MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Mar 2 20:46:29 2010
Length of input sequence	214 amino acids
Number of nanomers from input sequence	206
Number of nanomers with obligatory P1 anchor residue	69
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	21

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	YRKLSAQTA	205	3.3000	55.00
2	YVRADIQTV	94	1.4000	23.33
3	MRTLMETTL	159	0.2900	4.83
4	VLIHQPSLS	131	0.1000	1.67
5	YGIIDTVLE	196	0.1000	1.67
6	VLLAAGTPG	113	-0.0100	0
7	IQPQARYIL	7	-0.2000	0
8	FTSLMAIYD	82	-0.2000	0

9	YNKLFEERI	32	-0.6000	0
10	MYINSPGGG	73	-0.6600	0
11	VCLGQAASA	102	-0.7000	0
12	LIHQPSLSG	132	-0.7000	0
13	FIEHSSFGV	18	-0.8000	0
14	YINSPGGGF	74	-0.9000	0
15	IIFLGVQVD	40	-1.0000	0
16	LGQAASAAA	104	-1.1000	0
17	MAQLLVLES	56	-1.2000	0
18	MALPNARVL	124	-1.3100	0
19	LARHTGKDA	167	-1.5000	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	YRKLSAQTA	205	2.3000	38.33
2	MRTLMETTL	159	1.2900	21.50
3	VLIHQPSLS	131	1.1000	18.33
4	LLVLESLDP	59	1.0000	16.67
5	VLLAAGTPG	113	0.9900	16.50
6	IQPQARYIL	7	0.8000	13.33
7	YVRADIQTV	94	0.4000	6.67
8	MYINSPGGG	73	0.3400	5.67
9	VCLGQAASA	102	0.3000	5.00
10	LIHQPSLSG	132	0.3000	5.00
11	LGQAASAAA	104	-0.1000	0
12	MAQLLVLES	56	-0.2000	0
13	FTSLMAIYD	82	-0.2000	0
14	MALPNARVL	124	-0.3100	0
15	LARHTGKDA	167	-0.5000	0
16	FIEHSSFGV	18	-0.8000	0
17	LEIQAAEIE	149	-0.8000	0
18	MNSQNSQIQ	0	-0.9000	0

19	YGIIDTVLE	196	-0.9000	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	VLIHQPSLS	131	4.1700	43.89
2	VRADIQTVC	95	4.1000	43.16
3	ILPSFIEHS	14	3.6000	37.89
4	MYINSPGGG	73	3.6000	37.89
5	VQVDDASAN	45	3.4700	36.53
6	IQAAEIERM	151	2.8000	29.47
7	MAIYDTMQY	86	2.7000	28.42
8	YVRADIQTV	94	2.7000	28.42
9	MAQLLVLES	56	2.5000	26.32
10	IQPQARYIL	7	2.4100	25.37
11	IIFLGVQVD	40	2.4000	25.26
12	LLAAGTPGK	114	2.3000	24.21
13	YGIIDTVLE	196	2.2000	23.16
14	LIHQPSLSG	132	1.8000	18.95
15	IFLGVQVDD	41	1.6000	16.84
16	YINSPGGGF	74	1.6000	16.84
17	VLLAAGTPG	113	1.6000	16.84
18	LAAGTPGKR	115	1.6000	16.84
19	IQTVCLGQA	99	1.5000	15.79
20	VCLGQAASA	102	1.5000	15.79
21	IERMRTLME	156	1.5000	15.79

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	VRADIQTVC	95	3.1000	34.07

2	VLIHQPSLS	131	2.7700	30.44
3	YVRADIQTV	94	2.7000	29.67
4	ILPSFIEHS	14	2.2000	24.18
5	YRKLSAQTA	205	2.1000	23.08
6	FLGVQVDDA	42	1.8000	19.78
7	YGIIDTVLE	196	1.8000	19.78
8	VQVDDASAN	45	1.6700	18.35
9	MYINSPGGG	73	1.2000	13.19
10	LLAAGTPGK	114	1.2000	13.19
11	MAQLLVLES	56	1.1000	12.09
12	MQYVRADIQ	92	0.9000	9.89
13	YINSPGGGF	74	0.7000	7.69
14	IQTVCLGQA	99	0.5000	5.49
15	VCLGQAASA	102	0.5000	5.49
16	LPNARVLIH	126	0.4800	5.27
17	IQPQARYIL	7	0.4500	4.95
18	MAIYDTMQY	86	0.4000	4.40
19	MNSQNSQIQ	0	0.3000	3.30
20	IIFLGVQVD	40	0.3000	3.30
21	IQAAEIERM	151	0.3000	3.30

