MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Feb 17 20:36:08 2010
Length of input sequence	265 amino acids
Number of nanomers from input sequence	257
Number of nanomers with obligatory P1 anchor residue	81
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	26

ALLELE: DRB1_0101	Threshold for 3 % with score: 0.14	Highest Score achievable by any peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	1.4700	24.50
2	IRSASSNPA	130	0.9000	15.00
3	YSVLLSADV	168	0.8000	13.33
4	VRLRVPFTL	75	0.7000	11.67
5	YRDLAPVTE	4	0.4000	6.67
6	YTAEASVAL	254	0.2000	3.33
7	FEGYSAASI	119	-0.1000	0
8	IIWAPAIDG	202	-0.1000	0

9	FDLQLGTDV	221	-0.1100	0
10	LYLQETLTF	243	-0.3000	0
11	LRASKPLVR	68	-0.4000	0
12	IELEAARTF	18	-0.6100	0
13	LQLGTDVAI	223	-0.8000	0
14	VRLYLQETL	241	-0.8000	0
15	YLQETLTFL	244	-0.8100	0
16	FKRHIAGRR	26	-1.0000	0
17	FLCYTAEAS	251	-1.0000	0
18	IEGIRSASS	127	-1.1000	0
19	IAHLRASKP	65	-1.2000	0
20	VISQALSEL	151	-1.3000	0
21	LAGVDGPYS	161	-1.3800	0
22	IREHLNRLV	190	-1.4100	0
23	LNRLVDGDI	194	-1.7000	0
24	VLLSADVYT	170	-1.9000	0
25	LYRDLAPVT	3	-1.9300	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	2.4700	41.17
2	IRSASSNPA	130	1.9000	31.67
3	VRLRVPFTL	75	1.7000	28.33
4	IIWAPAIDG	202	0.9000	15.00
5	LYLQETLTF	243	0.7000	11.67
6	LRASKPLVR	68	0.6000	10.00
7	IELEAARTF	18	0.3900	6.50
8	LQLGTDVAI	223	0.2000	3.33
9	VRLYLQETL	241	0.2000	3.33
10	FEGYSAASI	119	-0.1000	0
11	IEGIRSASS	127	-0.1000	0
12	FDLQLGTDV	221	-0.1100	0

13	IAHLRASKP	65	-0.2000	0
14	YSVLLSADV	168	-0.2000	0
15	VISQALSEL	151	-0.3000	0
16	LAGVDGPYS	161	-0.3800	0
17	IREHLNRLV	190	-0.4100	0
18	YRDLAPVTE	4	-0.6000	0
19	LNRLVDGDI	194	-0.7000	0
20	YTAEASVAL	254	-0.8000	0
21	VLLSADVYT	170	-0.9000	0
22	LYRDLAPVT	3	-0.9300	0
23	FKRHIAGRR	26	-1.0000	0
24	LRLAGVDGP	159	-1.0000	0
25	FLCYTAEAS	251	-1.0000	0

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	4.2000	44.21
2	LYRDLAPVT	3	4.1000	43.16
3	LRASKPLVR	68	4.1000	43.16
4	LYLQETLTF	243	3.8000	40.00
5	LRLAGVDGP	159	3.5000	36.84
6	LGTDVAIGY	225	3.5000	36.84
7	LRVPFTLSR	77	3.2000	33.68
8	VRLRVPFTL	75	3.1600	33.26
9	FVEDRTIFE	112	3.1000	32.63
10	LVDGDIIWA	197	2.4000	25.26
11	IRSASSNPA	130	2.2100	23.26
12	LLSADVYTK	171	2.1500	22.63
13	LEAARTFKR	20	1.9000	20.00
14	VIAHLRASK	64	1.9000	20.00
15	IIWAPAIDG	202	1.9000	20.00
16	IEGIRSASS	127	1.8000	18.95

17	MNNLYRDLA	0	1.7000	17.89
18	VRLYLQETL	241	1.6600	17.47
19	FVLTTRGGD	212	1.6000	16.84
20	VISQALSEL	151	1.5300	16.11
21	VAIGYASHD	229	1.4700	15.47
22	FKRHIAGRR	26	1.4000	14.74
23	VERGSKDSD	91	1.4000	14.74
24	LAGVDGPYS	161	1.3000	13.68
25	VSTGRLIDV	49	1.1000	11.58
26	IFEGYSAAS	118	1.1000	11.58

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	FVEDRTIFE	112	2.7000	29.67
2	LVRLRVPFT	74	2.5000	27.47
3	LYRDLAPVT	3	2.4000	26.37
4	LRASKPLVR	68	1.6000	17.58
5	LRLAGVDGP	159	1.5000	16.48
6	FVLTTRGGD	212	1.5000	16.48
7	LVDGDIIWA	197	1.4000	15.38
8	IRSASSNPA	130	1.2100	13.30
9	VRLRVPFTL	75	1.2000	13.19
10	LGTDVAIGY	225	1.2000	13.19
11	LLSADVYTK	171	1.0500	11.54
12	FKRHIAGRR	26	0.9000	9.89
13	LYLQETLTF	243	0.9000	9.89
14	VIAHLRASK	64	0.8000	8.79
15	MNNLYRDLA	0	0.7000	7.69
16	LRVPFTLSR	77	0.7000	7.69
17	FLCYTAEAS	251	0.5000	5.49
18	IEGIRSASS	127	0.4000	4.40
19	YRDLAPVTE	4	-0.1000	0

20	YSAASIEGI	122	-0.1000	0
21	LAGVDGPYS	161	-0.1000	0
22	IFEGYSAAS	118	-0.3000	0
23	YASHDTDTV	233	-0.3000	0
24	VRLYLQETL	241	-0.3000	0
25	VISQALSEL	151	-0.4300	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRASKPLVR	68	3.1000	35.23
2	IRSASSNPA	130	2.9000	32.95
3	LRLAGVDGP	159	2.8000	31.82
4	LYLQETLTF	243	2.4000	27.27
5	LRVPFTLSR	77	2.2000	25.00
6	LVRLRVPFT	74	2.1000	23.86
7	LVDGDIIWA	197	2.0800	23.64
8	MNNLYRDLA	0	2.0000	22.73
9	LYRDLAPVT	3	2.0000	22.73
10	LGTDVAIGY	225	1.8800	21.36
11	VIAHLRASK	64	1.8000	20.45
12	IEGIRSASS	127	1.4000	15.91
13	FVEDRTIFE	112	1.3800	15.68
14	VRLYLQETL	241	1.1000	12.50
15	VKEAAKKLA	103	0.9000	10.23
16	LLSADVYTK	171	0.9000	10.23
17	VRLRVPFTL	75	0.7000	7.95
18	IFEGYSAAS	118	0.7000	7.95
19	VYTKVSETS	176	0.7000	7.95
20	VERGSKDSD	91	0.6000	6.82
21	LPEDPREIP	141	0.5000	5.68
22	LSRNEIDDV	83	0.3000	3.41
23	VISQALSEL	151	0.3000	3.41

24	IIWAPAIDG	202	0.1800	2.05
25	VAIGYASHD	229	0.1000	1.14
26	LQLGTDVAI	223	0.0800	0.91

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRASKPLVR	68	3.1000	35.23
2	IRSASSNPA	130	2.9000	32.95
3	LRLAGVDGP	159	2.8000	31.82
4	LYLQETLTF	243	2.4000	27.27
5	LRVPFTLSR	77	2.2000	25.00
6	LVRLRVPFT	74	2.1000	23.86
7	LVDGDIIWA	197	2.0800	23.64
8	MNNLYRDLA	0	2.0000	22.73
9	LYRDLAPVT	3	2.0000	22.73
10	LGTDVAIGY	225	1.8800	21.36
11	VIAHLRASK	64	1.8000	20.45
12	IEGIRSASS	127	1.4000	15.91
13	FVEDRTIFE	112	1.3800	15.68
14	VRLYLQETL	241	1.1000	12.50
15	VKEAAKKLA	103	0.9000	10.23
16	LLSADVYTK	171	0.9000	10.23
17	VRLRVPFTL	75	0.7000	7.95
18	IFEGYSAAS	118	0.7000	7.95
19	VYTKVSETS	176	0.7000	7.95
20	VERGSKDSD	91	0.6000	6.82
21	LPEDPREIP	141	0.5000	5.68
22	LSRNEIDDV	83	0.3000	3.41
23	VISQALSEL	151	0.3000	3.41
24	IIWAPAIDG	202	0.1800	2.05
25	VAIGYASHD	229	0.1000	1.14
26	LQLGTDVAI	223	0.0800	0.91

