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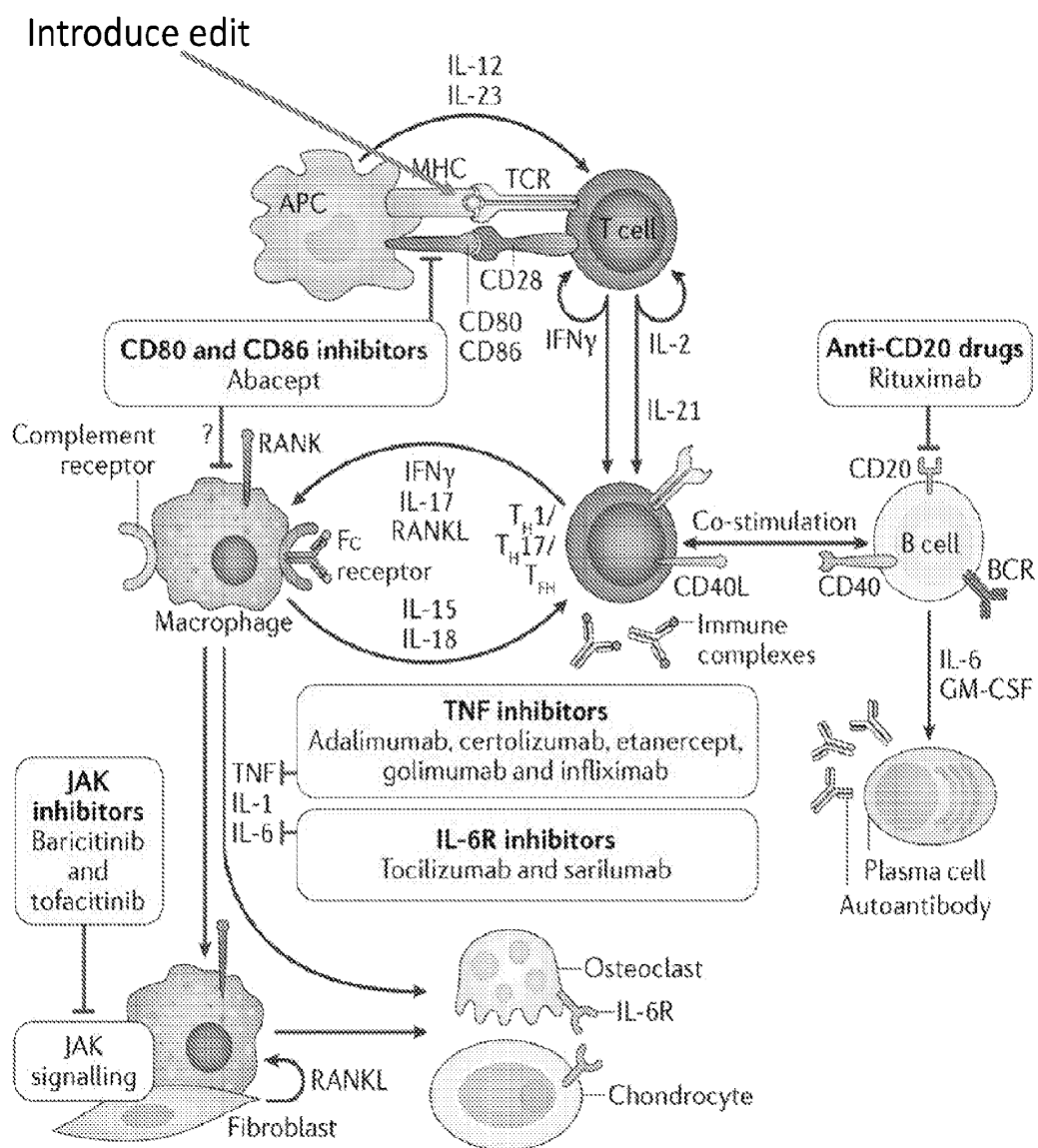


Fig. 1

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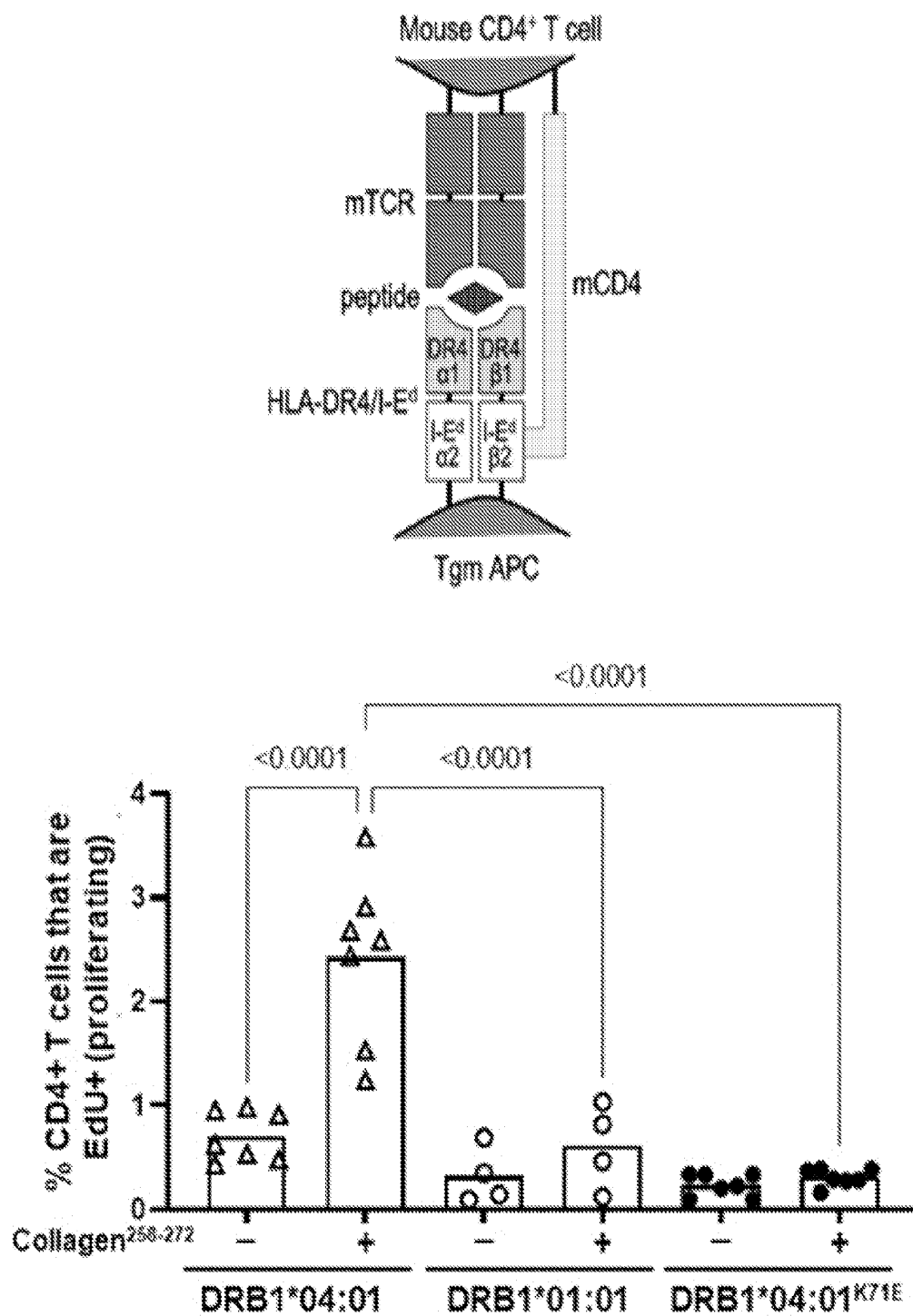


Fig. 2

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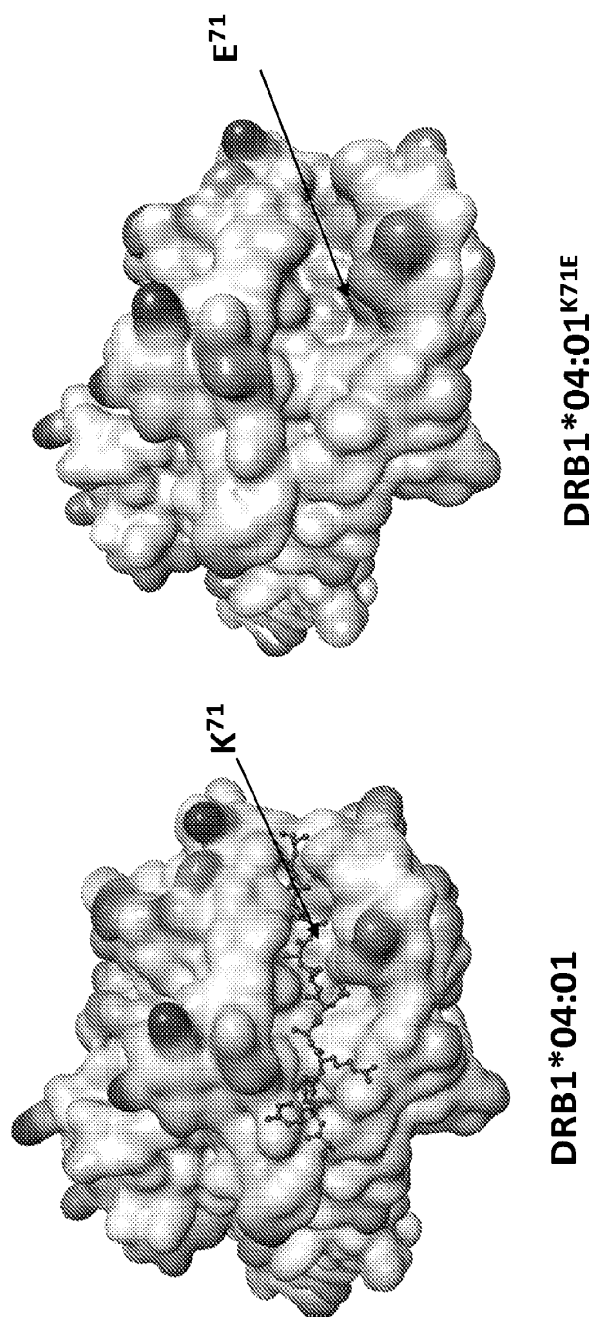


Fig.3A

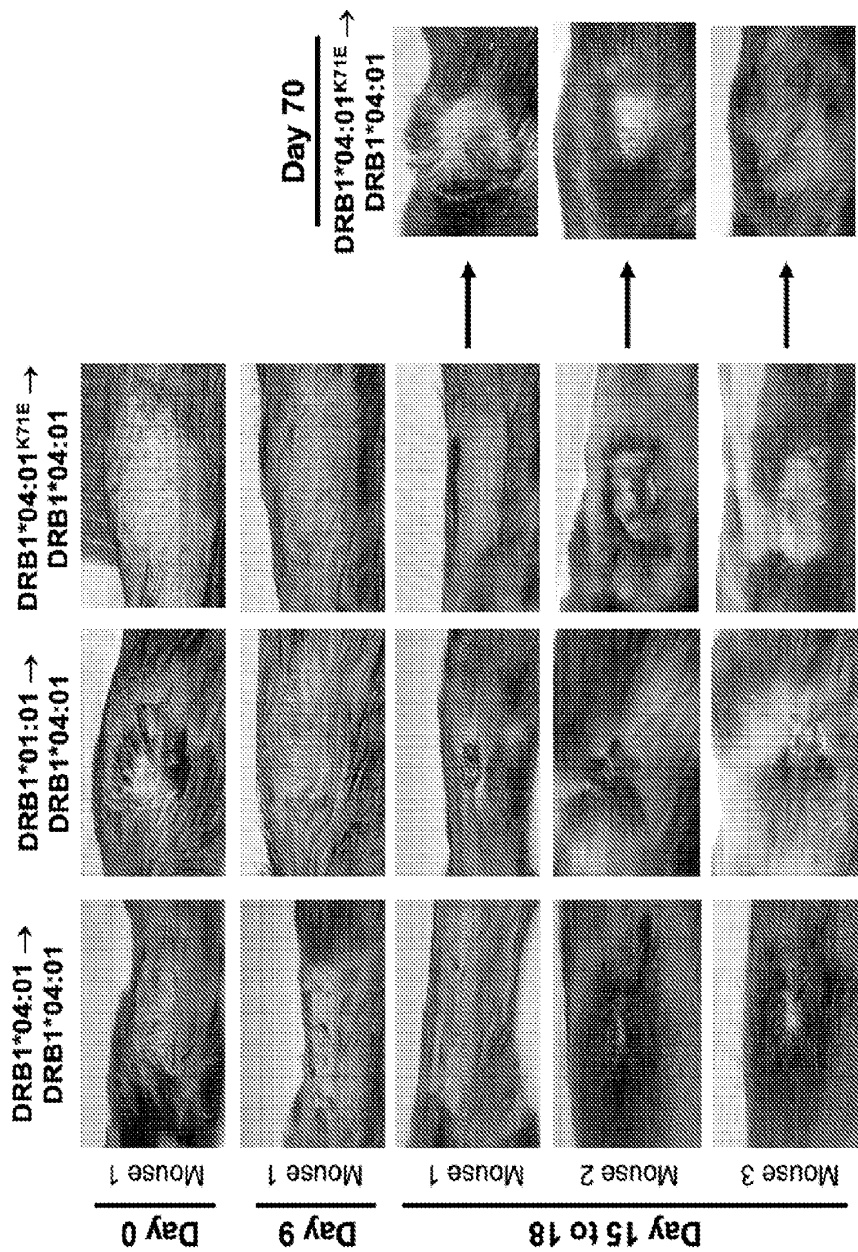


Fig.3B

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
AA Pos.	110	120	130	140	150	160	170	180	190	200
DRB1*01:01:01:01	V	I	P	E	R	T	O	P	L	O
DRB1*11:01:01:01	V	I	P	E	R	T	O	P	L	O
DRB1*15:01:01:01	V	I	P	E	R	T	O	P	L	O
AA Pos.	210	220	230							
DRB1*01:01:01:01	S	E	V	E	R	T	O	P	L	O
DRB1*11:01:01:01	S	E	V	E	R	T	O	P	L	O
DRB1*15:01:01:01	S	E	V	E	R	T	O	P	L	O