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	VRADIQTVC	95	4.1000	46.59
2	ILPSFIEHS	14	3.6000	40.91
3	VLIHQPSLS	131	3.5000	39.77
4	MAQLLVLES	56	2.6000	29.55
5	VQVDDASAN	45	2.4000	27.27
6	MQYVRADIQ	92	2.2000	25.00
7	LPNARVLIH	126	1.9800	22.50
8	YVRADIQTV	94	1.8000	20.45
9	IQAAEIERM	151	1.7000	19.32

10	VCLGQAASA	102	1.5000	17.05
11	MNSQNSQIQ	0	1.4000	15.91
12	IIFLGVQVD	40	1.4000	15.91
13	YRKLSAQTA	205	1.2000	13.64
14	FLGVQVDDA	42	1.1000	12.50
15	MAIYDTMQY	86	1.1000	12.50
16	LIHQPSLSG	132	0.9000	10.23
17	LLVLESLDP	59	0.8000	9.09
18	MYINSPGGG	73	0.8000	9.09
19	LLAAGTPGK	114	0.8000	9.09
20	VLEYRKLSA	202	0.8000	9.09
21	YGIIDTVLE	196	0.6800	7.73

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	VRADIQTVC	95	4.1000	46.59
2	ILPSFIEHS	14	3.6000	40.91
3	VLIHQPSLS	131	3.5000	39.77
4	MAQLLVLES	56	2.6000	29.55
5	VQVDDASAN	45	2.4000	27.27
6	MQYVRADIQ	92	2.2000	25.00
7	LPNARVLIH	126	1.9800	22.50
8	YVRADIQTV	94	1.8000	20.45
9	IQAAEIERM	151	1.7000	19.32
10	VCLGQAASA	102	1.5000	17.05
11	MNSQNSQIQ	0	1.4000	15.91
12	IIFLGVQVD	40	1.4000	15.91
13	YRKLSAQTA	205	1.2000	13.64
14	FLGVQVDDA	42	1.1000	12.50
15	MAIYDTMQY	86	1.1000	12.50
16	LIHQPSLSG	132	0.9000	10.23
17	LLVLESLDP	59	0.8000	9.09

18	MYINSPGGG	73	0.8000	9.09
19	LLAAGTPGK	114	0.8000	9.09
20	VLEYRKLSA	202	0.8000	9.09
21	YGIIDTVLE	196	0.6800	7.73

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	VRADIQTVC	95	4.1000	46.59
2	ILPSFIEHS	14	3.6000	40.91
3	VLIHQPSLS	131	3.5000	39.77
4	MAQLLVLES	56	2.6000	29.55
5	VQVDDASAN	45	2.4000	27.27
6	MQYVRADIQ	92	2.2000	25.00
7	LPNARVLIH	126	1.9800	22.50
8	YVRADIQTV	94	1.8000	20.45
9	IQAAEIERM	151	1.7000	19.32
10	VCLGQAASA	102	1.5000	17.05
11	MNSQNSQIQ	0	1.4000	15.91
12	IIFLGVQVD	40	1.4000	15.91
13	YRKLSAQTA	205	1.2000	13.64
14	FLGVQVDDA	42	1.1000	12.50
15	MAIYDTMQY	86	1.1000	12.50
16	LIHQPSLSG	132	0.9000	10.23
17	LLVLESLDP	59	0.8000	9.09
18	MYINSPGGG	73	0.8000	9.09
19	LLAAGTPGK	114	0.8000	9.09
20	VLEYRKLSA	202	0.8000	9.09
21	YGIIDTVLE	196	0.6800	7.73