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRASKPLVR	68	3.1000	35.23
2	IRSASSNPA	130	2.9000	32.95
3	LRLAGVDGP	159	2.8000	31.82
4	LYLQETLTF	243	2.4000	27.27
5	LRVPFTLSR	77	2.2000	25.00
6	LVRLRVPFT	74	2.1000	23.86
7	LVDGDIIWA	197	2.0800	23.64
8	MNNLYRDLA	0	2.0000	22.73
9	LYRDLAPVT	3	2.0000	22.73
10	LGTDVAIGY	225	1.8800	21.36
11	VIAHLRASK	64	1.8000	20.45
12	IEGIRSASS	127	1.4000	15.91
13	FVEDRTIFE	112	1.3800	15.68
14	VRLYLQETL	241	1.1000	12.50
15	VKEAAKKLA	103	0.9000	10.23
16	LLSADVYTK	171	0.9000	10.23
17	VRLRVPFTL	75	0.7000	7.95
18	IFEGYSAAS	118	0.7000	7.95
19	VYTKVSETS	176	0.7000	7.95
20	VERGSKDSD	91	0.6000	6.82
21	LPEDPREIP	141	0.5000	5.68
22	LSRNEIDDV	83	0.3000	3.41
23	VISQALSEL	151	0.3000	3.41
24	IIWAPAIDG	202	0.1800	2.05
25	VAIGYASHD	229	0.1000	1.14
26	LQLGTDVAI	223	0.0800	0.91

ALLELE: DRB1_0309	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	2.4	9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	FVEDRTIFE	112	4.1000	43.16
2	LVRLRVPFT	74	3.2000	33.68
3	LYRDLAPVT	3	3.1000	32.63
4	LRASKPLVR	68	3.1000	32.63
5	LYLQETLTF	243	2.8000	29.47
6	FVLTTRGGD	212	2.6000	27.37
7	LRLAGVDGP	159	2.5000	26.32
8	LGTDVAIGY	225	2.5000	26.32
9	FKRHIAGRR	26	2.4000	25.26
10	LRVPFTLSR	77	2.2000	23.16
11	VRLRVPFTL	75	2.1600	22.74
12	LVDGDIIWA	197	1.4000	14.74
13	YRDLAPVTE	4	1.3000	13.68
14	IRSASSNPA	130	1.2100	12.74
15	LLSADVYTK	171	1.1500	12.11
16	LEAARTFKR	20	0.9000	9.47
17	VIAHLRASK	64	0.9000	9.47
18	IIWAPAIDG	202	0.9000	9.47
19	FLCYTAEAS	251	0.9000	9.47
20	YSAASIEGI	122	0.8000	8.42
21	IEGIRSASS	127	0.8000	8.42
22	MNNLYRDLA	0	0.7000	7.37
23	YASHDTDTV	233	0.7000	7.37
24	VRLYLQETL	241	0.6600	6.95
25	YPIREHLNR	188	0.6000	6.32
26	VISQALSEL	151	0.5300	5.58

ALLELE: DRB1_0311	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score

1	LRASKPLVR	68	3.1000	35.23
2	IRSASSNPA	130	2.9000	32.95
3	LRLAGVDGP	159	2.8000	31.82
4	LYLQETLTF	243	2.4000	27.27
5	LRVPFTLSR	77	2.2000	25.00
6	LVRLRVPFT	74	2.1000	23.86
7	LVDGDIIWA	197	2.0800	23.64
8	MNNLYRDLA	0	2.0000	22.73
9	LYRDLAPVT	3	2.0000	22.73
10	LGTDVAIGY	225	1.8800	21.36
11	VIAHLRASK	64	1.8000	20.45
12	IEGIRSASS	127	1.4000	15.91
13	FVEDRTIFE	112	1.3800	15.68
14	VRLYLQETL	241	1.1000	12.50
15	VKEAAKKLA	103	0.9000	10.23
16	LLSADVYTK	171	0.9000	10.23
17	VRLRVPFTL	75	0.7000	7.95
18	IFEGYSAAS	118	0.7000	7.95
19	VYTKVSETS	176	0.7000	7.95
20	VERGSKDSD	91	0.6000	6.82
21	LPEDPREIP	141	0.5000	5.68
22	LSRNEIDDV	83	0.3000	3.41
23	VISQALSEL	151	0.3000	3.41
24	IIWAPAIDG	202	0.1800	2.05
25	VAIGYASHD	229	0.1000	1.14
26	LQLGTDVAI	223	0.0800	0.91

ALLELE: DRB1_0401	Threshold for 3 % with score: 1.48	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	3.3000	38.37
2	IRSASSNPA	130	3.0000	34.88
3	FVEDRTIFE	112	2.5800	30.00

4	YASHDTDTV	233	2.2000	25.58
5	IEGIRSASS	127	1.8000	20.93
6	LRASKPLVR	68	1.7000	19.77
7	LRVPFTLSR	77	1.7000	19.77
8	LVRLRVPFT	74	1.6000	18.60
9	FTLSRNEID	81	1.6000	18.60
10	YTAEASVAL	254	1.5800	18.37
11	LRLAGVDGP	159	1.5000	17.44
12	YSVLLSADV	168	1.3000	15.12
13	FKRHIAGRR	26	0.6000	6.98
14	LQETLTFLC	245	0.6000	6.98
15	IREHLNRLV	190	0.5000	5.81
16	YLQETLTFL	244	0.3000	3.49
17	FLCYTAEAS	251	0.3000	3.49
18	LYRDLAPVT	3	0.1000	1.16
19	VYTKVSETS	176	0.1000	1.16
20	YRDLAPVTE	4	0.0800	0.93
21	LGTDVAIGY	225	-0.0200	0
22	LLSADVYTK	171	-0.4000	0
23	VLLSADVYT	170	-0.4200	0
24	YSAASIEGI	122	-0.5000	0
25	IELEAARTF	18	-0.6000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	IREHLNRLV	190	4.5000	46.88
2	IRSASSNPA	130	4.0000	41.67
3	VRLRVPFTL	75	3.7000	38.54
4	LYLQETLTF	243	3.4000	35.42
5	LRVPFTLSR	77	3.3000	34.38
6	LLSADVYTK	171	2.7000	28.13
7	IEGIRSASS	127	2.0800	21.67

8	LQETLTFLC	245	1.9000	19.79
9	IAGRRVVDV	30	1.6000	16.67
10	LEAARTFKR	20	1.5000	15.62
11	VYTKVSETS	176	1.5000	15.62
12	LRASKPLVR	68	1.2000	12.50
13	LVRLRVPFT	74	0.9000	9.38
14	VPFTLSRNE	79	0.8000	8.33
15	LRLAGVDGP	159	0.7000	7.29
16	IFEGYSAAS	118	0.6000	6.25
17	IIWAPAIDG	202	0.6000	6.25
18	LVDGDIIWA	197	0.5000	5.21
19	LAFVEDRTI	110	0.4000	4.17
20	LQLGTDVAI	223	0.3000	3.12
21	VTAAVSTGR	45	0.1000	1.04
22	VIAHLRASK	64	-0.4000	0
23	YPIREHLNR	188	-0.4000	0
24	IDGAFVLTT	208	-0.4000	0
25	IELEAARTF	18	-0.5000	0

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IRSASSNPA	130	4.1000	46.59
2	IEGIRSASS	127	3.1000	35.23
3	LYLQETLTF	243	3.1000	35.23
4	LRVPFTLSR	77	2.6000	29.55
5	LVRLRVPFT	74	2.5000	28.41
6	LRLAGVDGP	159	1.6000	18.18
7	LLSADVYTK	171	1.6000	18.18
8	LEAARTFKR	20	0.9500	10.80
9	LQETLTFLC	245	0.9500	10.80
10	LRASKPLVR	68	0.8000	9.09
11	YSVLLSADV	168	0.5000	5.68

12	VTAAVSTGR	45	0.4000	4.55
13	IAHLRASKP	65	0.4000	4.55
14	VYTKVSETS	176	0.4000	4.55
15	IIWAPAIDG	202	0.1800	2.05
16	LNRLVDGDI	194	-0.1000	0
17	VRLRVPFTL	75	-0.2500	0
18	VISQALSEL	151	-0.3000	0
19	IREHLNRLV	190	-0.3000	0
20	VKAPTNGVI	57	-0.4000	0
21	VRLYLQETL	241	-0.4000	0
22	FLCYTAEAS	251	-0.4000	0
23	YRDLAPVTE	4	-0.9000	0
24	FVEDRTIFE	112	-0.9200	0
25	LAFVEDRTI	110	-1.0000	0

