

Table S1 Amino acid residues combinations with positive BLOSUM scores.

Residues	BLOSUM	Residues	BLOSUM
A-S	+1	I-M	+1
D-E	+2	I-V	+3
D-N	+1	K-Q	+1
D-T	+1	K-R	+2
E-K	+1	L-M	+2
E-Q	+2	L-V	+1
F-W	+1	M-V	+1
F-Y	+3	N-S	+1
G-T	+1	P-T	+1
H-N	+1	Q-R	+1
H-Y	+2	S-T	+1
I-L	+2	W-Y	+2

Table S2 Results of a BLAST analysis between DRB1*01:01, DQB1*02:01 and DPB1*01:01 sequences.

DRB1*01:01 vs DQB1*02:01 p=3e-100 Identities: 130/190 (68%) Positives: 152/190 (80%) Gaps:0/190	
1	GDTRPRFLWQLKFECHFFNGTERVRLLERCIYNQEE SVRFSDVGEYRAVTDLGRPD AEYWNSQ
	D+ F++Q K C+F NGTERVRL+ R IYN+EE VRFSDVGE+RAVT LG P AEYWNSQ
1	RDSPEDFVYQFKGMCYFTNGTERVRLVSRSIYNREEI VRFSDVGEFRAVTL LGLPAAEYWNSQ
65	KDLEQRRAAVD TYCRHNYGVGESFTVQRRVEPKVTVYPSKTQPLQHNNLLVCSVSGFYPGS I
	KD+LE++RAAVD CRHNY + T+QRRVEP VT+ PS+T+ L HNNLLVCSV+ FYP I
65	KDILERKRAAVDRVCRHNYQLELR TTLQRRVEPTVTI SPSRTEALNHHNNLLVCSV TDFYPAQI
128	EVRWFRNGQEEKAGVVSTGLI +NGDWFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA
	+VRWFRN QEE AGVVST LI NGDWFQ LVMLE P+ G+VYTC VEHP S+ SP+TVEWRA
128	KVRWFRNDQEETAGVVSTPLIRNGDWFQILVMLEMPQRGDVYTCHVEHPSLQSPITVEWRA
DRB1*01:01 vs DPB1*01:01 p=8e-95 Identities: 127/190 (67%) Positives: 151/190 (79%) Gaps:3/190	
1	GDTRPRFLWQLKFECHFFNGTERVRLLERCIYNQEE SVRFSDVGEYRAVTDLGRPD AEYWNSQKD
	T ++++Q +EC FNGT+R LER IYN+EE RFDSDVGE+RAVT LGRP AEYWNSQKD
1	RATPENYVYQGRQECYAFNGTQRxxFLERYIYNREEYARFSDVGEFRAVTELGRPAAEYWNSQKD
67	LLEQRRAAVD TYCRHNYGVGESFTVQRRVEPKVTVYPSKTQPLQHNNLLVCSVSGFYPGS I EV
	+LE++RA D CRHNY + E+ T+QRRV+PKV V PSK PLQHNNLLVC V+ FYPGSI +V
65	I LEEKRAVPDRVCRHNYEL+EA VTLQRRVQPKVNVSPSKKGPLQHNNLLVCHVTDFYPGS IQV
130	RWFRNGQEEKAGVVSTGLIQNGDWFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA
	RWF NGQEE AGVVST LI+NGDWF LVMLE P+ G+VY CQVEH S+ SP+TVEW A
128	RWFLNGQEETAGVVSTNLIRNGDWFxILVMLEMPQQGDVYICQVEHTSLDSPVTVEWKA
DQB1*02:01 vs DPB1*01:01 p=8e-103 Identities: 138/190 (73%) Positives: 152/190 (80%) Gaps:3/190	
1	RDSPEDFVYQFKGMCYFTNGTERVRLVSRSIYNREEI VRFSDVGEFRAVTL LGLPAAEYWNSQ
	R +PE++VYQ + CY NGT+R + R IYNREE RFDSDVGEFRAVT LG PAAEYWNSQ
1	RATPENYVYQGRQECYAFNGTQRxxFLERYIYNREEYARFSDVGEFRAVTELGRPAAEYWNSQ
65	KDILERKRAAVDRVCRHNYQLELR TTLQRRVEPTVTI SPSRTEALNHHNNLLVCSV TDFYPAQ
	KDILE KRA DRVCRHNY+L+ TLQRRV+P V +SPS L HNNLLVC VTDFYP
63	KDILEEKRAVPDRVCRHNYELDEAVTLQRRVQPKVNVSPSKKGPLQHNNLLVCHVTDFYPGS
127	IKVRWFRNDQEETAGVVSTPLIRNGDWFQILVMLEMPQRGDVYTCHVEHPSLQSPITVEWRA
	I+VRWF N QEETAGVVST LIRNGDWF ILVMLEMPQ+GDVY C VEH SL SP+TVEW A
125	IQVRWFLNGQEETAGVVSTNLIRNGDWFxILVMLEMPQQGDVYICQVEHTSLDSPVTVEWKA