Fig. 4

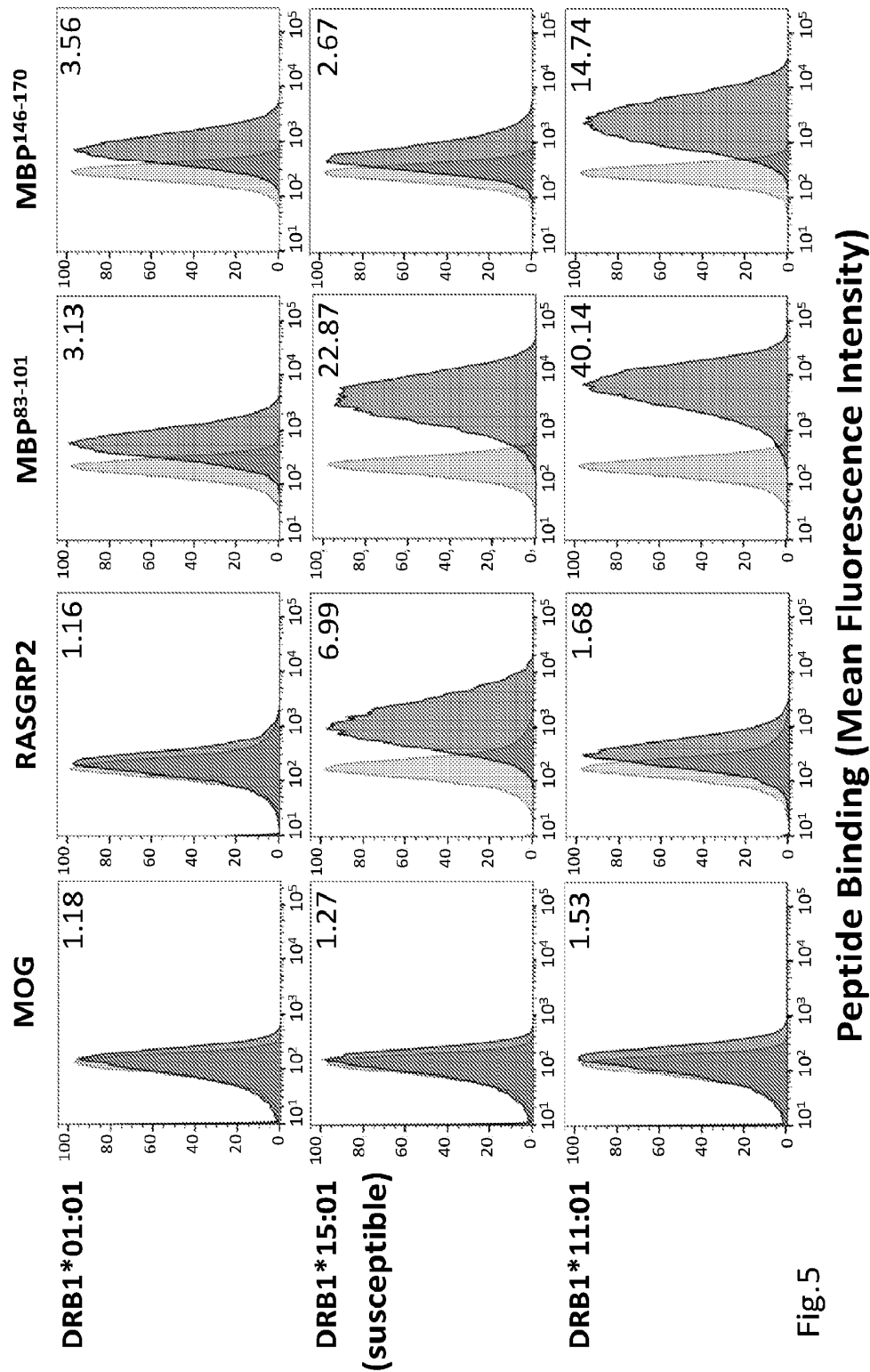


Fig.5

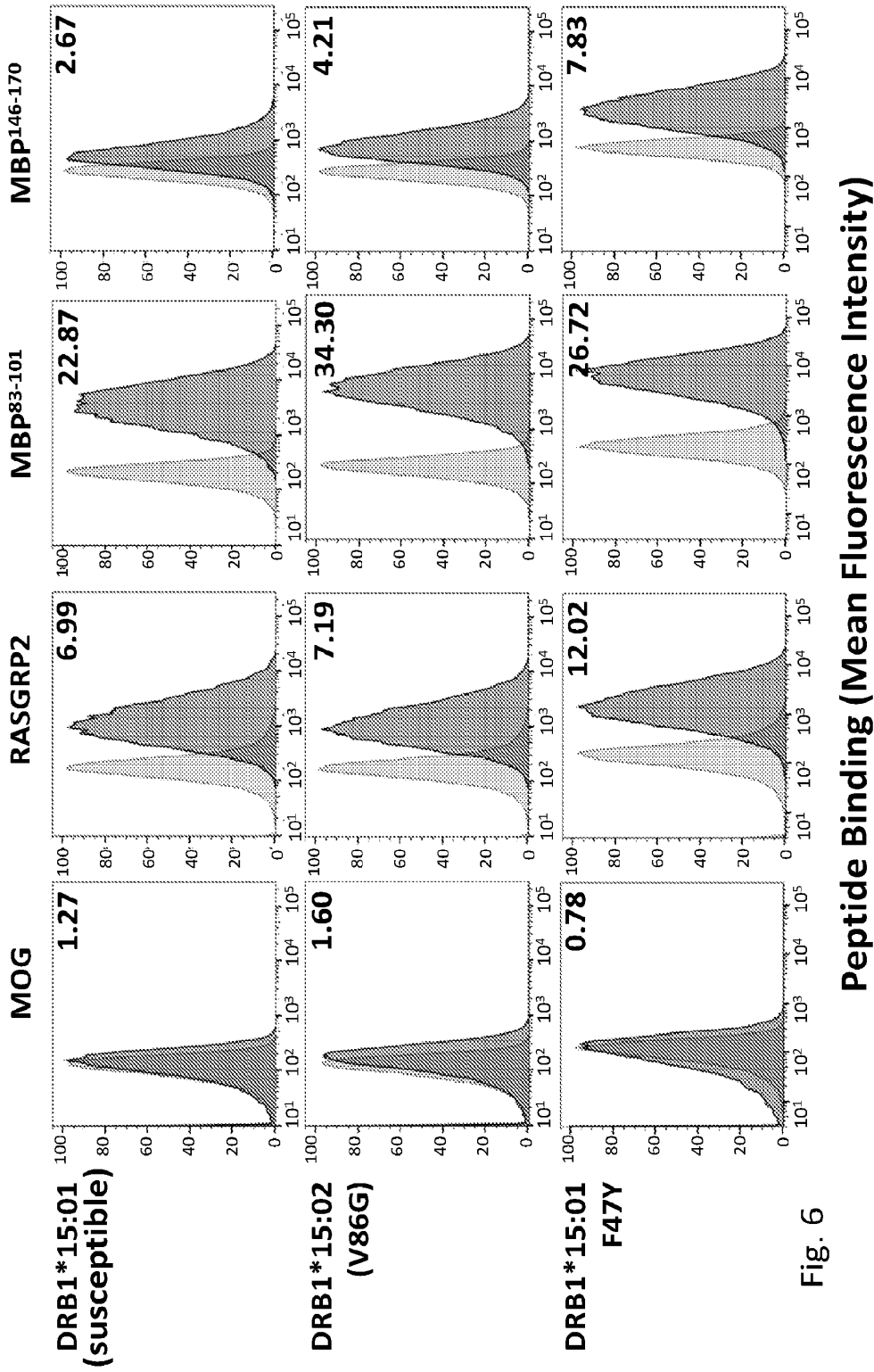


Fig. 6

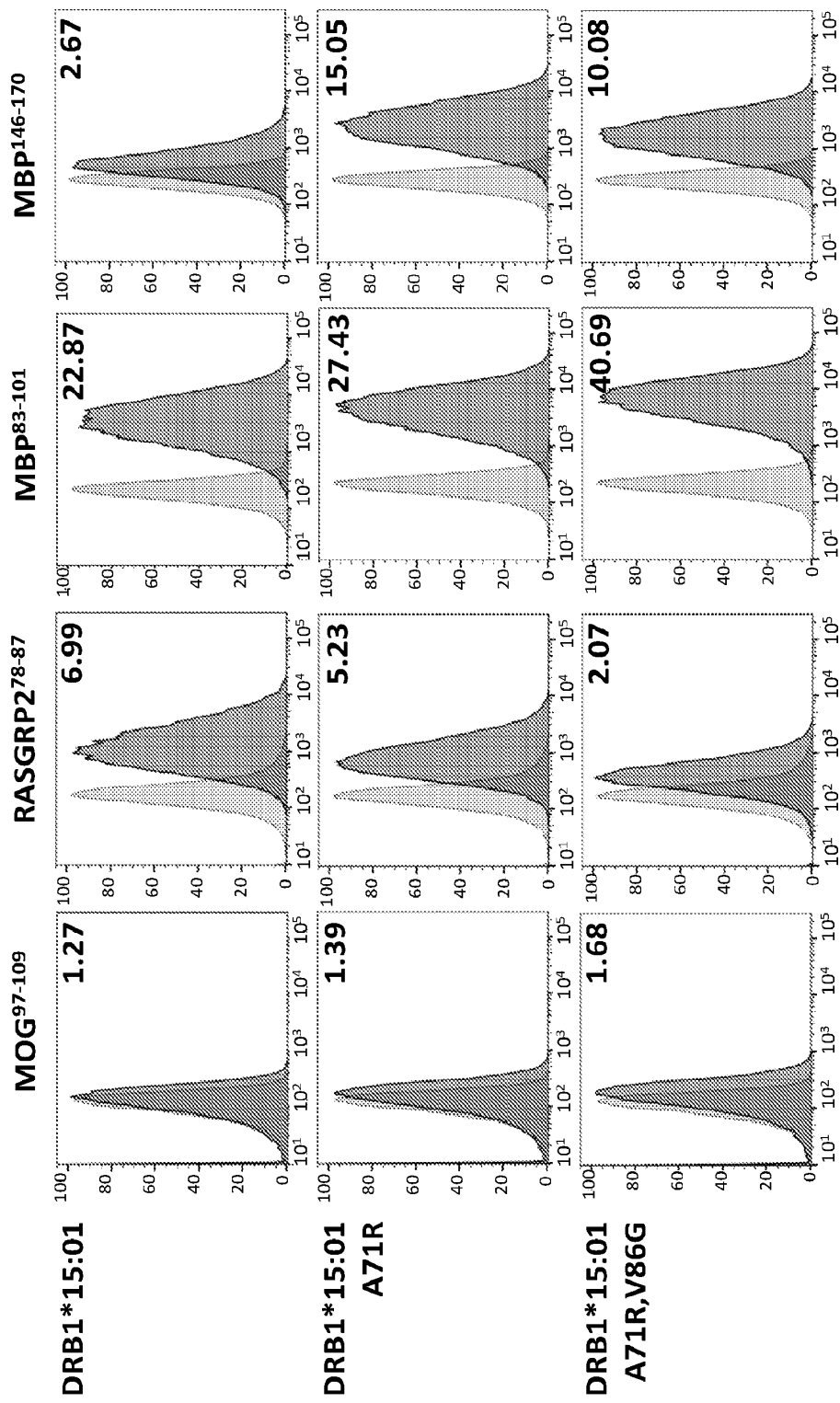


Fig.7 Peptide Binding (Mean Fluorescence Intensity)

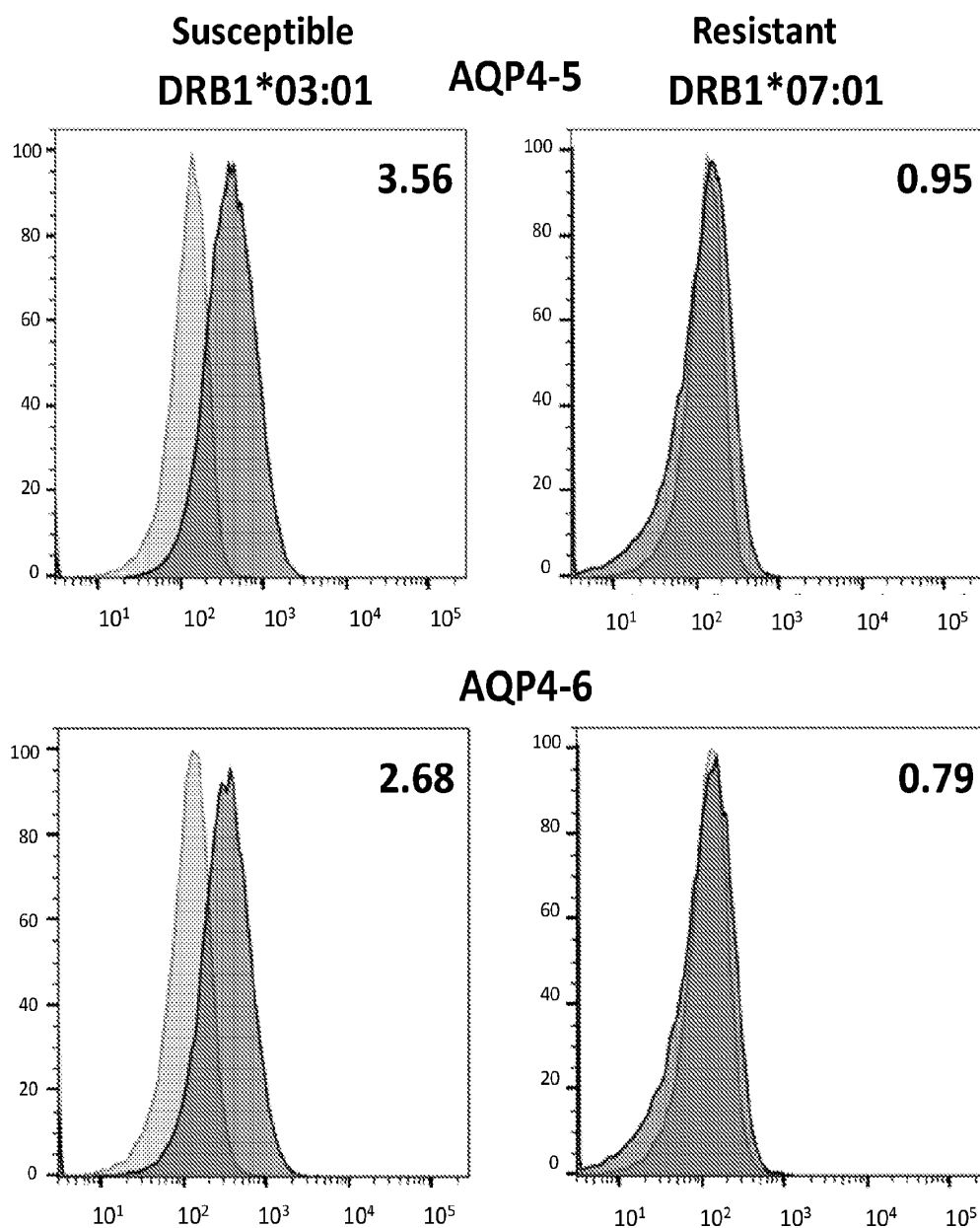
Sequence Alignment of DRB1*03:01 and DRB1*07:01

AA Pos.	10	20	30	40	50	60	70	80	90	100
DRB1*03:01:01:01	QUTRERLEY	SYSECHENG	TEAVVILRX	FMNQENVF	DSVGSFRAY	TELCRFRREY	WASQKLLIQ	WAGRVNICK	HNICVVESET	VSRPVHAYE
DRB1*07:01:01:01	---Q---	WQ	GNK	---QF-E-A	-F---	F---	---	I--D	R-Q--TV	-----E--
DRB1*03:01:02:01	---Q---	---	---	---	---	---	---	---	---	---
AA Pos.	110	120	130	140	150	160	170	180	190	200
DRB1*03:01:01:01	VPSVYCPDQ	HANILVSVS	GFPGSIEVR	WERNQSEET	GVVSTGLIIN	GNVFQIIVN	LETVESSEV	YTCQVSESV	TSPLIVSRA	ESSESQSSML
DRB1*07:01:01:01	---A---	---	---	---	---	---	---	---	---	---
DRB1*03:01:02:01	---	---	---	---	---	---	---	---	---	---
AA Pos.	210	220	230							
DRB1*03:01:01:01	SDPGSEVIGL	LELGADLEIV	FMQGNHSL	QPRGYS						
DRB1*07:01:01:01	---	---	---	---						
DRB1*03:01:02:01	---	---	---	---						

Fig. 8

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Binding of Aquaporin Peptides to DRB1 Alleles



Peptide Binding (Mean Fluorescence Intensity)
Fig.9

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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	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT
DRB1*04:05:01:01	GTGATGTTG	TTGACGCTG	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT
2A Ref.	110	120	130	140	150	160	170	180	190	200
DRB1*04:01:01:01	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT
DRB1*04:05:01:01	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT
2A Ref.	210	220	230							
DRB1*04:01:01:01	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT							
DRB1*04:05:01:01	TTGCTTGGT	TTGCTTGGT	TTGCTTGGT							

Fig.10

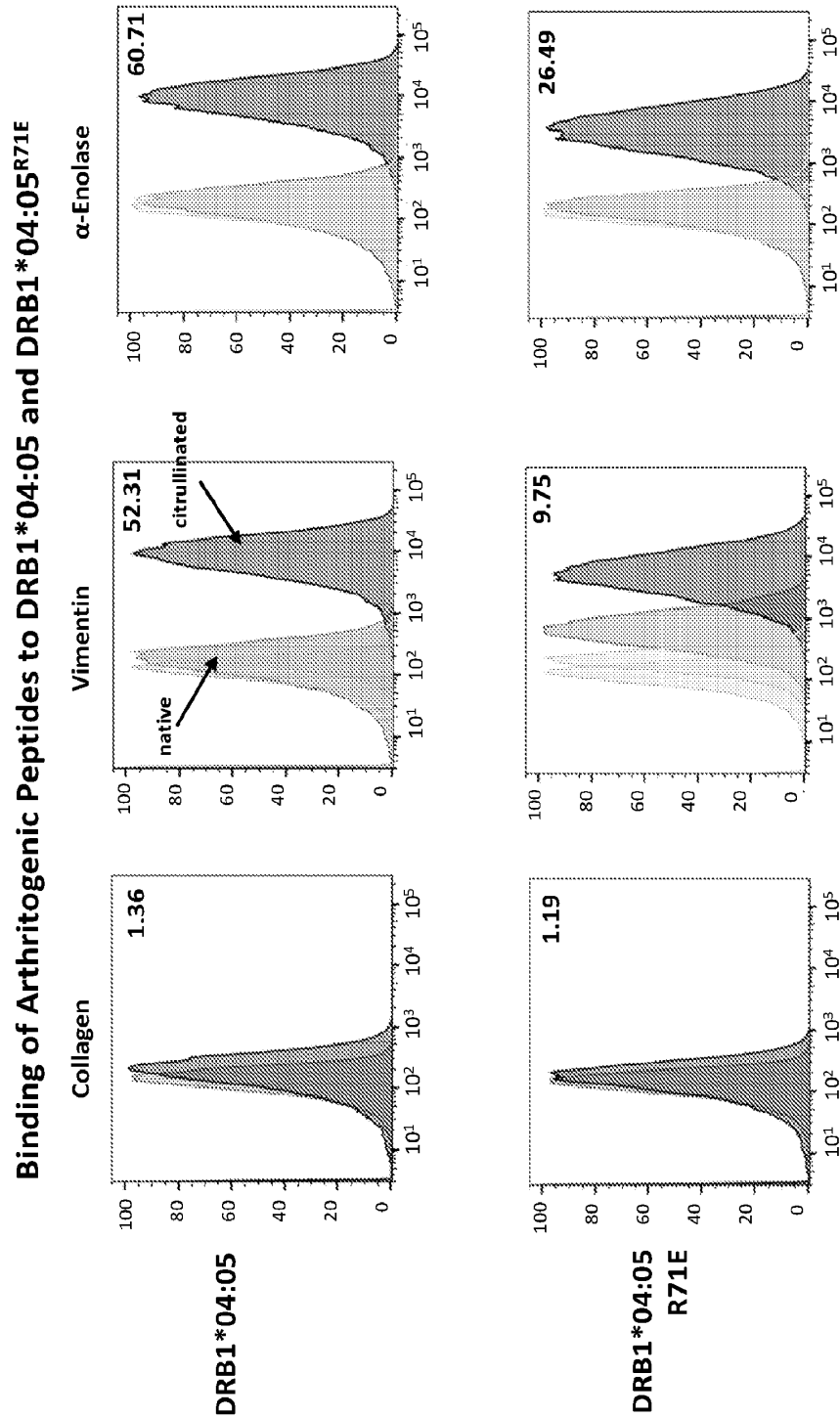


Fig. 11 Peptide Binding (Mean Fluorescence Intensity)