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	YRDLAPVTE	4	3.1000	32.98
2	IRSASSNPA	130	3.1000	32.98
3	FVEDRTIFE	112	3.0800	32.77
4	LYLQETLTF	243	3.0000	31.91
5	LVRLRVPFT	74	2.4000	25.53
6	IEGIRSASS	127	2.1000	22.34
7	FTLSRNEID	81	1.9000	20.21
8	YSVLLSADV	168	1.8000	19.15
9	LRVPFTLSR	77	1.6000	17.02
10	LRLAGVDGP	159	1.0000	10.64
11	LTFLCYTAE	249	1.0000	10.64
12	FLCYTAEAS	251	0.6000	6.38
13	IIWAPAIDG	202	0.4800	5.11
14	LEAARTFKR	20	-0.0500	0
15	LQETLTFLC	245	-0.0500	0

16	LLSADVYTK	171	-0.1000	0
17	IAHLRASKP	65	-0.2000	0
18	LRASKPLVR	68	-0.2000	0
19	VPFTLSRNE	79	-0.2000	0
20	FEGYSAASI	119	-0.2000	0
21	YTAEASVAL	254	-0.2000	0
22	VRLRVPFTL	75	-0.2500	0
23	VISQALSEL	151	-0.3000	0
24	FVLTTRGGD	212	-0.4000	0
25	VAIGYASHD	229	-0.4000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IRSASSNPA	130	3.1000	35.23
2	IEGIRSASS	127	2.1000	23.86
3	LYLQETLTF	243	2.1000	23.86
4	LRVPFTLSR	77	1.6000	18.18
5	LVRLRVPFT	74	1.5000	17.05
6	YSVLLSADV	168	1.5000	17.05
7	LRLAGVDGP	159	0.6000	6.82
8	LLSADVYTK	171	0.6000	6.82
9	FLCYTAEAS	251	0.6000	6.82
10	YRDLAPVTE	4	0.1000	1.14
11	FVEDRTIFE	112	0.0800	0.91
12	LEAARTFKR	20	-0.0500	0
13	LQETLTFLC	245	-0.0500	0
14	LRASKPLVR	68	-0.2000	0
15	FEGYSAASI	119	-0.4000	0
16	VTAAVSTGR	45	-0.6000	0
17	IAHLRASKP	65	-0.6000	0
18	VYTKVSETS	176	-0.6000	0
19	FTLSRNEID	81	-0.8000	0

20	YASHDTDTV	233	-0.8000	0
21	IIWAPAIDG	202	-0.8200	0
22	LNRLVDGDI	194	-1.1000	0
23	YTAEASVAL	254	-1.2000	0
24	VRLRVPFTL	75	-1.2500	0
25	VISQALSEL	151	-1.3000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	IRSASSNPA	130	4.1000	43.62
2	LYLQETLTF	243	4.0000	42.55
3	LVRLRVPFT	74	3.4000	36.17
4	IEGIRSASS	127	3.1000	32.98
5	LRVPFTLSR	77	2.6000	27.66
6	YRDLAPVTE	4	2.1000	22.34
7	FVEDRTIFE	112	2.0800	22.13
8	LRLAGVDGP	159	2.0000	21.28
9	LTFLCYTAE	249	2.0000	21.28
10	IIWAPAIDG	202	1.4800	15.74
11	LEAARTFKR	20	0.9500	10.11
12	LQETLTFLC	245	0.9500	10.11
13	FTLSRNEID	81	0.9000	9.57
14	LLSADVYTK	171	0.9000	9.57
15	IAHLRASKP	65	0.8000	8.51
16	LRASKPLVR	68	0.8000	8.51
17	VPFTLSRNE	79	0.8000	8.51
18	YSVLLSADV	168	0.8000	8.51
19	VRLRVPFTL	75	0.7500	7.98
20	VISQALSEL	151	0.7000	7.45
21	VAIGYASHD	229	0.6000	6.38
22	VRLYLQETL	241	0.6000	6.38
23	VTAAVSTGR	45	0.4000	4.26

24	VYTKVSETS	176	0.4000	4.26
25	LNRLVDGDI	194	0.1000	1.06

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	5.2000	57.78
2	FVEDRTIFE	112	3.9800	44.22
3	LRASKPLVR	68	3.2000	35.56
4	LRVPFTLSR	77	3.2000	35.56
5	YASHDTDTV	233	3.2000	35.56
6	IRSASSNPA	130	3.0000	33.33
7	FTLSRNEID	81	2.7000	30.00
8	YTAEASVAL	254	2.5400	28.22
9	LRLAGVDGP	159	2.5000	27.78
10	LVRLRVPFT	74	2.3000	25.56
11	YSVLLSADV	168	2.3000	25.56
12	IEGIRSASS	127	2.2000	24.44
13	FKRHIAGRR	26	2.1000	23.33
14	IREHLNRLV	190	1.5000	16.67
15	YRDLAPVTE	4	1.4800	16.44
16	IELEAARTF	18	1.3000	14.44
17	LGTDVAIGY	225	1.2800	14.22
18	YLQETLTFL	244	1.2600	14.00
19	LYRDLAPVT	3	0.8000	8.89
20	FLCYTAEAS	251	0.7000	7.78
21	LQETLTFLC	245	0.6000	6.67
22	IIWAPAIDG	202	0.5800	6.44
23	LEAARTFKR	20	0.5000	5.56
24	VYTKVSETS	176	0.5000	5.56
25	VTAAVSTGR	45	0.4000	4.44
26	YSAASIEGI	122	0.4000	4.44

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IRSASSNPA	130	4.1000	46.59
2	IEGIRSASS	127	3.1000	35.23
3	LYLQETLTF	243	3.1000	35.23
4	LRVPFTLSR	77	2.6000	29.55
5	LVRLRVPFT	74	2.5000	28.41
6	LRLAGVDGP	159	1.6000	18.18
7	LLSADVYTK	171	1.6000	18.18
8	LEAARTFKR	20	0.9500	10.80
9	LQETLTFLC	245	0.9500	10.80
10	LRASKPLVR	68	0.8000	9.09
11	YSVLLSADV	168	0.5000	5.68
12	VTAAVSTGR	45	0.4000	4.55
13	IAHLRASKP	65	0.4000	4.55
14	VYTKVSETS	176	0.4000	4.55
15	IIWAPAIDG	202	0.1800	2.05
16	LNRLVDGDI	194	-0.1000	0
17	VRLRVPFTL	75	-0.2500	0
18	VISQALSEL	151	-0.3000	0
19	IREHLNRLV	190	-0.3000	0
20	VKAPTNGVI	57	-0.4000	0
21	VRLYLQETL	241	-0.4000	0
22	FLCYTAEAS	251	-0.4000	0
23	YRDLAPVTE	4	-0.9000	0
24	FVEDRTIFE	112	-0.9200	0
25	LAFVEDRTI	110	-1.0000	0

ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	3.3000	38.37
2	IRSASSNPA	130	3.0000	34.88
3	FVEDRTIFE	112	2.5800	30.00
4	YASHDTDTV	233	2.2000	25.58
5	IEGIRSASS	127	1.8000	20.93
6	LRASKPLVR	68	1.7000	19.77
7	LRVPFTLSR	77	1.7000	19.77
8	LVRLRVPFT	74	1.6000	18.60
9	FTLSRNEID	81	1.6000	18.60
10	YTAEASVAL	254	1.5800	18.37
11	LRLAGVDGP	159	1.5000	17.44
12	YSVLLSADV	168	1.3000	15.12
13	FKRHIAGRR	26	0.6000	6.98
14	LQETLTFLC	245	0.6000	6.98
15	IREHLNRLV	190	0.5000	5.81
16	YLQETLTFL	244	0.3000	3.49
17	FLCYTAEAS	251	0.3000	3.49
18	LYRDLAPVT	3	0.1000	1.16
19	VYTKVSETS	176	0.1000	1.16
20	YRDLAPVTE	4	0.0800	0.93
21	LGTDVAIGY	225	-0.0200	0
22	LLSADVYTK	171	-0.4000	0
23	VLLSADVYT	170	-0.4200	0
24	YSAASIEGI	122	-0.5000	0
25	IELEAARTF	18	-0.6000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	6.1000	52.59
2	VRLYLQETL	241	4.5000	38.79
3	YTAEASVAL	254	4.2000	36.21

4	LYLQETLTF	243	3.6200	31.21
5	LRASKPLVR	68	3.6000	31.03
6	YSAASIEGI	122	3.5000	30.17
7	IRSASSNPA	130	3.4000	29.31
8	IPDVISQAL	148	3.2000	27.59
9	YLQETLTFL	244	3.0000	25.86
10	VLTTRGGDF	213	2.9000	25.00
11	FEGYSAASI	119	2.8000	24.14
12	LQLGTDVAI	223	2.6000	22.41
13	LQETLTFLC	245	2.4200	20.86
14	LAFVEDRTI	110	2.3000	19.83
15	VDGPYSVLL	164	2.3000	19.83
16	IREHLNRLV	190	2.2000	18.97
17	FVLTTRGGD	212	2.2000	18.97
18	YSVLLSADV	168	2.0000	17.24
19	VLLSADVYT	170	2.0000	17.24
20	IIWAPAIDG	202	1.9000	16.38
21	LRVPFTLSR	77	1.8200	15.69
22	IAGRRVVDV	30	1.8000	15.52
23	VKAPTNGVI	57	1.7000	14.66
24	VPFTLSRNE	79	1.7000	14.66
25	VISQALSEL	151	1.7000	14.66
26	FTLSRNEID	81	1.6000	13.79