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	YVRADIQTV	94	3.7000	38.95
2	YGIIDTVLE	196	3.2000	33.68
3	VLIHQPSLS	131	3.1700	33.37
4	VRADIQTVC	95	3.1000	32.63
5	ILPSFIEHS	14	2.6000	27.37
6	MYINSPGGG	73	2.6000	27.37
7	YINSPGGGF	74	2.6000	27.37
8	VQVDDASAN	45	2.4700	26.00
9	YRKLSAQTA	205	2.1000	22.11
10	FLGVQVDDA	42	1.8000	18.95
11	IQAAEIERM	151	1.8000	18.95
12	MAIYDTMQY	86	1.7000	17.89
13	MAQLLVLES	56	1.5000	15.79
14	IQPQARYIL	7	1.4100	14.84
15	IIFLGVQVD	40	1.4000	14.74
16	LLAAGTPGK	114	1.3000	13.68
17	LIHQPSLSG	132	0.8000	8.42
18	FIEHSSFGV	18	0.6000	6.32
19	IFLGVQVDD	41	0.6000	6.32
20	VLLAAGTPG	113	0.6000	6.32
21	LAAGTPGKR	115	0.6000	6.32

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	VRADIQTVC	95	4.1000	46.59
2	ILPSFIEHS	14	3.6000	40.91
3	VLIHQPSLS	131	3.5000	39.77
4	MAQLLVLES	56	2.6000	29.55
5	VQVDDASAN	45	2.4000	27.27
6	MQYVRADIQ	92	2.2000	25.00
7	LPNARVLIH	126	1.9800	22.50

8	YVRADIQTV	94	1.8000	20.45
9	IQAAEIERM	151	1.7000	19.32
10	VCLGQAASA	102	1.5000	17.05
11	MNSQNSQIQ	0	1.4000	15.91
12	IIFLGVQVD	40	1.4000	15.91
13	YRKLSAQTA	205	1.2000	13.64
14	FLGVQVDDA	42	1.1000	12.50
15	MAIYDTMQY	86	1.1000	12.50
16	LIHQPSLSG	132	0.9000	10.23
17	LLVLESLDP	59	0.8000	9.09
18	MYINSPGGG	73	0.8000	9.09
19	LLAAGTPGK	114	0.8000	9.09
20	VLEYRKLSA	202	0.8000	9.09
21	YGIIDTVLE	196	0.6800	7.73

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	VLIHQPSLS	131	3.1000	36.05
2	YGIIDTVLE	196	3.0800	35.81
3	YRKLSAQTA	205	3.0000	34.88
4	MNSQNSQIQ	0	2.3000	26.74
5	MAQLLVLES	56	2.1000	24.42
6	YVRADIQTV	94	2.0000	23.26
7	ILPSFIEHS	14	1.9000	22.09
8	LIHQPSLSG	132	1.8000	20.93
9	LLVLESLDP	59	1.7000	19.77
10	IERMRTLME	156	1.6000	18.60
11	VRADIQTVC	95	1.0000	11.63
12	IIFLGVQVD	40	0.9000	10.47
13	FLGVQVDDA	42	0.9000	10.47
14	LLAAGTPGK	114	0.9000	10.47
15	LPNARVLIH	126	0.6800	7.91

16	MAIYDTMQY	86	0.6000	6.98
17	VQVDDASAN	45	0.5000	5.81
18	LVLESLDPD	60	0.5000	5.81
19	LGQAASAAA	104	0.5000	5.81
20	FIEHSSFGV	18	0.3000	3.49
21	MQYVRADIQ	92	0.3000	3.49

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	VLIHQPSLS	131	4.0000	41.67
2	MNSQNSQIQ	0	3.2000	33.33
3	MAIYDTMQY	86	2.8000	29.17
4	IERMRTLME	156	2.6000	27.08
5	YVRADIQTV	94	2.1000	21.88
6	MAQLLVLES	56	2.0000	20.83
7	LPNARVLIH	126	1.9800	20.62
8	LIHQPSLSG	132	1.9000	19.79
9	YRKLSAQTA	205	1.7000	17.71
10	IIFLGVQVD	40	1.6000	16.67
11	LLVLESLDP	59	1.6000	16.67
12	LLAAGTPGK	114	1.6000	16.67
13	LGQAASAAA	104	1.5000	15.62
14	YGIIDTVLE	196	1.4800	15.42
15	FIEHSSFGV	18	0.9000	9.38
16	ITMYINSPG	71	0.9000	9.38
17	LEYRKLSAQ	203	0.9000	9.38
18	FGVKESNPY	24	0.7000	7.29
19	LMAIYDTMQ	85	0.6800	7.08
20	MALPNARVL	124	0.4000	4.17
21	LARHTGKDA	167	0.4000	4.17