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

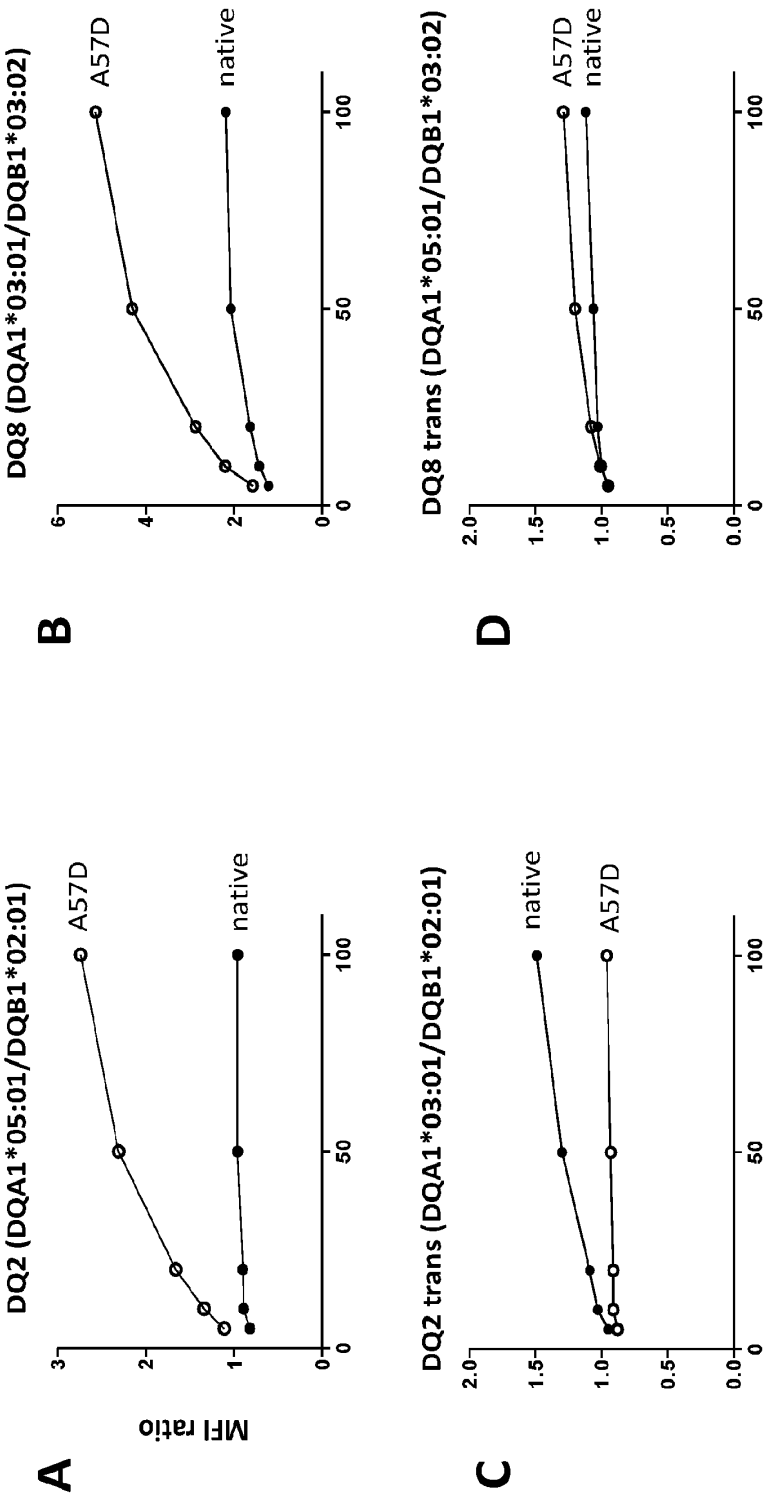


Fig. 12

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

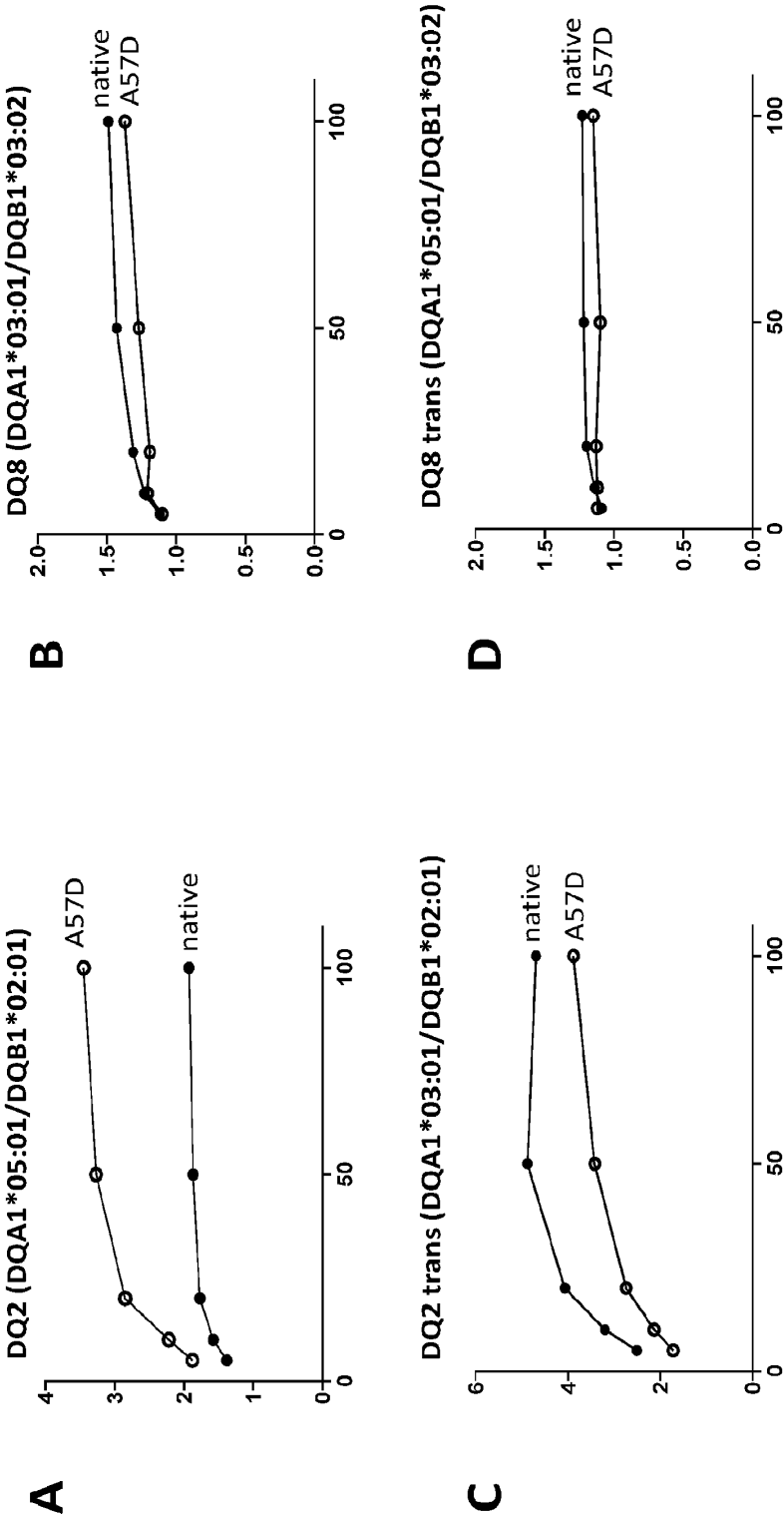


Fig.13

A57D Edit Inhibits Insulin Mimotope Binding to DQ8 and DQ2 Trans

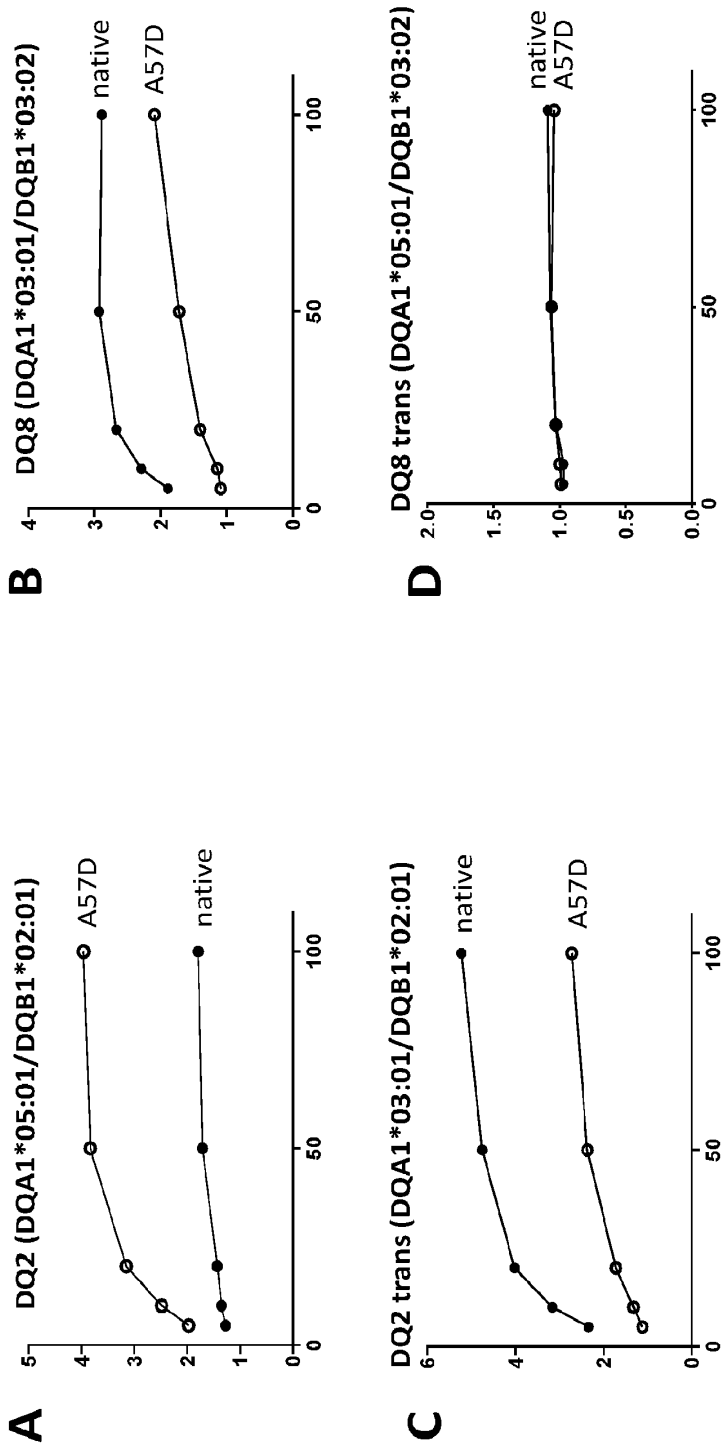


Fig.14

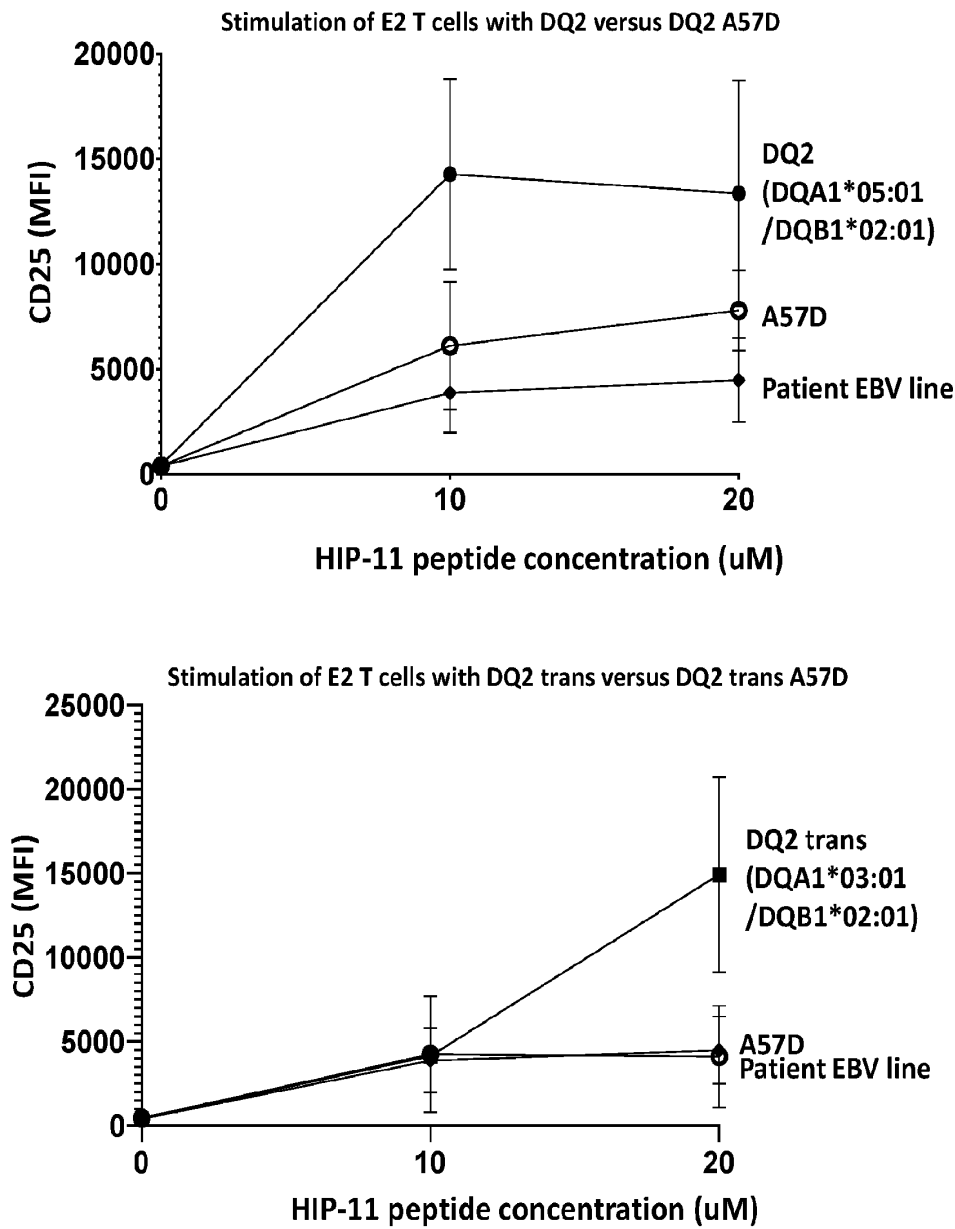


Fig.15

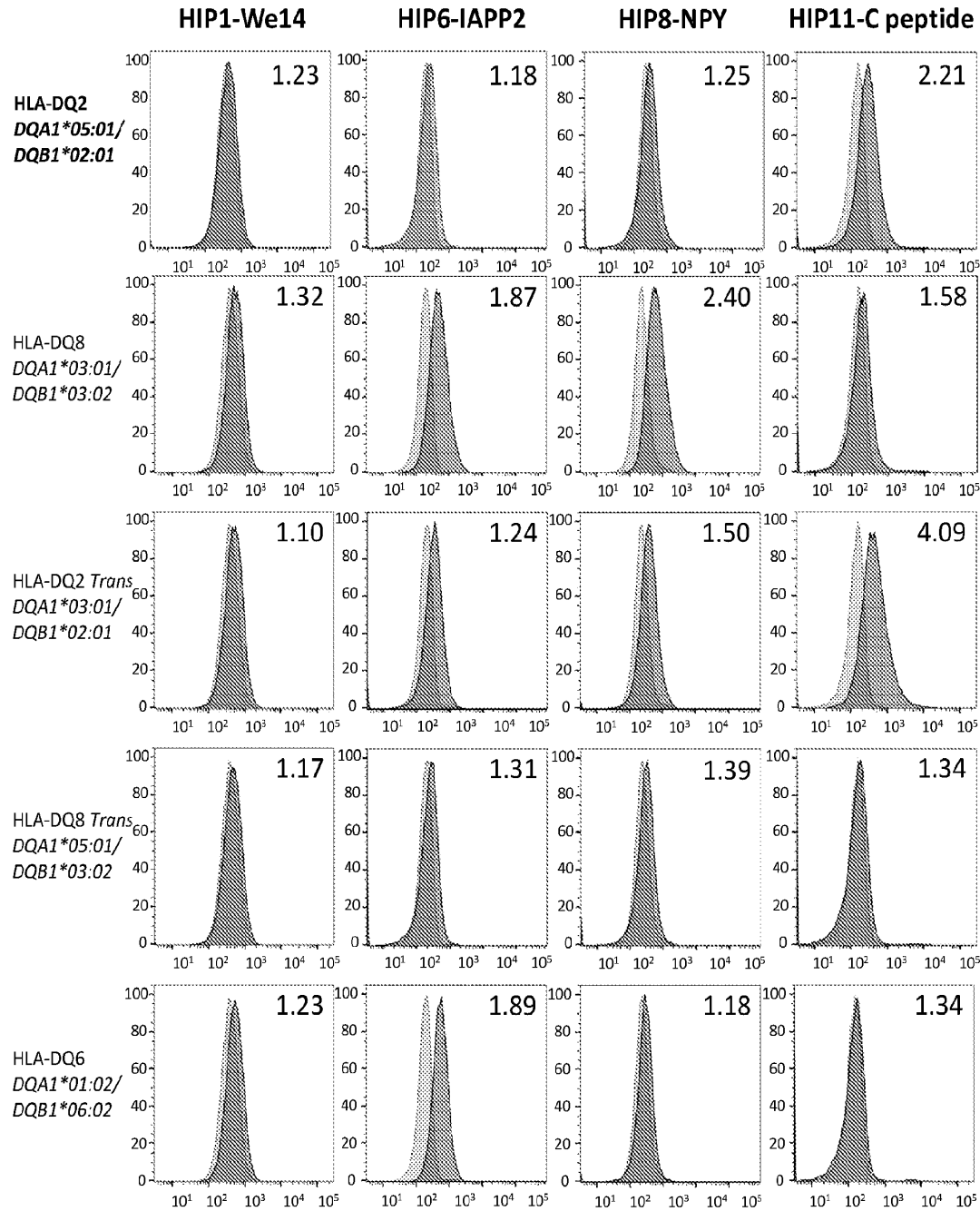


Fig.16

Peptide Binding (Mean Fluorescence Intensity)