Table S3 Results of a BLAST analysis between DRA1*01:01, DQA1*01:01 and DPA1*01:03 sequences.

DRA1*01:01 vs DPA1*01:03 p=2e-81 Identities:118/187 (63%) Positives: 139/187 (74%)

3	IKEEHVIIQAEFYLNPDQSGEFMFDFDGDDEIFHVDMAKKETVWRLEEFGRFASFEAQGAL	60
	IK +HV A F +GEFMF+FD DE+F+VD+ KKETVW LEEFG+ SFEAQG L	
3	IKADHVSTYAAFVQTHRPTGEFMFEFDEDEMFYVDLDDKKETVWHLEEFQAFSFEAQGG	60
61	ANIAVDKANLEIMTKRSNYTPITNVPPEVTVLTNSPVELREPNVLCIFIDKFTPPVVNVT	120
	ANIA+ NL + +RSN+T TN PPEVTV PVEL +PN LIC IDKF PPV+NVT	
61	ANIAILNNLNTLIQRSNHTQATNDPPEVTVFPKEPVELGQPNTLICHIDKFFPPVLNVT	120
121	WLRNGKPVTTGVSETVFLPREDHLFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEFDAPSPLP	187
	WL NG+ VT GV+E++FLPR D+ F KFHYL F+PS ED YDCRVEHWGLD+PLLKHWE P +P	
121	WLCNGELVTEGVAESLFLPRTDYSFHKFHYLTFVPSAEDFYDCRVEHWGLDQPLLKHWEAQEPIQMP	187

DRA1*01:01 vs DQA1*01:01 p=8e-77 Identities:99/168 (59%) Positives 122/168 (72%)

19	SGEFMFDFDGDDEIFHVDMAKKETVWRLEEFGRFASFEAQGALANIAVDKANLEIMTKRSN	78
	SG++ +FDGDE F+VD+ +KET WR EF +F F+ QGAL N+AV K NL IM KR N	
20	SGQYTHEFDGDEQFYVDLERKETAWRWPEFSKFGGDFDQGALRNMAVAKHNLNIMIKRYN	79
79	YTPITNVPPEVTVLTNSPVELREPNVLCIFIDKFTPPVVNVTWLRNGKPVTTGVSETVFL	138
	T TN PEVTV + SPV L +PN LIC +D PPVVN+TWL NG+ VT GVSET FL	
80	STAATNEVPEVTVFSKSPVTLGQPNTLICLDNIFPPVVNITWLSNGQSVTEGVSETSFL	139
139	PREDHLFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEFDAPSPL	186
	+ DH F K YL FLPS +++YDC+VEHWGLD+PLLKHWE + P+ +	
140	SKSDHSFFKISYLTFLPSADEIYDCKVEHWGLDQPLLKHWEPEIPAQM	187

DQA1*01:01 vs DPA1*01:03 p=1e-77 Identities:109/187 (58%) Positives:139/187 (74%)