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	6.1000	52.59
2	VRLYLQETL	241	4.5000	38.79
3	YTAEASVAL	254	4.2000	36.21
4	LYLQETLTF	243	3.6200	31.21
5	LRASKPLVR	68	3.6000	31.03
6	YSAASIEGI	122	3.5000	30.17

7	IRSASSNPA	130	3.4000	29.31
8	IPDVISQAL	148	3.2000	27.59
9	YLQETLTFL	244	3.0000	25.86
10	VLTTRGGDF	213	2.9000	25.00
11	FEGYSAASI	119	2.8000	24.14
12	LQLGTDVAI	223	2.6000	22.41
13	LQETLTFLC	245	2.4200	20.86
14	LAFVEDRTI	110	2.3000	19.83
15	VDGPYSVLL	164	2.3000	19.83
16	IREHLNRLV	190	2.2000	18.97
17	FVLTTRGGD	212	2.2000	18.97
18	YSVLLSADV	168	2.0000	17.24
19	VLLSADVYT	170	2.0000	17.24
20	IIWAPAIDG	202	1.9000	16.38
21	LRVPFTLSR	77	1.8200	15.69
22	IAGRRVVDV	30	1.8000	15.52
23	VKAPTNGVI	57	1.7000	14.66
24	VPFTLSRNE	79	1.7000	14.66
25	VISQALSEL	151	1.7000	14.66
26	FTLSRNEID	81	1.6000	13.79

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	4.1000	47.67
2	FVLTTRGGD	212	3.6000	41.86
3	FEGYSAASI	119	2.4000	27.91
4	YRDLAPVTE	4	2.3000	26.74
5	LVRLRVPFT	74	2.2000	25.58
6	YPIREHLNR	188	1.9000	22.09
7	VRLYLQETL	241	1.7000	19.77
8	FLCYTAEAS	251	1.5000	17.44
9	IAGRRVVDV	30	1.2000	13.95

10	FVEDRTIFE	112	1.2000	13.95
11	YSVLLSADV	168	0.4000	4.65
12	VYTKVSETS	176	0.4000	4.65
13	LYLQETLTF	243	0.3000	3.49
14	LRVPFTLSR	77	0.2000	2.33
15	VEDRTIFEG	113	0.2000	2.33
16	IEGIRSASS	127	0.2000	2.33
17	LRLAGVDGP	159	0.1000	1.16
18	MNNLYRDLA	0	-0.4000	0
19	IIWAPAIDG	202	-0.4000	0
20	LRASKPLVR	68	-0.6000	0
21	VKEAAKKLA	103	-0.6000	0
22	FKRHIAGRR	26	-0.7000	0
23	LLSADVYTK	171	-0.7000	0
24	LTTRGGDFD	214	-0.8000	0

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	3.1000	38.75
2	FEGYSAASI	119	2.2000	27.50
3	YPIREHLNR	188	1.9000	23.75
4	FLCYTAEAS	251	1.5000	18.75
5	LVRLRVPFT	74	1.3000	16.25
6	IAGRRVVDV	30	0.9000	11.25
7	FVLTTRGGD	212	0.9000	11.25
8	VRLYLQETL	241	0.7000	8.75
9	VYTKVSETS	176	0.4000	5.00
10	LRVPFTLSR	77	0.2000	2.50
11	IEGIRSASS	127	0.2000	2.50
12	YSVLLSADV	168	0.1000	1.25
13	VIAHLRASK	64	-0.2000	0
14	LRLAGVDGP	159	-0.3000	0

15	MNNLYRDLA	0	-0.4000	0
16	LRASKPLVR	68	-0.6000	0
17	VKEAAKKLA	103	-0.6000	0
18	LYLQETLTF	243	-0.6000	0
19	YRDLAPVTE	4	-0.7000	0
20	FKRHIAGRR	26	-0.7000	0
21	WEPVKEAAK	100	-1.0000	0
22	VEDRTIFEG	113	-1.1000	0
23	LVDGDIIWA	197	-1.3000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	4.1000	51.25
2	LVRLRVPFT	74	2.3000	28.75
3	IAGRRVVDV	30	1.9000	23.75
4	VRLYLQETL	241	1.7000	21.25
5	VYTKVSETS	176	1.4000	17.50
6	LRVPFTLSR	77	1.2000	15.00
7	FEGYSAASI	119	1.2000	15.00
8	IEGIRSASS	127	1.2000	15.00
9	IRSASSNPA	130	1.0000	12.50
10	LLSADVYTK	171	1.0000	12.50
11	YPIREHLNR	188	0.9000	11.25
12	VIAHLRASK	64	0.8000	10.00
13	LRLAGVDGP	159	0.7000	8.75
14	MNNLYRDLA	0	0.6000	7.50
15	FLCYTAEAS	251	0.5000	6.25
16	LRASKPLVR	68	0.4000	5.00
17	VKEAAKKLA	103	0.4000	5.00
18	LYLQETLTF	243	0.4000	5.00
19	VEDRTIFEG	113	-0.1000	0
20	FVLTTRGGD	212	-0.1000	0

21	LVDGDIIWA	197	-0.3000	0
22	LAGVDGPYS	161	-0.7000	0
23	IIWAPAIDG	202	-0.7000	0
24	IFEGYSAAS	118	-0.8000	0
25	YSVLLSADV	168	-0.9000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	5.1000	59.30
2	LVRLRVPFT	74	3.2000	37.21
3	VRLYLQETL	241	2.7000	31.40
4	FVLTTRGGD	212	2.6000	30.23
5	IAGRRVVDV	30	2.2000	25.58
6	FEGYSAASI	119	1.4000	16.28
7	VYTKVSETS	176	1.4000	16.28
8	YRDLAPVTE	4	1.3000	15.12
9	LYLQETLTF	243	1.3000	15.12
10	LRVPFTLSR	77	1.2000	13.95
11	VEDRTIFEG	113	1.2000	13.95
12	IEGIRSASS	127	1.2000	13.95
13	LRLAGVDGP	159	1.1000	12.79
14	IRSASSNPA	130	1.0000	11.63
15	YPIREHLNR	188	0.9000	10.47
16	MNNLYRDLA	0	0.6000	6.98
17	IIWAPAIDG	202	0.6000	6.98
18	FLCYTAEAS	251	0.5000	5.81
19	LRASKPLVR	68	0.4000	4.65
20	VKEAAKKLA	103	0.4000	4.65
21	LLSADVYTK	171	0.3000	3.49
22	FVEDRTIFE	112	0.2000	2.33
23	LTTRGGDFD	214	0.2000	2.33
24	VAIGYASHD	229	0.2000	2.33

25	VIAHLRASK	64	0.1000	1.16

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	3.9500	45.40
2	FLCYTAEAS	251	3.2000	36.78
3	YPIREHLNR	188	2.5000	28.74
4	VRLYLQETL	241	2.4000	27.59
5	FEGYSAASI	119	2.2000	25.29
6	VYTKVSETS	176	2.1000	24.14
7	IRSASSNPA	130	2.0000	22.99
8	IAGRRVVDV	30	1.9000	21.84
9	LVRLRVPFT	74	1.5000	17.24
10	LRLAGVDGP	159	0.9000	10.34
11	LLSADVYTK	171	0.9000	10.34
12	MNNLYRDLA	0	0.8000	9.20
13	LRVPFTLSR	77	0.8000	9.20
14	IDVKAPTNG	55	0.4000	4.60
15	YRDLAPVTE	4	0.3000	3.45
16	IEGIRSASS	127	0.2000	2.30
17	FVLTTRGGD	212	0.2000	2.30
18	YSVLLSADV	168	0.1000	1.15
19	VIAHLRASK	64	-0.2000	0
20	VEDRTIFEG	113	-0.2500	0
21	YLQETLTFL	244	-0.4000	0
22	LVDGDIIWA	197	-0.4200	0
23	YSAASIEGI	122	-0.6000	0