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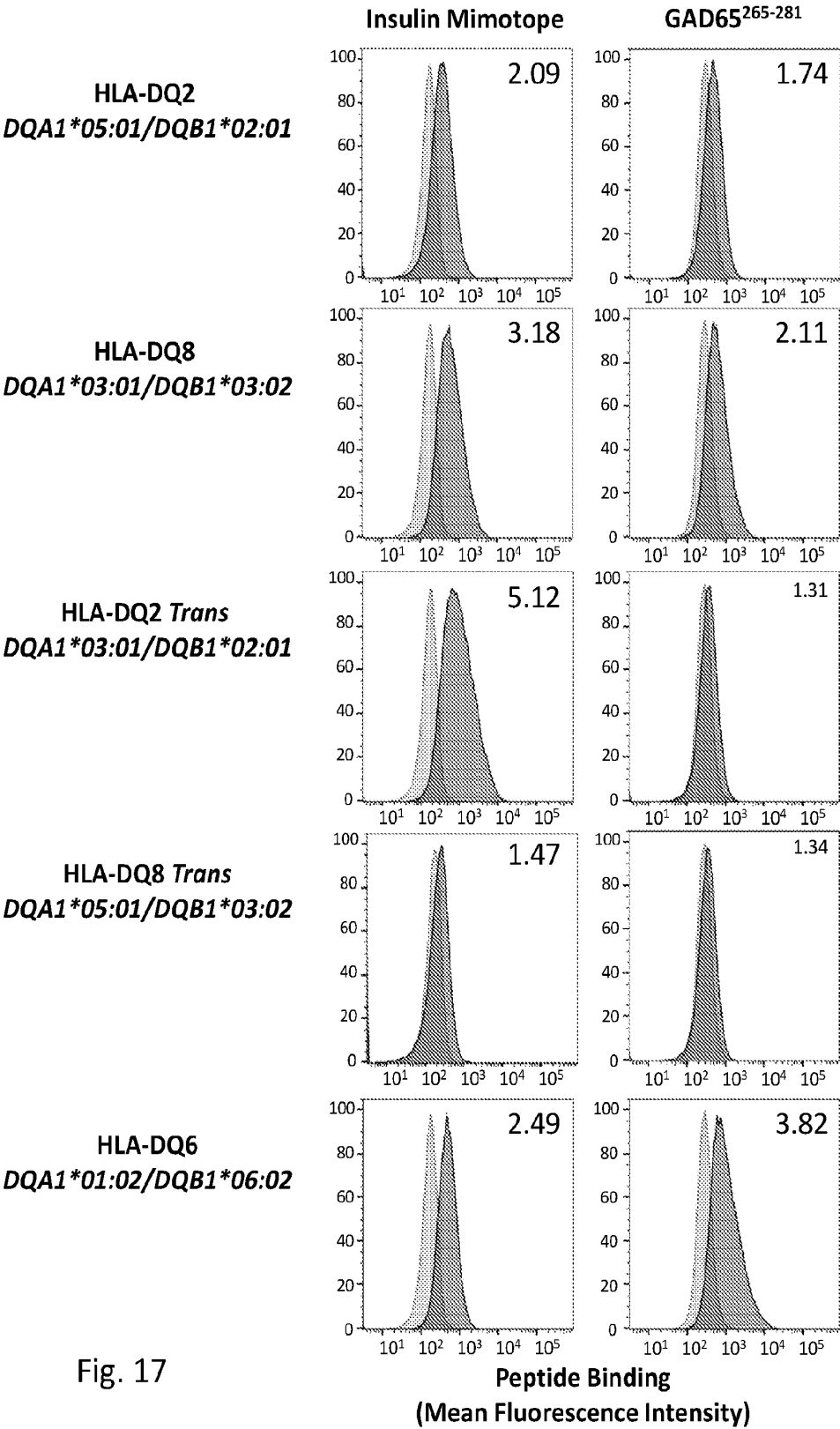


Fig. 17

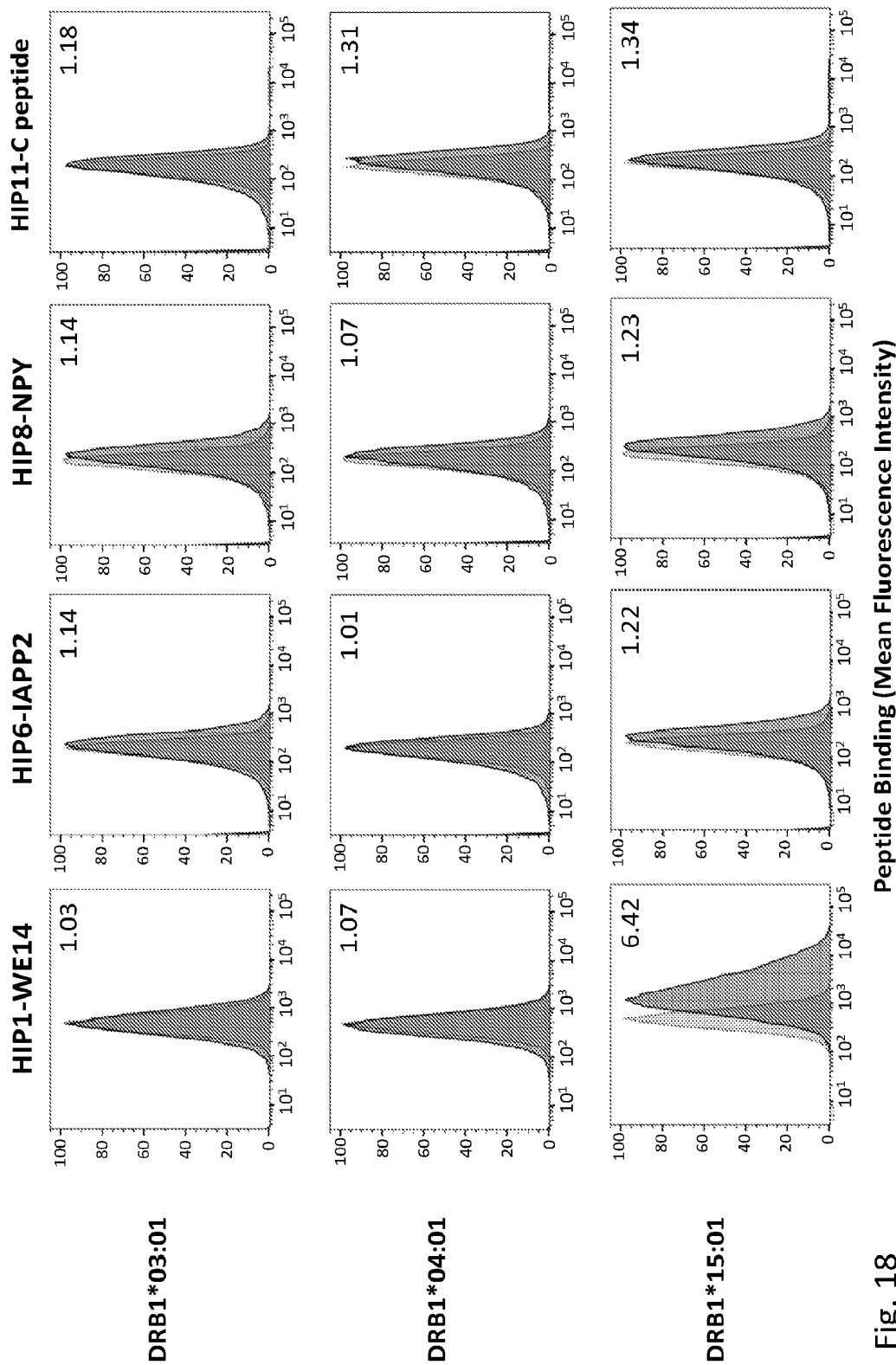


Fig. 18

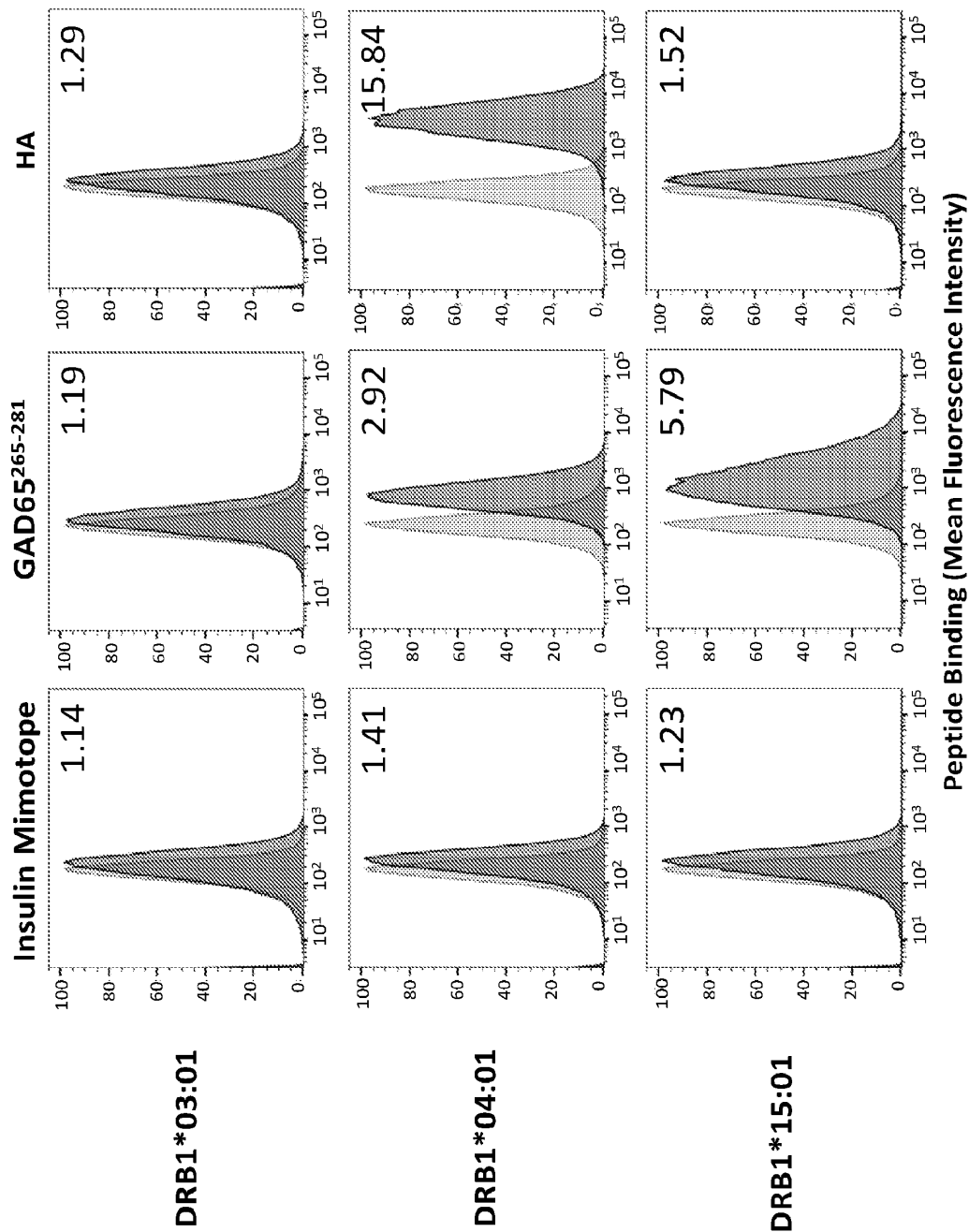


Fig. 19

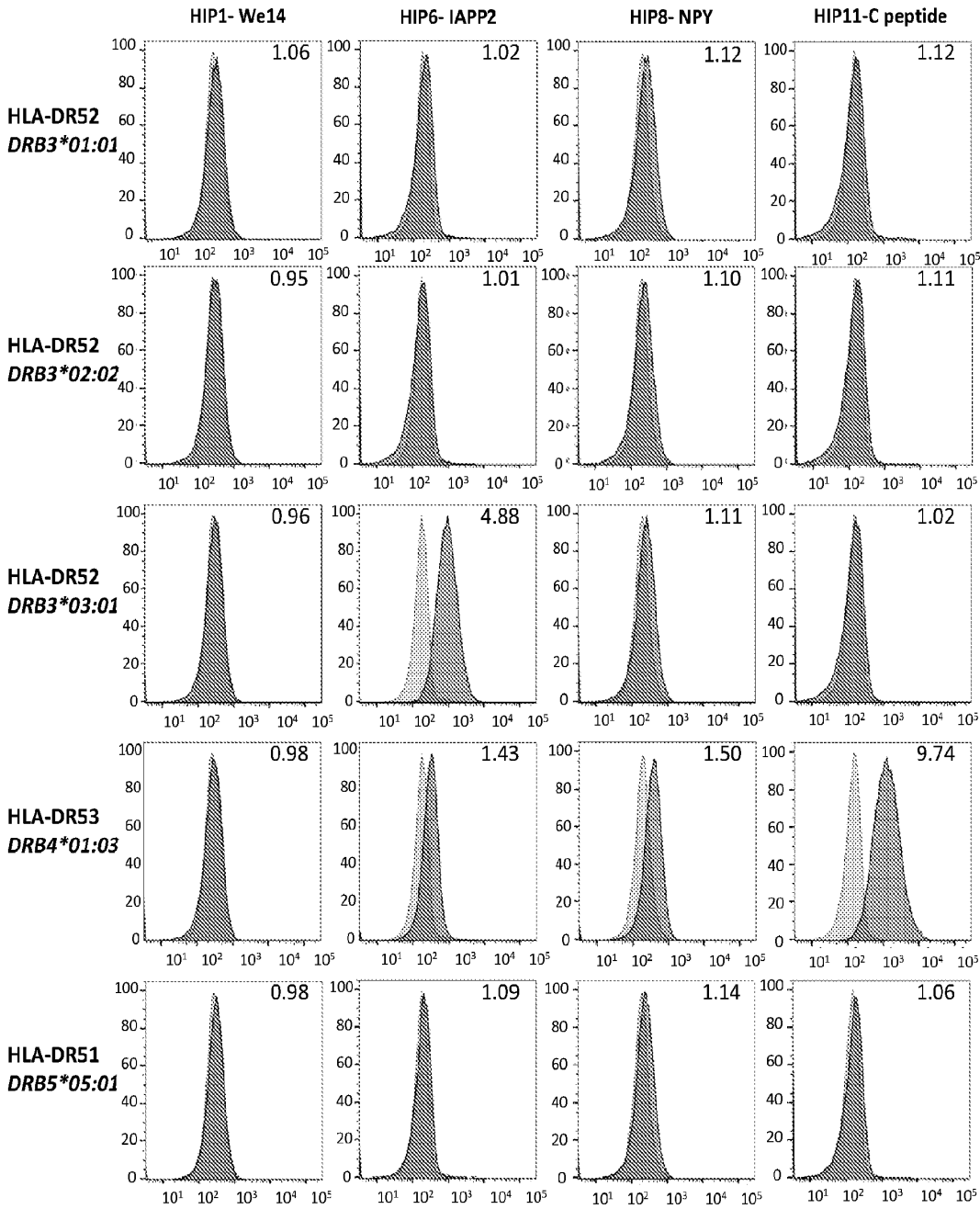


Fig. 20

Peptide Binding (Mean Fluorescence Intensity)

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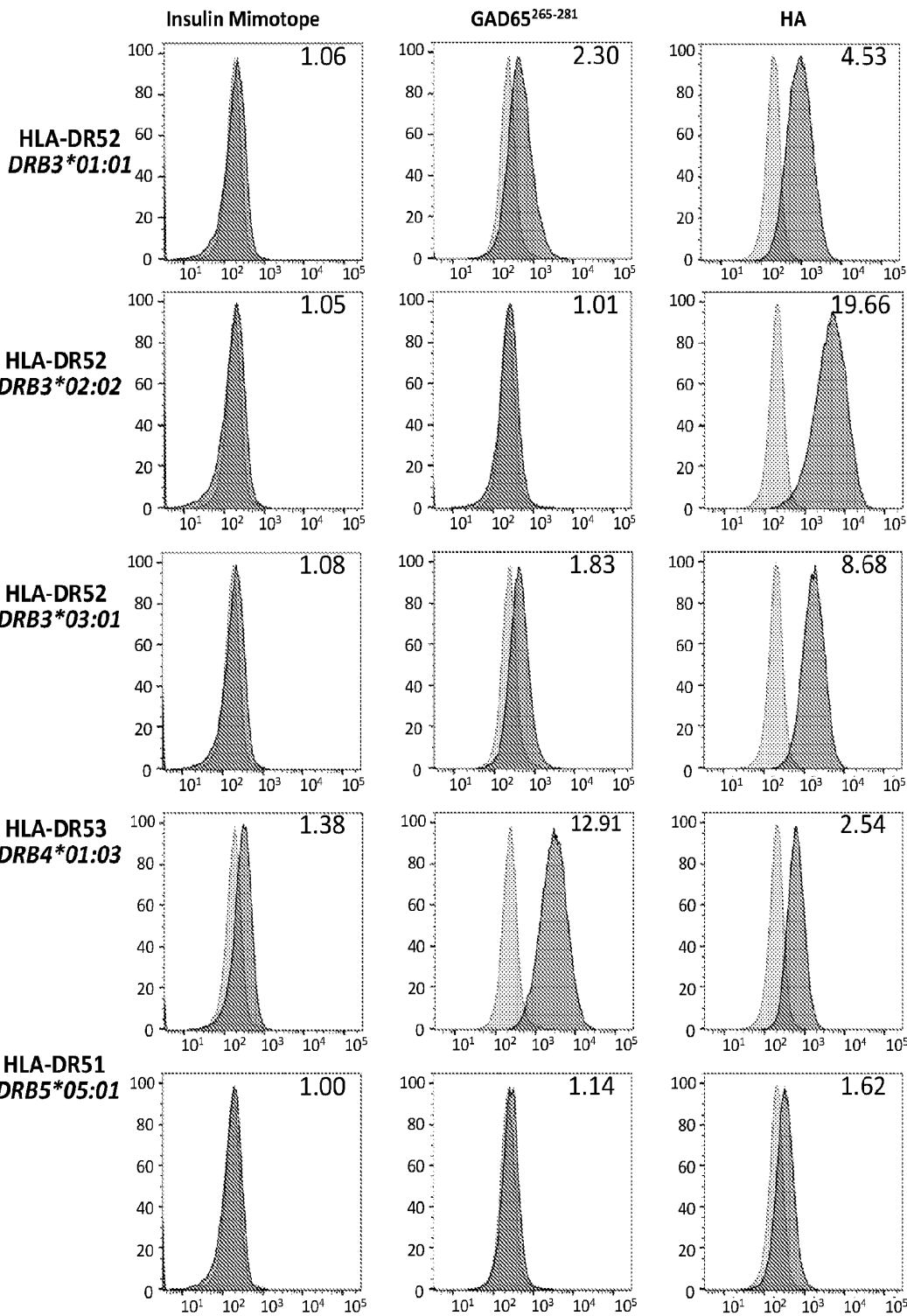