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	IERMRTLME	156	3.1000	35.23
2	MAQLLVLES	56	2.9000	32.95
3	MAIYDTMQY	86	2.7000	30.68
4	VLIHQPSLS	131	2.7000	30.68
5	LLVLESLDP	59	2.5000	28.41
6	MNSQNSQIQ	0	2.3000	26.14
7	YGIIDTVLE	196	2.2000	25.00
8	LMAIYDTMQ	85	2.0000	22.73
9	YRKLSAQTA	205	2.0000	22.73
10	IIFLGVQVD	40	1.9000	21.59
11	ITMYINSPG	71	1.8000	20.45
12	MQYVRADIQ	92	1.8000	20.45
13	LLAAGTPGK	114	1.6000	18.18
14	LIHQPSLSG	132	1.6000	18.18
15	LGQAASAAA	104	1.5000	17.05
16	LPNARVLIH	126	1.2800	14.55
17	YVRADIQTV	94	0.8000	9.09
18	ILPSFIEHS	14	0.5000	5.68
19	FLGVQVDDA	42	0.4000	4.55
20	MRTLMETTL	159	0.2000	2.27

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	YGIIDTVLE	196	6.2000	65.96
2	IERMRTLME	156	5.1000	54.26
3	IIFLGVQVD	40	3.6000	38.30
4	YRKLSAQTA	205	3.0000	31.91
5	MAIYDTMQY	86	2.8000	29.79

6	FTSLMAIYD	82	2.2800	24.26
7	MNSQNSQIQ	0	2.1000	22.34
8	ITMYINSPG	71	2.1000	22.34
9	YVRADIQTV	94	2.1000	22.34
10	MAQLLVLES	56	1.9000	20.21
11	LLVLESLDP	59	1.9000	20.21
12	LIHQPSLSG	132	1.9000	20.21
13	LMAIYDTMQ	85	1.8000	19.15
14	VLIHQPSLS	131	1.7000	18.09
15	MQYVRADIQ	92	1.6000	17.02
16	LPNARVLIH	126	1.5000	15.96
17	IQGQFSDLE	142	1.5000	15.96
18	FLGVQVDDA	42	1.4000	14.89
19	FGVKESNPY	24	1.3000	13.83
20	LEIQAAEIE	149	1.2000	12.77
21	YILPSFIEH	13	1.0800	11.49

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	YGIIDTVLE	196	3.2000	36.36
2	YRKLSAQTA	205	3.0000	34.09
3	IERMRTLME	156	2.1000	23.86
4	MAQLLVLES	56	1.9000	21.59
5	YVRADIQTV	94	1.8000	20.45
6	MAIYDTMQY	86	1.7000	19.32
7	VLIHQPSLS	131	1.7000	19.32
8	LLVLESLDP	59	1.5000	17.05
9	FLGVQVDDA	42	1.4000	15.91
10	MNSQNSQIQ	0	1.3000	14.77
11	LMAIYDTMQ	85	1.0000	11.36
12	IIFLGVQVD	40	0.9000	10.23
13	ITMYINSPG	71	0.8000	9.09

14	MQYVRADIQ	92	0.8000	9.09
15	LLAAGTPGK	114	0.6000	6.82
16	LIHQPSLSG	132	0.6000	6.82
17	LGQAASAAA	104	0.5000	5.68
18	LPNARVLIH	126	0.2800	3.18
19	FGVKESNPY	24	0.2000	2.27
20	YILPSFIEH	13	-0.1400	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	IERMRTLME	156	6.1000	64.89
2	YGIIDTVLE	196	5.2000	55.32
3	IIFLGVQVD	40	4.6000	48.94
4	MAIYDTMQY	86	3.8000	40.43
5	MNSQNSQIQ	0	3.1000	32.98
6	ITMYINSPG	71	3.1000	32.98
7	MAQLLVLES	56	2.9000	30.85
8	LLVLESLDP	59	2.9000	30.85
9	LIHQPSLSG	132	2.9000	30.85
10	LMAIYDTMQ	85	2.8000	29.79
11	VLIHQPSLS	131	2.7000	28.72
12	MQYVRADIQ	92	2.6000	27.66
13	LPNARVLIH	126	2.5000	26.60
14	IQGQFSDLE	142	2.5000	26.60
15	LEIQAAEIE	149	2.2000	23.40
16	VIRKDTDRD	177	2.0000	21.28
17	YRKLSAQTA	205	2.0000	21.28
18	VQVDDASAN	45	1.7000	18.09
19	LGQAASAAA	104	1.5000	15.96
20	FTSLMAIYD	82	1.2800	13.62
21	IMAQLLVLE	55	1.2000	12.77