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	4.6000	45.54
2	YPIREHLNR	188	3.7000	36.63
3	FVLTTRGGD	212	3.7000	36.63
4	LVRLRVPFT	74	3.3500	33.17
5	YRDLAPVTE	4	2.8000	27.72
6	FVEDRTIFE	112	2.8000	27.72
7	VRLYLQETL	241	2.8000	27.72
8	FLCYTAEAS	251	2.6000	25.74
9	FEGYSAASI	119	2.4000	23.76
10	LYLQETLTF	243	2.1000	20.79
11	LRVPFTLSR	77	2.0000	19.80
12	IAGRRVVDV	30	1.7000	16.83
13	VYTKVSETS	176	1.5000	14.85
14	LRASKPLVR	68	1.2000	11.88
15	IIWAPAIDG	202	1.2000	11.88
16	VEDRTIFEG	113	0.7000	6.93
17	YSVLLSADV	168	0.4000	3.96
18	IRSASSNPA	130	0.3000	2.97
19	LVDGDIIWA	197	0.3000	2.97
20	IDGAFVLTT	208	0.3000	2.97
21	IEGIRSASS	127	0.2000	1.98
22	LRLAGVDGP	159	-0.2000	0

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	2.8500	34.34
2	LYLQETLTF	243	1.8000	21.69
3	LRASKPLVR	68	1.5000	18.07
4	FVLTTRGGD	212	1.4000	16.87
5	LRVPFTLSR	77	1.3000	15.66
6	IEGIRSASS	127	0.8000	9.64

7	LLSADVYTK	171	0.7000	8.43
8	YPIREHLNR	188	0.7000	8.43
9	VRLRVPFTL	75	0.6000	7.23
10	YSVLLSADV	168	0.5000	6.02
11	IRSASSNPA	130	0.3000	3.61
12	YRDLAPVTE	4	0.2000	2.41
13	VIAHLRASK	64	0.2000	2.41
14	IIWAPAIDG	202	-0.1000	0
15	FKRHIAGRR	26	-0.2000	0
16	MNNLYRDLA	0	-0.3000	0
17	FLCYTAEAS	251	-0.3000	0
18	LVDGDIIWA	197	-0.4000	0
19	LAGVDGPYS	161	-0.4500	0
20	LRLAGVDGP	159	-0.6000	0
21	IDGAFVLTT	208	-0.6000	0
22	FEGYSAASI	119	-0.7000	0
23	WEPVKEAAK	100	-0.9000	0
24	FVEDRTIFE	112	-0.9000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	3.5000	41.67
2	VIAHLRASK	64	3.3000	39.29
3	LVRLRVPFT	74	2.7000	32.14
4	LYLQETLTF	243	2.7000	32.14
5	IRSASSNPA	130	2.4000	28.57
6	IREHLNRLV	190	2.4000	28.57
7	LLSADVYTK	171	1.9000	22.62
8	LRLAGVDGP	159	1.6000	19.05
9	LRASKPLVR	68	1.5000	17.86
10	LRVPFTLSR	77	1.4000	16.67
11	VYTKVSETS	176	1.3000	15.48

12	VRLYLQETL	241	1.3000	15.48
13	MNNLYRDLA	0	1.2000	14.29
14	VKEAAKKLA	103	1.2000	14.29
15	IAGRRVVDV	30	0.8000	9.52
16	LEAARTFKR	20	0.5000	5.95
17	IEGIRSASS	127	0.3000	3.57
18	LQETLTFLC	245	0.3000	3.57
19	IELEAARTF	18	0.2000	2.38
20	VISQALSEL	151	0.2000	2.38
21	FLCYTAEAS	251	0.1000	1.19
22	FKRHIAGRR	26	-0.2000	0
23	IIWAPAIDG	202	-0.4000	0
24	YPIREHLNR	188	-0.5000	0
25	LVDGDIIWA	197	-0.5000	0

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	3.8500	46.39
2	LYLQETLTF	243	2.8000	33.73
3	LRASKPLVR	68	2.5000	30.12
4	LRVPFTLSR	77	2.3000	27.71
5	IEGIRSASS	127	1.8000	21.69
6	LLSADVYTK	171	1.7000	20.48
7	VRLRVPFTL	75	1.6000	19.28
8	IRSASSNPA	130	1.3000	15.66
9	VIAHLRASK	64	1.2000	14.46
10	VKEAAKKLA	103	1.0000	12.05
11	IIWAPAIDG	202	0.9000	10.84
12	MNNLYRDLA	0	0.7000	8.43
13	LVDGDIIWA	197	0.6000	7.23
14	LAGVDGPYS	161	0.5500	6.63
15	LRLAGVDGP	159	0.4000	4.82

16	IDGAFVLTT	208	0.4000	4.82
17	FVLTTRGGD	212	0.4000	4.82
18	VRLYLQETL	241	-0.1000	0
19	LQETLTFLC	245	-0.2000	0
20	VYTKVSETS	176	-0.3000	0
21	YPIREHLNR	188	-0.3000	0
22	LEAARTFKR	20	-0.5000	0
23	YSVLLSADV	168	-0.5000	0
24	LNRLVDGDI	194	-0.5000	0
25	IAGRRVVDV	30	-0.6000	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	3.8500	46.39
2	LYLQETLTF	243	2.8000	33.73
3	LRASKPLVR	68	2.5000	30.12
4	LRVPFTLSR	77	2.3000	27.71
5	IEGIRSASS	127	1.8000	21.69
6	LLSADVYTK	171	1.7000	20.48
7	VRLRVPFTL	75	1.6000	19.28
8	IRSASSNPA	130	1.3000	15.66
9	VIAHLRASK	64	1.2000	14.46
10	VKEAAKKLA	103	1.0000	12.05
11	IIWAPAIDG	202	0.9000	10.84
12	MNNLYRDLA	0	0.7000	8.43
13	LVDGDIIWA	197	0.6000	7.23
14	LAGVDGPYS	161	0.5500	6.63
15	LRLAGVDGP	159	0.4000	4.82
16	IDGAFVLTT	208	0.4000	4.82
17	FVLTTRGGD	212	0.4000	4.82
18	VRLYLQETL	241	-0.1000	0
19	LQETLTFLC	245	-0.2000	0

20	VYTKVSETS	176	-0.3000	0
21	YPIREHLNR	188	-0.3000	0
22	LEAARTFKR	20	-0.5000	0
23	YSVLLSADV	168	-0.5000	0
24	LNRLVDGDI	194	-0.5000	0
25	IAGRRVVDV	30	-0.6000	0

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	3.5000	38.46
2	LYRDLAPVT	3	3.4000	37.36
3	LRASKPLVR	68	2.6000	28.57
4	LRLAGVDGP	159	2.5000	27.47
5	LVDGDIIWA	197	2.4000	26.37
6	IRSASSNPA	130	2.2100	24.29
7	VRLRVPFTL	75	2.2000	24.18
8	LGTDVAIGY	225	2.2000	24.18
9	LLSADVYTK	171	2.0500	22.53
10	LYLQETLTF	243	1.9000	20.88
11	VIAHLRASK	64	1.8000	19.78
12	MNNLYRDLA	0	1.7000	18.68
13	LRVPFTLSR	77	1.7000	18.68
14	FVEDRTIFE	112	1.7000	18.68
15	IEGIRSASS	127	1.4000	15.38
16	LAGVDGPYS	161	0.9000	9.89
17	IFEGYSAAS	118	0.7000	7.69
18	VRLYLQETL	241	0.7000	7.69
19	VISQALSEL	151	0.5700	6.26
20	IIWAPAIDG	202	0.5000	5.49
21	FVLTTRGGD	212	0.5000	5.49
22	LEAARTFKR	20	0.4000	4.40
23	VAIGYASHD	229	0.3700	4.07

24	VERGSKDSD	91	0.3000	3.30
25	VKEAAKKLA	103	0.3000	3.30
26	VYTKVSETS	176	0.3000	3.30

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	2.5000	29.76
2	VIAHLRASK	64	2.3000	27.38
3	LVRLRVPFT	74	1.7000	20.24
4	LYLQETLTF	243	1.7000	20.24
5	IRSASSNPA	130	1.4000	16.67
6	IREHLNRLV	190	1.4000	16.67
7	FLCYTAEAS	251	1.1000	13.10
8	LLSADVYTK	171	0.9000	10.71
9	FKRHIAGRR	26	0.8000	9.52
10	LRLAGVDGP	159	0.6000	7.14
11	LRASKPLVR	68	0.5000	5.95
12	YPIREHLNR	188	0.5000	5.95
13	LRVPFTLSR	77	0.4000	4.76
14	FEGYSAASI	119	0.4000	4.76
15	VYTKVSETS	176	0.3000	3.57
16	YASHDTDTV	233	0.3000	3.57
17	VRLYLQETL	241	0.3000	3.57
18	MNNLYRDLA	0	0.2000	2.38
19	VKEAAKKLA	103	0.2000	2.38
20	IAGRRVVDV	30	-0.2000	0
21	YSVLLSADV	168	-0.2000	0
22	FVLTTRGGD	212	-0.2000	0
23	LEAARTFKR	20	-0.5000	0
24	IEGIRSASS	127	-0.7000	0

