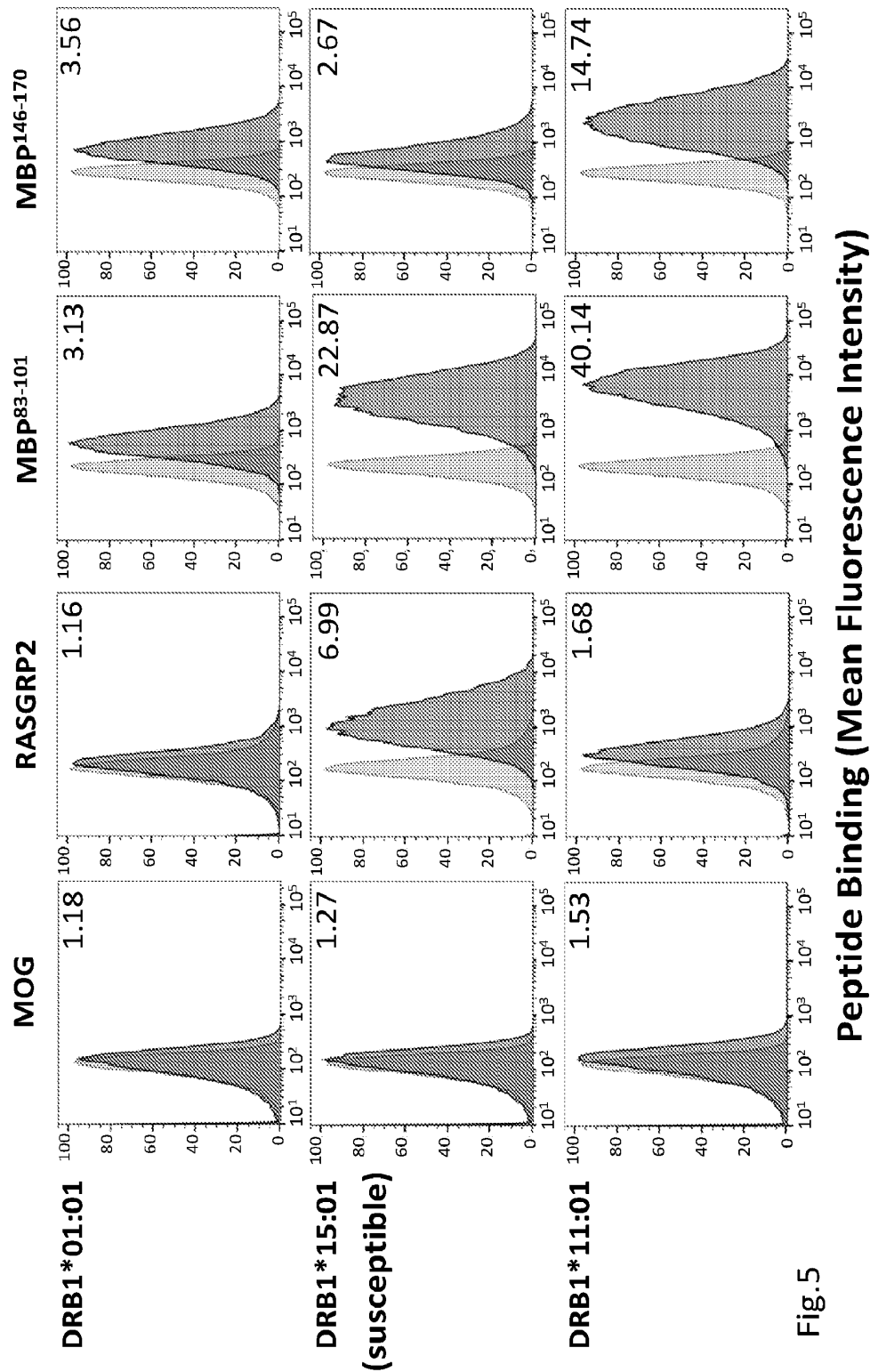


Fig.5

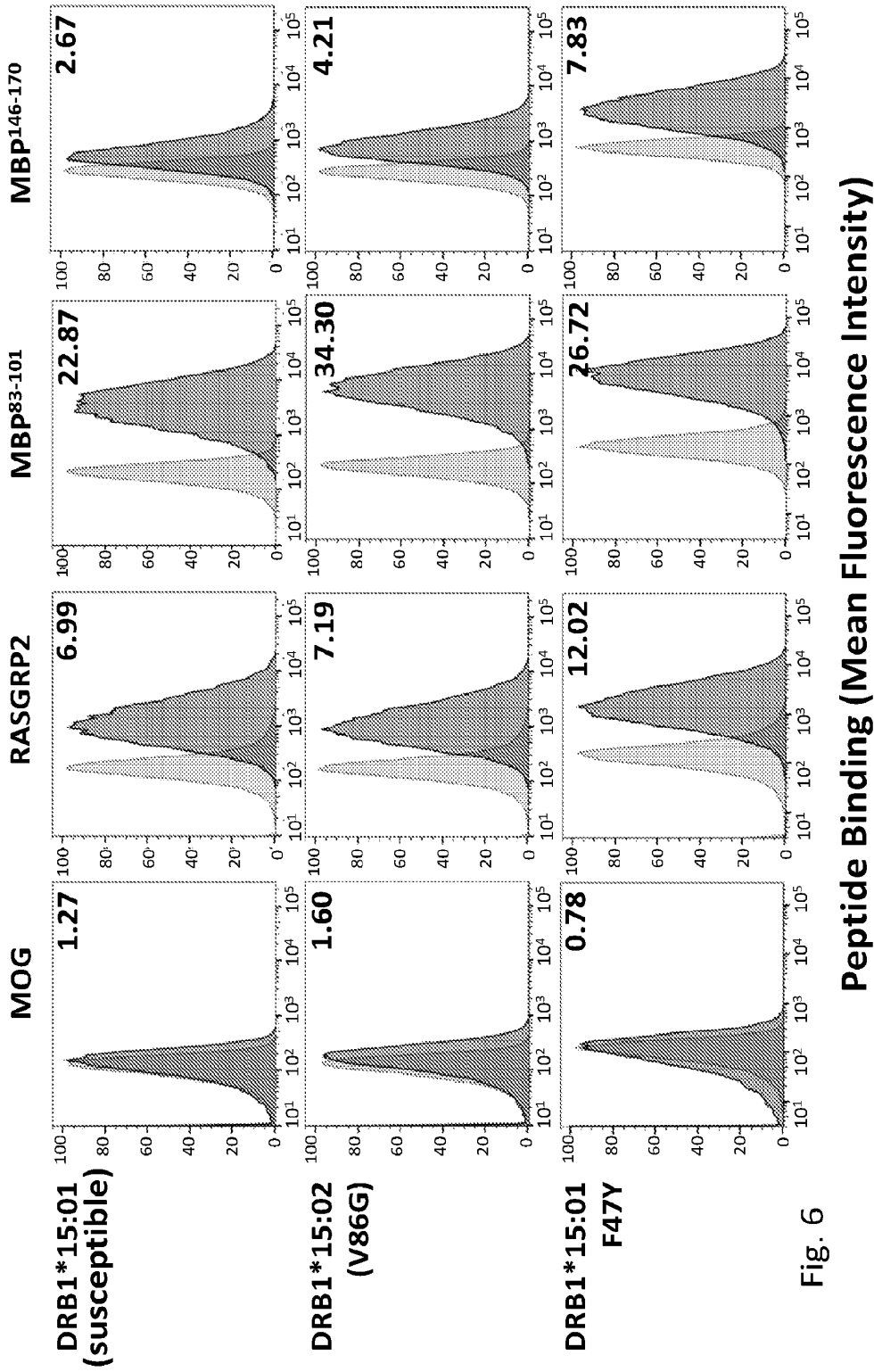


Fig. 6

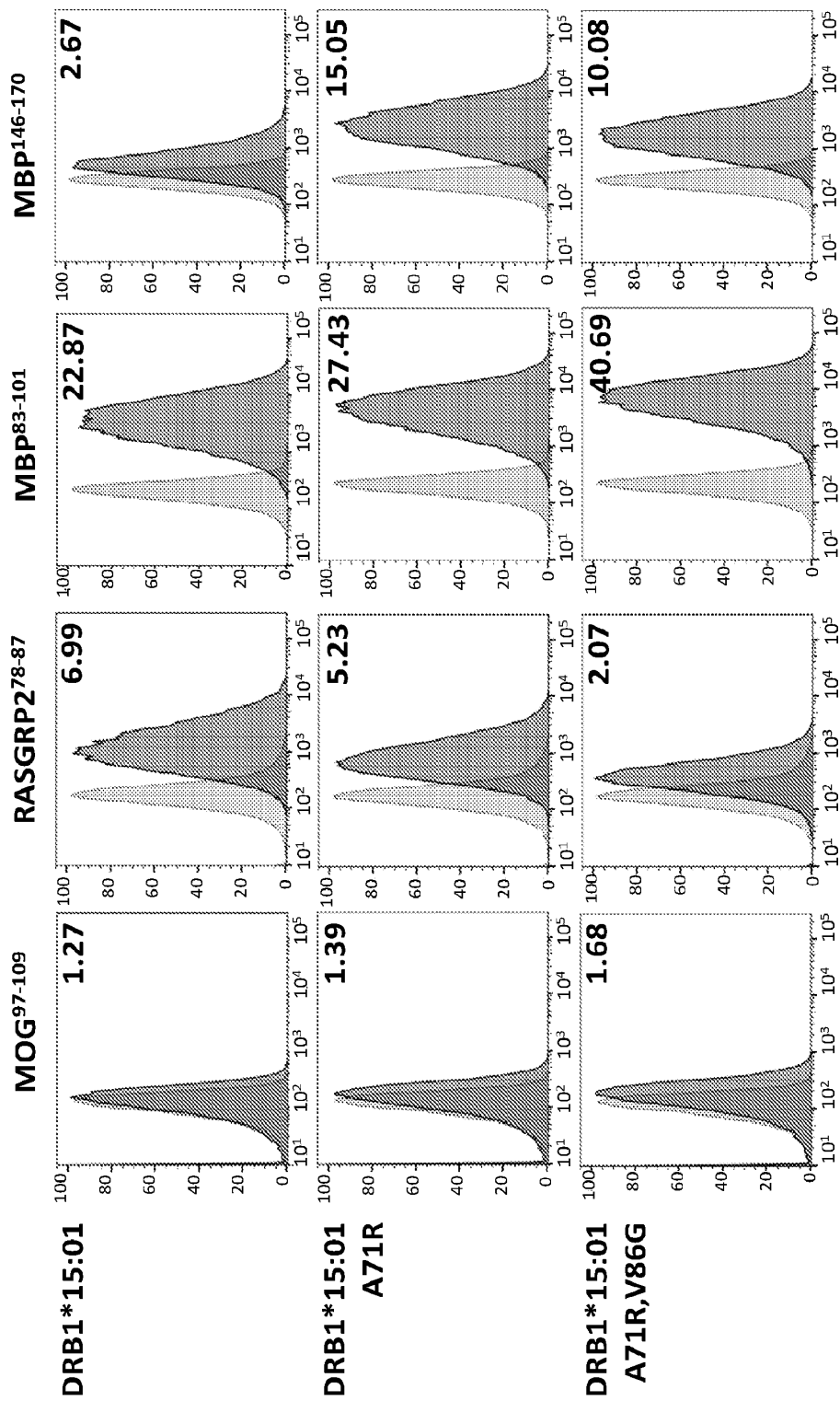


Fig.7

Peptide Binding (Mean Fluorescence Intensity)

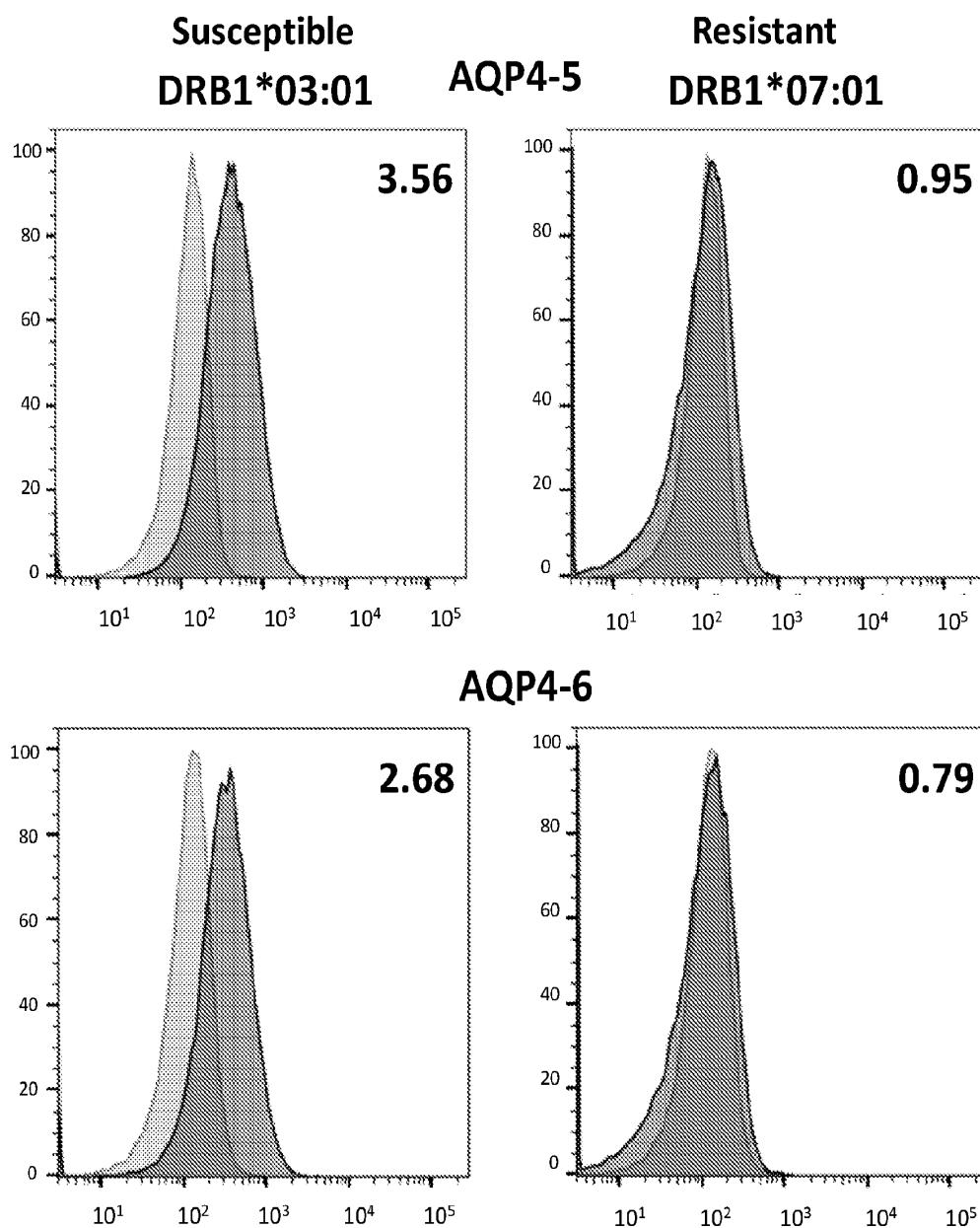
Sequence Alignment of DRB1*03:01 and DRB1*07:01

AA Pos.	10	20	30	40	50	60	70	80	90	100
DRB1*03:01:01:01	QUTRERLEY	SYSCCHENG	TEAVVILRX	FMNQENVF	DSVGSFRV	TELCRFRREY	WASQKLLQ	WAGRVNICK	HNICVLEST	VSRVYHAYE
DRB1*07:01:01:01	---Q---	WQ	GNK	---QF-E-A	-Y---	---Y--S	---I--D	R-Q--TV	---G---	-----E--
DRB1*03:01:02:01	---Q---	---Q	DRF	---H-G	LY	---Y---	---P--R	R-EE--TV	---G---	-----E--
AA Pos.	110	120	130	140	150	160	170	180	190	200
DRB1*03:01:01:01	VPSVYCPDQ	HANILVSVS	GFPGSIEVR	WRNGQERT	GVVSTGLIH	GNVFQILVA	LETVESSEV	YTCQVSESV	TSPLIVSRA	ESSESQSMIL
DRB1*07:01:01:01	---A-----	-----	-----	-----A	-----Q-	-----	-----	-----	N-----	-----
DRB1*03:01:02:01	---A-----	-----	-----	-----A	-----Q-	-----	-----	-----	N-----	-----
AA Pos.	210	220	230							
DRB1*03:01:01:01	SDPGSEVLS	LELGADSELY	FMQGNHSL	QPGTSL						
DRB1*07:01:01:01	-----	-----	-----	---T---						
DRB1*03:01:02:01	-----	-----	-----	---T---						