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	YGIIDTVLE	196	4.4800	49.78
2	VLIHQPSLS	131	3.5000	38.89
3	LIHQPSLSG	132	3.2000	35.56
4	YVRADIQTV	94	3.0000	33.33
5	IERMRTLME	156	3.0000	33.33
6	YRKLSAQTA	205	3.0000	33.33
7	LLVLESLDP	59	2.7000	30.00
8	MAQLLVLES	56	2.5000	27.78
9	ILPSFIEHS	14	2.3000	25.56
10	IIFLGVQVD	40	2.0000	22.22
11	MAIYDTMQY	86	1.9000	21.11
12	MNSQNSQIQ	0	1.6000	17.78
13	LVLESLDPD	60	1.6000	17.78
14	IQGQFSDLE	142	1.6000	17.78
15	MYINSPGGG	73	1.4000	15.56
16	IQAAEIERM	151	1.4000	15.56
17	FIEHSSFGV	18	1.3000	14.44
18	VQVDDASAN	45	1.3000	14.44
19	LEIQAAEIE	149	1.3000	14.44
20	FGVKESNPY	24	1.2000	13.33
21	VRADIQTVC	95	1.0000	11.11

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	IERMRTLME	156	3.1000	35.23
2	MAQLLVLES	56	2.9000	32.95
3	MAIYDTMQY	86	2.7000	30.68

4	VLIHQPSLS	131	2.7000	30.68
5	LLVLESLDP	59	2.5000	28.41
6	MNSQNSQIQ	0	2.3000	26.14
7	YGIIDTVLE	196	2.2000	25.00
8	LMAIYDTMQ	85	2.0000	22.73
9	YRKLSAQTA	205	2.0000	22.73
10	IIFLGVQVD	40	1.9000	21.59
11	ITMYINSPG	71	1.8000	20.45
12	MQYVRADIQ	92	1.8000	20.45
13	LLAAGTPGK	114	1.6000	18.18
14	LIHQPSLSG	132	1.6000	18.18
15	LGQAASAAA	104	1.5000	17.05
16	LPNARVLIH	126	1.2800	14.55
17	YVRADIQTV	94	0.8000	9.09
18	ILPSFIEHS	14	0.5000	5.68
19	FLGVQVDDA	42	0.4000	4.55
20	MRTLMETTL	159	0.2000	2.27

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	VLIHQPSLS	131	3.1000	36.05
2	YGIIDTVLE	196	3.0800	35.81
3	YRKLSAQTA	205	3.0000	34.88
4	MNSQNSQIQ	0	2.3000	26.74
5	MAQLLVLES	56	2.1000	24.42
6	YVRADIQTV	94	2.0000	23.26
7	ILPSFIEHS	14	1.9000	22.09
8	LIHQPSLSG	132	1.8000	20.93
9	LLVLESLDP	59	1.7000	19.77
10	IERMRTLME	156	1.6000	18.60
11	VRADIQTVC	95	1.0000	11.63
12	IIFLGVQVD	40	0.9000	10.47

13	FLGVQVDDA	42	0.9000	10.47
14	LLAAGTPGK	114	0.9000	10.47
15	LPNARVLIH	126	0.6800	7.91
16	MAIYDTMQY	86	0.6000	6.98
17	VQVDDASAN	45	0.5000	5.81
18	LVLESLDPD	60	0.5000	5.81
19	LGQAASAAA	104	0.5000	5.81
20	FIEHSSFGV	18	0.3000	3.49
21	MQYVRADIQ	92	0.3000	3.49