3	IVADHVASCNVLYQFYGPSGQYTHEFDGDEQFYVDLERKETAWRWPEFSKFGGDFDQGA	60
	I ADHV++ Q + P+G++ EFD DE FYVDL++KET W EF + F+ QG	
3	IKADHVSTYAA-FVQTHRPTGEFMFEFDEDEMFYVDLDDKKETVWHLEEFQAFSFEAQGG	59
61	LRNMAVAKHNLNIMIKRYNSTAATNEVPEVTVFSKSPVTLGQPNTLICLDNIFPPVVNI	120
	L N+A+ +NLN +I+R N T ATN+ PEVTVF K PV LGQPNTLIC +D FPPV+N+	
60	LANIAILNNLNTLIQRSNHTQATNDPPEVTVFPKEPVELGQPNTLICHIDKFFPPVLNV	119
121	TWLSNGQSVTEGVSETSFLSKSDHSFFKISYLTFLPSADEIYDCKVEHWGLDQPLLKHWEPEIPAQM	187
	TWL NG+ VTEGV+E+ FL ++D+SF K YLTF+PSA++ YDC+VEHWGLDQPLLKHWE + P QM	
120	TWLCNGELVTEGVAESLFLPRTDYSFHKFHYLTFVPSAEDFYDCRVEHWGLDQPLLKHWEAQEPIQM	186

Table S4 Allele sharing between interlocus class II eplets and amino acid residues within a 3.5 Ångstrom radius.

	14	24	25	26	27	40	42		
	E	V	R	Residue	V	F	S	Eplet	
DRB1*03:01	-	-	-	26Y	-	-	-	rq26Y	
DRB1*09:01	-	-	-	26Y	-	-	-	rq26Y	
DRB3*01:01	-	-	-	26Y	-	-	-	rq26Y	
DQB1*03:01	M	-	-	26Y	-	-	-	rq26Y	
DQB1*06:01	M	-	-	26Y	-	-	-	rq26Y	
	30	35	36	3738	39	48	50	54	
	Y	E	E	Residues	R	R	V	G	Eplet
DRB1*07:01	L	-	-	37F38V	-	-	-	-	rp37FV
DRB1*14:01	-	-	-	37F38V	-	-	-	-	rp37FV
DRB1*14:54	-	-	-	37F38V	-	-	-	-	rp37FV
DRB3*03:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*02:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*03:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*04:02	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*06:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*08:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*09:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*10:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*14:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*16:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*17:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*18:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*19:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*20:01	-	-	-	37F38V	-	-	-	-	rp37FV
DPB1*23:01	-	-	-	37F38V	-	-	-	-	rp37FV
	30	35	36	3738	39	48	50	54	
	Y	E	E	Residues	R	R	V	G	Eplet
DRB1*10:01	R	-	-	37Y38A	-	-	-	-	raqp37YA
DRB3*02:02	H*	-	-	37Y38A	-	-	-	-	raqp37YA
DRB4*01:01	-	-	-	37Y38A	-	Q*	-	-	raqp37YA
DRB4*01:03	-	-	-	37Y38A	-	Q*	-	-	raqp37YA
DQB1*03:01	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*03:02	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*03:03	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*04:01	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*04:02	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*06:02	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*06:03	H*	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*06:04	H*	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*06:05	-	-	-	37Y38A	-	-	-	-	raqp37YA
DQB1*06:09	-	-	-	37Y38A	-	-	-	-	raqp37YA
DPB1*01:01	-	-	-	37Y38A	-	-	-	-	raqp37YA
DPB1*11:01	-	-	-	37Y38A	-	-	-	-	raqp37YA
DPB1*13:01	-	-	-	37Y38A	-	-	-	-	raqp37YA
DPB1*15:01	-	-	-	37Y38A	-	-	-	-	raqp37YA

	30	35	36	3738	39	48	50	54	
	Y	E	E	Residues	R	R	V	G	Eplet
DRB1*04:01	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*04:02	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*04:03	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*04:04	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*04:05	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*08:01	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*08:02	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*11:01	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*11:02	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*11:04	-	-	-	37Y38V	-	-	-	-	rq37YV
DRB1*13:03	-	-	-	37Y38V	-	-	-	-	rq37YV
DQB1*05:01	H*	-	-	37Y38V	-	-	-	-	rq37YV
DQB1*05:02	H*	-	-	37Y38V	-	-	-	-	rq37YV