Fig. 8

10/45

Binding of Aquaporin Peptides to DRB1 Alleles



Peptide Binding (Mean Fluorescence Intensity)
Fig.9

SUBSTITUTE SHEET (RULE 26)

Sequence alignment DRB1*04:01 and *04:05

2A Ref.	10	20	30	40	50	60	70	80	90	100
DRB1*04:01:01:01	GTGATGTTG	TTGACGCTG	CTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG
DRB1*04:05:01:01	GTGATGTTG	TTGACGCTG	CTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG
2A Ref.	110	120	130	140	150	160	170	180	190	200
DRB1*04:01:01:01	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG
DRB1*04:05:01:01	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG
2A Ref.	210	220	230							
DRB1*04:01:01:01	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG							
DRB1*04:05:01:01	TTGCTGCTG	TTGCTGCTG	TTGCTGCTG							

Fig.10

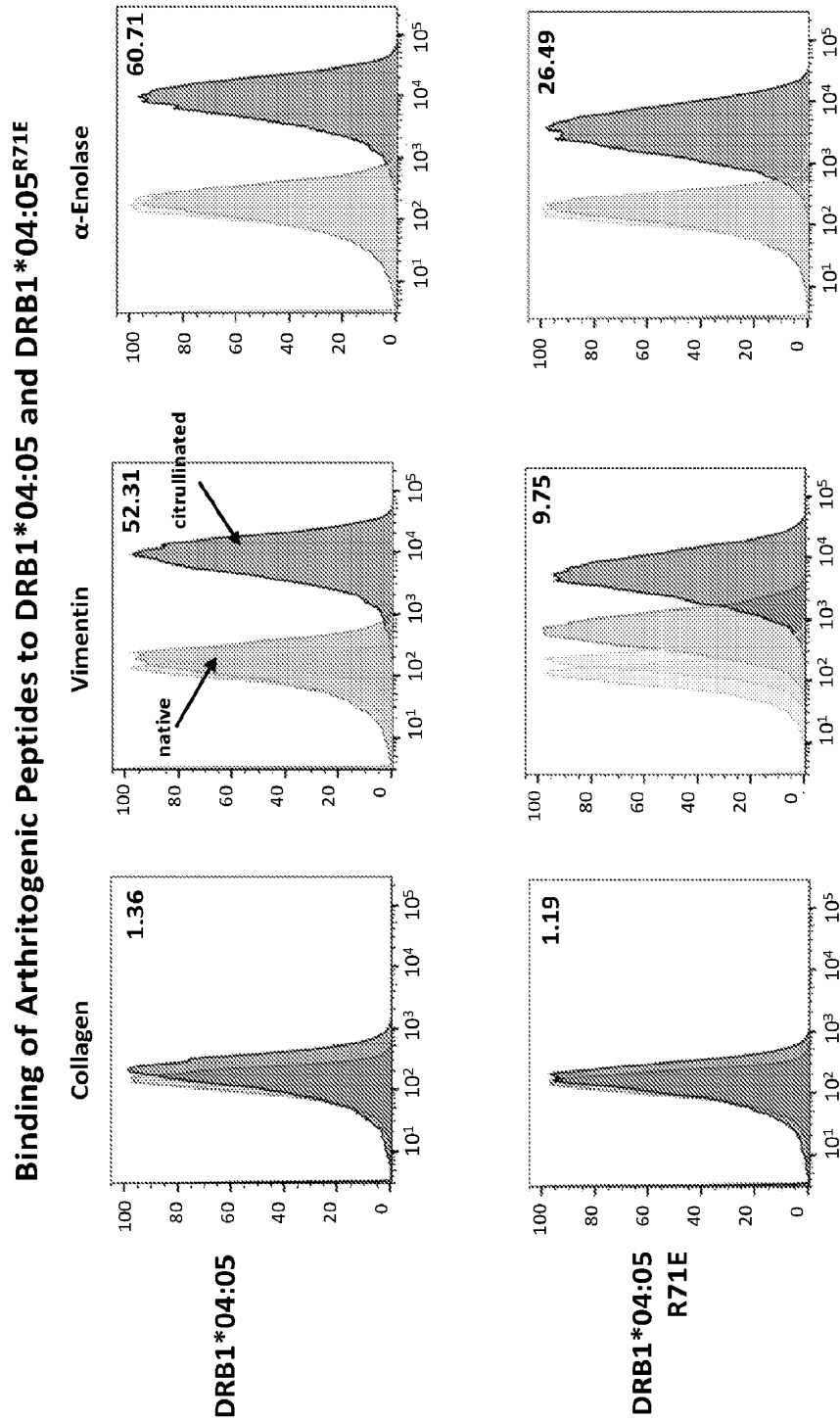


Fig. 11 Peptide Binding (Mean Fluorescence Intensity)