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	3.6000	40.91
2	VRLRVPFTL	75	3.4600	39.32
3	VIAHLRASK	64	2.4000	27.27
4	LVRLRVPFT	74	2.4000	27.27
5	IREHLNRLV	190	2.4000	27.27
6	FKRHIAGRR	26	2.3000	26.14
7	LRASKPLVR	68	2.0000	22.73
8	YPIREHLNR	188	2.0000	22.73
9	LRVPFTLSR	77	1.9000	21.59
10	LRLAGVDGP	159	1.6000	18.18
11	FLCYTAEAS	251	1.5000	17.05
12	YRDLAPVTE	4	1.4000	15.91
13	IRSASSNPA	130	1.4000	15.91
14	FEGYSAASI	119	1.3000	14.77
15	YASHDTDTV	233	1.3000	14.77
16	VRLYLQETL	241	1.2600	14.32
17	IELEAARTF	18	1.1000	12.50
18	LEAARTFKR	20	1.0000	11.36
19	LLSADVYTK	171	1.0000	11.36
20	FVLTTRGGD	212	0.9000	10.23
21	IAGRRVVDV	30	0.8000	9.09
22	YSVLLSADV	168	0.8000	9.09
23	VYTKVSETS	176	0.7000	7.95
24	MNNLYRDLA	0	0.2000	2.27
25	VKEAAKKLA	103	0.2000	2.27
26	VISQALSEL	151	0.1600	1.82

ALLELE: DRB1_1121	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	3.5000	41.67
2	VIAHLRASK	64	3.3000	39.29
3	LVRLRVPFT	74	2.7000	32.14
4	LYLQETLTF	243	2.7000	32.14
5	IRSASSNPA	130	2.4000	28.57
6	IREHLNRLV	190	2.4000	28.57
7	LLSADVYTK	171	1.9000	22.62
8	LRLAGVDGP	159	1.6000	19.05
9	LRASKPLVR	68	1.5000	17.86
10	LRVPFTLSR	77	1.4000	16.67
11	VYTKVSETS	176	1.3000	15.48
12	VRLYLQETL	241	1.3000	15.48
13	MNNLYRDLA	0	1.2000	14.29
14	VKEAAKKLA	103	1.2000	14.29
15	IAGRRVVDV	30	0.8000	9.52
16	LEAARTFKR	20	0.5000	5.95
17	IEGIRSASS	127	0.3000	3.57
18	LQETLTFLC	245	0.3000	3.57
19	IELEAARTF	18	0.2000	2.38
20	VISQALSEL	151	0.2000	2.38
21	FLCYTAEAS	251	0.1000	1.19
22	FKRHIAGRR	26	-0.2000	0
23	IIWAPAIDG	202	-0.4000	0
24	YPIREHLNR	188	-0.5000	0
25	LVDGDIIWA	197	-0.5000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	3.7000	42.53
2	LVRLRVPFT	74	3.5500	40.80
3	LRASKPLVR	68	3.0000	34.48

4	LRVPFTLSR	77	2.8000	32.18
5	FVLTTRGGD	212	2.5000	28.74
6	YPIREHLNR	188	2.2000	25.29
7	YRDLAPVTE	4	1.6000	18.39
8	VRLRVPFTL	75	1.5600	17.93
9	YSVLLSADV	168	1.5000	17.24
10	FKRHIAGRR	26	1.3000	14.94
11	IIWAPAIDG	202	1.3000	14.94
12	IEGIRSASS	127	1.2000	13.79
13	LLSADVYTK	171	0.8000	9.20
14	FVEDRTIFE	112	0.5000	5.75
15	LRLAGVDGP	159	0.4000	4.60
16	VIAHLRASK	64	0.3000	3.45
17	IRSASSNPA	130	0.3000	3.45
18	FEGYSAASI	119	0.2000	2.30
19	IDGAFVLTT	208	0.1000	1.15
20	FLCYTAEAS	251	0.1000	1.15
21	LAGVDGPYS	161	-0.0500	0
22	VRLYLQETL	241	-0.1400	0
23	MNNLYRDLA	0	-0.3000	0

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	4.6000	52.27
2	VRLRVPFTL	75	4.4600	50.68
3	VIAHLRASK	64	3.4000	38.64
4	LVRLRVPFT	74	3.4000	38.64
5	IREHLNRLV	190	3.4000	38.64
6	LRASKPLVR	68	3.0000	34.09
7	LRVPFTLSR	77	2.9000	32.95
8	LRLAGVDGP	159	2.6000	29.55
9	IRSASSNPA	130	2.4000	27.27

10	VRLYLQETL	241	2.2600	25.68
11	IELEAARTF	18	2.1000	23.86
12	LEAARTFKR	20	2.0000	22.73
13	LLSADVYTK	171	2.0000	22.73
14	IAGRRVVDV	30	1.8000	20.45
15	VYTKVSETS	176	1.7000	19.32
16	FKRHIAGRR	26	1.3000	14.77
17	MNNLYRDLA	0	1.2000	13.64
18	VKEAAKKLA	103	1.2000	13.64
19	VISQALSEL	151	1.1600	13.18
20	YPIREHLNR	188	1.0000	11.36
21	IIWAPAIDG	202	1.0000	11.36
22	VEDRTIFEG	113	0.7000	7.95
23	IEGIRSASS	127	0.7000	7.95
24	FLCYTAEAS	251	0.5000	5.68
25	YRDLAPVTE	4	0.4000	4.55
26	FEGYSAASI	119	0.3000	3.41

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	3.6000	40.91
2	VRLRVPFTL	75	3.4600	39.32
3	VIAHLRASK	64	2.4000	27.27
4	LVRLRVPFT	74	2.4000	27.27
5	IREHLNRLV	190	2.4000	27.27
6	FKRHIAGRR	26	2.3000	26.14
7	LRASKPLVR	68	2.0000	22.73
8	YPIREHLNR	188	2.0000	22.73
9	LRVPFTLSR	77	1.9000	21.59
10	LRLAGVDGP	159	1.6000	18.18
11	FLCYTAEAS	251	1.5000	17.05
12	YRDLAPVTE	4	1.4000	15.91

13	IRSASSNPA	130	1.4000	15.91
14	FEGYSAASI	119	1.3000	14.77
15	YASHDTDTV	233	1.3000	14.77
16	VRLYLQETL	241	1.2600	14.32
17	IELEAARTF	18	1.1000	12.50
18	LEAARTFKR	20	1.0000	11.36
19	LLSADVYTK	171	1.0000	11.36
20	FVLTTRGGD	212	0.9000	10.23
21	IAGRRVVDV	30	0.8000	9.09
22	YSVLLSADV	168	0.8000	9.09
23	VYTKVSETS	176	0.7000	7.95
24	MNNLYRDLA	0	0.2000	2.27
25	VKEAAKKLA	103	0.2000	2.27
26	VISQALSEL	151	0.1600	1.82

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	4.5000	50.00
2	LVRLRVPFT	74	3.6000	40.00
3	LYLQETLTF	243	3.6000	40.00
4	IREHLNRLV	190	2.7000	30.00
5	VIAHLRASK	64	2.6000	28.89
6	IRSASSNPA	130	2.4000	26.67
7	VRLYLQETL	241	2.3000	25.56
8	YRDLAPVTE	4	2.0000	22.22
9	LRLAGVDGP	159	2.0000	22.22
10	VPFTLSRNE	79	1.6000	17.78
11	LRASKPLVR	68	1.5000	16.67
12	FVLTTRGGD	212	1.5000	16.67
13	LRVPFTLSR	77	1.4000	15.56
14	VYTKVSETS	176	1.3000	14.44
15	MNNLYRDLA	0	1.2000	13.33

16	VKEAAKKLA	103	1.2000	13.33
17	VISQALSEL	151	1.2000	13.33
18	LLSADVYTK	171	1.2000	13.33
19	IELEAARTF	18	1.1000	12.22
20	IAGRRVVDV	30	1.1000	12.22
21	IIWAPAIDG	202	0.9000	10.00
22	IGYASHDTD	231	0.7000	7.78
23	VEDRTIFEG	113	0.6000	6.67
24	LEAARTFKR	20	0.5000	5.56
25	IEGIRSASS	127	0.3000	3.33
26	LQETLTFLC	245	0.3000	3.33