	64	65	66	6770	68	69	71	72	73	
	Q	K	D	Residues	L	E	K	R	A	Eplet
DQB1*04:01	-	-	-	67I70E	-	-	D	-	-	qp67IE
DQB1*04:02	-	-	-	67I70E	-	-	D	-	-	qp67IE
DPB1*01:01	-	-	-	67I70E	-	-	-	-	-	qp67IE
DPB1*02:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*02:02	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*04:01	-	-	-	67I70E	-	-	-	-	-	qp67IE
DPB1*04:02	-	-	-	67I70E	-	-	-	-	-	qp67IE
DPB1*05:01	-	-	-	67I70E	-	-	-	-	-	qp67IE
DPB1*08:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*09:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*10:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*13:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*17:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*18:01	-	-	-	67I70E	-	-	-	-	-	qp67IE
DPB1*19:01	-	-	-	67I70E	-	-	E*	-	-	qp67IE
DPB1*23:01	-	-	-	67I70E	-	-	-	-	-	qp67IE

	64	65	66	6771	68	69	70	72	73	
	Q	K	D	Residue	L	E	E	R	A	Eplet
DRB1*13:03	-	-	-	67I71K	-	-	D*	-	-	rqp67IK
DQB1*02:01	-	-	-	67I71K	-	-	R	-	-	rqp67IK
DQB1*02:02	-	-	-	67I71K	-	-	R	-	-	rqp67IK
DPB1*01:01	-	-	-	67I71K	-	-	-	-	-	rqp67IK
DPB1*04:01	-	-	-	67I71K	-	-	-	-	-	rqp67IK
DPB1*04:02	-	-	-	67I71K	-	-	-	-	-	rqp67IK
DPB1*05:01	-	-	-	67I71K	-	-	-	-	-	rqp67IK
DPB1*18:01	-	-	-	67I71K	-	-	-	-	-	rqp67IK

	64	65	66	6771	68	69	70	72	73	
	Q	K	D	Residues	L	E	Q	R	G	Eplet
DRB1*03:01	-	-	-	67L71K	-	-	-	-	-	rp67LK
DRB1*03:02	-	-	-	67L71K	-	-	-	-	-	rp67LK
DRB1*04:01	-	-	-	67L71K	-	-	-	-	A	rp67LK
DRB3*01:01	-	-	-	67L71K	-	-	-	-	-	rp67LK
DRB3*02:01	-	-	-	67L71K	-	-	-	-	-	rp67LK
DRB3*02:02	-	-	-	67L71K	-	-	-	-	-	rp67LK
DRB3*03:01	-	-	-	67L71K	-	-	-	-	-	rp67LK
DPB1*03:01	-	-	-	67L71K	-	-	E*	-	A	rp67LK
DPB1*14:01	-	-	-	67L71K	-	-	E*	-	A	rp67LK
DPB1*28:01	-	-	-	67L71K	-	-	E*	-	A	rp67LK

	64	65	66	6771	68	69	70	72	73	
	Q	K	D	Residues	L	E	Q	R	A	Eplet
DRB1*01:01	-	-	-	67L71R	-	-	-	-	-	rp67LR
DRB1*01:02	-	-	-	67L71R	-	-	-	-	-	rp67LR
DRB1*04:03	-	-	-	67L71R	-	-	-	-	-	rp67LR
DRB1*04:05	-	-	-	67L71R	-	-	-	-	-	rp67LR
DRB1*10:01	-	-	-	67L71R	-	-	R*	-	-	rp67LR
DRB1*14:01	-	-	-	67L71R	-	-	R*	-	-	rp67LR
DRB1*14:02	-	-	-	67L71R	-	-	-	-	-	rp67LR
DRB4*01:01	-	-	-	67L71R	-	-	R*	-	-	rp67LR
DPB1*11:01	-	-	-	67L71R	-	-	E*	-	-	rp67LR