A57D Edit Does Not Block HIP8-NPY Binding to DQ2 or DQ8

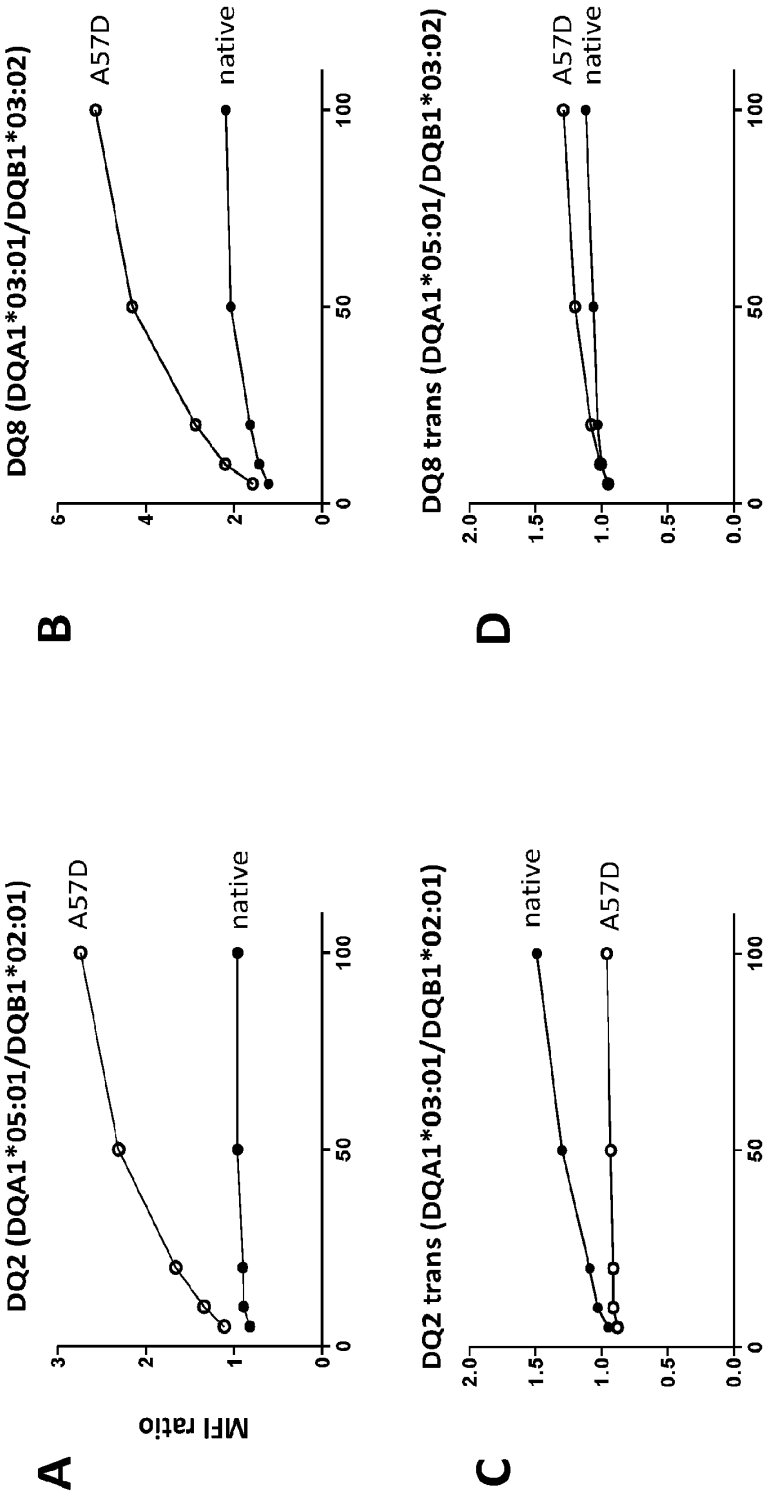


Fig. 12

A57D Edit Does Not Block HIP11-C Binding to DQ2 or DQ8

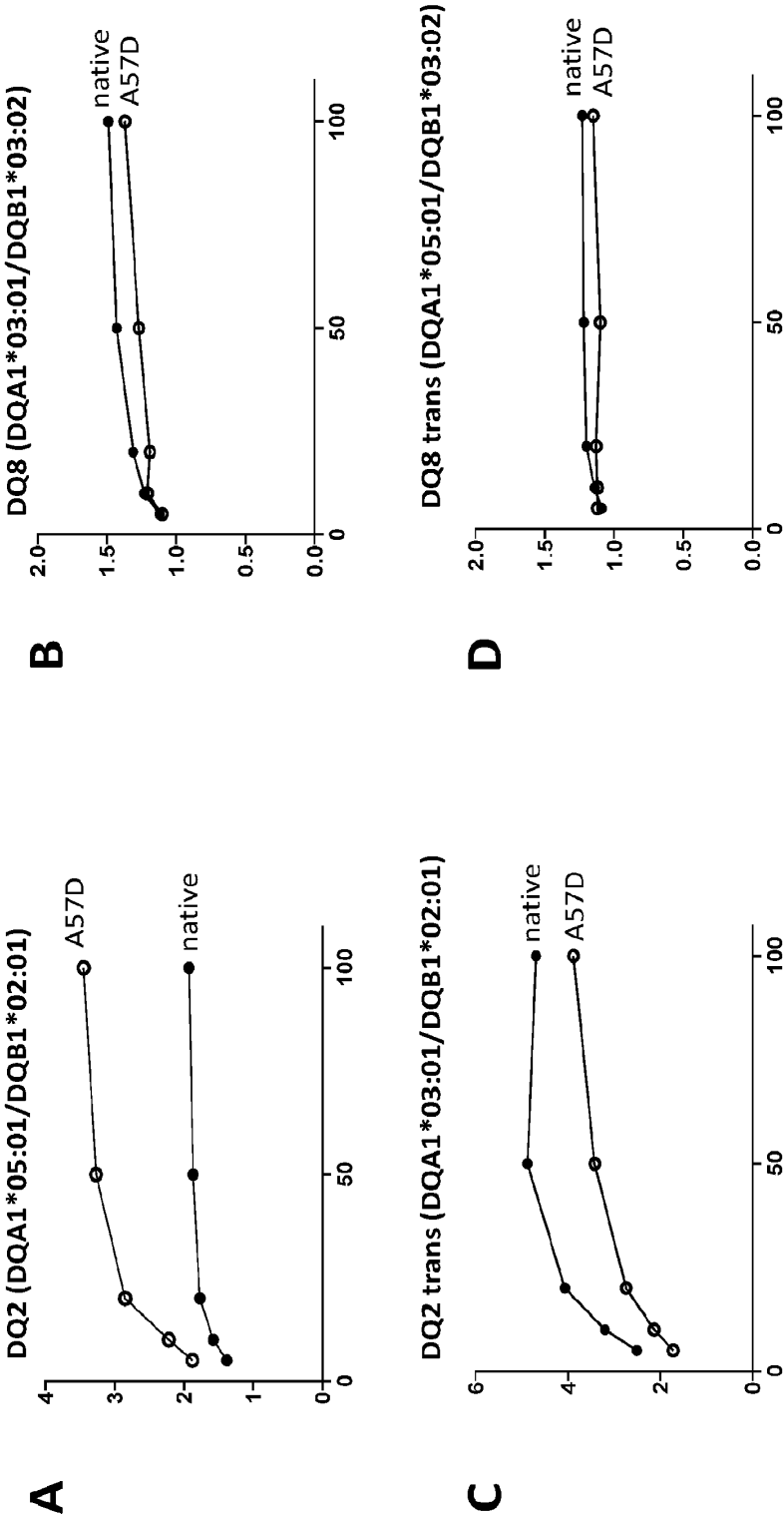


Fig.13

A57D Edit Inhibits Insulin Mimotope Binding to DQ8 and DQ2 Trans

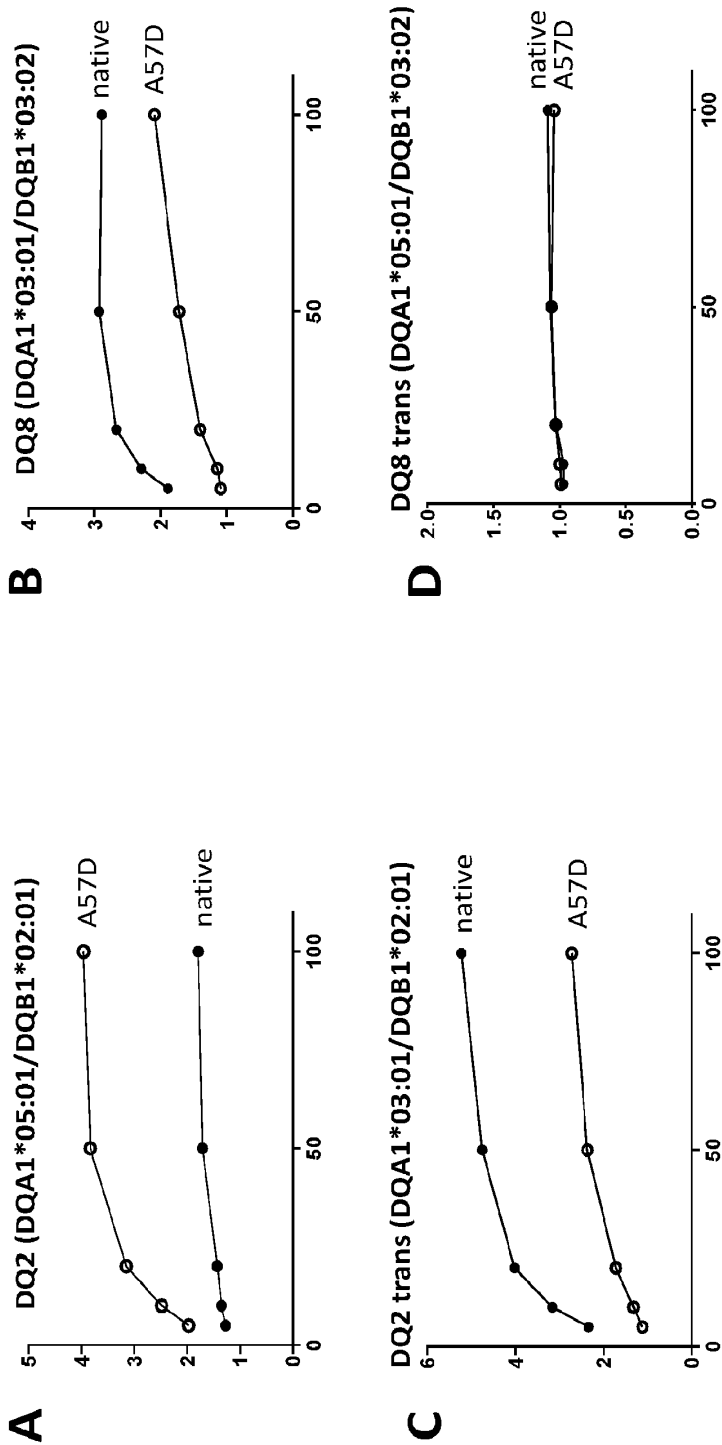


Fig.14

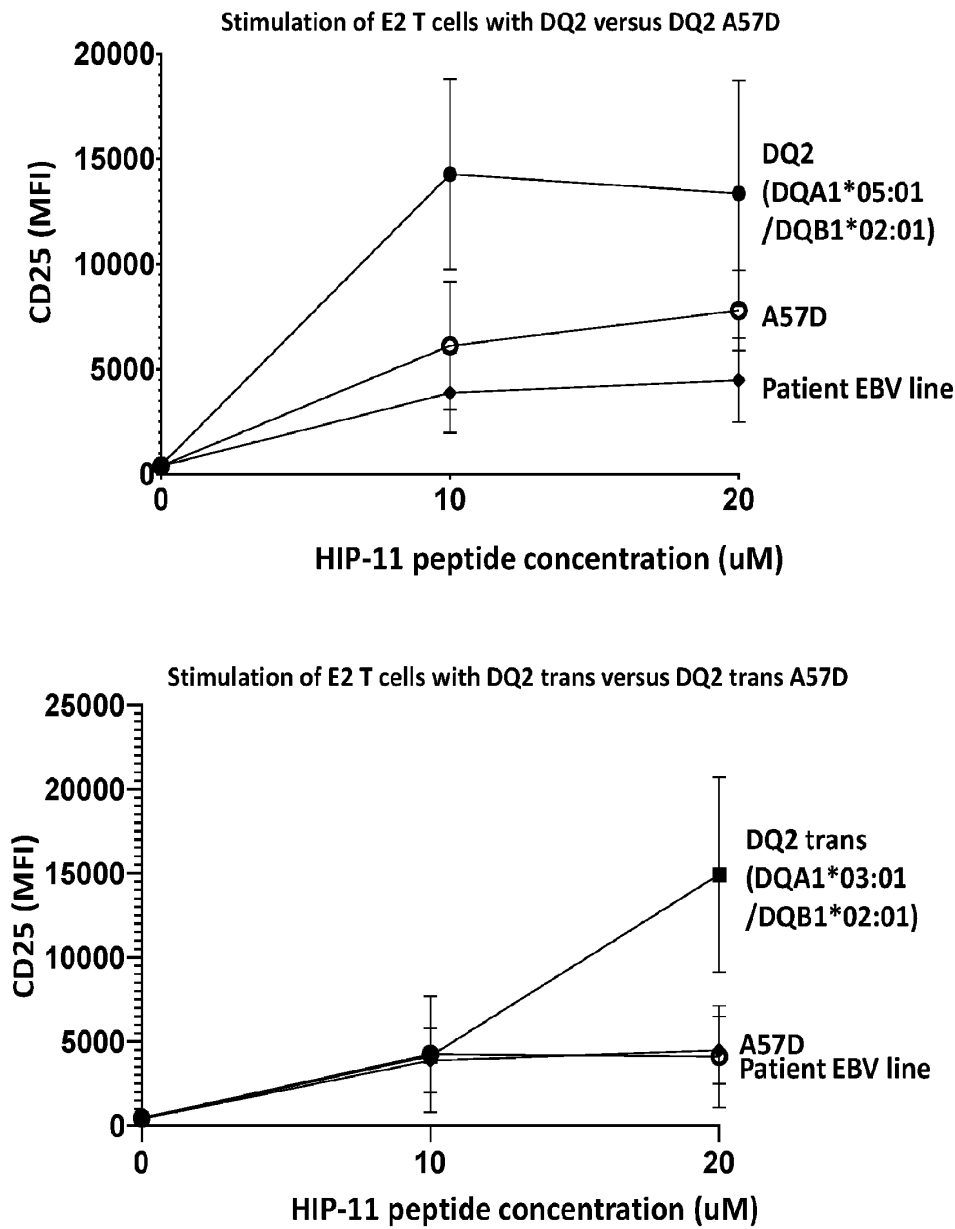


Fig.15

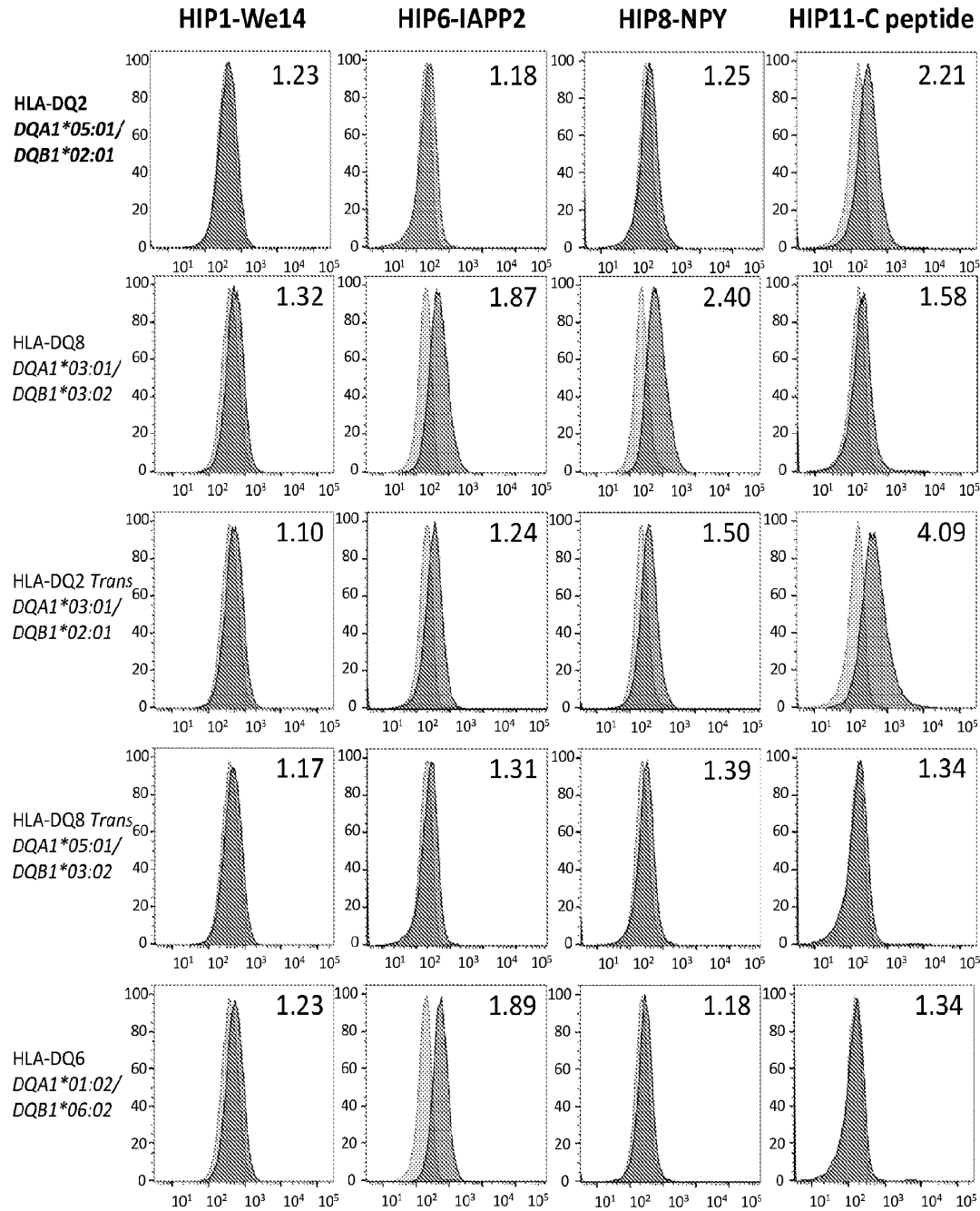


Fig.16 Peptide Binding (Mean Fluorescence Intensity)