Fig. 21 Peptide Binding (Mean Fluorescence Intensity)

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<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	AQGTLSKIFKLGGDRSRSRGSPMARR
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 a 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

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Novel Constructs for DRB1 Pocket 1 Gene Editing

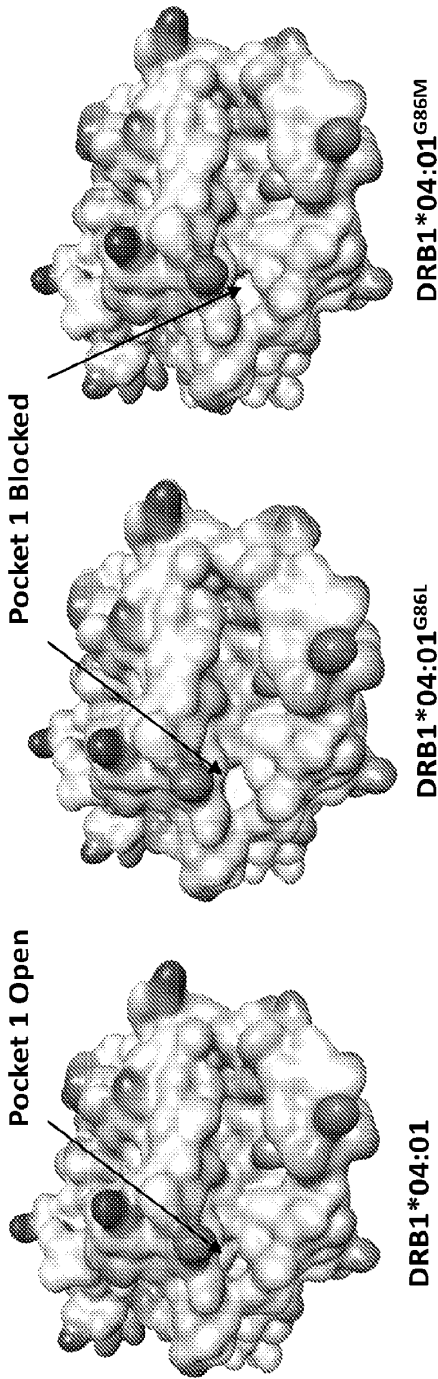


Fig. 23A

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

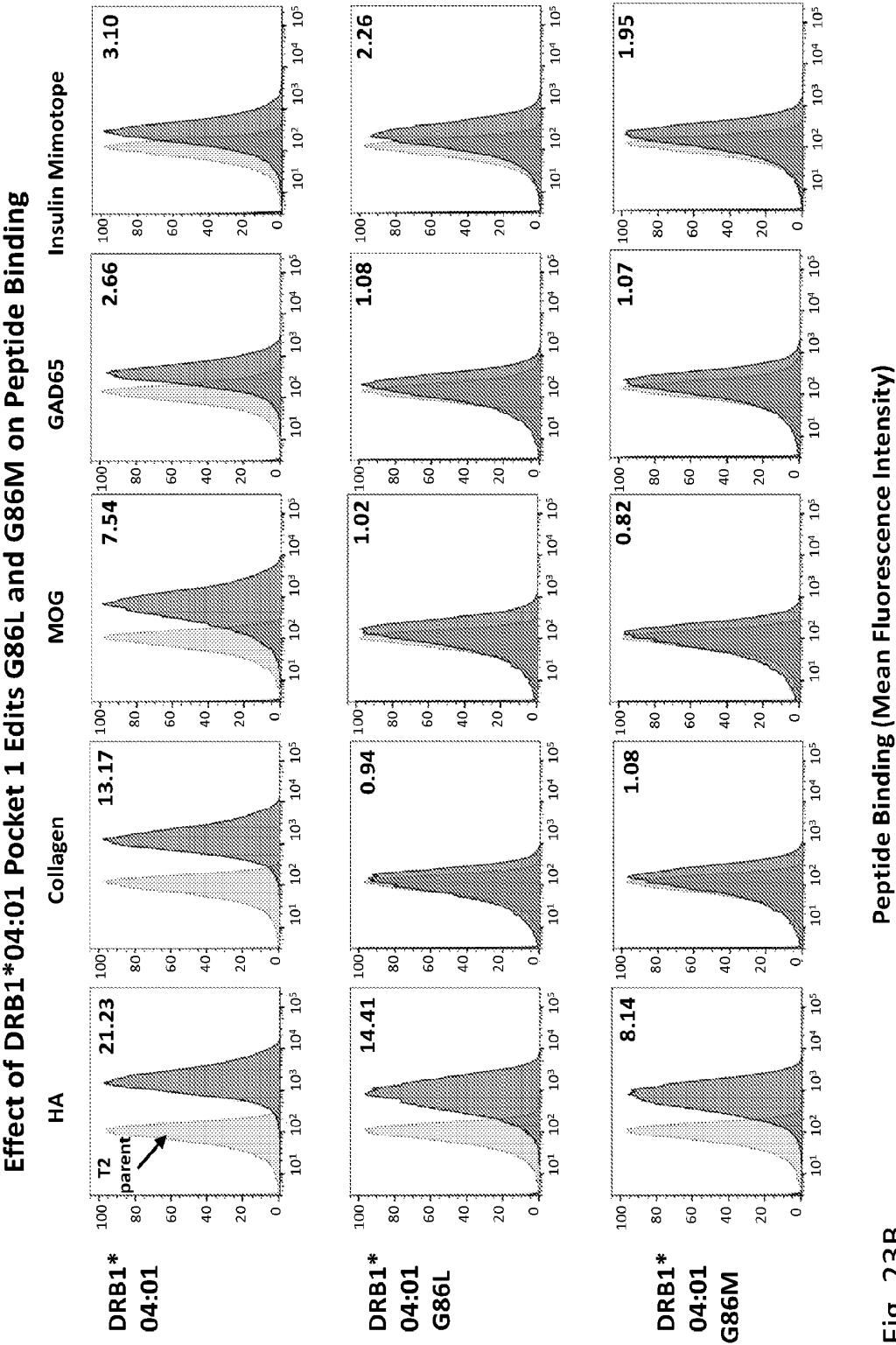


Fig. 23B

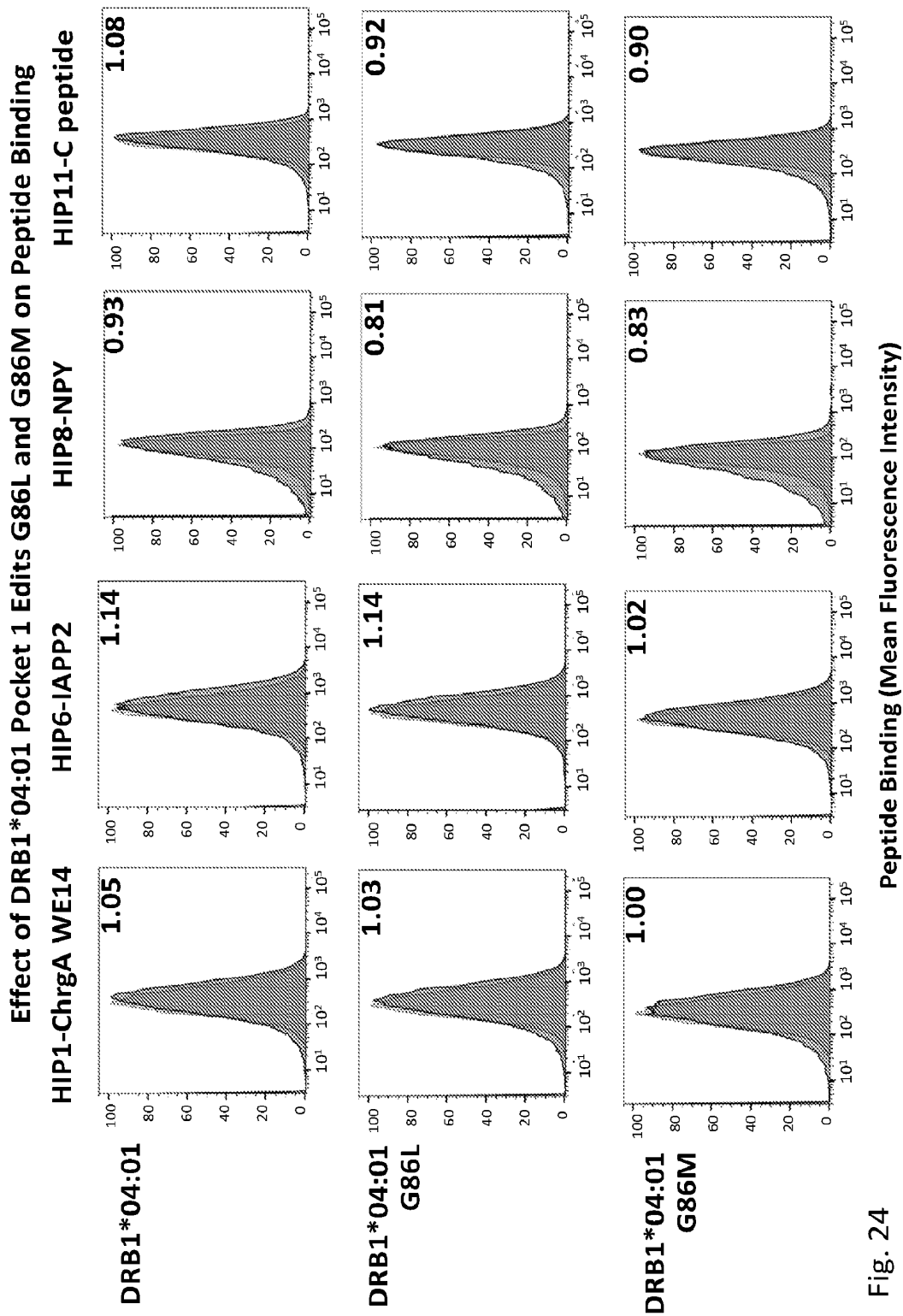


Fig. 24

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

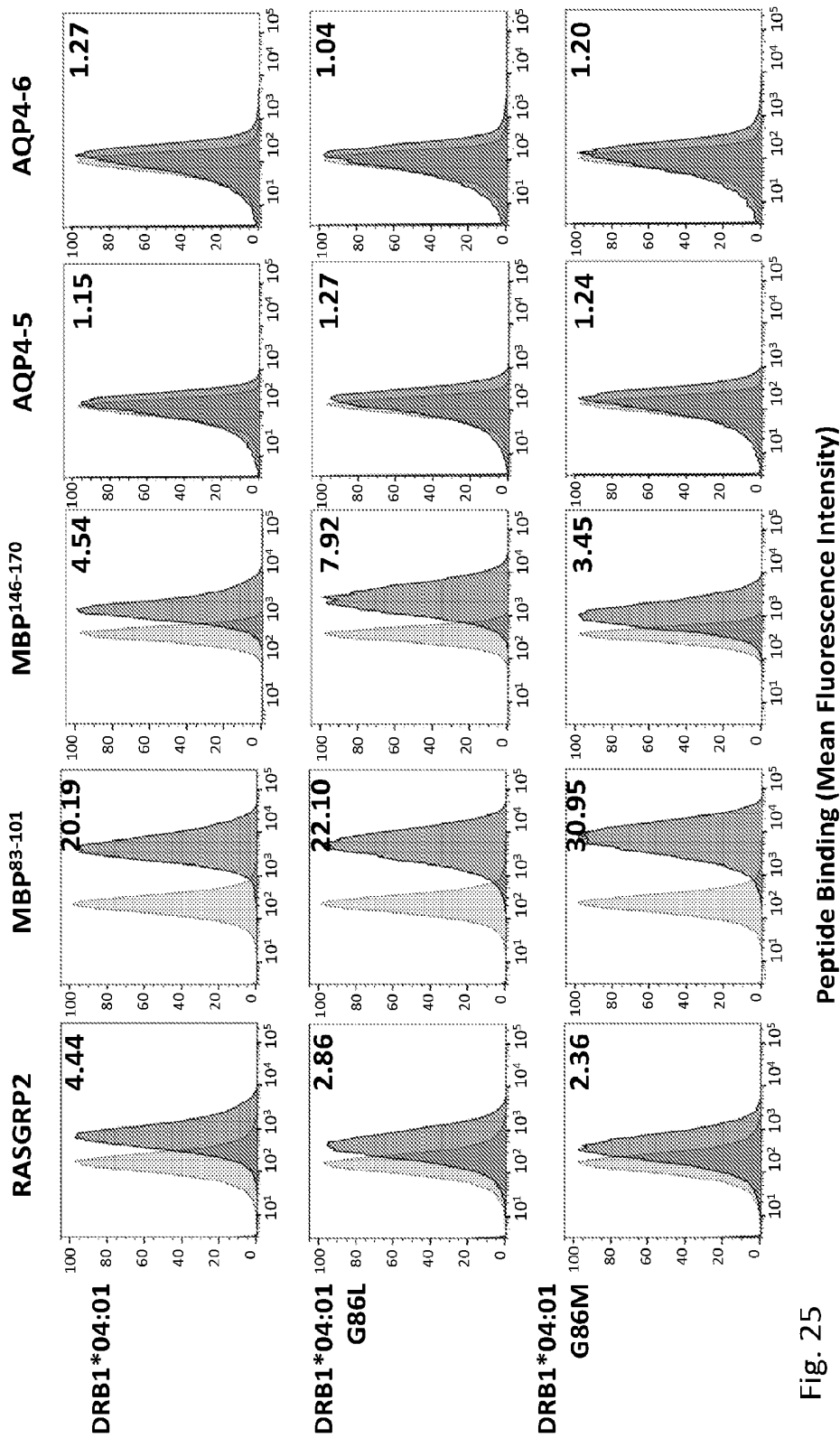
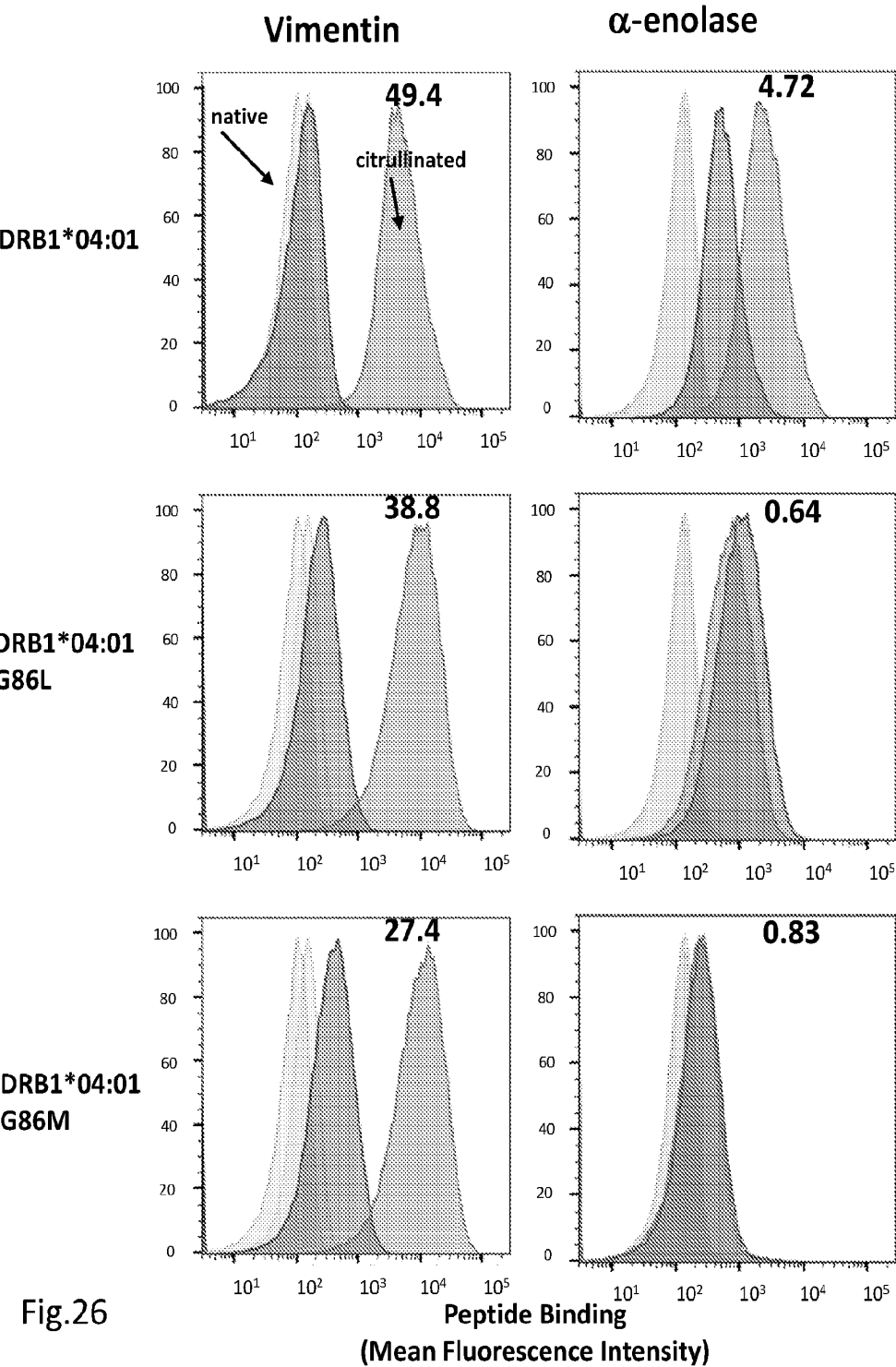