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	3.7000	42.53
2	LVRLRVPFT	74	3.5500	40.80
3	LRASKPLVR	68	3.0000	34.48
4	LRVPFTLSR	77	2.8000	32.18
5	FVLTTRGGD	212	2.5000	28.74
6	YPIREHLNR	188	2.2000	25.29
7	YRDLAPVTE	4	1.6000	18.39
8	VRLRVPFTL	75	1.5600	17.93
9	YSVLLSADV	168	1.5000	17.24
10	FKRHIAGRR	26	1.3000	14.94
11	IIWAPAIDG	202	1.3000	14.94
12	IEGIRSASS	127	1.2000	13.79
13	LLSADVYTK	171	0.8000	9.20
14	FVEDRTIFE	112	0.5000	5.75
15	LRLAGVDGP	159	0.4000	4.60
16	VIAHLRASK	64	0.3000	3.45
17	IRSASSNPA	130	0.3000	3.45
18	FEGYSAASI	119	0.2000	2.30

19	IDGAFVLTT	208	0.1000	1.15
20	FLCYTAEAS	251	0.1000	1.15
21	LAGVDGPYS	161	-0.0500	0
22	VRLYLQETL	241	-0.1400	0
23	MNNLYRDLA	0	-0.3000	0

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	1.7000	25.00
2	FVLTTRGGD	212	1.3000	19.12
3	IEGIRSASS	127	0.8000	11.76
4	YSVLLSADV	168	0.5000	7.35
5	VIAHLRASK	64	0.2000	2.94
6	VRLRVPFTL	75	0.1000	1.47
7	YRDLAPVTE	4	-0.3000	0
8	FKRHIAGRR	26	-0.3000	0
9	LRASKPLVR	68	-0.3000	0
10	LRLAGVDGP	159	-0.3000	0
11	LRVPFTLSR	77	-0.5000	0
12	VKEAAKKLA	103	-0.6000	0
13	FEGYSAASI	119	-0.7000	0
14	WEPVKEAAK	100	-0.9000	0
15	YPIREHLNR	188	-1.1000	0
16	FLCYTAEAS	251	-1.4000	0
17	LAGVDGPYS	161	-1.6000	0
18	LNRLVDGDI	194	-1.6000	0
19	IIWAPAIDG	202	-1.7000	0
20	LQETLTFLC	245	-1.7000	0
21	LSELRLAGV	156	-1.9000	0

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLRVPFT	74	3.8500	46.39
2	LYLQETLTF	243	2.8000	33.73
3	LRASKPLVR	68	2.5000	30.12
4	LRVPFTLSR	77	2.3000	27.71
5	IEGIRSASS	127	1.8000	21.69
6	LLSADVYTK	171	1.7000	20.48
7	VRLRVPFTL	75	1.6000	19.28
8	IRSASSNPA	130	1.3000	15.66
9	VIAHLRASK	64	1.2000	14.46
10	VKEAAKKLA	103	1.0000	12.05
11	IIWAPAIDG	202	0.9000	10.84
12	MNNLYRDLA	0	0.7000	8.43
13	LVDGDIIWA	197	0.6000	7.23
14	LAGVDGPYS	161	0.5500	6.63
15	LRLAGVDGP	159	0.4000	4.82
16	IDGAFVLTT	208	0.4000	4.82
17	FVLTTRGGD	212	0.4000	4.82
18	VRLYLQETL	241	-0.1000	0
19	LQETLTFLC	245	-0.2000	0
20	VYTKVSETS	176	-0.3000	0
21	YPIREHLNR	188	-0.3000	0
22	LEAARTFKR	20	-0.5000	0
23	YSVLLSADV	168	-0.5000	0
24	LNRLVDGDI	194	-0.5000	0
25	IAGRRVVDV	30	-0.6000	0

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9

Rank	Sequence	At Position	Score	% of Highest Score

1	FVLTTRGGD	212	4.1000	46.07
2	LVRLRVPFT	74	3.7500	42.13
3	YRDLAPVTE	4	3.2000	35.96
4	LYLQETLTF	243	2.7000	30.34
5	FVEDRTIFE	112	2.1000	23.60
6	VRLRVPFTL	75	1.6000	17.98
7	LRASKPLVR	68	1.5000	16.85
8	LRVPFTLSR	77	1.3000	14.61
9	IIWAPAIDG	202	1.2000	13.48
10	IEGIRSASS	127	0.8000	8.99
11	YSVLLSADV	168	0.8000	8.99
12	YPIREHLNR	188	0.7000	7.87
13	IRSASSNPA	130	0.3000	3.37
14	IDGAFVLTT	208	0.3000	3.37
15	VRLYLQETL	241	-0.1000	0
16	FKRHIAGRR	26	-0.2000	0
17	LRLAGVDGP	159	-0.2000	0
18	LIDVKAPTN	54	-0.2500	0
19	MNNLYRDLA	0	-0.3000	0
20	FLCYTAEAS	251	-0.3000	0
21	LVDGDIIWA	197	-0.4000	0
22	LAGVDGPYS	161	-0.4500	0
23	VIAHLRASK	64	-0.5000	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	3.5000	41.67
2	VIAHLRASK	64	3.3000	39.29
3	LVRLRVPFT	74	2.7000	32.14
4	LYLQETLTF	243	2.7000	32.14
5	IRSASSNPA	130	2.4000	28.57
6	IREHLNRLV	190	2.4000	28.57

7	LLSADVYTK	171	1.9000	22.62
8	LRLAGVDGP	159	1.6000	19.05
9	LRASKPLVR	68	1.5000	17.86
10	LRVPFTLSR	77	1.4000	16.67
11	VYTKVSETS	176	1.3000	15.48
12	VRLYLQETL	241	1.3000	15.48
13	MNNLYRDLA	0	1.2000	14.29
14	VKEAAKKLA	103	1.2000	14.29
15	IAGRRVVDV	30	0.8000	9.52
16	LEAARTFKR	20	0.5000	5.95
17	IEGIRSASS	127	0.3000	3.57
18	LQETLTFLC	245	0.3000	3.57
19	IELEAARTF	18	0.2000	2.38
20	VISQALSEL	151	0.2000	2.38
21	FLCYTAEAS	251	0.1000	1.19
22	FKRHIAGRR	26	-0.2000	0
23	IIWAPAIDG	202	-0.4000	0
24	YPIREHLNR	188	-0.5000	0
25	LVDGDIIWA	197	-0.5000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	2.5000	29.76
2	VIAHLRASK	64	2.3000	27.38
3	LVRLRVPFT	74	1.7000	20.24
4	LYLQETLTF	243	1.7000	20.24
5	IRSASSNPA	130	1.4000	16.67
6	IREHLNRLV	190	1.4000	16.67
7	FLCYTAEAS	251	1.1000	13.10
8	LLSADVYTK	171	0.9000	10.71
9	FKRHIAGRR	26	0.8000	9.52
10	LRLAGVDGP	159	0.6000	7.14

11	LRASKPLVR	68	0.5000	5.95
12	YPIREHLNR	188	0.5000	5.95
13	LRVPFTLSR	77	0.4000	4.76
14	FEGYSAASI	119	0.4000	4.76
15	VYTKVSETS	176	0.3000	3.57
16	YASHDTDTV	233	0.3000	3.57
17	VRLYLQETL	241	0.3000	3.57
18	MNNLYRDLA	0	0.2000	2.38
19	VKEAAKKLA	103	0.2000	2.38
20	IAGRRVVDV	30	-0.2000	0
21	YSVLLSADV	168	-0.2000	0
22	FVLTTRGGD	212	-0.2000	0
23	LEAARTFKR	20	-0.5000	0
24	IEGIRSASS	127	-0.7000	0

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	4.6000	52.27
2	VRLRVPFTL	75	4.4600	50.68
3	VIAHLRASK	64	3.4000	38.64
4	LVRLRVPFT	74	3.4000	38.64
5	IREHLNRLV	190	3.4000	38.64
6	LRASKPLVR	68	3.0000	34.09
7	LRVPFTLSR	77	2.9000	32.95
8	LRLAGVDGP	159	2.6000	29.55
9	IRSASSNPA	130	2.4000	27.27
10	VRLYLQETL	241	2.2600	25.68
11	IELEAARTF	18	2.1000	23.86
12	LEAARTFKR	20	2.0000	22.73
13	LLSADVYTK	171	2.0000	22.73
14	IAGRRVVDV	30	1.8000	20.45
15	VYTKVSETS	176	1.7000	19.32

16	FKRHIAGRR	26	1.3000	14.77
17	MNNLYRDLA	0	1.2000	13.64
18	VKEAAKKLA	103	1.2000	13.64
19	VISQALSEL	151	1.1600	13.18
20	YPIREHLNR	188	1.0000	11.36
21	IIWAPAIDG	202	1.0000	11.36
22	VEDRTIFEG	113	0.7000	7.95
23	IEGIRSASS	127	0.7000	7.95
24	FLCYTAEAS	251	0.5000	5.68
25	YRDLAPVTE	4	0.4000	4.55
26	FEGYSAASI	119	0.3000	3.41