18/45

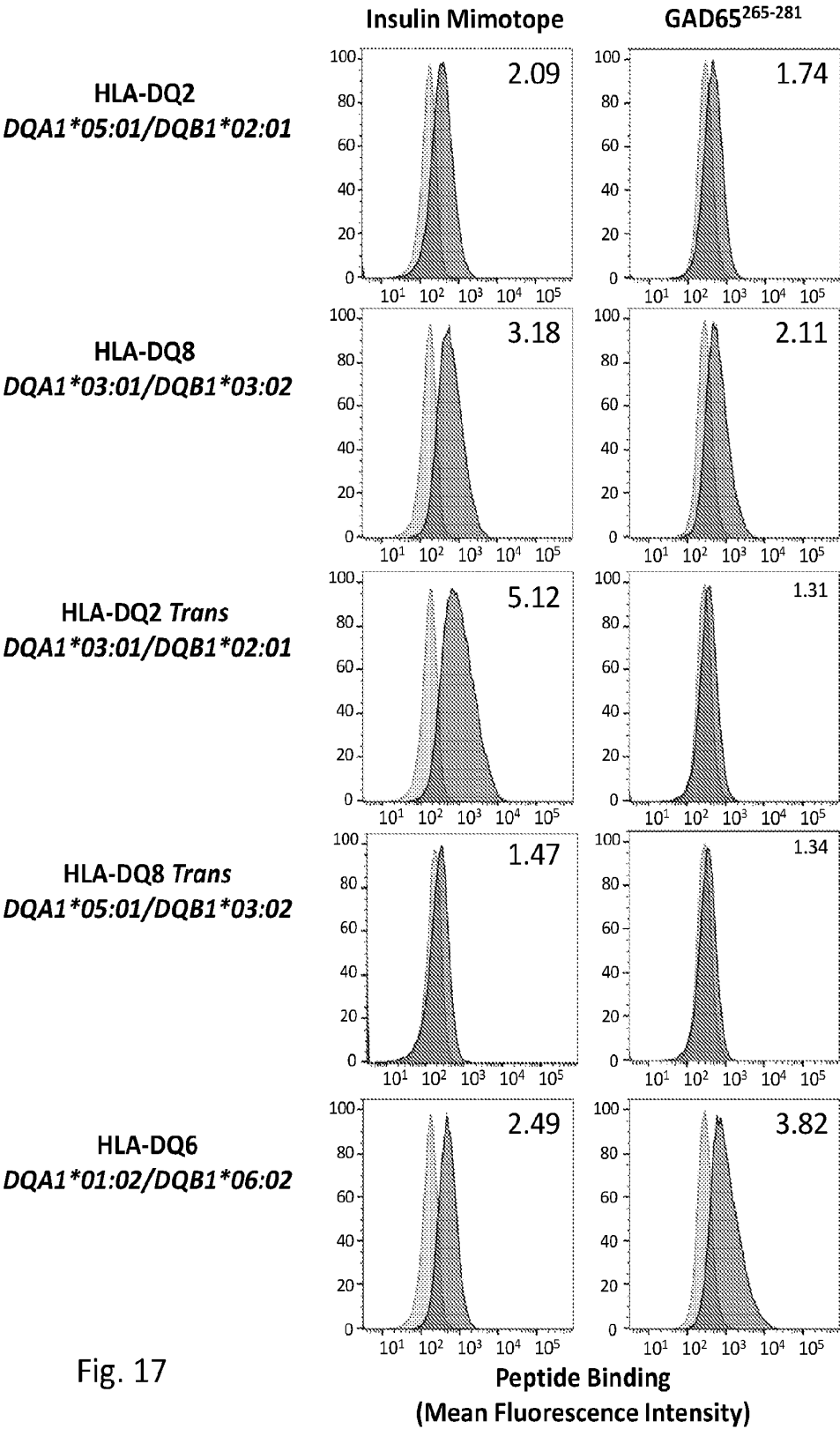


Fig. 17

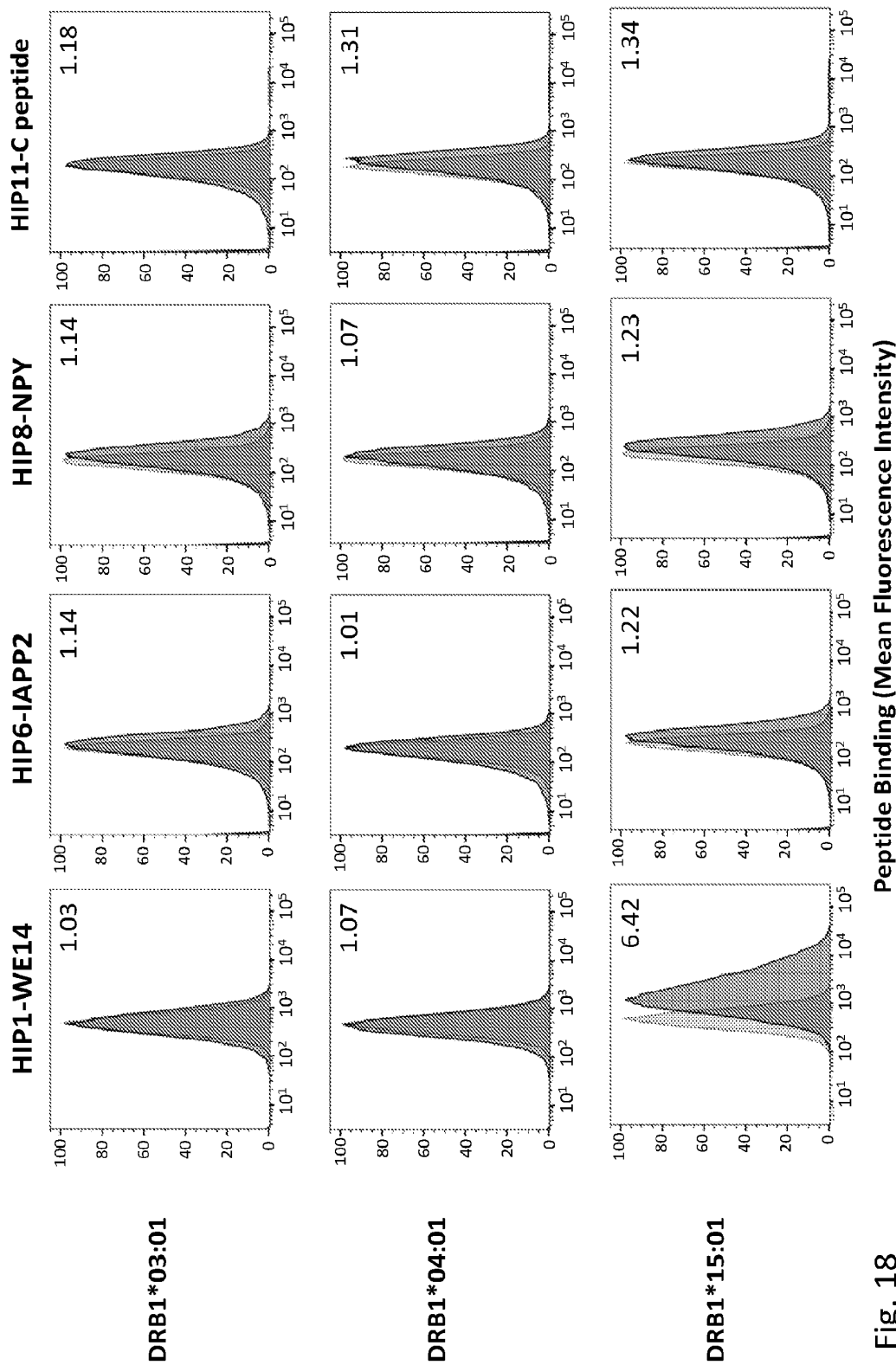


Fig. 18

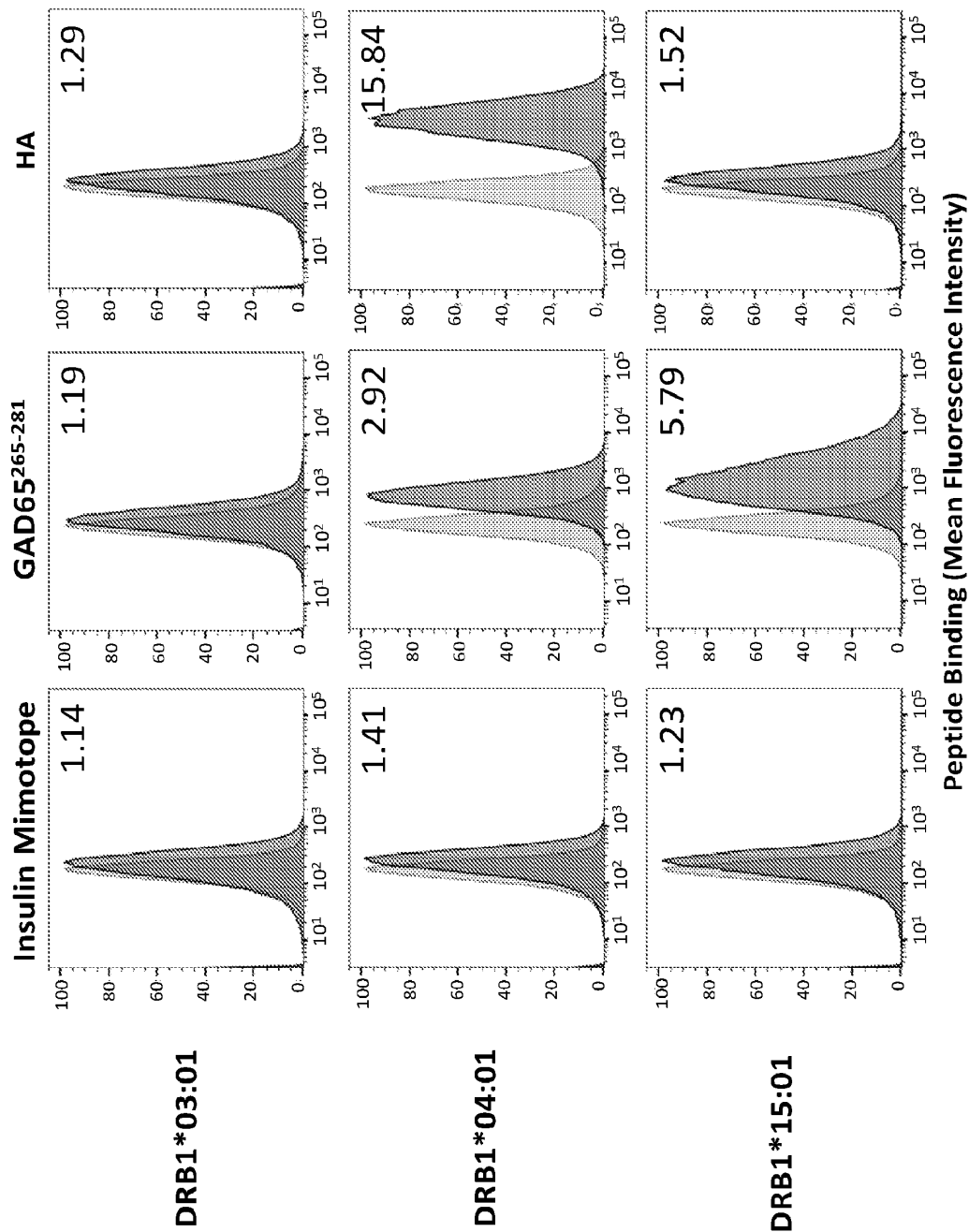


Fig. 19

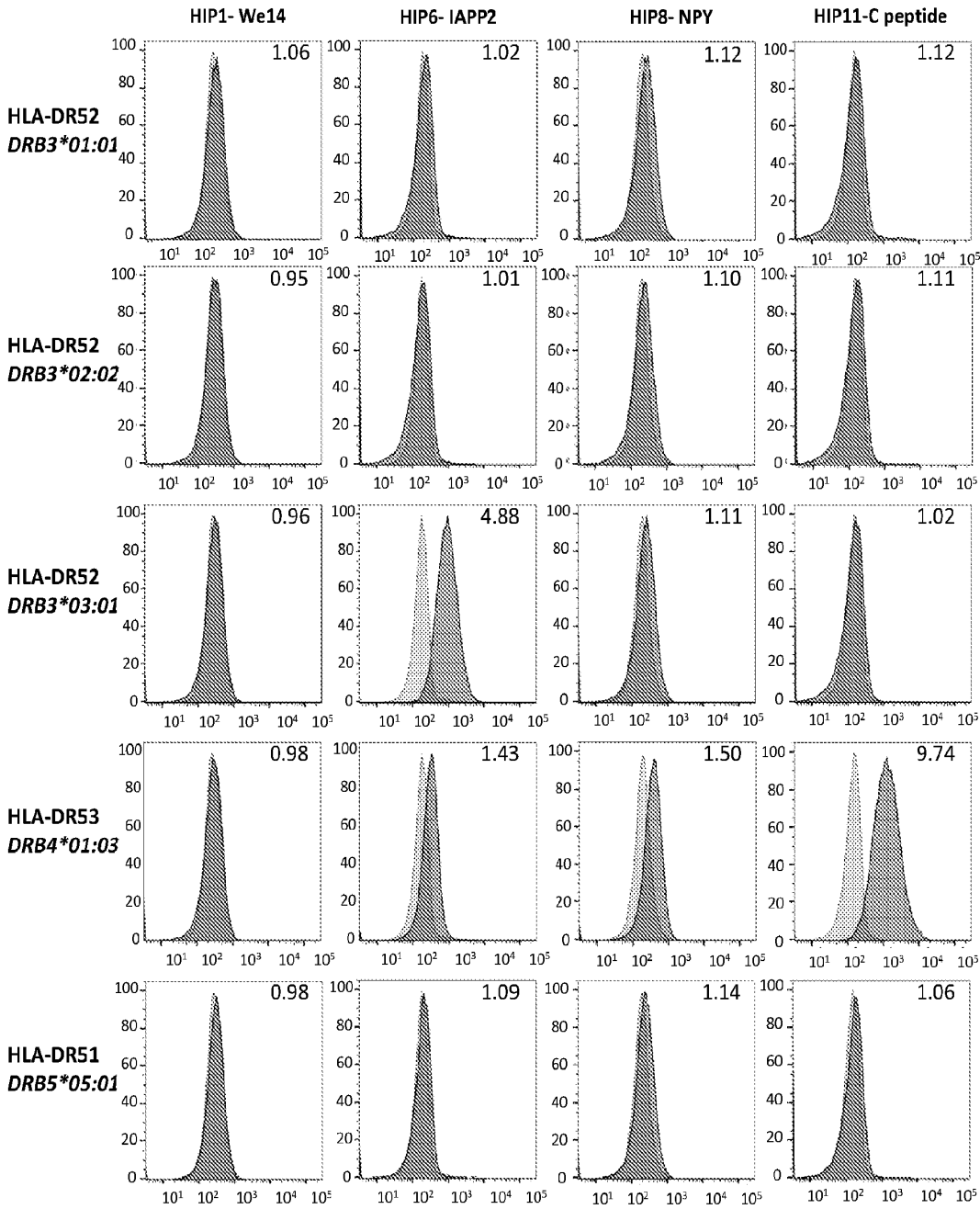


Fig. 20

Peptide Binding (Mean Fluorescence Intensity)

SUBSTITUTE SHEET (RULE 26)

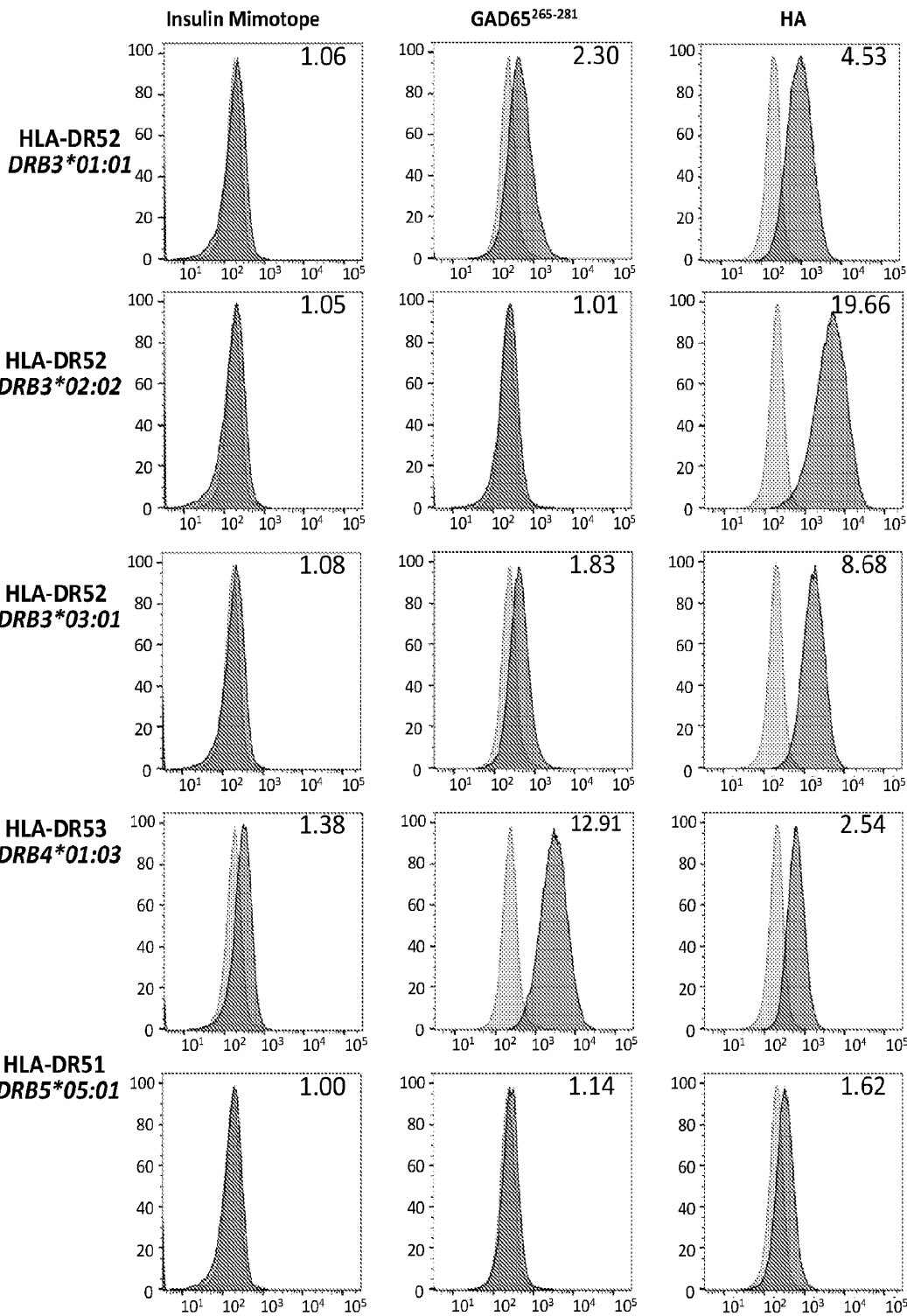


Fig. 21 Peptide Binding (Mean Fluorescence Intensity)

23/45

<u>Disease</u>	<u>Peptide</u>	<u>Sequence</u>
MS	MBP ⁸³⁻¹⁰¹	ENPVVHFFKNIVTPRTPPP
	RASGRP2 ⁷⁸⁻⁸⁷	LVRYWISAFP
	MOG ⁹⁷⁻¹⁰⁹	FFRDHSYQEEA
	MBP ¹⁴⁶⁻¹⁷⁰	AQGTLISKIFKLGGDRSRSRGSPMARR
Diabetes	HIP 1	GQVELGG-WSKMDQLA
	HIP6	GQVELGGG-NAVEVLK
	HIP8	GQVELGGG-SSPETLI
	HIP11	SLQPLA-LEAEDLQV
	Insulin Mimotope	HLVEELYLVAGEEG
	GAD65 ²⁶⁵⁻²⁸¹	AMMIARFKMFPEVKEKG
	Insulin B9-23	SHLVEALYLVCGERG
NMO	AQP4 ²⁸⁴⁻²⁹⁸ (AQP4-5)	RSQVETDDLILKPGV
	AQP4 ²⁸⁵⁻²⁹⁹ (AQP4-6)	SQVETDDLILKPGVV
RA	Type II Collagen ²⁵⁸⁻²⁷²	PGIAGFKGEQGPKE
	carbamyated collagen	
	alpha enolase ¹¹⁻²⁵	IFDSRGNPTVEVDLF
	citrullinated alpha enolase	IFDS{CIT}GNPTVEVDLF
	Native Vimentin ⁶⁶⁻⁷⁸	SAVRLRSSVPGVR
	Citrullinated vimentin	SAVRL{CIT}SSVPGVR
	carbamyated vimentin	
	fibrinogen ⁷⁹⁻⁹¹	QDFTNRINKLKNS
	citrullinated fibrinogen ⁷⁹⁻⁹¹	QDFTN{CIT}INKLKNS
	carbamyated fibrinogen ⁷⁹⁻⁹¹	
	aggrecan ⁸⁹⁻¹⁰³	ATEGRVRVNSAYQDK
	citrullinated aggrecan	ATEG{CIT}VRVNSAYQDK
	cartilage intermediate layer protein - CILP ²⁹⁷⁻³¹¹	ATIKAEFVRAETPYM
	citrullinated CILP	ATIKAEFV{CIT}AETPYM
	Asparagine Synthase Peptide Derived from Streptomyces	AVRLQGSVAGVR
Other	BK virus	PYHFKYHEKHANAI
	CLIP	PVSKMRMATPLLMQA
	Influenza hemagglutinin (HA ³⁰⁶⁻³¹⁸)	PKYVKQNTLKLAT

Fig. 22

SUBSTITUTE SHEET (RULE 26)

Novel Constructs for DRB1 Pocket 1 Gene Editing

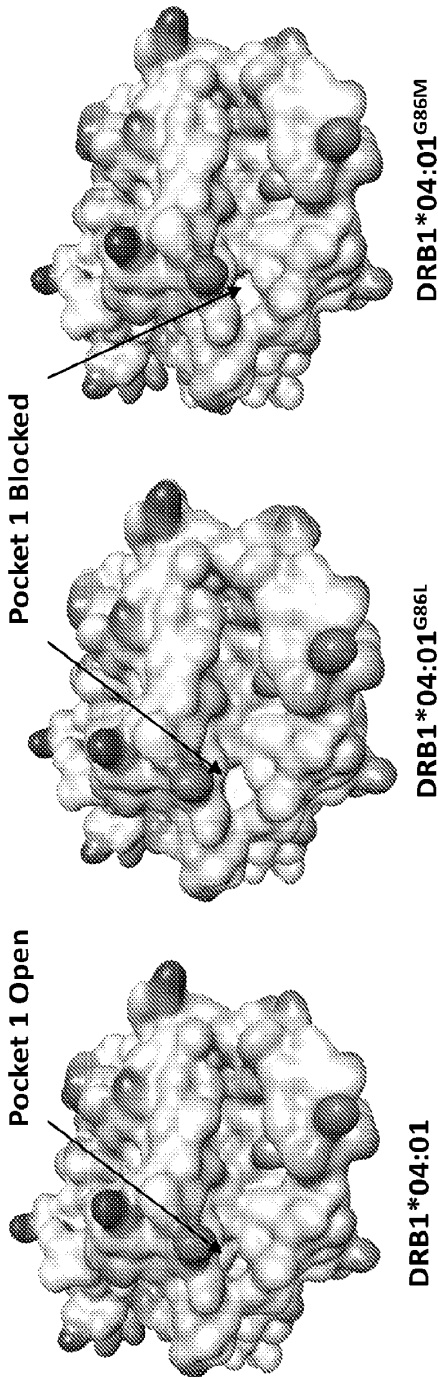
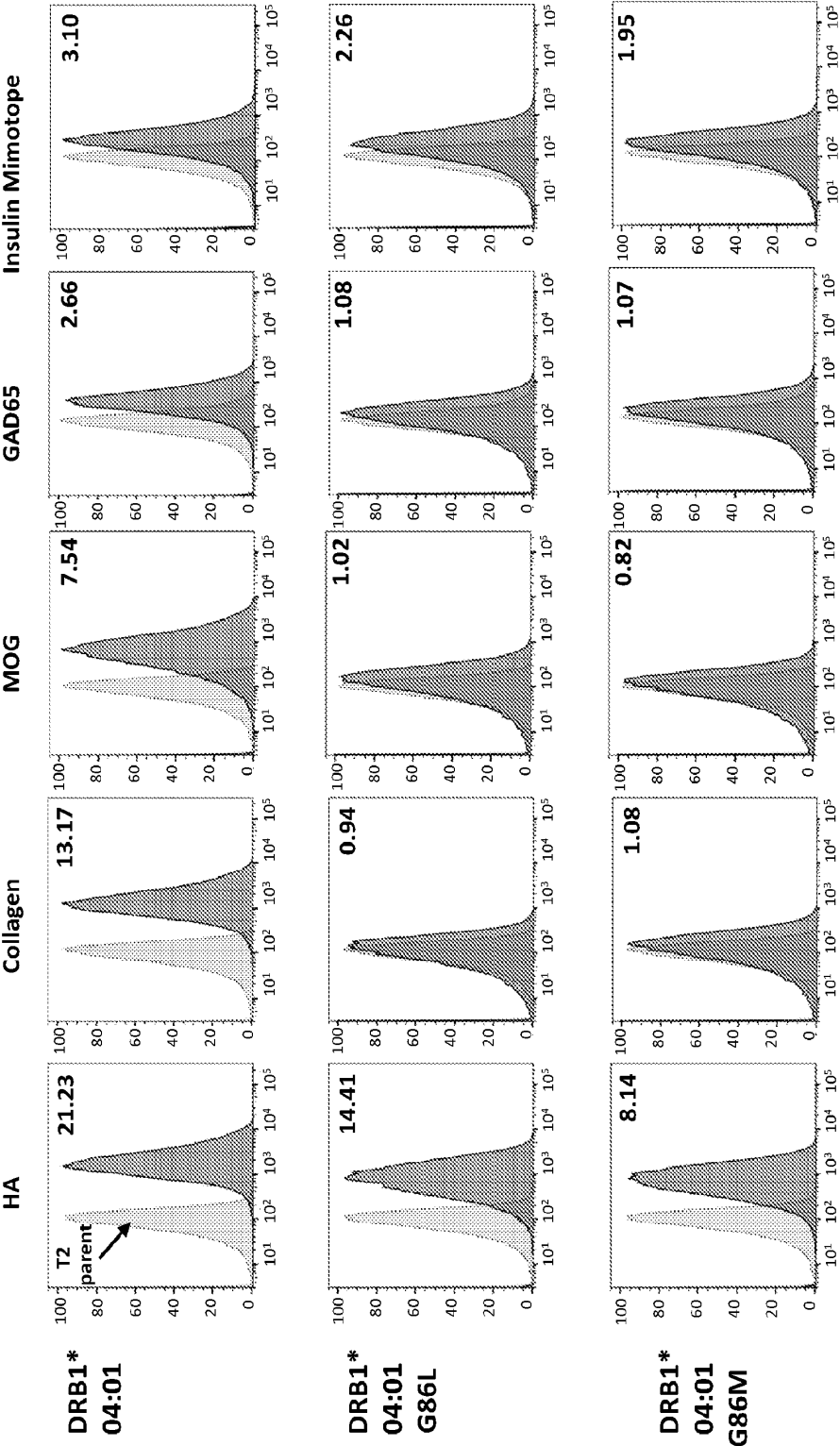