Fig. 25

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



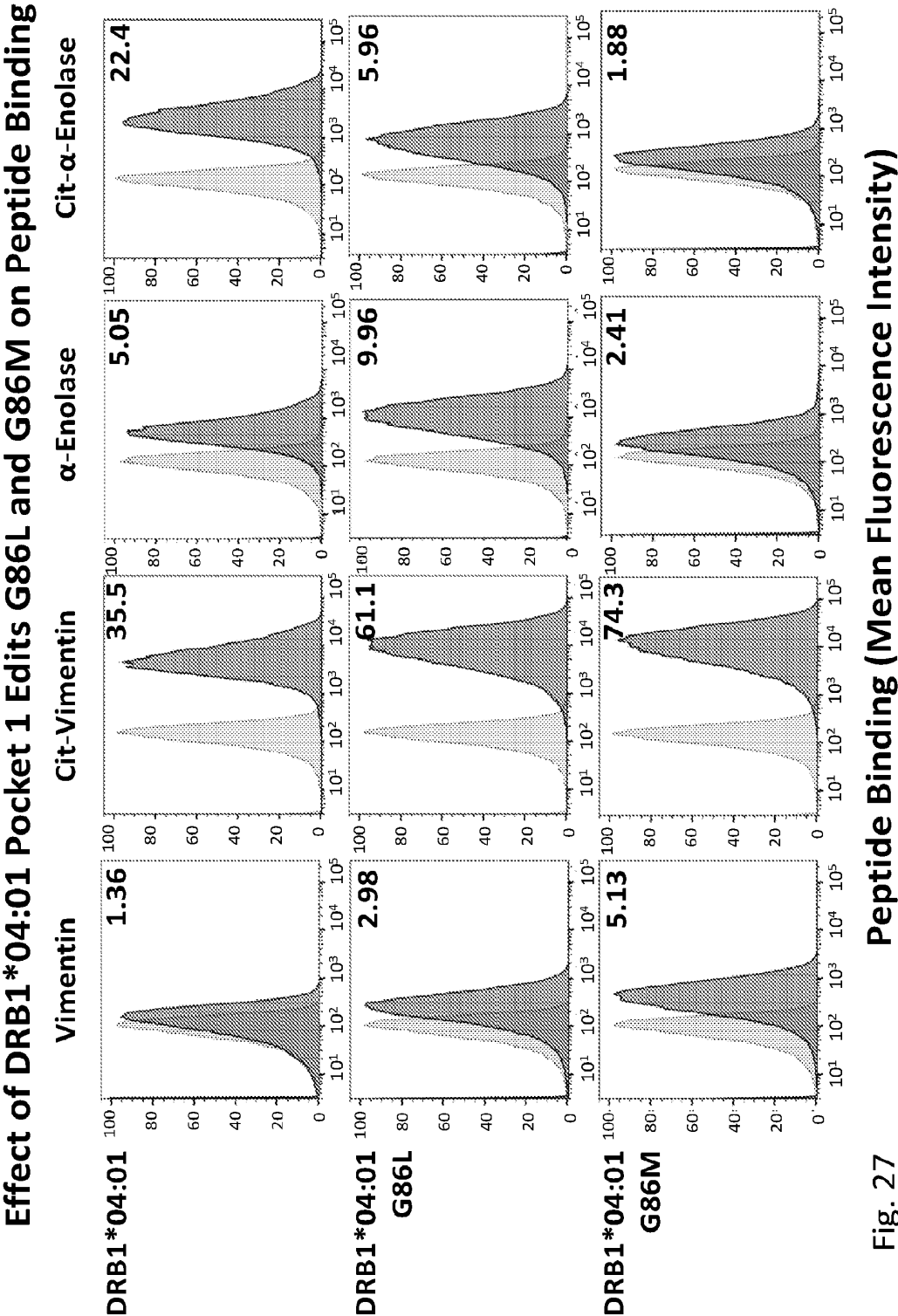


Fig. 27

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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

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SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
1	A*02:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DGETRNVKHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSQWFLRGYHQYAYDG KDYIALKEDLRSWTAADMAAQTTKHKWLAHVAEQLRAYLESTCVENLRRYLENGKETLQ RTDAPKTHMTHHVAVSDEATLRCWALSFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVLFGLAVITG AVVAAVMWRKSSDRKGGSSYSQAASSDSAQGSQVSLTACKV
2	A*03:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DGETRNVKHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSQWFLRGYHQYAYDG KDYIALNEDLRSWTAADMAAQITKRWLAARVAEQLRAYLESTCVENLRRYLENGKETLQ RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVLLGLAVITG AVVAAVMWRKSSDRKGGSSYSQAASSDSAQGSQVSLTACKV
3	A*29:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DLQTRNVKHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSQWFLRGYHQYAYDG KDYIALNEDLRSWTAADMAAQITQKRWLAARVAEQLRAYLESTCVENLRRYLENGKETLQ RTDAPKTHMTHHVAVSDEATLRCWALSFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVLFGLAVFAG AVVAAVMWRKSSDRKGGSSYSQAASSDSAQGSQVSLTACKV
4	B*07:02:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DRNTQIKKAAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCQVGPDSGRLLRGHGDQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARVAEQLRAYLESTCVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA
5	E*08:01:01:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DRNTQIKKAAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCQVGPDSGRLLRGHGDQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARVAEQLRAYLESTCVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA
6	B*27:09:02:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DRETQICKAKAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCQVGPDSGRLLRGHGDQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARVAEQLRAYLESTCVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA
7	B*27:01	GSLSMRYFFTSVSRPGRGEPFRLAVGYVDDTQFVRFDSDAASQRMPPAPWIEQEGPEYW DRETQICKAKAQTYRNLRLALRYNQSEAGSHTLQSMYGCQVGPDSGRLLRGHGDQYAYDG KDYIALNEDLRSWTAADTAQAQITQKRWLAARVAEQLRAYLESTCVENLRRYLENGKETLQ RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAQDGT FQKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRNEPSSQPTIPIVGIAGLVAVLVVVG AVVAAVMCRKSSGGKGGSSYSQAACSDSAQGSQVSLTA

Fig. 29

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SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
8	B*27:03	GSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRREEPRAPWIEQEGPEYHW DRETQICAKAKAQIDREDLRILLAYYNQSEAGSHLQNMVYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAARVAEQRAYLEGECEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
9	B*27:05:02:01	GSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRREEPRAPWIEQEGPEYHW DRETQICAKAKAQIDREDLRILLAYYNQSEAGSHLQNMVYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAARVAEQRAYLEGECEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
10	B*27:09	GSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRREEPRAPWIEQEGPEYHW DRETQICAKAKAQIDREDLRILLAYYNQSEAGSHLQNMVYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAARVAEQRAYLEGECEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
11	B*51:01:01:01	GSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRTEEPRAPWIEQEGPEYHW DRNTQIFWNTNTQTYRENLRILALAYYNQSEAGSHWQTMVYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAAREAEQRAYLEGCEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVATVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
12	B*54:01:01:01	GSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRTEEPRAPWIEQEGPEYHW DRNTQIYKAQAQITRESLRNLRGYYNQSEAGSHWQTMVYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAARVAEQRAYLEGCEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVATVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
13	B*57:01:01:01	GSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRTEPRAPWIEQEGPEYHW DGETANMKASQTYRENLRILALAYYNQSEAGSHIIQVMYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAARVAEQRAYLEGCEVWLRRLYLENGKETLQ RADPPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIG AVVAAVMCRKSSGGKGGSYSAACSDSAQGS DVSLTA
14	C*06:02:01:01	CSNSMRYFTHTSVSRPGRGEPFRFIVGVVDITLQVRFDSDAASPRTEEPRAPWIEQEGPEYHW DRETQIKYKQAQADRVNLRNLRGYYNQSEAGSHLQNMVYCDVGFPGRLLRGYNQDAYDG KDYIALNEDLSSWTAADTAAQITQKWEAAREAEQRAYLEGCEVWLRRLYLENGKETLQ RAEHPKTHVTHHPISDHEATLRQWALGFYPAEITLTWQRDGEDQTQDTLVEITRPAGERT FQKWAARVVVPSGEEQRYTCHVQHEGLPEPLTLRWEPSSQSTVPIVGIVAGLAVLAVLAVL GAVMAVVMCRKSSGGKGGSCSAACSDSAQGS DESLIACKR

Fig. 29 continued

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SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
15	C*18:01:01:01	CSRSRMRYFDITAVSRPGRSEPRFISVGYVDDTQFVRFSDASERGEPRAPVWEQESPEYWDRETQNYKRAQADRWNLRLKRGYYNQSEDSHTLQRMFGCDLSPDGLLLRGYNQFAYDGGDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQRPAYLEGTCVFWLRRVLENGKETLQRAERPKTHVTHHEVSDHEATLRCAWALGFYFAEITLTWQWDGEDQGTQDTLQVETREAGDGTFOKNAAVVVVSSEGEQRYTCHVQHEGLPEPLTLNKPSSQPIIPIVGVIVAGLAVLVVLAVLGAVVAVVMCRKSSGGGSGGSCQAASNSAQQSDSLIACKA
16	DFA1*02:01:01:01	IKADHVSTYAAAFVQTRPTGEFMEFDEDSQFFVVDLQKKEIVWHLEEFGRAPSFZTAQGGALANIALNNMLNTLIQRSNHTQAANDPPEVTVFPREPVELGQPNILICHIDRFPFVPLNVTWLCNGEPVTEGVAESLFLPRTBYSFHKPHVLTFPVPSAEDVVDCEVHNGLDQPLLNHWEAQEPIQMPETTETVLCALGLVLGLVGIIVGTVLIIKSLRSGHDPFAQGGPL
17	DFB1*13:01:01:01	RATPENYVQLRQCEYAFNGTQRFLERYIVNREEYARFDSVGEFRAVTEIGRPAEAYWN SQHDILEEERAVFDRICRHHYELDEAVTLQRVQPKVNVSPSHNGPLQHHNLLVCHVTDF YPGSIQVRNFWLNGQEETAGVVTNLIIRNGDWTFOILVMLEMTPOQSGVYICQVEHTSLDS PVTVEWKAQSDSARSKTITGAGGFVLGLITCGVGIFMHRRSKRVQGRSA
18	DQA1*01:01:01:01	EDIVADHVASCGVNLVQFYGPSGQYTHEFDGDEEFYVDLERKETAWRWFEPSKFGGFDPO GALRNMVAVAKHNINIMIKRYNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGQSVTEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHNGLDQPLLNH WEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIGGLRSVGASRRHQGGL
19	DQA1*01:02:01:01	EDIVADHVASCGVNLVQFYGPSGQYTHEFDGDEEFYVDLERKETAWRWFEPSKFGGFDPO GALRNMVAVAKHNINIMIKRYNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGQSVTEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHNGLDQPLLNH WEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIGGLRSVGASRRHQGGL
20	DQA1*02:01:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWKLFLFRLREDPOF ALTNIHAVLKHNLNLIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHNGLDQPLLNH WEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
21	DQA1*03:01:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWQLPLFRFRFRFDPOF FALTNIHAVLKHNLNLIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHNGLDQPLLNH WEPEIPTPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
22	DQA1*05:01:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWCLFVLRLQFREDPOF ALTNIHAVLKHNLNLIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTLLPSAEEIYDCKVEHNGLDQPLLNH WEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
23	DQA1*05:05:01:01	EDIVADHVASYGVNLVQSYGPSGQYTHEFDGDEEFYVDLERKETVWCLFVLRLQFREDPOF ALTNIHAVLKHNLNLIKRSNSTAATNEVPEVTVFSKSPVTLGQPNILICLVNIFPPVWNITWLSNGHSTVEGVSETSFLSKSDHSFFKISYLTLLPSAEEIYDCKVEHNGLDQPLLNH WEPEIPAPMSELTETVVCALGLSVGLVGIIVGTVFIIRGLRSVGASRRHQGGL
24	DQB1*02:01:01:01	RDSPEDFVYQFKGWCYFTNGTERVRLVSRSIYNREEIVRFDSDVGEFRAVTEILLGLPAAEY WNSQNDILERKRAAVDRVCRHNYQLELRITTLQPRVEPTVILSPORTEALNHHNLLVCSVT DFYPAQIKVNRWFRNDQEETAGVVTSTPLIRNGDWTFOILVMLEMTPOQSGVYTCHEHPSL QSPITVENPAQSESAQSKMLSGIGGFVLGLIFLGLGLIIHHRSSQKGLH

Fig. 29 continued

SUBSTITUTE SHEET (RULE 26)

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SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
25	DQB1*03:01:01:01	RDSPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTELGPPDAEY WNSQKEVLETRAEELDTVCRHNYQLELRITLQRRVEPTVTISPSRTAEALNHNHLLVCSVT DFYPAQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QNPITVWRAQSESAQSKMLSGIGGFVLGLIFLGLGLIITHRSQKGLLH
26	DQB1*03:02:01:01	RDSPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTELGPPAAEY WNSQKEVLETRAEELDTVCRHNYQLELRITLQRRVEPTVTISPSRTAEALNHNHLLVCSVT DFYPAQIKVRFNRNDQEETIGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QNPITVWRAQSESAQSKMLSGIGGFVLGLIFLGLGLIITHRSQKGLLH
27	DQB1*05:01:01:01	RDSPEDFVYQFKGLCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTEPGRFPAEY WNSQKEVLEGRASVDRVCRHNYEVAAGILQRRVEPTVTISPSRTAEALNHNHLLVCSVT DFYPSQIKVRFNRNDQEETAGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QSPITVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSQKGPQPPFAGLLH
28	DQB1*06:01:01:01	RDPPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEDVARFDSDEGVYRAVTEPGRPDAAEY WNSQKDLERTRAEELDTVCRHNYEVAFRGILQRRVEPTVTISPSRTAEALNHNHLLVCSVT DFYPSQIKVRFNRNDQEETAGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QSPITVWRAQSESAQSKMLSGIGGFVLGLIFLGLGLIIRQRSQKGPQPPFAGLLH
29	DQB1*06:02:01:01	RDSPEDFVYQFKAMCYFTNGTERVRYVTRYIYNREEVARFDSDEGVYRAVTEPGRPDAAEY WNSQKEVLEGRASVDRVCRHNYEVAFRGILQRRVEPTVTISPSRTAEALNHNHLLVCSVT DFYPSQIKVRFNRNDQEETAGVVSTPLIRNGDWTFQILVMLEMTPOHGDVYTCHVEHPSL QSPITVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRQRSQKGPQPPFAGLLH
30	DRB1*01:01:01:01	GDTRPRFLWQLKTECHFFNGTERVRLLERCIYNQEESEVRFDSDEGVYRAVTELGPRDAAEY WNSQKDLLEQRAAADVTYCRHNYGVGESFTVQRARVEPKVTIYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKAGVVSTGLIQNGDWTFQILVMLETVPRSGEVYTCCQVEHPSV TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIYFRNQKQGHSGLQPTGFSL
31	DRB1*01:02:01:01	GDTRPRFLWQLKTECHFFNGTERVRLLERCIYNQEESEVRFDSDEGVYRAVTELGPRDAAEY WNSQKDLLEQRAAADVTYCRHNYGVGESFTVQRARVEPKVTIYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKAGVVSTGLIQNGDWTFQILVMLETVPRSGEVYTCCQVEHPSV TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIYFRNQKQGHSGLQPTGFSL
32	DRB1*01:03:01	GDTRPRFLWQLKTECHFFNGTERVRLLERCIYNQEESEVRFDSDEGVYRAVTELGPRDAAEY WNSQKDLLEQRAAADVTYCRHNYGVGESFTVQRARVEPKVTIYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKAGVVSTGLIQNGDWTFQILVMLETVPRSGEVYTCCQVEHPSV TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIYFRNQKQGHSGLQPTGFSL
33	DRB1*03:01:01:01	GDTRPRFLEYSTSECHFFNGTERVRYLDRIYFHQEEENVRFDSDVGEYRAVTELGPRDAAEY WNSQKDLLEQKGRVVDNYCRHNYGVGESFTVQRARVHPKVTIYPSKIQPLQHHNLLVCSVS GFYPSGIEVRNFRNGQEEKIGVVSTGLIRNGDWTFQILVMLETVPRSGEVYTCCQVEHPSL TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIYFRNQKQGHSGLQPTGFSL
34	DRB1*04:01:01:01	GDTRPRFLEQVKKHECHFFNGTERVRLDRYFHQEEYVRFDSDEGVYRAVTELGPRDAAEY WNSQKDLLEQKRAAADVTYCRHNYGVGESFTVQRARVPEVTIYPSKIQPLQHHNLLVCSVN GFYPSGIEVRNFRNGQEEKIGVVSTGLIQNGDWTFQILVMLETVPRSGEVYTCCQVEHPSL TSPLTVWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIYFRNQKQGHSGLQPTGFSL

Fig. 29 continued

SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
35	DRB1*04:02:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRFYFHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDILEERRAAVDITYCRHNYGVVESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
36	DRB1*04:03:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRFYFHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVVESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
37	DRB1*04:04:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRFYFHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVVESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
38	DRB1*04:05:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRFYFHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVGESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
39	DRB1*04:06:01:01	GDTRPRFLEQVNHCHFFNGSTERVRFLEDRFYFHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVGESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVN GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSL TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
40	DRB1*07:01:01:01	GDTRPRFLWQKYNCHFFNGSTERVQFLERLFYHQQEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLLEQRAAEVDITYCRHNYGVGESFTVQRRVYPEVTIVYPANTQPLQHHNLLVCSVS GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSV MSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
41	DRB1*08:01:01	GDTRPRFLEYSSTGEYFFNGSTERVRFLEDRFYFHQEEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLFLEERRALVDITYCRHNYGVGESFTVQRRVHPEVTIVYPANTQPLQHHNLLVCSVS GFYFGSIEVRWFRNGQEEKTVGVSTGLIHNGDWTFQILVMLETIVPRSGEVYTCQVEHPSV TSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
42	DRB1*09:01:02:01	GDTRPRFLKQDKECHFFNGSTERVRYLHRIYHQQEYVRFDSDVGEYRAVTELGREDAEY WNSQNDLFLEERRAEVDITYCRHNYGVGESFTVQRRVHPEVTIVYPANTQPLQHHNLLVCSVS GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSV MSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS
43	DRB1*10:01:01:01	GDTRPRFLEEVNFECHFFNGSTERVRLERRVHQQEYVARYDSDVGEYRAVTELGREDAEY WNSQNDLLEERRAAVDITYCRHNYGVGESFTVQRRVQPKVTIVYPANTQPLQHHNLLVCSVN GFYFGSIEVRWFRNGQEEKTVGVSTGLIQNGDWTFQILVMLETIVPRSGEVYTCQVEHPSV MSPLTIVENRARSESAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKGHSGLQPTGFLS

Fig. 29 continued

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

Fig. 29 continued

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SEQ ID NO.	HLA Allele Name	Mature Protein Sequence
53	DRB1*16:01:01:01	GDTRPRFLWQPKRECHFFNGTIERVRFDRYFYNGQESVRFDSVGEYRAVTELGPRPDAEY WNSQKDFLEDRAAAYDTYCRHNYGVGESFTVQRRVQPKVTVYPSKTPQLQHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSV TSPLTVEWRARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGQLQPTGFLS
54	DRB3*01:01:02:01	GDTRPRFLELRKSECHFFNGTIERVRYLDRYFHNQEEFLRDSVGEYRAVTELGPRPVAES WNSQKDLLEQKRGRVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTPQLQHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSV TSALTVEWRARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGQLQPTGFLS
55	DRB3*02:02:01:01	GDTRPRFLELLKSECHFFNGTIERVRFLEHFNQEEYARFDSVGEYRAVTELGPRPDAEY WNSQKDLLEQNRGQVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTPQLQHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSV TSPLTVEWSARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGQLQPTGFLS
56	DRB3*03:01:01:01	GDTRPRFLELLKSECHFFNGTIERVRFLEHFNQEEFVRFDSVGEYRAVTELGPRPVAES WNSQKDLLEQNRGQVDNYCRHNYGVGESFTVQRRVHPQVTVYPAKTPQLQHNLLVCSVS GFYPGSIIEVRNFFNGQEEKAGVSTGLIHNGDWTFQTLVMLETVPRSGEVYTCQVEHPSV TSPLTVEWRARSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGQLQPTGFLS
57	DRB4*01:03:01:01	GDTQPRFLEQAKCECHFFNGTIERVWNLIRVIYNGQEEVARYNSDLGEYQAVTELGPRPDAEY WNSQKDLLEERRAEVDITYCRINYGVGESFTVQRRVQPKVTVYPSKTPQLQHNLLVCSVN GFYPGSIIEVRNFFNGQEEKAGVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSM NSPLTVQWSARSESQAQSKMLSGVGGFVLGLLFLGTGLFIYFRNQKHSGQLQPTGLLS
58	DRB5*01:01:01:01	GDTRPRFLQDQKYECHFFNGTIERVRFLEHDIYNGQEEELRFDSVGEYRAVTELGPRPDAEY WNSQKDFLEDRAAAYDTYCRHNYGVGESFTVQRRVEPKVTVYPAKTPQLQHNLLVCSVN GFYPGSIIEVRNFFNSQZEKAGVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSV TSPLTVEWRAQSESQAQSKMLSGVGGFVLGLLFLGAGLFIYFRNQKHSGSLHPTGLVS

Fig. 29 continued

[illegible]

Fig. 30

DQA1* 05.05	GATCAGATCTACCCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACCCCGTATGAGCCCTGTGGAGGTGAAGAC ATTGTGGCTGACCCATGCTGCTCTTATGCTGTAAACTTGTACCACTCTTACGCTCCCTCTGGCCAGTACACCCATGAATTTGATGGAGATGAG CAGTTCTACGTGACCTGGGGAGGAAGGAGACTGCTGTGTTTGGCTGTCTCAGACAATTTAGATTGACCCGCAATTTGCACTGACAAA CATGCTGTCTCTAAACATAACTTGAACAGTGTGATTAAGGCTCTCAACTCTACCGCTGCTACCAATGAGGTTCTGAGGTCCAGTGTCTTTCC AAGTCTCCCGTGACACTGGGTGAGGCCAAGATCTCATCTGTGTTGTGGACAAACATCTTCTCCTGTGGTCAACATCAGATGCTGAGCAAT GGGCACTCAGTACAGAAAGGTGTTTCTGAGACCAAGCTTCTCTCCAAAGTGTATCTCTCTTCAAGATCAGTTACCTCAACCTCTCTCTCT CTGCTGAGGAGAGTTATGACTGCAAGGTGGAGCACTGGGGACTGGACAAGCCCTCTCTGAAACACTGGGGAGCCCTGAGATTCCAGCCCTA TGTACAGAGCTCACAGAGAGTGTGCTGCGCCCTGGGGTGTGTTGTGGGCTCTGTTGGCAATGTGGTGGGCACTGTCTTCTATCATCCGAG GCCCTGCTTCAGTTGTGCTTCCAGACACCAAGGGCCCTGTGTACTGGAGGATC	63
DQA1*0 5.05	GATCAGATCTACCCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACCCCGTATGAGCCCTGTGGAGGTGAAGAC ATTGTGGCTGACCCATGCTGCTCTTATGCTGTAAACTTGTACCACTCTTACGCTCCCTCTGGCCAGTACACCCATGAATTTGATGGAGATGAG CAGTTCTACGTGACCTGGGGAGGAAGGAGACTGCTGTGTTTGGCTGTCTCAGACAATTTAGATTGACCCGCAATTTGCACTGACAAA CATGCTGTCTCTAAACATAACTTGAACAGTGTGATTAAGGCTCTCAACTCTACCGCTGCTACCAATGAGGTTCTGAGGTCCAGTGTCTTTCC AAGTCTCCCGTGACACTGGGTGAGGCCAAGATCTCATCTGTGTTGTGGACAAACATCTTCTCCTGTGGTCAACATCAGATGCTGAGCAAT GGGCACTCAGTACAGAAAGGTGTTTCTGAGACCAAGCTTCTCTCCAAAGTGTATCTCTCTTCAAGATCAGTTACCTCAACCTCTCTCTCT CTGCTGAGGAGAGTTATGACTGCAAGGTGGAGCACTGGGGACTGGACAAGCCCTCTCTGAAACACTGGGGAGCCCTGAGATTCCAGCCCTA TGTACAGAGCTCACAGAGAGTGTGCTGCGCCCTGGGGTGTGTTGTGGGCTCTGTTGGCAATGTGGTGGGCACTGTCTTCTATCATCCGAG GCCCTGCTTCAGTTGTGCTTCCAGACACCAAGGGCCCTGTGTACTGGAGGATC	64
DQB1*0 2.01 K71E	GATCAGATCTACCCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACCCCGTATGAGCCCTGTGGAGGTGAAGAC AGCACCCCATGCTGGTGAAGGGCAGAGACTCTCCGAGGATTTCTGTACCACTTTAAGGGCATGTGCTACTTCCACCAACGGGACAGAGCCG GTGCTGCTTGTGAGCAGAGGATCTATAACCGAGAGAGAGATGCTGCGCTTCCAGACGCGACGTGGGGGGAGTTCCGGGGGGTGAAGCTGCT GGGGCTGGCTGCGCGAGTACTGTGAACAGCCAGGAAGGACATCTGTGAGAGGGGAACGGGGCGGGGTGGACAGGGTGTGCAAGACACA ACTATCAGTTTGAAGCTCCGACAGACTGTGCAAGCGGGAGTGGAGGCCAGAGTACCATCTCCCATCCAGGACAGAGGGCCCTCAACCAAC ACAACCTGTGCTGCTGCTGGTACAGATTTCTATCCAGCCAGATCAAAAGTCCGGTGGTTTGGGAATGACCAAGAGGAGACAGCTGGGG TTGTGCTCACCCCTCTTATTAGGAATGGTGTACTGGACCTTCCAGATCTGTGATGCTGGAATGACTCCCAAGCGTGGAGACGCTACACCC TGCACAGTGGAGCACCCAGCCCTCAGAGCCCATCACCCGTGGAGTGGCGGGCTCAATCTGAATCTGCCAGAGCAAGATGCTGAGTGG CAATTGGAGGCTTGTGCTGGGGCTGATCTCTCTGGGCTGGCCCTTATCATCATCAGAGGATCAGAAAGGGCTCTGCACTGACTGAG GATC	65
DQB1*0 2.01 K71T	GATCAGATCTACCCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACCCCGTATGAGCCCTGTGGAGGTGAAGAC AGCACCCCATGCTGGTGAAGGGCAGAGACTCTCCGAGGATTTCTGTACCACTTTAAGGGCATGTGCTACTTCCACCAACGGGACAGAGCCG GTGCTGCTTGTGAGCAGAGGATCTATAACCGAGAGAGAGATGCTGCGCTTCCAGACGCGACGTGGGGGGAGTTCCGGGGGGTGAAGCTGCT GGGGCTGGCTGCGCGAGTACTGTGAACAGCCAGGAAGGACATCTGTGAGAGGGGAACGGGGCGGGGTGGACAGGGTGTGCAAGACACA CTACCAAGTTGGAGCTCCGACAGACTTGTGAGCGGGGAGTGGAGGCCACAGTGACCATCTCCCATCCAGGACAGAGGGCCCTCAACCAACCA CAACCTGTGCTGCTGCTGGTACAGATTTCTATCCAGCCAGATCAAAAGTCCGGTGGTTTCTGGAATGACCAAGGAGAGACAGCTGGGGTT GTGCTCACCCCTCTTATTAGGAATGGTGTACTGTGACCTTCCAGATCTGTGATGCTGGAATGACTCCCAAGCGTGGAGAGCTACACCT GCCAGCTGGAGCACCCAGCCCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAATCTGCCAGAGCAAGATGCTGAGTGGC ATTGGAGGCTTGTGCTGGGGCTGATCTTCTCGGGCTGGGCTTATCATCATCAGAGGATCAGAAAGGGCTCTGCACTGACTGAG GATC	66
DQB1*0 301	GATCAGATCTACCCATGATCCAAACAAAGCTGTGATGCTGGGGACCCCTGCCCCGACCCCGTATGAGCCCTGTGGAGGTGAAGAC AGCACCCCATGCTGGTGAAGGGCAGAGACTCTCCGAGGATTTCTGTACCACTTTAAGGGCATGTGCTACTTCCACCAACGGGACAGAGCCG GTGCTGCTTGTGAGCAGAGGATCTATAACCGAGAGAGAGATGCTGCGCTTCCAGACGCGACGTGGGGGGAGTTCCGGGGGGTGAAGCTGCT GGGGCTGGCTGCGCGAGTACTGTGAACAGCCAGGAAGGACATCTGTGAGAGGGGAACGGGGCGGGGTGGACAGGGTGTGCAAGACACA CTACCAAGTTGGAGCTCCGACAGACTTGTGAGCGGGGAGTGGAGGCCACAGTGACCATCTCCCATCCAGGACAGAGGGCCCTCAACCAACCA CAACCTGTGCTGCTGCTGGTACAGATTTCTATCCAGCCAGATCAAAAGTCCGGTGGTTTCTGGAATGACCAAGGAGAGACAGCTGGGGTT GTGCTCACCCCTCTTATTAGGAATGGTGTACTGTGACCTTCCAGATCTGTGATGCTGGAATGACTCCCAAGCGTGGAGAGCTACACCT GCCAGCTGGAGCACCCAGCCCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAATCTGCCAGAGCAAGATGCTGAGTGGC GCCAGCTGGAGCACCCAGCCCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAATCTGCCAGAGCAAGATGCTGAGTGGC ATTGGAGGCTTGTGCTGGGGCTGATCTTCTCGGGCTGGGCTTATCATCATCAGAGGATCAGAAAGGGCTCTGCACTGACTGAG GATC	67

Fig. 30 continued

DQB1*0302A57D	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCACCDCCGTGCTGAGSGCCAGAGACTCTCCGAGGATTTCGTGTACCAAGTTTAAGGGCATGTGCTACTTCAACCAACGGGACGGGAGCGCGTGTGGCTCTGTGTAGCAGATACATCTATAACDGGAGAGAGTACGCAAGCTTGGACAGGACGTTGGGGTGTATGGGGCGGTGACGCGGCCTGGGGCGGCGCTGACGCGAGTACTGGAACAGCCAG AAGTCTCTGGAGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACCTTGCAGGCGGAGAGTGGAGGCCACAGTGACCATCTCCCATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGCTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGACCCAGAGGAGACAACTGSGCTTGTGTCCACCCCGCTTATTAGGAACGGGTGACTGGACCTTCAGATCCTGTGTATGCTGGAAATGACTCCOCAGCGTGGAGACGTCTACACCTGCCACGSGAGGACCCAGCGCTCCAGAACCCCATGCTGSGAGTGGCGGGCTGATGAAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGTGTGTGGGCTGATCTCCGCGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTGTGCACTGACTCGAGGATGGCTGTGCACTGACTCGAGGATC	68
DQB1*0357	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCACCDCCGTGCTGAGSGCCAGAGACTCTCCGAGGATTTCGTGTACCAAGTTTAAGGGCATGTGCTACTTCAACCAACGGGACGGGAGCGCGTGTGGCTCTGTGTAGCAGATACATCTATAACDGGAGAGAGTACGCAAGCTTGGACAGGACGTTGGGGTGTATGGGGCGGTGACGCGGCCTGGGGCGGCGCTGACGCGAGTACTGGAACAGCCAG AAGTCTCTGGAGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACCTTGCAGGCGGAGAGTGGAGGCCACAGTGACCATCTCCCATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGCTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGACCCAGAGGAGACAACTGSGCTTGTGTCCACCCCGCTTATTAGGAACGGGTGACTGGACCTTCAGATCCTGTGTATGCTGGAAATGACTCCOCAGCGTGGAGACGTCTACACCTGCCACGSGAGGACCCAGCGCTCCAGAACCCCATGCTGSGAGTGGCGGGCTGATGAAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGTGTGTGGGCTGATCTCCGCGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTGTGCACTGACTCGAGGATC	69
DQB1*0604	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCCTCCTACTGCTGAGGGGACAGAGACTCTCCGAGGATTTCGTGTACCAAGTTTAAGGGCATGTGCTACTTCAACCAACGGGACGGGAGCGCGCTGTGGCTCTGTGTAGCAGATACATCTATAACDGGAGAGAGTACGCAAGCTTGGACAGGACGTTGGGGTGTATGGGGCGGTGACGCGGCCTGGGGCGGCGCTTGGCGAGTACTGGAACAGCCAG AAGTCTCTGGAGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACCTTGCAGGCGGAGAGTGGAGGCCACAGTGACCATCTCCCATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGCTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGATCCAGAGGAGACAGCCGCGCTGTGTGTCCACCCCGCTTATTAGGAATGGTGTACTGGACCTTCAGATCCTGTGTATGCTGGAAATGACTCCOCAGCGTGGAGATGCTACACCTTGGCACGSGAGGACCCAGCGCTCCAGAACCCCATCAGGSGAGTGGCGGGCTGATGAAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGTGTGTGGGCTGATCTCCGCGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTGTGCACTGACTCGAGGATC	70
DRB1*0301V86L	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCCTCCTACTGCTGAGGGGACACAGACCAAGCTTTCGTGGAGTACTCTAGCTGTGTCATTTCTCAATGGGACGGAGCGGGTGGGGTACCCTGGACAGATACTTCCATAACAGGAGGAGAGAGTGGCTTGGACAGCGAGCTGGGGGAGTTCCGGGGCGGTGACGGAGCTGGGGGCGGCTGTGATGCTGGAGTACTGGAACAGCCAG AAGTCTCTGGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACCTTGCAGGCGGAGTGGAGGCCACAGTGACCATCTCCCATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGATCCAGAGGAGACAGCCGCGCTGTGTGTCCACCCCGCTTATTAGGAATGGTGTACTGGACCTTCAGATCCTGTGTATGCTGGAAATGACTCCOCAGCGTGGAGATGCTACACCTTGGCACGSGAGGACCCAGCGCTCCAGAACCCCATCAGGSGAGTGGCGGGCTGATGAAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGTGTGTGGGCTGATCTCCGCGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTGTGCACTGACTCGAGGATC	71
DRB1*0301V86M	GATCAGATCTACCCACCATGTCCTTGG AAG AAGGCTTTGCGGATCCCTGGAGGCTTGGGGTAGCAACTGTGACCTTGATGCTGGCGATGCTGAGCCTCCTACTGCTGAGGGGACACAGACCAAGCTTTCGTGGAGTACTCTAGCTGTGTCATTTCTCAATGGGACGGAGCGGGTGGGGTACCCTGGACAGATACTTCCATAACAGGAGGAGAGAGTGGCTTGGACAGCGAGCTGGGGGAGTTCCGGGGCGGTGACGGAGCTGGGGGCGGCTGTGATGCTGGAGTACTGGAACAGCCAG AAGTCTCTGGAGGACCCGGGCGGAGTTGGACACGGTGTGTCAGACACA ACTACCAGTTG GAGCTCCGCAAGACCTTGCAGGCGGAGTGGAGGCCACAGTGACCATCTCCCATCCAGSACAGAGGCGCCCAACCAACCACCAACCTGCTGGCTGTGTCAGTACAGATTCTATCCAGCCAGATCAAGTCCGCTGGTTTGGGAATGATCCAGAGGAGACAGCCGCGCTGTGTGTCCACCCCGCTTATTAGGAATGGTGTACTGGACCTTCAGATCCTGTGTATGCTGGAAATGACTCCOCAGCGTGGAGATGCTACACCTTGGCACGSGAGGACCCAGCGCTCCAGAACCCCATCAGGSGAGTGGCGGGCTGATGAAATGTGCCAGAGCAAGATGCTGAGTGGCTATTGGAGGCTTGTGTGTGGGCTGATCTCCGCGGCTGGGCTTATTATCCATCAGAGGAGTCAGAAAGGGCTCTGTGCACTGACTCGAGGATC	72