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LYLQETLTF	243	4.6000	52.27
2	VRLRVPFTL	75	4.4600	50.68
3	VIAHLRASK	64	3.4000	38.64
4	LVRLRVPFT	74	3.4000	38.64
5	IREHLNRLV	190	3.4000	38.64
6	LRASKPLVR	68	3.0000	34.09
7	LRVPFTLSR	77	2.9000	32.95
8	LRLAGVDGP	159	2.6000	29.55
9	IRSASSNPA	130	2.4000	27.27
10	VRLYLQETL	241	2.2600	25.68
11	IELEAARTF	18	2.1000	23.86
12	LEAARTFKR	20	2.0000	22.73
13	LLSADVYTK	171	2.0000	22.73
14	IAGRRVVDV	30	1.8000	20.45
15	VYTKVSETS	176	1.7000	19.32
16	FKRHIAGRR	26	1.3000	14.77
17	MNNLYRDLA	0	1.2000	13.64
18	VKEAAKKLA	103	1.2000	13.64

19	VISQALSEL	151	1.1600	13.18
20	YPIREHLNR	188	1.0000	11.36
21	IIWAPAIDG	202	1.0000	11.36
22	VEDRTIFEG	113	0.7000	7.95
23	IEGIRSASS	127	0.7000	7.95
24	FLCYTAEAS	251	0.5000	5.68
25	YRDLAPVTE	4	0.4000	4.55
26	FEGYSAASI	119	0.3000	3.41

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	5.1000	52.04
2	VRLYLQETL	241	4.7000	47.96
3	IRSASSNPA	130	3.7000	37.76
4	LRVPFTLSR	77	3.2600	33.27
5	LVRLRVPFT	74	3.1000	31.63
6	LQLGTDVAI	223	2.8000	28.57
7	LRASKPLVR	68	2.6000	26.53
8	IREHLNRLV	190	2.6000	26.53
9	LYLQETLTF	243	2.5600	26.12
10	FEGYSAASI	119	2.5000	25.51
11	LVDGDIIWA	197	2.3500	23.98
12	LNRLVDGDI	194	2.3000	23.47
13	VKAPTNGVI	57	2.2000	22.45
14	MNNLYRDLA	0	2.1000	21.43
15	IIWAPAIDG	202	1.8000	18.37
16	VSTGRLIDV	49	1.7000	17.35
17	VIAHLRASK	64	1.5000	15.31
18	VISQALSEL	151	1.5000	15.31
19	FLCYTAEAS	251	1.5000	15.31
20	VLLSADVYT	170	1.4000	14.29
21	LYRDLAPVT	3	1.3000	13.27

22	IEGIRSASS	127	1.2000	12.24
23	LRLAGVDGP	159	1.1000	11.22
24	LQETLTFLC	245	1.0600	10.82
25	FKRHIAGRR	26	0.9000	9.18
26	LAGVDGPYS	161	0.9000	9.18

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	4.1000	41.84
2	VRLYLQETL	241	3.7000	37.76
3	FEGYSAASI	119	3.5000	35.71
4	IRSASSNPA	130	2.7000	27.55
5	FLCYTAEAS	251	2.5000	25.51
6	LRVPFTLSR	77	2.2600	23.06
7	LVRLRVPFT	74	2.1000	21.43
8	FKRHIAGRR	26	1.9000	19.39
9	FVLTTRGGD	212	1.9000	19.39
10	LQLGTDVAI	223	1.8000	18.37
11	LRASKPLVR	68	1.6000	16.33
12	YSVLLSADV	168	1.6000	16.33
13	YPIREHLNR	188	1.6000	16.33
14	IREHLNRLV	190	1.6000	16.33
15	LYLQETLTF	243	1.5600	15.92
16	LVDGDIIWA	197	1.3500	13.78
17	LNRLVDGDI	194	1.3000	13.27
18	YLQETLTFL	244	1.3000	13.27
19	VKAPTNGVI	57	1.2000	12.24
20	MNNLYRDLA	0	1.1000	11.22
21	YASHDTDTV	233	0.8600	8.78
22	IIWAPAIDG	202	0.8000	8.16
23	YTAEASVAL	254	0.8000	8.16
24	VSTGRLIDV	49	0.7000	7.14

25	VIAHLRASK	64	0.5000	5.10
26	VISQALSEL	151	0.5000	5.10

ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRVPFTL	75	5.1000	52.04
2	VRLYLQETL	241	4.7000	47.96
3	IRSASSNPA	130	3.7000	37.76
4	LRVPFTLSR	77	3.2600	33.27
5	LVRLRVPFT	74	3.1000	31.63
6	LQLGTDVAI	223	2.8000	28.57
7	LRASKPLVR	68	2.6000	26.53
8	IREHLNRLV	190	2.6000	26.53
9	LYLQETLTF	243	2.5600	26.12
10	FEGYSAASI	119	2.5000	25.51
11	LVDGDIIWA	197	2.3500	23.98
12	LNRLVDGDI	194	2.3000	23.47
13	VKAPTNGVI	57	2.2000	22.45
14	MNNLYRDLA	0	2.1000	21.43
15	IIWAPAIDG	202	1.8000	18.37
16	VSTGRLIDV	49	1.7000	17.35
17	VIAHLRASK	64	1.5000	15.31
18	VISQALSEL	151	1.5000	15.31
19	FLCYTAEAS	251	1.5000	15.31
20	VLLSADVYT	170	1.4000	14.29
21	LYRDLAPVT	3	1.3000	13.27
22	IEGIRSASS	127	1.2000	12.24
23	LRLAGVDGP	159	1.1000	11.22
24	LQETLTFLC	245	1.0600	10.82
25	FKRHIAGRR	26	0.9000	9.18
26	LAGVDGPYS	161	0.9000	9.18

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRASKPLVR	68	4.0000	40.82
2	FKRHIAGRR	26	3.5000	35.71
3	VRLRVPFTL	75	3.5000	35.71
4	LLSADVYTK	171	2.8000	28.57
5	LRVPFTLSR	77	2.5000	25.51
6	LEAARTFKR	20	2.3000	23.47
7	WEPVKEAAK	100	2.2000	22.45
8	VLTTRGGDF	213	1.8000	18.37
9	IIWAPAIDG	202	1.7000	17.35
10	LAFVEDRTI	110	1.4000	14.29
11	IRSASSNPA	130	1.4000	14.29
12	IELEAARTF	18	1.3000	13.27
13	VTAAVSTGR	45	1.3000	13.27
14	YPIREHLNR	188	1.2000	12.24
15	FVLTTRGGD	212	1.2000	12.24
16	LYLQETLTF	243	1.2000	12.24
17	FEGYSAASI	119	0.9000	9.18
18	LNRLVDGDI	194	0.9000	9.18
19	YRDLAPVTE	4	0.8000	8.16
20	IEGIRSASS	127	0.8000	8.16
21	VRLYLQETL	241	0.6000	6.12
22	LVRLRVPFT	74	0.3000	3.06
23	YLQETLTFL	244	0.3000	3.06
24	FLCYTAEAS	251	0.2000	2.04
25	VIAHLRASK	64	0.1000	1.02
26	LAGVDGPYS	161	0.1000	1.02

ALLELE: DRB5_0105	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRASKPLVR	68	4.0000	40.82
2	FKRHIAGRR	26	3.5000	35.71
3	VRLRVPFTL	75	3.5000	35.71
4	LLSADVYTK	171	2.8000	28.57
5	LRVPFTLSR	77	2.5000	25.51
6	LEAARTFKR	20	2.3000	23.47
7	WEPVKEAAK	100	2.2000	22.45
8	VLTTRGGDF	213	1.8000	18.37
9	IIWAPAIDG	202	1.7000	17.35
10	LAFVEDRTI	110	1.4000	14.29
11	IRSASSNPA	130	1.4000	14.29
12	IELEAARTF	18	1.3000	13.27
13	VTAAVSTGR	45	1.3000	13.27
14	YPIREHLNR	188	1.2000	12.24
15	FVLTTRGGD	212	1.2000	12.24
16	LYLQETLTF	243	1.2000	12.24
17	FEGYSAASI	119	0.9000	9.18
18	LNRLVDGDI	194	0.9000	9.18
19	YRDLAPVTE	4	0.8000	8.16
20	IEGIRSASS	127	0.8000	8.16
21	VRLYLQETL	241	0.6000	6.12
22	LVRLRVPFT	74	0.3000	3.06
23	YLQETLTFL	244	0.3000	3.06
24	FLCYTAEAS	251	0.2000	2.04
25	VIAHLRASK	64	0.1000	1.02
26	LAGVDGPYS	161	0.1000	1.02