Fig. 23A

NON-POLAR			
	Glycine {Gly : G}		Alanine {Ala : A}
	Leucine {Leu : L}		Isoleucine {Ile : I}
	Methionine {Met : M}		Tryptophan {Trp : W}
	Phenylalanine {Phe : F}		Proline {Pro : P}
	Cysteine {Cys : C}		Valine {Val : V}

Effect of DRB1*04:01 Pocket 1 Edits G86L and G86M on Peptide Binding



Peptide Binding (Mean Fluorescence Intensity)

Fig. 23B

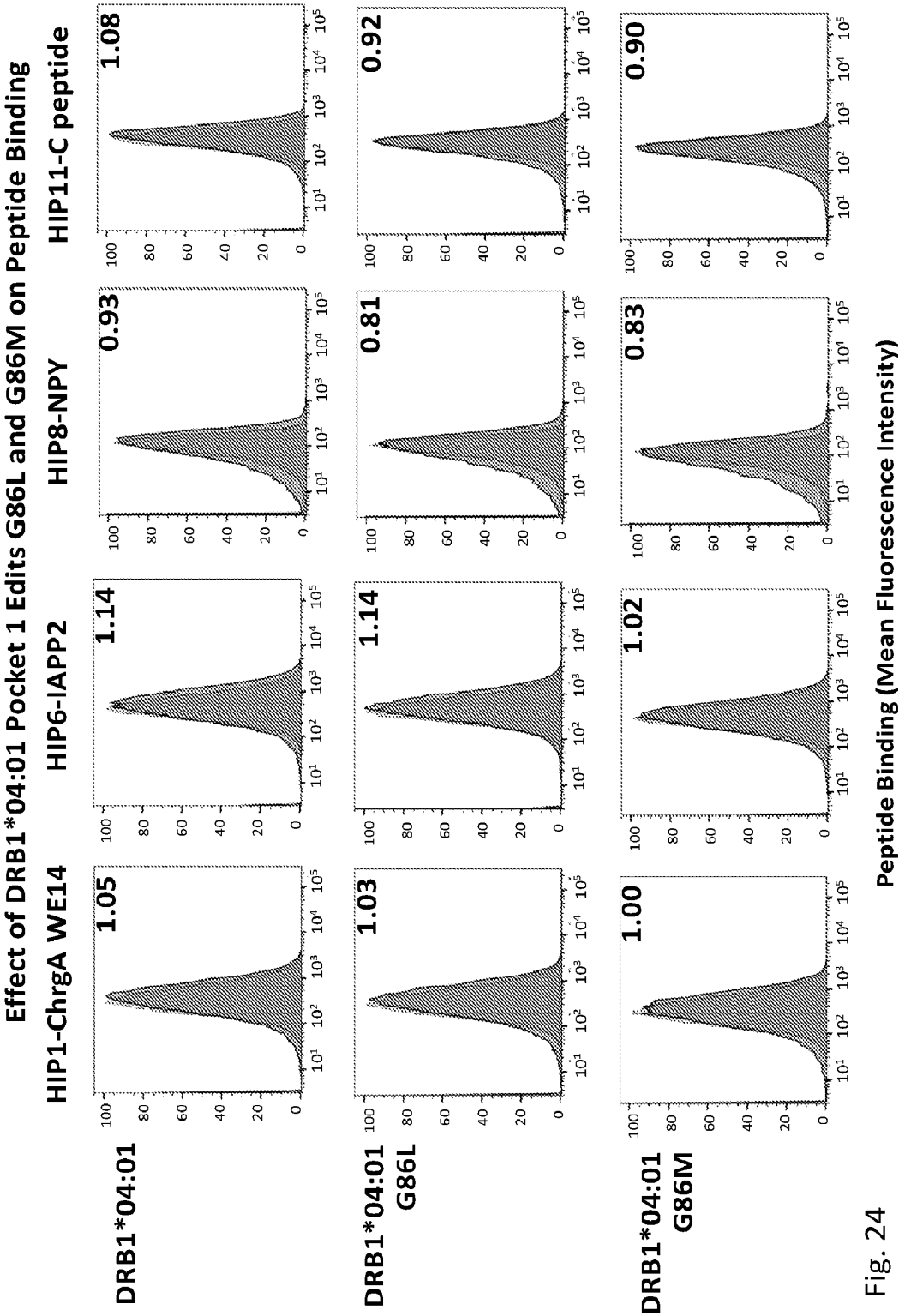


Fig. 24

Effect of DRB1*04:01 Pocket 1 Edits G86L and G86M on Peptide Binding

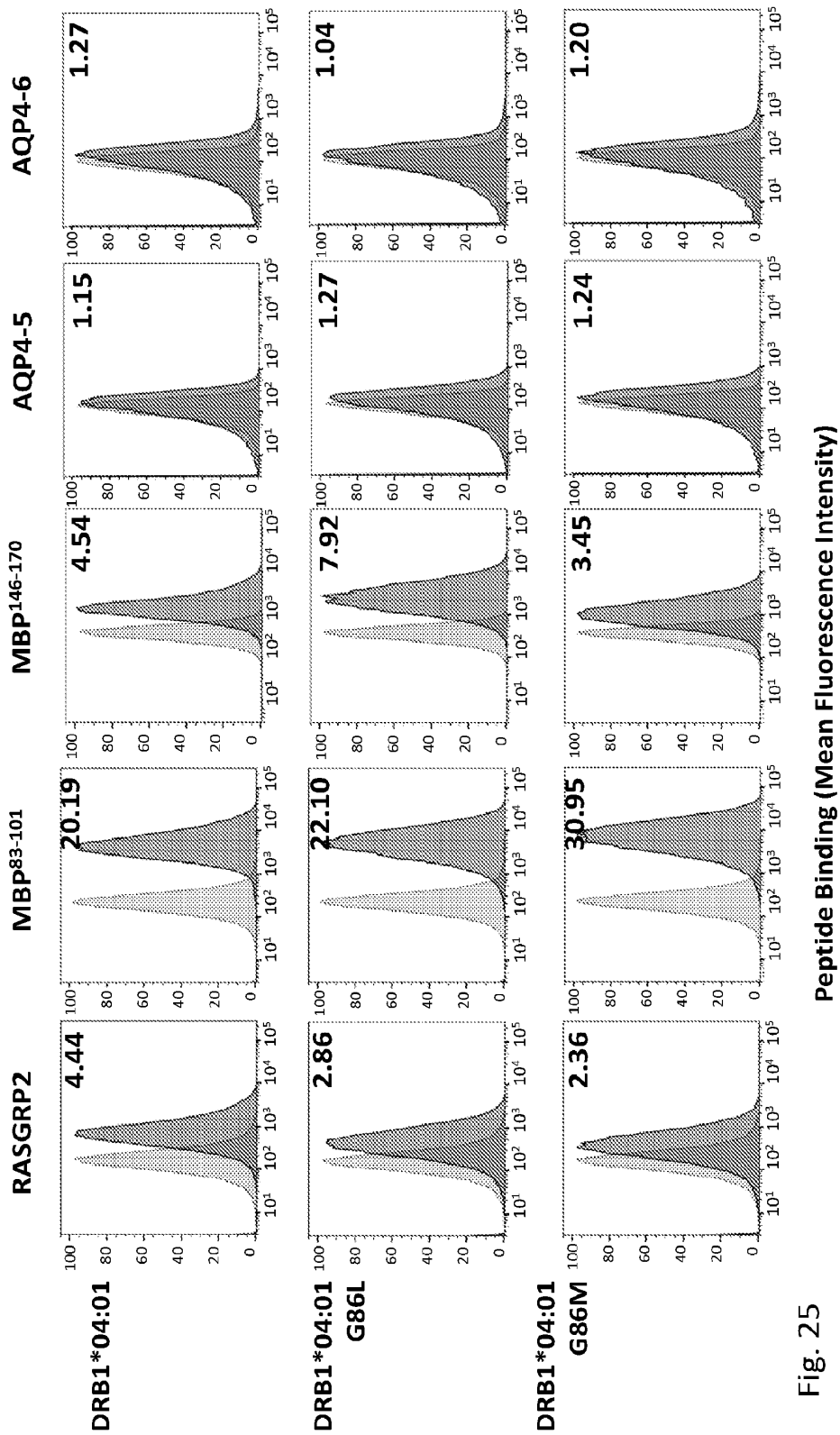
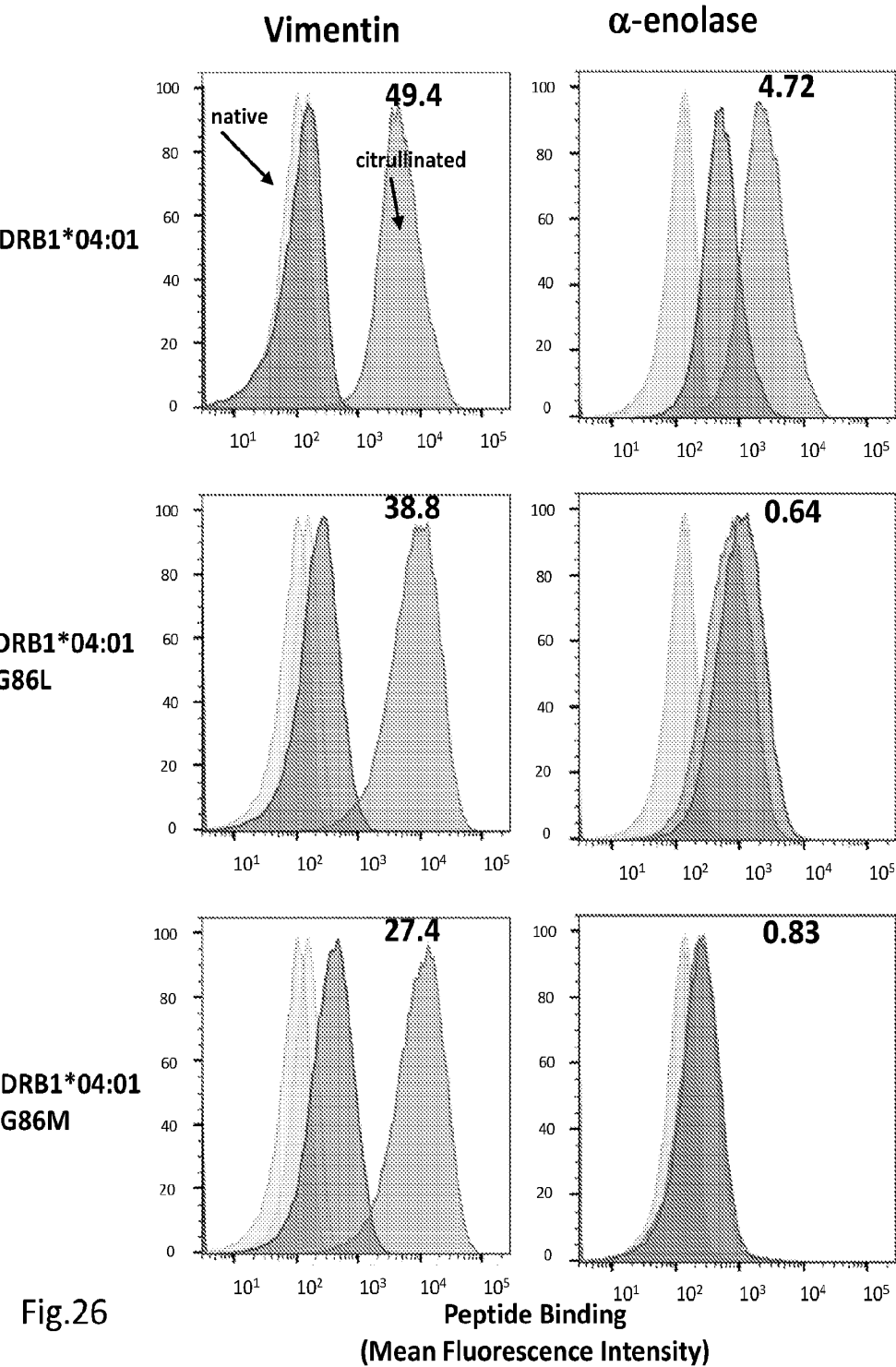