Fig. 30 continued

DRS1*Q 4.01 G86F	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TTTTSAGAGCTTCACAGTG CAGCGGGGAGTCTATCCTGAGGTGACTG TGATCTCTGCAAGAGACCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGCTTCGGGAACGGCCAGGAAGAGAACTGGGGTGTGTCCACA GGCTGTATCCAGAAAGGAGACTGAGCTTCACAGACCTCTGAGTCTGCTGCTGGAAGAGTTCTCTGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGAGGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGGAATCTGACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTCGTGCTGGGGCTGCTCTCTCTGGGGGGGGCTGTTTCTACTCTCAGGAATCAGAAAGGACACTCTGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	73
DRS1*Q 4.01 G86L	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TCTTGAAGAGTTCTACAGTGCGAGGGCGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGCTTCGGGAACGGCCAGGAAGAGAACTGGGGTGTGTCCACA GGCTGTATCCAGAAAGGAGACTGAGCTTCACAGACCTCTGAGTCTGCTGCTGGAAGAGTTCTCTGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGAGGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGGAATCTGACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTCGTGCTGGGGCTGCTCTCTCTGGGGGGGGCTGTTTCTACTCTCAGGAATCAGAAAGGACACTCTGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	74
DRS1*Q 4.01 G86M	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TATGAGAGAGCTTCACAGTGCGAGGGCGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGCTTCGGGAACGGCCAGGAAGAGAACTGGGGTGTGTCCACA GGCTGTATCCAGAAAGGAGACTGAGCTTCACAGACCTCTGAGTCTGCTGCTGGAAGAGTTCTCTGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGAGGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGGAATCTGACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTCGTGCTGGGGCTGCTCTCTCTGGGGGGGGCTGTTTCTACTCTCAGGAATCAGAAAGGACACTCTGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	75
DRS1*Q 4.03 R71E	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TGTGAGAGAGCTTCACAGTGCGAGGGCGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGCTTCGGGAACGGCCAGGAAGAGAACTGGGGTGTGTCCACA GGCTGTATCCAGAAAGGAGACTGAGCTTCACAGACCTCTGAGTCTGCTGCTGGAAGAGTTCTCTGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGAGGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGGAATCTGACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTCGTGCTGGGGCTGCTCTCTCTGGGGGGGGCTGTTTCTACTCTCAGGAATCAGAAAGGACACTCTGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	76
DRS1*Q 4.04 R71E	GATCAGATCTACCCACCATGCTG TGTCGAAGTTCCCTGGAGGCTCCTGCATGSCAGCTCTGACAGTGACACTGATGCTGCTGAGCTCCCCA CTGGCTTTGGCTGSGGACACCCGACCCAGCTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGGGGCTGGCTTC CTGGACAGATACCTTCTATCACCAGAGGAGTACGTGCGCTTCGACAGCGACGTGGGGAGTACCGGGGGCTGACGGAGCTGGGGGGC CTGATGCCAGTACTGGAACAGCCAGAGGACCTCCTGAGCAGAGCGGGGGGGCTGGACACCTACTGACAGACACAACTACGGGGT TGTGAGAGAGCTTCACAGTGCGAGGGCGAGTCTATCCTGAGGTGACTGCTGATCTCTGCAAGAGCCAGCCCCCTGACGACCCACAACTCCTG GTCTGCTCTGTAATGCTTCTATCCAGGCGAGCATGGAAGTCAGGTGCTTCGGGAACGGCCAGGAAGAGAACTGGGGTGTGTCCACA GGCTGTATCCAGAAAGGAGACTGAGCTTCACAGACCTCTGAGTCTGCTGCTGGAAGAGTTCTCTGGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCAAAGCCTGAGGAGCCCTCTACAGTGGAATGGAGAGCAGGCTCTGGAATCTGACAGAGCAAGATGCTGAGTGGAGTGGGG GCTTCGTGCTGGGGCTGCTCTCTCTGGGGGGGGCTGTTTCTACTCTCAGGAATCAGAAAGGACACTCTGACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	77

Fig. 30 continued

DRB1*0 4.05 R71E	GATCAGATCTACCCATGGTG TGCTGAAGTTCCCTCGAGGCTCCTG CATGGCAGCTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGGACACCCGACCACTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGCGGGTGCGGTTT CTGGACAGATACCTTATCAACAGAGGAGTAGTGCTGCTTGACAGCGACGTGGGGAGTACCGGGCGGTGACGGAGCTGGGGGGG CTAGCGCGAGTACTGSAACAGCCAGAGGACCTCTCTGAGCAGGAGCGGGCGGGTGAGACCTACTGACAGACAACTACGGGGT TGGTGAGAGCTTACAGTGCGAGCGCGAGTCTATCCTGAGGTTGACTGTATCTCTGCAAGAGCCAGCCCTGCGAGCACACAACTCTCTG GTCTGCTCTGTGAATGGTTTCTATCCAGGAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAAGAAAGTGGGGTGTTCCACA GGCCTGATCCAGAAATGGAGACTGGACCTCCAGACCTGGTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCCAAGCTGACGAGCCCTCTACAGTGGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGAGTGCGGG GCTTGGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCTACTACTTACAGGAATCAGAAAGGACACTCTGSACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	78
DRB1*0 4.08 R71E	GATCAGATCTACCCATGGTG TGCTGAAGTTCCCTCGAGGCTCCTG CATGGCAGCTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGGACACCCGACCACTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGCGGGTGCGGTTT CTGGACAGATACCTTATCAACAGAGGAGTAGTGCTGCTTGACAGCGAGTGCGGGAGTACCGGGCGGTGACGGAGCTGGGGGGG CTGATGCCAGTACTGSAACAGCCAGAGGACCTCTCTGAGCAGGAGCGGGCGGGTGAGACCTACTGACAGACAACTACGGGGT TGGTGAGAGCTTACAGTGCGAGCGCGAGTCTATCCTGAGGTTGACTGTATCTCTGCAAGAGCCAGCCCTGCGAGCACACAACTCTCTG GTCTGCTCTGTGAATGGTTTCTATCCAGGAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAAGAAAGTGGGGTGTTCCACA GGCCTGATCCAGAAATGGAGACTGGACCTCCAGACCTGGTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGTG GAGCACCCCAAGCTGACGAGCCCTCTACAGTGGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGAGTGCGGG GCTTGGTGCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCTACTACTTACAGGAATCAGAAAGGACACTCTGSACTTCAGCCACAGGATTC CTGAGCTGACTCGAGGATC	79
DRB1*0 7.01	GATCAGATCTACCCATGGTG TGCTGAAGTTCCCTCGAGGCTCCTG CATGGCAGCTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGGACACCCGACCACTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGCGGGTGCGGTTT TGGAAGAGCTTCTATCAACAGGAGGAGTTCTGCTGCTTGACAGCGAGTGCGGGAGTACCGGGCGGTGACGGAGCTAGGGCGGGC TGTCGCCAGTCTGSAACAGCCAGAGGACATCTCTGAGGAGCAGGCGGGGGCCAGGTGGACACCGTGTCAGACACAACTACGGGGT GGTGAGAGCTTCTACAGTGCGAGCGCGAGTCTATCCTGAGGTTGACTGTATCTCTGCAAGAGCTTACCGCCCTGCGAGGACCACTCTCTG GTCTGCTCTGTGAATGGTTTCTATCCAGGAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAAGAAAGTGGGGTGTTCCACA AGGCCCTGATCCAGAAATGGAGACTGGACCTCTCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGT GGAGCACCCCAAGTGTGATGAGCCCTCTCAGAGTGGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGAGTGCGGG GGCTTTGTCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCTACTACTTACAGGAATCAGAAAGGACACTCTGSACTTCAGCCACAGGATT CTGAGCTGACTCGAGGATC	80
DRB1*0 9.01	GATCAGATCTACCCATGGTG TGCTGAAGTTCCCTCGAGGCTCCTG CATGGCAGCTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGGACACCCGACCACTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGCGGGTGCGGTTT TGACAGAGGAGCTTATCAACAGAGGAGGAACCTGCTGCTTGACAGCGAGTGCGGGAGTACCGGGCGGTGACGGAGCTGGGGGGG CTGTGCGCGAGTCTGSAACAGCCAGAGGACCTCTCTGAGCGGAGCGGGCGCGAGGTGACACCGTGTCAGACACAACTACGGGGT TGGTGAGAGCTTACAGTGCGAGCGCGAGTCTATCCTGAGGTTGACTGTATCTCTGCAAGAGCTTACCGCCCTGCGAGGACCACTCTCTG GTCTGCTCTGTGAATGGTTTCTATCCAGGAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAAGAAAGTGGGGTGTTCCACA AGGCCCTGATCCAGAAATGGAGACTGGACCTCTCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGT GGAGCACCCCAAGTGTGATGAGCCCTCTCAGAGTGGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGAGTGCGGG GGCTTTGTCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCTACTACTTACAGGAATCAGAAAGGACACTCTGSACTTCAGCCACAGGATT CTGAGCTGACTCGAGGATC	81
DRB1*1 0.01	GATCAGATCTACCCATGGTG TGCTGAAGTTCCCTCGAGGCTCCTG CATGGCAGCTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGGACACCCGACCACTTTCTTGGAGCAGGTTAAACATGAGTGTCATTCTTCAACGGGACGGAGCGGGTGCGGTTT CTGGAAAGAGCGGCTTCAACCAAGAGGAGTAGTGCTGCTTGACAGCGAGTGCGGGAGTACCGGGCGGTGACGGAGCTGGGGGGG GCTGATGGAGTACTGSAACAGCCAGAGGACCTCTCTGAGCGGAGCGGGCGGGTGAGACCTACTGACAGACAACTACGGGGT GTTGGTGAGAGCTTACAGTGCGAGCGCGAGTTCAACCTAAGGTGACTGTATCTCTTCAAGAGCCAGCCCTGCGAGCACCAACCTCTG TGGTCTGTTCTGTGAATGGTTTCTATCCAGGAGCATTTGAATCAGGTGGTTCCGGAACGGCCAGGAAAGAAAGTGGGGTGTTCCACA CGGGCCTGATCCAGAAATGGAGACTGGACCTCTCAGACCTGCTGATGCTGGAAACAGTTCTCTCGAGTGGAGAGGTTTACACCTGCCAAGT TGGAGACCCCAAGTGTGATGAGCCCTCTCAGAGTGGAATGGAGAGCAAGCTCTGAATCTGCACAGAGCAAGATGCTGAGTGAGTGCGGG GGCTTTGTCTGGGCCCTGCTCTCTTGGGGCGGGGCTGTTCTACTACTTACAGGAATCAGAAAGGACACTCTGSACTTCAGCCACAGGATT CTGAGCTGACTCGAGGATC	82

Fig. 30 continued

DRB1*1 1.01	GATCAGATCTACCAACATGGTGTGCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTATACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GGTGAGAGCTTACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	83
DRB1*1 1.02	GATCAGATCTACCAACATGGTGTGCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTATACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GTGGAGAGCTTACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	84
DRB1*1 1.03	GATCAGATCTACCAACATGGTGTGCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTATACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GTGGAGAGCTTACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	85
DRB1*1 2.01	GATCAGATCTACCAACATGGTGTGCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTATACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GTGGAGAGCTTACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	86
DRB1*1 501 A71R	GATCAGATCTACCAACATGGTGTGCTGAGGCTCCCTGAGGCTCCCTGATGGCAGTTCTGACAGTGACACTGATGGTGCTGAGCTCCCA CTGGCTTTGGCTGGGACACACAGACCAGTTTCTGGAGTACTCTACGCTGAGTGTCAATTCCTCAATGGGACGGAGCGGGTGCGGTTCC TGGACAGATACCTTATACCAAGAGGAGTACGCTGGCTTGGACAGCGACGTTGGGGAGTTCCGGGGCGGTGACGAGCTGGGGCGGG TGATGAGGAGTACTGGAACAGCCAGAAAGACTTCTGGAAGACAGCGGGCGGGGGTGAGACACTACTGCAGACACAACCTACGGGGTT GTGGAGAGCTTACAGTGCAGCGGGGAGTCCATCCTAAGGTGACTGTGTATCCTTCAAAGACCCAGCCCCCTGCAGCACCAACCTCCTGG TCTGTCTGTGAGTGGTTTCTATCCAGGCAGCATTTGAAGTCAAGGTGGTTCCGGAAATGGCCAGGAAGAGAAAGACTGGGGTGTTCCACAG GCCGTATCCACAATGGAGACTGGACCTTCCAGACCTGGTGTATGCTGGAAACAGTTCCCTGGAGTGGAGAGGTTTACACCTGCCAAGTGS AGCACCCAAAGCGTGACAAGCCCTCTCAGTGGAAATGGAGAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTGGGG CTTTGTGCTGGGCCCTGCTCTCTTGGGGCGGGCTGTTCACTACTTCAGGAATCAGAAAGGACACTCTGGGACTTCAGCCAGAGGATTCC TGAGCTGACTGAGGATC	87

Fig. 30 continued

0 RB1 *1 5.01 F47Y	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTTCAATGGAGCGGAGCGGGTGGCTTC CTGGACAGATCTTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGCGCGCTGGACACCTACTGACAGACAACTACGGGG TTGCTGAGAGCTTACAGTGCAGCGGGAGTCCAACTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCAC AGGCTGATCCAGAAATGGAGACTGACCTTCACAGACCTGCTGATGCTGGAAACAGTTCTGGAAGTGAGAGGTTTACACCTGCAAGT GGAGCACCCAGCGTGACAAAGCCCTCTCACAGTGGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGAGTCTGGG GGCTTTGCTGCTGGGCTGCTCTCTGCTGGGGCGGGCTGTCATCTACTTCAAGGAATCAGAAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	88
0 RB1 *1 501 V86L	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TCTGAGAGAGCTTACAGTGCAGCGGGAGTCCAACTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GAGCACCAGCGTGACAAAGCCCTCTCACAGTGGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGAGTCTGGGG GGCTTTGCTGCTGGGCTGCTCTCTGCTGGGGCGGGCTGTCATCTACTTCAAGGAATCAGAAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	89
0 RB1 *1 501 V86M	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TATGAGAGAGCTTACAGTGCAGCGGGAGTCCAACTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GAGCACCAGCGTGACAAAGCCCTCTCACAGTGGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGAGTCTGGGG GGCTTTGCTGCTGGGCTGCTCTCTGCTGGGGCGGGCTGTCATCTACTTCAAGGAATCAGAAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	90
0 RB1 *1 5.02_85 G [Gly@ pos85]	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TGGTGAGAGAGCTTACAGTGCAGCGGGAGTCCAACTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GAGCACCAGCGTGACAAAGCCCTCTCACAGTGGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGAGTCTGGGG GGCTTTGCTGCTGGGCTGCTCTCTGCTGGGGCGGGCTGTCATCTACTTCAAGGAATCAGAAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	91
0 RB1 *1 5.122_7 1R/86D {Arg@po s71/Gly @pos85 }	GATCAGATCTACCCACCATGCTGCTGTAAGCTCCCTGAGGGCTCTGCTGATGACACCGCTGACAGTGACACTGATGGTCTGAGCTCCCA CTGGCTTTGCTGCTGGGACACCCGACCCAGTTTCTGCTGGCAGCCTAAGAGGAGTGTCATTCTTCAATGGAGCGAGCGGGTGGCTTC CTGGACAGATCTTCTATAACDAGGAGGAGTCCGTCGCTTCGACAGCGAGCTGGGGAGTACCBSGGCGSTAGCGAGCTGGGGGG CCTGACGCTGAGTACTGGAACAGCCAGAGGACATCTGAGCAGCGCGGGCGCGCTGGACACCTACTGACAGACAACTACGGGGT TGGTGAGAGAGCTTACAGTGCAGCGGGAGTCCAACTAAGGCTGCTGATATCTTCAAGAGCCAGCCCTGCGAGCAACCAACCTCT GTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GGCTCTGCTCTGAGTGGTTTCTATCTCAGGCGAGCATTCAGTCAAGCTAGGCTTCTCTGAAAGCGCCAGGAAGAGAGGCTGGGATGGTGCACA GAGCACCAGCGTGACAAAGCCCTCTCACAGTGGAATGAGAGCAGGCTCTGAACTGACAGAGCAAGATGCTGAGTGAGTCTGGGG GGCTTTGCTGCTGGGCTGCTCTCTGCTGGGGCGGGCTGTCATCTACTTCAAGGAATCAGAAAGGACACTGCTGACTTCAAGCCACAGGATT CCTGAGCTGACTGAGGATC	92

Fig. 30 continued