	70	71	72	73	7475	76	77	78	79	80	
	Q	K	R	A	Residues	D	T	Y	C	R	Eplet
DRB1*01:01/02	-	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*01:03	D	E*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*04:01	-	-	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*04:02	D	E*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*04:04/05	-	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*10:01	R*	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*11:01/04	D	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*11:02	D	E*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*12:01/02	D	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*13:01/02	D	E*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*13:03	D	-	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*14:02	-	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*15:01/02/03	-	A	-	-	74A75V	-	-	-	-	-	rq74AV
DRB1*16:01/02	D	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB5*01:01	D	R*	-	-	74A75V	-	-	-	-	-	rq74AV
DRB5*02:02	-	A	-	-	74A75V	-	-	-	-	-	rq74AV
DQB1*02:01	R*	-	-	-	74A75V	-	R	V	-	-	rq74AV
DQB1*02:02	R*	-	-	-	74A75V	-	R	V	-	-	rq74AV

	73	74	75	76	7778	79	80	81	
	A	V	P	D	Residues	C	H	N	Eplet
DQB1*02:01	-	A*	V	-	77R78V	-	-	-	qp77RV
DQB1*02:02	-	A*	V	-	77R78V	-	-	-	qp77RV
DQB1*05:01	-	S	V	-	77R78V	-	-	-	qp77RV
DQB1*05:02	-	S	V	-	77R78V	-	-	-	qp77RV
DPB1*01:01	-	-	-	-	77R78V	-	-	-	qp77RV
DPB1*03:01	-	-	-	-	77R78V	-	-	-	qp77RV
DPB1*08:01	-	-	-	-	77R78V	-	-	-	qp77RV
DPB1*09:01	-	-	-	-	77R78V	-	-	-	qp77RV
DPB1*10:01	-	-	-	-	77R78V	-	-	-	qp77RV
DPB1*14:01	-	-	-	-	77R78V	-	-	-	qp77RV

	73	74	75	76	7778	79	80	81	
	A	E	L	D	Residues	C	H	N	Eplet
DRB1*07:01	G	Q*	V*	-	77T78V	-	-	-	rq77TV
DRB1*09:01	-	-	V*	-	77T78V	-	-	-	rq77TV
DRB1*09:02	-	-	V*	-	77T78V	-	-	-	rq77TV
DQB1*03:01	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*03:02	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*03:03	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*04:01	-	S	V*	-	77T78V	-	-	-	rq77TV
DQB1*04:02	-	S	V*	-	77T78V	-	-	-	rq77TV
DQB1*06:01	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*06:02	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*06:03	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*06:04	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*06:05	-	-	-	-	77T78V	-	-	-	rq77TV
DQB1*06:09	-	-	-	-	77T78V	-	-	-	rq77TV

	139	141	140142	143	159	160		
	K	G	Residues	V	V	M	Eplet	
DRB1*03:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*03:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*04:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*04:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*04:03	-	-	140T142V	-	-	-	rq140TV	
DRB1*04:04	-	-	140T142V	-	-	-	rq140TV	
DRB1*04:05	-	-	140T142V	-	-	-	rq140TV	
DRB1*08:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*08:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*10:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*11:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*11:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*11:04	-	-	140T142V	-	-	-	rq140TV	
DRB1*12:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*12:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*13:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*13:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*13:03	-	-	140T142V	-	-	-	rq140TV	
DRB1*14:01	-	-	140T142V	-	-	-	rq140TV	
DRB1*14:02	-	-	140T142V	-	-	-	rq140TV	
DRB1*14:54	-	-	140T142V	-	-	-	rq140TV	
DRB3*03:01	-	-	140T142V	-	-	-	rq140TV	
DQB1*03:01	T	-	140T142V	-	-	-	rq140TV	
DQB1*03:02	T	-	140T142V	-	-	-	rq140TV	
DQB1*03:03	T	-	140T142V	-	-	-	rq140TV	
DQB1*04:01	T	-	140T142V	-	-	-	rq140TV	
DQB1*04:02	T	-	140T142V	-	-	-	rq140TV	
	27	32	33	34	35	36	47	
	H	D	E	Residue	F	Y	C	Eplet
DQA1*0102	-	-	-	34Q	-	-	R	pq34Q
DQA1*0103	-	-	-	34Q	-	-	R	pq34Q
DQA1*0401	-	-	-	34Q	-	-	-	pq34Q
DQA1*0501	-	-	-	34Q	-	-	-	pq34Q
DQA1*0503	-	-	-	34Q	-	-	-	pq34Q
DQA1*0505	-	-	-	34Q	-	-	-	pq34Q
DQA1*0601	-	-	-	34Q	-	-	-	pq34Q
DPA1*0201	F	-	-	34Q	-	-	H	pq34Q
DPA1*0202	F	-	-	34Q	-	-	H	pq34Q

Table S5 Amino acid residues within a 3.5 Ångstroms of β chain eplets that are monomorphic at other loci.