Fig. 25

Effect of DRB1*04:01 Pocket 1 Edits G86L and G86M on Peptide Binding



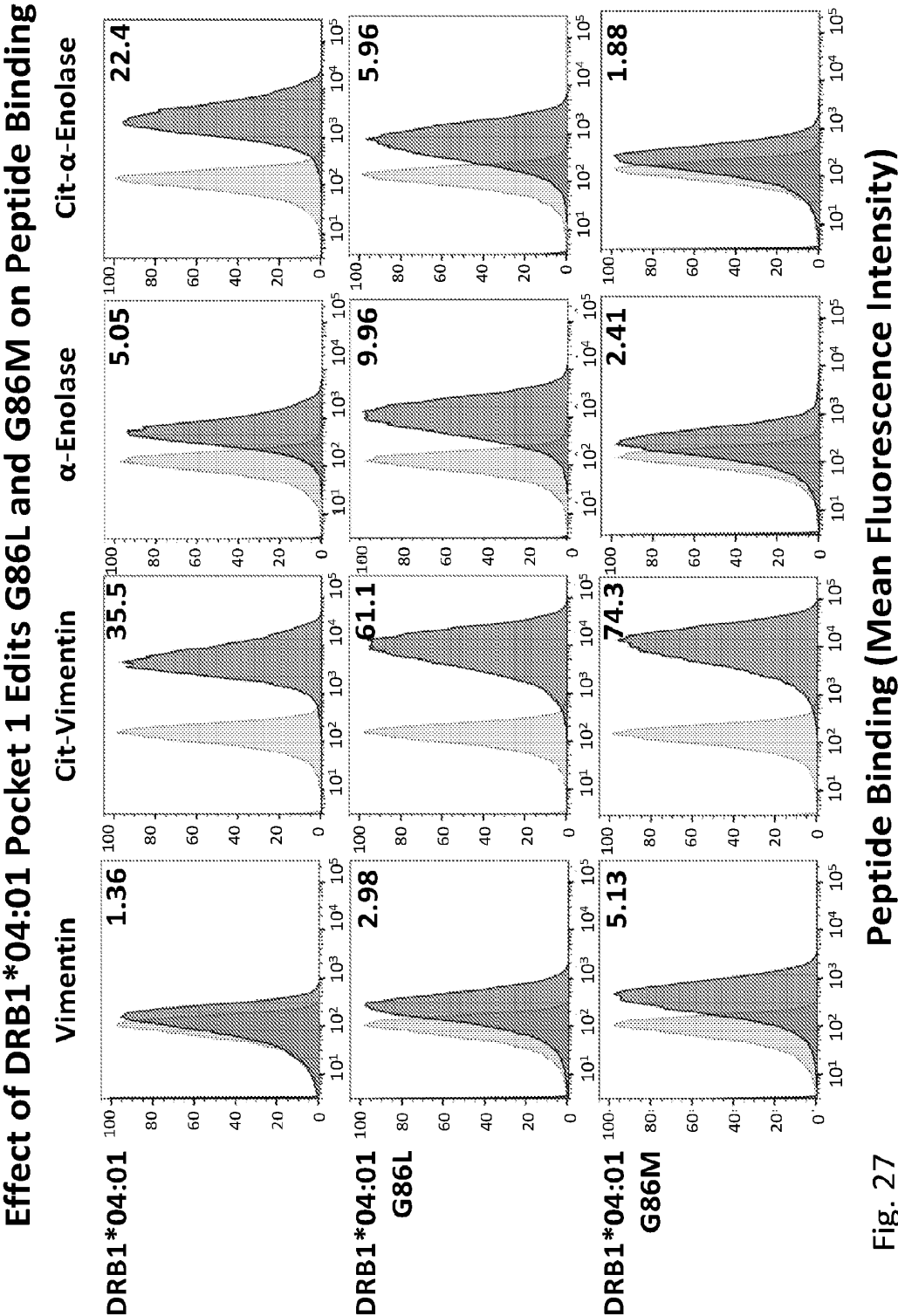


Fig. 27

30/45

Representative alleles, positions, mutations

<u>Allele</u>	<u>Specific positions/specific mutations</u>												
DRB1*01:01	L67I	Q70D	V85A	G86V	R71E								
DRB1*01:02													
DRB1*01:03													
DRB1*03:01	V86L	V86M											
DRB1*04:01	L67I	Q70D	K71E	G86V	K71R	L67F	A74L	G86M	G86L	A74E	G86F	L67I-Q70D	L67F-A74F
DRB1*04:02													
DRB1*04:03	R71E												
DRB1*04:04	R71E												
DRB1*04:05	R71E												
DRB1*04:08	R71E												
DRB1*07:01													
DRB1*09:01													
DRB1*10:01													
DRB1*11:01													
DRB1*11:02													
DRB1*11:03													
DRB1*12:01													
DRB1*13:01	V86L	V86M											
DRB1*14:01													
DRB1*15:01	F47Y	A71R	A71R-V86G	{DRB1*15:122}									
DRB1*15:02													
DRB1*16:01													
DRB3*01:01													
DRB3*02:02													
DRB3*03:01													
DRB4*01:03													
DRB5*01:01													
<u>Alleles</u>	<u>DQA1</u>	<u>DQB1</u>	<u>Specific positions/specific mutations</u>										
DQ5	DQA1*01:01	DQB1*05:01											
DQ6	DQA1*01:02	DQB1*06:02											
DQ2	DQA1*05:01	DQB1*02:01	A57D	K71E	K71T								
DQ2 Trans	DQA1*03:01	DQB1*02:01	A57D										
DQ8	DQA1*03:01	DQB1*03:02	A57D										
DQ8 trans	DQA1*05:01	DQB1*03:02	A57D										
	DQA1*05:05	DQB1*03:01											
	DQA1*03:01	DQB1*03:01											
<u>Alleles</u>	<u>Specific positions/specific mutations</u>												
B27:03													
B27:05	V59H	{E D116H	{B*27:09}										
B27:09													

Fig.28

31/45

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
1	A*02:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DGETRNVKHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSQWFLRGYHQYAYDG KDYIALKEDLRSWTAADMAAQTTKHKWLAHVAEQLRAYLESTCVENLRRYLENGKETLQ RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTLVEITRPAGDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVLFGLAVITG AVVAAVMWRKSSDRKGGSSYSQAASSDSAQGSQVSLTACKV
2	A*03:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DGETRNVKHSQTHRVDLGTLRGYYNQSEAGSHTIQTMYGCDVGSQWFLRGYHQYAYDG KDYIALNEDLRSWTAADMAAQITKRWLAARAEQLRAYLESTCVENLRRYLENGKETLQ RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVLLGLAVITG AVVAAVMWRKSSDRKGGSSYSQAASSDSAQGSQVSLTACKV
3	A*29:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DLQTRNVKHSQTHRVDLGTLRGYYNQSEAGSHTIQTMYGCHVGSQWFLRGYHQYAYDG KDYIALNEDLRSWTAADMAAQITQKRWLAARAEQLRAYLESTCVENLRRYLENGKETLQ RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTLVEITRPAGDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVLFGLAVFAG AVVAAVMWRKSSDRKGGSSYSQAASSDSAQGSQVSLTACKV
4	B*07:02:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASPREPAPWIEQEGPEYW DRNTQIKKAAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCQVGPGRILLRGHGDQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARAEQRRAYLEGECEVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGDRT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQSTVPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA
5	E*08:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASPREPAPWIEQEGPEYW DRNTQIKKAAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCQVGPGRILLRGHGDQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARAEQDRAYLEGECEVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGDRT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQSTVPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA
6	B*27:09:02:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASPREPAPWIEQEGPEYW DRETQICKAKAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCQVGPGRILLRGYHQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARAEQLRAYLEGECEVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGDRT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQSTVPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA
7	B*27:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASPREPAPWIEQEGPEYW DRETQICKAKAQTYRNLRTALRYNQSEAGSHTLQSMYGCQVGPGRILLRGYHQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARAEQLRAYLEGECEVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGDRT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQSTVPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA

Fig. 29

SUBSTITUTE SHEET (RULE 26)

32/45

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
8	B*27:03	GSRSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRREEPRAPWIEQEGPEYHW DRETQICAKAKQIDREDLRITLLAYYNQSEAGSHLQNMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQRLRAYLEGECEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
9	B*27:05:02:01	GSRSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRREEPRAPWIEQEGPEYHW DRETQICAKAKQIDREDLRITLLAYYNQSEAGSHLQNMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQRLRAYLEGECEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
10	B*27:09	GSRSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRREEPRAPWIEQEGPEYHW DRETQICAKAKQIDREDLRITLLAYYNQSEAGSHLQNMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQRLRAYLEGECEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
11	B*51:01:01:01	GSRSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRTEPRAPWIEQEGPEYHW DRNTQIFWNTNTQTYRENLRALAYYNQSEAGSHWQTMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQRLRAYLEGCEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVATVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
12	B*54:01:01:01	GSRSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRGEPRAPWIEQEGPEYHW DRNTQIYKAQAQITRESLRNLRGYYNQSEAGSHWQTMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQRLRAYLEGCEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVATVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
13	B*57:01:01:01	GSRSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRMAPRAPWIEQEGPEYHW DGETANMKASQTYRENLRALAYYNQSEAGSHIIQVMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQRLRAYLEGCEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
14	C*06:02:01:01	CSHSRYFTHTSVSRPGRGEPFRFIVGVVDITLFVRFDSDAASPRGEPRAPWIEQEGPEYHW DRETQIKYKQAQADRVNLRNLRGYYNQSEAGSHLQNMVGCDFGPDGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQRLRAYLEGCEVWLRRLYLENGKETLQ RAEHPKTHVTHHPISDHEATLRCAWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPEPLTLRWEPSSQSTVPIVGIVAGLAVLAVLAVL GAVMAVVMCRKSSGGKGGSCSAACSDSAQGS DESLIACKR

Fig. 29 continued

33/45

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
15	C*18:01:01:01	CSRSRMRYFDITAVSRPGRSEPRFISVGYVDDTQFVRFSDASERGEPRAPVWEQESPEYWDRETQNYKRAQADRVNLRKLRGYYNQSEDSHTLQRMFGCDLSPDGLLLRGYNQFAYDGRDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQRPAYLEGTCVWEWLRRLVLENGKETLQRAERPKTHVTHHEVSDHEATLRCAWALGFYFAEITLTWQWDGEDQGTQDTLQVETREAGDGTFOKNAAVVVVSSEGEQRYTCHVQHEGLPEPLTLRNKPSQPIIPIVGVIVAGLAVLVVLAVLGAVVAVVMCRKSSGGWGGSCSQAAASNSAQQSDLSLACKA
16	DPA1*02:01:01:01	IKADHVSTYAAFVQTHRPTGEFMEFDEDSQFFVVDLQKKEIVWHLEEFGRAPSFZTAQGGALANIALNNMLNTLIQRSNHTQAANDPPEVTVFPREPVELGQPNILICIDRFTPPVNLNVTWLCNGEPVTEGVAESLFLPRTBYSFHKPHYLTFPVPSAEDVDCEVHEHWGLDQPLLNHWEAQEPIQMPETTETVLCALGLVLGLVGIIVGTVLIIKSLRSGHDPRAQGGPL
17	DEB1*13:01:01:01	RATPENYVQLRQCEYAFNGTQRFLERYIVNREEYARFDSVGEFRAVTELCRPAEAYWN SQNDILEEERAVFDRICRHHYELDEAVTLQRVQPKVNVVSPSHNGPLQHHNLLVCHVTDF YPGSIQVRNFWLNGQEETAGVVTNLIIRNGDWTFOILVMLEMTPOQGSVYICQVEHTSLDS PVTVEWKAQSDSARSKTITGAGGFVLGLITCGVGIFMHRRSKRVQRGSA
18	DQA1*01:01:01:01	EDIVADHVASCGVNLVQFYGPSGQYTHEFDGDEEFYVDLERKETAWRWFEPSKFGGFDPO GALRNMAVAKHNINIMIKRYNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGQSVTEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHWGLDQPLLNHWEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIGGLRSVGASRRHQGGL
19	DQA1*01:02:01:01	EDIVADHVASCGVNLVQFYGPSGQYTHEFDGDEEFYVDLERKETAWRWFEPSKFGGFDPO GALRNMAVAKHNINIMIKRYNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGQSVTEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHWGLDQPLLNHWEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIGGLRSVGASRRHQGGL
20	DQA1*02:01:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWKLFLFRLREDPOF ALTNI AVLKHNINILIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHWGLDQPLLNHWEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
21	DQA1*03:01:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWQLPLFRFRFRFDPOFALTNI AVLKHNINIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHWGLDQPLLNHWEPEIPTPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
22	DQA1*05:01:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWCLFVLRLQFREDPOFALTNI AVLKHNINSLIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTLLPSADESYDCKVEHWGLDQPLLNHWEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
23	DQA1*05:05:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWCLFVLRLQFREDPOFALTNI AVLKHNINSLIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTLLPSADESYDCKVEHWGLDQPLLNHWEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
24	DQB1*02:01:01:01	RDSPEDFVYQFKGWCYFTNGTERVRLVSRSIYNREEIVRFDSDVGEFRAVTELLGLPAAEYWN SQNDILEKRAAVDRVCRHNYQLELRITTLQPRVEPTVILSPORTEALNNHNLVCSVTDFYPAQIKVNRWFRNDQEETAGVVTPLIRNGDWTFOILVMLEMTPOQGSVYTCHEHPSLQSPITVENPAQSESAQSKMLSGIGGFVLGLIFLGLGLIIHHRSSQWGLH

Fig. 29 continued

SUBSTITUTE SHEET (RULE 26)

34/45

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
25	DQB1*03:01:01:01	RDSPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTPLGPPDAEY WNSQKEVLERIRAEELDTVCRHNYQLELRITLQRRVEPTVTISPSRTIENLNHNLLVCSVT DFYPAQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QNPITVWRAQSESAQSKMLSGIGGFVLGLIFLGLGLIIRHRSQKGLLH
26	DQB1*03:02:01:01	RDSPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTPLGPPAAEY WNSQKEVLERIRAEELDTVCRHNYQLELRITLQRRVEPTVTISPSRTIENLNHNLLVCSVT DFYPAQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QNPITVWRAQSESAQSKMLSGIGGFVLGLIFLGLGLIIRHRSQKGLLH
27	DQB1*05:01:01:01	RDSPEDFVYQFKGLCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTPOGRFPAEY WNSQKEVLEGRASVDRVCRHNYEVAAGILQRRVEPTVTISPSRTIENLNHNLLVCSVT DFYPSQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QSPITVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH
28	DQB1*06:01:01:01	RDPPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEDVARFDSDEGVYRAVTPOGRPDAEY WNSQKDLERIRAEELDTVCRHNYEVAFRGILQRRVEPTVTISPSRTIENLNHNLLVCSVT DFYPSQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QSPITVWRAQSESAQSKMLSGIGGFVLGLIFLGLGLIIRQRSEKGLLH
29	DQB1*06:02:01:01	RDSPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTPOGRPDAEY WNSQKEVLEGRIRAEELDTVCRHNYEVAFRGILQRRVEPTVTISPSRTIENLNHNLLVCSVT DFYPSQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QSPITVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH
30	DRB1*01:01:01:01	GDTRPRFLWQLKTECHFFNGTERVRLLERCIYNQEESEVRFDSDEGVYRAVTPLGRPDAEY WNSQKDLLEQRRAAVDITYCRHNYGVGESFTVQRARVEPKVTIVYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKAGVVSTGLIQNGDWTFQILVMLEMTVPRSGEVYTCCQVEHPSV TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH
31	DRB1*01:02:01:01	GDTRPRFLWQLKTECHFFNGTERVRLLERCIYNQEESEVRFDSDEGVYRAVTPLGRPDAEY WNSQKDLLEQRRAAVDITYCRHNYGVGESFTVQRARVEPKVTIVYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKAGVVSTGLIQNGDWTFQILVMLEMTVPRSGEVYTCCQVEHPSV TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH
32	DRB1*01:03:01	GDTRPRFLWQLKTECHFFNGTERVRLLERCIYNQEESEVRFDSDEGVYRAVTPLGRPDAEY WNSQKDLLEQRRAAVDITYCRHNYGVGESFTVQRARVEPKVTIVYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKAGVVSTGLIQNGDWTFQILVMLEMTVPRSGEVYTCCQVEHPSV TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH
33	DRB1*03:01:01:01	GDTRPRFLEYSTSECHFFNGTERVRYLDRIYHNGEENVRFDSDVGEYRAVTPLGRPDAEY WNSQKDLLEQRRGRVDITYCRHNYGVGESFTVQRARVPEKVTIVYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKIGVVSTGLIRNGDWTFQILVMLEMTVPRSGEVYTCCQVEHPSL TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH
34	DRB1*04:01:01:01	GDTRPRFLEQVKKHECHFFNGTERVRLDRYFYHNGEYVRFDSDEGVYRAVTPLGRPDAEY WNSQKDLLEQRRAAVDITYCRHNYGVGESFTVQRARVPEKVTIVYPSKIQPLQHHNLLVCSVN GFYPSGIEVRNFRNGQEEKIGVVSTGLIQNGDWTFQILVMLEMTVPRSGEVYTCCQVEHPSL TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSEKGLLH

Fig. 29 continued

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
35	DRB1*04:02:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRYFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDILEERRAAVDITYCRHNYGVVESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYPGSIIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
36	DRB1*04:03:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRYFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVVESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYPGSIIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
37	DRB1*04:04:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRYFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVVESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYPGSIIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
38	DRB1*04:05:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRYFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVGESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYPGSIIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
39	DRB1*04:06:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRYFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVGESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYPGSIIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
40	DRB1*07:01:01:01	GDTRPRFLWQKYNCHFFNGSTERVQFLERLFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDILEERRAQVDITYCRHNYGVGESFTVQRRVHPEVTIVYPANTQPLQHHNLLVCSVS GFYPGSIIEVRWFRNGQEEKAGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSV MSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
41	DRB1*08:01:01	GDTRPRFLEYSTGEYFFNGSTERVRFLEDRYFYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQKDFLEERRALVDITYCRHNYGVGESFTVQRRVHPEVTIVYPANTQPLQHHNLLVCSVS GFYPGSIIEVRWFRNGQEEKTVGVSTGLIHNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSV TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
42	DRB1*09:01:02:01	GDTRPRFLKQDKECHFFNGSTERVRYLHRIYHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQKDFLEERRAEVDITYCRHNYGVGESFTVQRRVHPEVTIVYPANTQPLQHHNLLVCSVS GFYPGSIIEVRWFRNGQEEKAGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSV MSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
43	DRB1*10:01:01:01	GDTRPRFLEEVNFECHFFNGSTERVRLERRVHNQEEYARYDSDVGEYRAVTELGREDAEY WNSQKDLLEERRAAVDITYCRHNYGVGESFTVQRRVQPKVTIVYPANTQPLQHHNLLVCSVN GFYPGSIIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCCQVEHPSV MSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS

Fig. 29 continued

36/45

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
44	DRB1*11:01:01:01	GDTRPRFLEYSTSECHFFNGSTERVRFLEDRYFYNQEEYVRFDSVVGGEFRAVTELGPRDEEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
45	DRB1*11:02:01:01	GDTRPRFLEYSTSECHFFNGSTERVRFLEDRYFYNQEEYVRFDSVVGGEFRAVTELGPRDEEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
46	DRB1*11:03:01	GDTRPRFLEYSTSECHFFNGSTERVRFLEDRYFYNQEEYVRFDSVVGGEFRAVTELGPRDEEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
47	DRB1*11:04:01:01	GDTRPRFLEYSTSECHFFNGSTERVRFLEDRYFYNQEEYVRFDSVVGGEFRAVTELGPRDEEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
48	DRB1*12:01:01:01	GDTRPRFLEYSTSECHFFNGSTERVRLLEHNFHNGEELLREDSVVGGEFRAVTELGPRDAES WNSQKDFLEDERAAVDITYCRHNYGAVESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
49	DRB1*13:01:01:01	GDTRPRFLEYSTSECHFFNGSTERVRFLEDRYFYHNGEENVREDSVVGGEFRAVTELGPRDAEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
50	DRB1*14:01:01	GDTRPRFLEYSTSECHFFNGSTERVRFLEDRYFYHNGEESVRFDSVVGGEYRAVTELGPRAAEH WNSQKDLLEERRAEVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKTGVSSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPRGFLS
51	DRB1*15:01:01:01	GDTRPRFLWQPKRECHFFNGSTERVRFLEDRYFYNQEEYVRFDSVVGGEFRAVTELGPRDAEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKAGMVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPTGFLS
52	DRB1*15:02:02:01	GDTRPRFLWQPKRECHFFNGSTERVRFLEDRYFYNQEEYVRFDSVVGGEFRAVTELGPRDAEY WNSQKDFLEDERAAVDITYCRHNYGVGESFTVQRRVHPKVTIVYPSKTQPLQHHNLLVCSVS GFYPGSIIEVRWFNNGQEEKAGMVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHP3V TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFTIYFRNQKHSGQLQPTGFLS

Fig. 29 continued

37/45

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
53	DRB1*16:01:01:01	GDTRPRFLWQPKRECHFFNGTERVRFLDRYFYNGQESVRFDSWGEYRAVTELGRPDAEY WNSQKDFLEDRAAAYDTYCRHNYGVGESFTVQRRVQPKVTVYPSKTPQLQHHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVWLETVPRSGEVYTCQVEHPSPV TSPLTVEWRARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGSLQPTGFLS
54	DRB3*01:01:02:01	GDTRPRFLELRKSECHFFNGTERVRFLDRYFHNQEEFLRFDSWGEYRAVTELGRPVAES WNSQKDLLEQKRGRVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTPQLQHHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVWLETVPRSGEVYTCQVEHPSPV TSALTVEWRARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGSLQPTGFLS
55	DRB3*02:02:01:01	GDTRPRFLELLKSECHFFNGTERVRFLERHFNQEEYARFDSWGEYRAVRELGRPDAEY WNSQKDLLEQNRGQVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTPQLQHHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVWLETVPRSGEVYTCQVEHPSPV TSPLTVEWSARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGSLQPTGFLS
56	DRB3*03:01:01:01	GDTRPRFLELLKSECHFFNGTERVRFLERYFHNQEEFVRFDSWGEYRAVTELGRPVAES WNSQKDLLEQNRGQVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTPQLQHHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIHNGDWTFQTLVWLETVPRSGEVYTCQVEHPSPV TSPLTVEWRARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGSLQPTGFLS
57	DRB4*01:03:01:01	GDTQPRFLEQAKCECHFFNGTERVWNLIRVIYNGQEEVARYNSDLGEYQAVTELGRPDAEY WNSQKDLLEERRAEVDITYCRINYGVGESFTVQRRVQPKVTVYPSKTPQLQHHNLLVCSVN GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVWLETVPRSGEVYTCQVEHPSM NSPLTVQWSARSESQAQSKMLSGVGGFVLGLLFLGTGLFIYFRNQKHSGSLQPTGLLS
58	DRB5*01:01:01:01	GDTRPRFLQDQKYECHFFNGTERVRFLHRDIYNGQEEQLRFDSWGEYRAVTELGRPDAEY WNSQKDFLEDRAAAYDTYCRHNYGVGESFTVQRRVEPKVTVYPAKTPQLQHHNLLVCSVN GFYPGSIIEVRNFFNSQZEKAGVSTGLIQNGDWTFQTLVWLETVPRSGEVYTCQVEHPSV TSPLTVEWRAQSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGSLHPTGLVS

Fig. 29 continued

[illegible]

Fig. 30

DQA1* 05.05	GATCAGATCTACCACCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACACCGTGATGAGCCCTGTGGAGGTGAAGAC ATTGTGGCTGACACCGTCGCTCTTATGCTGTAAACTTGTACCACTCTTACGCTCCCTCTGGCCAGTACACCCATGAATTTGATGGAGATGAG CAGTTCTACGTGACCTGGGGAGGAAGGAGACTGTCTGTGTTTCCCTGTCTCAGACAAATTAGATTGACCCGCAATTTGCACTGACAAA CATGCTGTCTCTAAACATAACTTGAACAGTGTGATTAAGGCTCCAACTCTACCGCTGCTACCAATGAGGTTCTGAGGTCCACAGTGTCTTTCC AAGTCTCCCGTGACACTGGGTGAGGCCAACATCTCATCTGTCTGTGTGGACAAACATCTTCTCCTGTGGTCAACATCAGATGCTGAGCAAT GGGCACTCAGTACAGAAAGGTGTTTCTGAGACCGCTTCTCTCCAAAGTGTATCTCTCTTCAAGATCAGTTACCTCAACCTCTCTCTCT CTGTGTAGGAGAGTTATGACTGCAAGGTGGAGCACTGGGGACTGGACAAGCCTCTCTGAAACACTGGGGAGCCGTGAGATTCCAGCCCTA TGTACAGAGCTCACAGAGAGTGTGTGTGCGCCCTGGGGTGTGTGTGGGCTCTGTGGCAATGTGTGGGCACTGTCTTCTATCATCCGAG GCCGTGCTTCAGTTGTGTCTCCAGACACCAAGGGCCCTGTGTACTGGAGATC	63
DQA1*0 5.05	GATCAGATCTACCACCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACACCGTGATGAGCCCTGTGGAGGTGAAGAC ATTGTGGCTGACACCGTCGCTCTTATGCTGTAAACTTGTACCACTCTTACGCTCCCTCTGGCCAGTACACCCATGAATTTGATGGAGATGAG CAGTTCTACGTGACCTGGGGAGGAAGGAGACTGTCTGTGTTTCCCTGTCTCAGACAAATTAGATTGACCCGCAATTTGCACTGACAAA CATGCTGTCTCTAAACATAACTTGAACAGTGTGATTAAGGCTCCAACTCTACCGCTGCTACCAATGAGGTTCTGAGGTCCACAGTGTCTTTCC AAGTCTCCCGTGACACTGGGTGAGGCCAACATCTCATCTGTCTGTGTGGACAAACATCTTCTCCTGTGGTCAACATCAGATGCTGAGCAAT GGGCACTCAGTACAGAAAGGTGTTTCTGAGACCGCTTCTCTCCAAAGTGTATCTCTCTTCAAGATCAGTTACCTCAACCTCTCTCTCT CTGTGTAGGAGAGTTATGACTGCAAGGTGGAGCACTGGGGACTGGACAAGCCTCTCTGAAACACTGGGGAGCCGTGAGATTCCAGCCCTA TGTACAGAGCTCACAGAGAGTGTGTGTGCGCCCTGGGGTGTGTGTGGGCTCTGTGGCAATGTGTGGGCACTGTCTTCTATCATCCGAG GCCGTGCTTCAGTTGTGTCTCCAGACACCAAGGGCCCTGTGTACTGGAGATC	64
DQB1*0 2.01 K71E	GATCAGATCTACCACCATGATCTTGGAAAAAGGCTTGTGGATCCCGGAGGGCTTGGGGCAGCAACTGTGACCTTGTGATGCTGTGGATGCTG AGCACCCAGTGGCTGAGGGCAGAGACTCTCCGAGGATTTCTGTACCACTTAAAGGCCATGTGCTACTTCCACACCGGAGAGAGGCG GTGCTGTCTGTGAGCAGAGCATCTATAACCGAGAGAGATGTGCGCTTCCAGACGAGCGTGGGGGAGTTCCGGGGCGGTGAGCGCTGCT GGGGCTGCTGCTGCGCGAGTACTGTGAGCAGCCAGGAAGGACATCTGTGAGAGGGGAACGGGCGCGGTGGGACAGGGTGTGAGAGACAA ACTACAGTTTGGAGCTCCGACAGACTTGTGAGCGGGAGTGGAGGCCAGATGACCATCTCCCATCCAGGACAGAGGGCCCTCAACCA ACAACCTGTGTGTGCTGCTGAGACAGATTTCTATCCAGCCAGATCAAAAGTCCGGTGGTTTGGGAATGACCGAGAGAGACAGCTGCG TTGTGCTCCACCCCTTATTAGGAATGGTGTGACTGGACCTTCCAGATCTGTGTATGTGCTGGAATGACTCCCGAGCGTGGAGACGTCTACAC TGCACAGTGGAGCACCCAGCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAATCTGCCAGAGCAAGATGCTGAGTGG CAATTGGAGGCTTGTGTGTGGCTGTATCTCTCTGGGCTTGTATCATCATCAGAGAGTCCAGAAAGGGCTCTGTGCTGACTGACTGAG GATC	65
DQB1*0 2.01 K71T	GATCAGATCTACCACCATGATCTTGGAAAAAGGCTTGTGGATCCCGGAGGGCTTGGGGCAGCAACTGTGACCTTGTGATGCTGTGGATGCTG AGCACCCAGTGGCTGAGGGCAGAGACTCTCCGAGGATTTCTGTACCACTTAAAGGCCATGTGCTACTTCCACACCGGAGAGAGGCG GTGCTGTCTGTGAGCAGAGCATCTATAACCGAGAGAGATGTGCGCTTCCAGACGAGCGTGGGGGAGTTCCGGGGCGGTGAGCGCTGCT GGGGCTGCTGCTGCGCGAGTACTGTGAGCAGCCAGGAAGGACATCTGTGAGAGGGAGACAGGGCGGGGTGGACAGGGTGTGAGACACAA CTACAGTTTGGAGCTCCGACAGACTTGTGAGCGGGAGTGGAGGCCACAGTACCATCTCCCATCCAGAGAGGGCCCTCAACCA CAACCTGTGCTGCTGCTGCTGAGTACAGATTTCTATCCAGCCAGATCAAAAGTCCGGTGGTTTCTGGAATGACCAAGGAGAGACAGCTGCGGT GTGTGCGACCCCTTATTAGGAATGTGTGACTGTGACCTTCCAGATCTGTGTGTGTGGAATGACTCCCGAGCGTGGAGAGCTTACACCT GCCAGCTGGAGCACCCAGCCCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAAATCTGCCAGAGCAAGATGCTGAGTGGC ATTGGAGGCTGTGTGCTGGGCTGATCTTCTGCGGCTGGGCTTATCATCATCAGAGAGTCCAGAAAGGGCTCTGCTGACTGACTGAG GATC	66
DQB1*0 301	GATCAGATCTACCACCATGATCTTGGAAAAAGGCTTGTGGATCCCGGAGGGCTTGGGGCAGCAACTGTGACCTTGTGATGCTGTGGATGCTG AGCACCCAGTGGCTGAGGGCAGAGACTCTCCGAGGATTTCTGTACCACTTAAAGGCCATGTGCTACTTCCACACCGGAGAGAGGCG GTGCTGTATGTGAGCAGATACATCTATAACCGAGAGAGATGTGCGCTTCCAGACGAGCGTGGGGGAGTTCCGGGGCGGTGAGCGCTGCT GGGGCTGCTGCTGCGCGAGTACTGTGAGCAGCCAGGAAGGACATCTGTGAGAGGGAGCCGGCGGGAGTTGGACAGGGTGTGAGACACAA CTACAGTTTGGAGCTCCGACAGACTTGTGAGCGGGAGTGGAGGCCACAGTACCATCTCCCATCCAGAGAGGGCCCTCAACCA CAACCTGTGCTGCTGCTGCTGAGTACAGATTTCTATCCAGCCAGATCAAAAGTCCGGTGGTTTCTGGAATGACCAAGGAGAGACAGCTGCGGT GTGTGCGACCCCTTATTAGGAATGTGTGACTGTGACCTTCCAGATCTGTGTGTGTGGAATGACTCCCGAGCGTGGAGAGCTTACACCT GCCAGCTGGAGCACCCAGCCCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAAATCTGCCAGAGCAAGATGCTGAGTGGC GCCAGCTGGAGCACCCAGCCCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAAATCTGCCAGAGCAAGATGCTGAGTGGC ATTGGAGGCTGTGTGCTGGGCTGATCTTCTGCGGCTGGGCTTATCATCATCAGAGAGTCCAGAAAGGGCTCTGCTGACTGACTGAG GATC	67

Fig. 30 continued

DQB1*0302A57D	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCACCDCCGTGCTGAGSGCCASAGACTCTCCGAGGATTTCGTGTACCAAGTTTAAGGGCATGTGCTACTTCAACCAACGGGACGGGAGCGCGTGTGGCTCTGTGTAGCAGATACATCTATAACDGGAGAGGAGTAACGCAAGCTTGGACAGGACGTTGGGGGTGTATGGGGCGGTGACGCGGCCTGGGGCGGCGCTGACGCGAGTACTGGAACAGCCAG AAGG AAGTCTCTGGAGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACTTTGCAGGCGGCGAGTGGAGGCCACAGTGACCATCTCCCAATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGCTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGACCCAGAGGAGACAACTGSGCTTGTGTCCACCCCGCTTATTAGGAACGGGTGACTGGACCTTCAGATCCCTGGTGTATGCTGGAAATGACTCCCAAGCGTGGAGACGTCACACCTGCCACGSGAGGACCCAGCGCTCCAGAACCCCATGCTGSGAGTGGCGGGCTCAGTGTGAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGGTGTGGGGCTGATCTCCCTGGGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTCTGCACTGACTCGAGGATGGCTGGCTGCACTGACTCGAGGATC	68
DQB1*0357	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCACCDCCGTGCTGAGSGCCAGAGACTCTCCGAGGATTTCGTGTACCAAGTTTAAGGGCATGTGCTACTTCAACCAACGGGACGGGAGCGCGTGTGGCTCTGTGTAGCAGATACATCTATAACDGGAGAGGAGTAACGCAAGCTTGGACAGGACGTTGGGGGTGTATGGGGCGGTGACGCGGCCTGGGGCGGCGCTGACGCGAGTACTGGAACAGCCAG AAGG AAGTCTCTGGAGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACTTTGCAGGCGGCGAGTGGAGGCCACAGTGACCATCTCCCAATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGCTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGACCCAGAGGAGACAACTGSGCTTGTGTCCACCCCGCTTATTAGGAACGGGTGACTGGACCTTCAGATCCCTGGTGTATGCTGGAAATGACTCCCAAGCGTGGAGACGTCACACCTGCCACGSGAGGACCCAGCGCTCCAGAACCCCATGCTGSGAGTGGCGGGCTCAGTGTGAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGGTGTGGGGCTGATCTCCCTGGGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTCTGCACTGACTCGAGGATC	69
DQB1*0604	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCCTCCTACTGCTGAGGGGACAGAGACTCTCCGAGGATTTCGTGTACCAAGTTTAAGGGCATGTGCTACTTCAACCAACGGGACGGGAGCGCGCTGTGGCTCTGTGTAGCAGATACATCTATAACDGGAGAGGAGTAACGCAAGCTTGGACAGGACGTTGGGGGTGTATGGGGCGGTGACGCGGCCTGGGGCGGCGCTTGGCGAGTACTGGAACAGCCAG AAGG AAGTCTCTGGAGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACTTTGCAGGCGGCGAGTGGAGGCCACAGTGACCATCTCCCAATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGCTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGATCCAGAGGAGACAGCCGCGCTGTGTGTCCACCCCGCTTATTAGGAATGGTGTACTGGACCTTCAGATCCCTGGTGTATGCTGGAAATGACTCCCAAGCGTGGAGATGTCACACCTTGGCAGGSGAGGACCCAGCGCTCCAGAACCCCATCAGCTGGAGTGGCGGGCTCAGTGTGAATGTGCCAGAGCAAGATGCTGAGTGGCGCTTTGGAGGCTTCTGTGCTGGGCTGATCTCCCTGGGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTCTGCACTGACTCGAGGATC	70
DRB1*0301V86L	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCCTCCTACTGCTGAGGGGACACAGACCAAGCTTTCGTGGAGTACTCTAGCTGTGTCATTTCTCAATGGGACGGAGCGGGTGGGGTACCCTGGACAGATACTTCCATAACAGGAGGAGAGAGTGCGCTTGGACAGCGAGCTGGGGGAGTTCCGGGGCGGTGACGGAGCTGGGGGCGGCTGTGATGCGCGAGTACTGGAACAGCCAG AAGG AAGTCTCTGGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACTTTGCAGGCGGCGAGTGGAGGCCACAGTGACCATCTCCCAATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGATGCTGTCTATCCAGGCGAGCATGGAAGTCAGGCTGGTTCCGGAATGGCCAGG AAGAG AAGACTGGGGTGTGTCCACA GGCTGTATCCACAATGGAGACTGSACTTCCAGACCCCTGGTGTATGCTGGAGAGTTTACACCTGCGCAAGTGGAGCACCAGCGGTGACAAAGCGGTGACAAAGCGCTCTCACAGTGG AATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGGGCTTTGTGCTGGGCTCTCTCTCTGGGGCGGGCTGTCTATCTACTTGAAG AATCAGAAAGGACACTCTGACTTCAACCAAGAGGATTCCTGAGCTGACTCGAGGATC	71
DRB1*0301V86M	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCCTCCTACTGCTGAGGGGACACAGACCAAGCTTTCGTGGAGTACTCTAGCTGTGTCATTTCTCAATGGGACGGAGCGGGTGGGGTACCCTGGACAGATACTTCCATAACAGGAGGAGAGAGTGCGCTTGGACAGCGAGCTGGGGGAGTTCCGGGGCGGTGACGGAGCTGGGGGCGGCTGTGATGCGCGAGTACTGGAACAGCCAG AAGG AAGTCTCTGGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACTTTGCAGGCGGCGAGTGGAGGCCACAGTGACCATCTCCCAATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGATGCTGTCTATCCAGGCGAGCATGGAAGTCAGGCTGGTTCCGGAATGGCCAGG AAGAG AAGACTGGGGTGTGTCCACA GGCTGTCTGTGAGTGGTTTCTATCCAGGCGAGCATGGAAGTCAGGCTGGTTCCGGAATGGCCAGG AAGAG AAGACTGGGGTGTGTCCACA GGCTGTGATCCACAATGGAGACTGGACCTTCAGACCCCTGGTGTATGCTGGAGAGTTTACACCTGCGCAAGTGGAGTGGGGGCTTTGTGCTGGGCTCTCTCTCTGGGGCGGGCTGTCTATCTACTTGAAG AATCAGAAAGGACACTCTGACTTCAACCAAGAGGATTCCTGAGCTGACTCGAGGATC	72