	12	27	Eplet	29	39	40	47
All DPB1	R	L	28E	R	R	F	F
DRB1*01:01	K*	-	28E	-	-	-	Y* monoP
DRB1*01:02	K*	-	28E	-	-	-	Y* monoP
DRB1*01:03	K*	-	28E	-	-	-	Y* monoP
DRB1*03:02	T	-	28E	-	-	-	Y* monoP
DRB1*07:01	K*	-	28E	-	-	-	Y* monoP
DRB1*10:01	K*	-	28E	-	-	Y*	Y* monoP
DRB1*12:01	T	-	28E	-	-	-	Y* monoP
DRB1*14:02	T	-	28E	-	-	-	Y* monoP
DRB3*02:02	K*	-	28E	-	-	-	Y* monoP
DRB3*03:01	K*	-	28E	-	-	-	Y* monoP
	103	Eplet	105	106	107	114	
All DQB	P	104S	R	T	E	L	
DRB1*01	-	104S	K*	`	Q*	-	monoQ
DRB1*03	-	104S	K*	`	Q*	-	monoQ
DRB1*08	-	104S	K*	`	Q*	-	monoQ
DRB1*10	-	104S	K*	`	Q*	-	monoQ
DRB1*11	-	104S	K*	`	Q*	-	monoQ
DRB1*12	-	104S	K*	`	Q*	-	monoQ
DRB1*13	-	104S	K*	`	Q*	-	monoQ
DRB1*14	-	104S	K*	`	Q*	-	monoQ
DRB1*15	-	104S	K*	`	Q*	-	monoQ
DRB1*16	-	104S	K*	`	Q*	-	monoQ
DRB4	-	104S	K*	`	Q*	-	monoQ
		132	Eplet	134	135		
All DPB		F	133L	N	G		
DRB1*15:01		-	133L	-	-		monoP
DRB1*16:01		-	133L	-	-		monoP

	9	10	29	Eplet	36	37	38	
All DPB1	Y	Q	R	30YI	E	Y	A	
DRB4*01:01	E	-	-	30YI	-	-	-	monoP
DQB1*0301	-	-	-	30YI	-	-	-	monoP
DQB1*0302	-	-	-	30YI	-	-	-	monoP
DQB1*0303	-	-	-	30YI	-	-	-	monoP
DQB1*0401	F*	-	-	30YI	-	-	-	monoP
DQB1*0402	F*	-	-	30YI	-	-	-	monoP
DQB1*0601	L	-	-	30YI	-	D	-	monoP
DQB1*0602	F*	-	-	30YI	-	-	-	monoP
DQB1*0605	-	-	-	30YI	-	-	-	monoP
DQB1*0609	-	-	-	30YI	-	-	-	monoP

	40	41	44	Eplet	47	48	
All DRB1	F	D	V	45GE	F	R	
All DPB1	F	D	V	45GE	F	R	
DQB1*0201	-	-	-	45GE	-	-	monoRP
DQB1*0202	-	-	-	45GE	-	-	monoRP

	101	102	115	Eplet	117	160	
All DPB	V*	S	L	116V	C	M	
nonDQB1*05	I*	-	-	116V	-	-	monoP

	138	139	Eplet	141	142	143	144	145	
All DPB1	E	T	140A	G	V	V	S	T	
DQB1*02:01	-	-	140A	-	-	-	-	-	monoP
DQB1*02:02	-	-	140A	-	-	-	-	-	monoP
DQB1*05:01	-	-	140A	-	-	-	-	-	monoP
DQB1*05:02	-	-	140A	-	-	-	-	-	monoP
DQB1*06:01	-	-	140A	-	-	-	-	-	monoP
DQB1*06:02	-	-	140A	-	-	-	-	-	monoP
DQB1*06:03	-	-	140A	-	-	-	-	-	monoP
DQB1*06:04	-	-	140A	-	-	-	-	-	monoP
DQB1*06:05	-	-	140A	-	-	-	-	-	monoP
DQB1*06:09	-	-	140A	-	-	-	-	-	monoP

Table S6 Amino acid residues within a 3.5 Ångstroms of alpha chain eplets that are monomorphic at other loci.