Fig. 30 continued

DRS1*Q 4.01 G86F	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCGAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TTTTSAGAGCTTCACAGTG CAGCGGGGAGTCTATCCTGAGGTGACTG TGATCTCTGCAAGAGACCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGGTTCCGGAACGGCCAGGAAGAGAACTGGGGTGGTGTCCACA GGCTGTATCCAGAAAGGAGACTGGACCTTCAGAGCCCTGCTGATGCTGGAAACAGTTCTCGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGACGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGAACTCTGCACAGAGCAAGATGCTGAGTGAGTGGGG GCTTCGTGCTGGGCTGCTCTCTCTGGGGGGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	73
DRS1*Q 4.01 G86L	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCGAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TCTTGAAGAGTTCAAGTGCGAGGCGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGGTTCCGGAACGGCCAGGAAGAGAACTGGGGTGGTGTCCACA GGCTGTATCCAGAAAGGAGACTGGACCTTCAGAGCCCTGCTGATGCTGGAAACAGTTCTCGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGACGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGAACTCTGCACAGAGCAAGATGCTGAGTGAGTGGGG GCTTCGTGCTGGGCTGCTCTCTCTGGGGGGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	74
DRS1*Q 4.01 G86M	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCGAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TATGAGAGAGCTTCACAGTGACGGGGGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGGTTCCGGAACGGCCAGGAAGAGAACTGGGGTGGTGTCCACA GGCTGTATCCAGAAAGGAGACTGGACCTTCAGAGCCCTGCTGATGCTGGAAACAGTTCTCGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGACGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGAACTCTGCACAGAGCAAGATGCTGAGTGAGTGGGG GCTTCGTGCTGGGCTGCTCTCTCTGGGGGGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	75
DRS1*Q 4.03 R71E	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCGAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TGTGAGAGAGCTTCACAGTGACGGGGGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGGTTCCGGAACGGCCAGGAAGAGAACTGGGGTGGTGTCCACA GGCTGTATCCAGAAAGGAGACTGGACCTTCAGAGCCCTGCTGATGCTGGAAACAGTTCTCGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGACGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGAACTCTGCACAGAGCAAGATGCTGAGTGAGTGGGG GCTTCGTGCTGGGCTGCTCTCTCTGGGGGGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	76
DRS1*Q 4.04 R71E	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCGAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TGTGAGAGAGCTTCACAGTGACGGGGGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGGTTCCGGAACGGCCAGGAAGAGAACTGGGGTGGTGTCCACA GGCTGTATCCAGAAAGGAGACTGGACCTTCAGAGCCCTGCTGATGCTGGAAACAGTTCTCGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGACGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGAACTCTGCACAGAGCAAGATGCTGAGTGAGTGGGG GCTTCGTGCTGGGCTGCTCTCTCTGGGGGGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	77

Fig. 30 continued

DRB1*0 4.05 R71E	GATCAGATCTACCAACATGGTGTGCTGAAGTTCCCTGAGGCTCCTGATGCGCAGCTCTGACAGTGACACTGATGGTGTGAGCTGCCA CTGGCTTTGGCTGGGGACACCCGACCAAGTTTCTTGGAGCAGGTTAAACATGAGTGTCAATTTCTCAACGGGACGGAGCGGGTGGGTTT CTGGACAGATACCTTATCAACCAAGAGGAGTAGTGGCTTGGACAGCGACGTGGGGAGTACCGGGGGGTGACGGAGCTGGGGGGGG CTAGCGCGAGTACTGGAACAGCCAGAAAGSACCTCCTGGAAGCAGGAGCGGGCGGGTGGACACCTACTGACAGACAACTACGGGGT TGGTGAAGAGCTTACAGTGCAGCGGCGAGTCTATCCTGAGGTGACTGTGTATCTCTGCAAGSADCCAGCCCTGCGAGCACCACAACCTCTG GTCTGCTCTGTGAATGCTTCTATCCAGGCAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAGAAAGTCTGGGGTGGTGTGCCACA GGCCTGATCCAGAAATGGAGACTGGACCTTCCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCCAAGCTGACGAGCCCTCTACAGTGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTGGTGTCTGGCCCTGCTCTCTTGGGGCGGGGCTGTTCATCTACTTACAGGAATCAGAAAGGACACTCTGSACTTCCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	78
DRB1*0 4.08 R71E	GATCAGATCTACCAACATGGTGTGCTGAAGTTCCCTGAGGCTCCTGATGCGCAGCTCTGACAGTGACACTGATGGTGTGAGCTGCCA CTGGCTTTGGCTGGGGACACCCGACCAAGTTTCTTGGAGCAGGTTAAACATGAGTGTCAATTTCTCAACGGGACGGAGCGGGTGGGTTT CTGGACAGATACCTTATCAACCAAGAGGAGTAGTGGCTTGGACAGCGAGTGGGGAGTACCGGGGGGTGACGGAGCTGGGGGGGG CTGATGCCAGTACTGGAACAGCCAGAAAGSACCTCCTGGAAGCAGGAGCGGGCGGGTGGACACCTACTGACAGACAACTACGGGGT TGGTGAAGAGCTTACAGTGCAGCGGCGAGTCTATCCTGAGGTGACTGTGTATCTCTGCAAGSADCCAGCCCTGCGAGCACCACAACCTCTG GTCTGCTCTGTGAATGCTTCTATCCAGGCAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAGAAAGTCTGGGGTGGTGTGCCACA GGCCTGATCCAGAAATGGAGACTGGACCTTCCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCCAAGCTGACGAGCCCTCTACAGTGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTGGTGTCTGGCCCTGCTCTCTTGGGGCGGGGCTGTTCATCTACTTACAGGAATCAGAAAGGACACTCTGSACTTCCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	79
DRB1*0 7.01	GATCAGATCTACCAACATGGTGTGCTGAAGTTCCCTGAGGCTCCTGATGCGCAGCTCTGACAGTGACACTGATGGTGTGAGCTGCCA CTGGCTTTGGCTGGGGACACCCGACCAAGTTTCTTGGAGCAGGTTAAACATGAGTGTCAATTTCTCAACGGGACGGAGCGGGTGGGTTT TGGAAAGACTTCTATACCAAGAGGAGTAGTGGCTTGGACAGCGAGTGGGGAGTACCGGGGGGTGACGGAGCTAGGGCGGGCT TGTGCGCGAGTCTGGAACAGCCAGAAAGACATCTCTGAGSAGCAGGCGGGGGCCAGGTGGACACCGTGTGCAGACAACTACGGGGT GGTGAAGACTTCTACAGTGCAGCGGCGAGTCTATCCTGAGGTGACTGTGTATCTCTGCAAGSADCCAGCCCTGCGAGCACCACAACCTCTG GTCTGCTCTGTGAATGCTTCTATCCAGGCAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAGAAAGTCTGGGGTGGTGTGCCACA AGGCCCTGATCCAGAAATGGAGACTGGACCTTCCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGT GGAGCACCCCAAGTGTGATGAGCCCTCTACAGTGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG GGCTTTGTCTGGCCCTGCTCTCTTGGGGCGGGGCTGTTCATCTACTTACAGGAATCAGAAAGGACACTCTGSACTTCCAGCCACAGGATT CTGAGCTGACTCGAGGATC	80
DRB1*0 9.01	GATCAGATCTACCAACATGGTGTGCTGAAGTTCCCTGAGGCTCCTGATGCGCAGCTCTGACAGTGACACTGATGGTGTGAGCTGCCA CTGGCTTTGGCTGGGGACACCCGACCAAGTTTCTTGGAGCAGGTTAAACATGAGTGTCAATTTCTCAACGGGACGGAGCGGGTGGGTTT TGCACAGAGGCTCTATACCAAGAGGAGAAAGTGGCTTGGACAGCGAGTGGGGAGTACCGGGGGGTGACGGAGCTGGGGGGGG CTGTGCGCGAGTCTGGAACAGCCAGAAAGGACTTCTGGAAGCGGAGGGGGCCAGGTGGACACCGTGTGCAGACAACTACGGGGT TGGTGAAGAGCTTACAGTGCAGAGGCGAGTCTATCCTGAGGTGACTGTGTATCTCTGCAAGSADCCAGCCCTGCGAGCACCACAACCTCTG GTCTGCTCTGTGAATGCTTCTATCCAGGCAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAGAAAGTCTGGGGTGGTGTGCCACA AGGCCCTGATCCAGAAATGGAGACTGGACCTTCCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGT GGAGCACCCCAAGTGTGATGAGCCCTCTACAGTGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG GGCTTTGTCTGGCCCTGCTCTCTTGGGGCGGGGCTGTTCATCTACTTACAGGAATCAGAAAGGACACTCTGSACTTCCAGCCACAGGATT CTGAGCTGACTCGAGGATC	81
DRB1*1 0.01	GATCAGATCTACCAACATGGTGTGCTGAAGTTCCCTGAGGCTCCTGATGCGCAGCTCTGACAGTGACACTGATGGTGTGAGCTGCCA CTGGCTTTGGCTGGGGACACCCGACCAAGTTTCTTGGAGCAGGTTAAACATGAGTGTCAATTTCTCAACGGGACGGAGCGGGTGGGTTT CTGGAAAGAGCGGCTTATACCAAGAGGAGAAAGTGGCTTGGACAGCGAGTGGGGAGTACCGGGGGGTGACGGAGCTGGGGGGGG GGCTGATGGAGTACTGGAACAGCCAGAAAGSACCTCCTGGAAGCGGAGGGCGGGTGGGGTGGACACCTACTGACAGACAACTACGGGG GTTGGTGAAGAGCTTACAGTGCAGCGGCGAGTCTATCCTGAGGTGACTGTGTATCTCTGCAAGSADCCAGCCCTGCGAGCACCACAACCTCTG TGGTCTGTCTGTGAATGCTTCTATCCAGGCAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAGAAAGTCTGGGGTGGTGTGCCACA CGGGCCTGATCCAGAAATGGAGACTGGACCTTCCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGT TGGAGCACCCCAAGTGTGATGAGCCCTCTACAGTGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG GGCTTTGTCTGGCCCTGCTCTCTTGGGGCGGGGCTGTTCATCTACTTACAGGAATCAGAAAGGACACTCTGSACTTCCAGCCACAGGATT CTGAGCTGACTCGAGGATC	82

Fig. 30 continued

DRB1*1 1.01	GATCAGATCTACCAACATGGTGTGTCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTCTATAACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GGTGAGAGCTTTCACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGTAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCACTACTTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	83
DRB1*1 1.02	GATCAGATCTACCAACATGGTGTGTCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTCTATAACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GTGGAGAGCTTTCACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGTAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCACTACTTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	84
DRB1*1 1.03	GATCAGATCTACCAACATGGTGTGTCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTCTATAACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GTGGAGAGCTTTCACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGTAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCACTACTTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	85
DRB1*1 2.01	GATCAGATCTACCAACATGGTGTGTCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTCTATAACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG CTGTGCGCGGAGTCCGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGACACACAACCTACGGGGCT GTGGAGAGCTTTCACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGTAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCACTACTTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	86
DRB1*1 501 A71R	GATCAGATCTACCAACATGGTGTGTCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTCTATAACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG CTGACCGCTGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGT TGTGGAGAGCTTTCACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG GTCTGTCTGTGTAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCACTACTTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC CTGAGCTGACTGAGGATC	87

Fig. 30 continued

0 RB1 *1 5.01 F47Y	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTCTCAATGGAGCGGAGCGGGTGGCTTC CTGGACAGATCTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGGGCGCGCTGGACACCTACTGACAGACAACTACGGGG TTGCTGAGAGCTTACAGTGCAGCGGGAGTCCACCTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCAC AGGCTGATCCAGAAATGGAGACTGACCTTCACAGACCTGCTGATGCTGGAAACAGTTCTCTGAAGTGAGAGGTTTACACCTGCAAGT GGAGCACCCAGCGTGACAGCCCTCTCAGAGTGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGGAGTCGGG GGCTTTGCTGCTGGGGCTGCTCTCTGCTGGGGGGCTGCTTCTACTTCAAGGAATGAGGAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	88
0 RB1 *1 501 V86L	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTCTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TCTGAGAGAGCTTACAGTGCAGCGGGAGTCCACCTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GGCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGGAGTCGGG GGCTTTGCTGCTGGGGCTGCTCTCTGCTGGGGGGCTGCTTCTACTTCAAGGAATGAGGAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	89
0 RB1 *1 501 V86M	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTCTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TATGAGAGAGCTTACAGTGCAGCGGGAGTCCACCTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GGCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGGAGTCGGG GGCTTTGCTGCTGGGGCTGCTCTCTGCTGGGGGGCTGCTTCTACTTCAAGGAATGAGGAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	90
0 RB1 *1 5.02_85 G [Gly@ pos85]	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTCTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TGGTGAGAGAGCTTACAGTGCAGCGGGAGTCCACCTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GGCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGGAGTCGGG GGCTTTGCTGCTGGGGCTGCTCTCTGCTGGGGGGCTGCTTCTACTTCAAGGAATGAGGAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	91
0 RB1 *1 5.122_7 1R/86D {Arg@po s71/Gly @pos85 }	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTCTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TGGTGAGAGAGCTTACAGTGCAGCGGGAGTCCACCTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GGCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGGAGTCGGG GGCTTTGCTGCTGGGGCTGCTCTCTGCTGGGGGGCTGCTTCTACTTCAAGGAATGAGGAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	92

Fig. 30 continued