	36	43	44	Eplet	46					
All DPA1	Y	E	T	45V	W					
non DQA1*01	-	-	-	45V	-	monoP				
	57	58	59	60	Eplet	62	63	64		
DRA1* 01:01	F	E	A	Q	61G	A	L	A		
DQA1*01	-	D*	P	-	61G	-	-	-	monoR	
	61	62	63	64	65	Eplet	67	68	69	
DRA1* 01:01	G	A	L	A	N	66I	A	V	D	
DQA1*0201	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0301	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0302	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0303	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0401	F	-	-	T	-	66I	-	-	T*	monoR
DQA1*0402	F	-	-	T	-	66I	-	-	T*	monoR
DQA1*0404	F	-	-	T	-	66I	-	-	T*	monoR
DQA1*0501	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0502	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0503	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0504	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0505	F	-	-	T	-	66I	-	-	L	monoR
DQA1*0601	F	-	-	T	-	66I	-	-	T*	monoR
DQA1*0602	F	-	-	T	-	66I	-	-	T*	monoR
	76	77	78	79	Eplet	81	82			
DRA1* 01:01	M	T	K	R	80S	N	Y			
DQA1*0201	L*	I	-	-	80S	-	S	monoR		
DQA1*0301	V*	I	-	-	80S	-	S	monoR		
DQA1*0302	V*	I	-	-	80S	-	S	monoR		
DQA1*0303	V*	I	-	-	80S	-	S	monoR		
DQA1*0401	L*	I	-	-	80S	-	S	monoR		
DQA1*0402	L*	I	-	-	80S	-	S	monoR		
DQA1*0404	L*	I	-	-	80S	-	S	monoR		
DQA1*0501	L*	I	-	-	80S	-	S	monoR		
DQA1*0502	L*	I	-	-	80S	-	S	monoR		
DQA1*0503	L*	I	-	-	80S	-	S	monoR		
DQA1*0504	L*	I	-	-	80S	-	S	monoR		
DQA1*0505	L*	I	-	-	80S	-	S	monoR		
DQA1*0601	L*	I	-	-	80S	-	S	monoR		
DQA1*0602	L*	I	-	-	80S	-	S	monoR		

	106	155	Eplet	157	
DRA1* 01:01	N	P	156F	L	
nonDQA1*05	-	T*	156F	-	monoR
	127	159	Eplet	162	
AI DPA1	N	S	160AE	E	
DQA1*0501	-	-	160AE	D*	monoP
DQA1*0505	-	-	160AE	-	monoP
	173	174	Eplet	176	
DRA1* 01:01	L	D	175E	P	
DQA1*02:01	-	-	175E	-	monoR
DQA1*03:01	-	-	175E	-	monoR
DQA1*03:02	-	-	175E	-	monoR
DQA1*03:03	-	-	175E	-	monoR
DQA1*04:01	-	-	175E	-	monoR
DQA1*04:02	-	-	175E	-	monoR
DQA1*04:04	-	-	175E	-	monoR
DQA1*06:01	-	-	175E	-	monoR
DQA1*06:02	-	-	175E	-	monoR
	173	174	Eplet	176	
All DPA1	L	D	175Q	P	
DQA1*01:01	-	-	175Q	-	monoP
DQA1*01:02	-	-	175Q	-	monoP
DQA1*01:03	-	-	175Q	-	monoP
DQA1*01:04	-	-	175Q	-	monoP
DQA1*01:05	-	-	175Q	-	monoP
DQA1*01:06	-	-	175Q	-	monoP
DQA1*01:07	-	-	175Q	-	monoP
	85	Eplet	87	88	116
All DQA1	A	86T	N	D	F
DPA1*01:03	-	86T	-	-	- monoQ
DPA1*01:04	-	86T	-	-	- monoQ
DPA1*03:01	-	86T	-	-	- monoQ