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	YVRADIQTV	94	5.4000	46.55
2	FIEHSSFGV	18	4.7000	40.52
3	YINSPGGGF	74	4.6000	39.66
4	YGIIDTVLE	196	4.3200	37.24
5	IQPQARYIL	7	3.0000	25.86
6	MALPNARVL	124	2.9000	25.00
7	FGVKESNPY	24	2.8000	24.14
8	IQAAEIERM	151	2.6000	22.41
9	LFEERIIFL	35	2.5000	21.55
10	YRKLSAQTA	205	2.5000	21.55
11	MAIYDTMQY	86	2.4200	20.86
12	YILPSFIEH	13	2.3000	19.83
13	MRTLMETTL	159	2.2000	18.97
14	VIQGQFSDL	141	2.0000	17.24
15	ILPSFIEHS	14	1.9000	16.38
16	LLVLESLDP	59	1.9000	16.38
17	YNKLFEERI	32	1.8000	15.52
18	METTLARHT	163	1.6000	13.79
19	IERMRTLME	156	1.2200	10.52
20	VDDASANDI	47	1.2000	10.34

21	VLIHQPSLS	131	1.2000	10.34

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	YVRADIQTV	94	5.4000	46.55
2	FIEHSSFGV	18	4.7000	40.52
3	YINSPGGGF	74	4.6000	39.66
4	YGIIDTVLE	196	4.3200	37.24
5	IQPQARYIL	7	3.0000	25.86
6	MALPNARVL	124	2.9000	25.00
7	FGVKESNPY	24	2.8000	24.14
8	IQAAEIERM	151	2.6000	22.41
9	LFEERIIFL	35	2.5000	21.55
10	YRKLSAQTA	205	2.5000	21.55
11	MAIYDTMQY	86	2.4200	20.86
12	YILPSFIEH	13	2.3000	19.83
13	MRTLMETTL	159	2.2000	18.97
14	VIQGQFSDL	141	2.0000	17.24
15	ILPSFIEHS	14	1.9000	16.38
16	LLVLESLDP	59	1.9000	16.38
17	YNKLFEERI	32	1.8000	15.52
18	METTLARHT	163	1.6000	13.79
19	IERMRTLME	156	1.2200	10.52
20	VDDASANDI	47	1.2000	10.34
21	VLIHQPSLS	131	1.2000	10.34

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	MAIYDTMQY	86	3.3000	38.37

2	YGIIDTVLE	196	3.3000	38.37
3	IERMRTLME	156	3.0000	34.88
4	IIFLGVQVD	40	2.6000	30.23
5	VIRKDTDRD	177	2.5000	29.07
6	LEYRKLSAQ	203	2.4000	27.91
7	FGVKESNPY	24	2.0000	23.26
8	VLEYRKLSA	202	2.0000	23.26
9	YVRADIQTV	94	1.9000	22.09
10	MYINSPGGG	73	1.7000	19.77
11	YRKLSAQTA	205	1.7000	19.77
12	FEERIIFLG	36	1.3000	15.12
13	MAQLLVLES	56	1.3000	15.12
14	LPNARVLIH	126	1.2000	13.95
15	FTSLMAIYD	82	1.1000	12.79
16	ITMYINSPG	71	1.0000	11.63
17	VLIHQPSLS	131	0.4000	4.65
18	FLGVQVDDA	42	0.3000	3.49
19	YILPSFIEH	13	0.2000	2.33
20	MQYVRADIQ	92	0.2000	2.33
21	IQTVCLGQA	99	0.2000	2.33

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	MAIYDTMQY	86	2.2000	27.50
2	VLEYRKLSA	202	2.0000	25.00
3	YRKLSAQTA	205	1.7000	21.25
4	YVRADIQTV	94	1.6000	20.00
5	LEYRKLSAQ	203	1.6000	20.00
6	MAQLLVLES	56	1.3000	16.25
7	FGVKESNPY	24	0.9000	11.25
8	MYINSPGGG	73	0.4000	5.00
9	VLIHQPSLS	131	0.4000	5.00

10	FLGVQVDDA	42	0.3000	3.75
11	YGIIDTVLE	196	0.3000	3.75
12	IQTVCLGQA	99	0.2000	2.50
13	LPNARVLIH	126	-0.0200	0
14	IIFLGVQVD	40	-0.1000	0
15	VIRKDTDRD	177	-0.2000	0
16	ITMYINSPG	71	-0.3000	0
17	LLVLESLDP	59	-0.5000	0
18	MQYVRADIQ	92	-0.6000	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	MAIYDTMQY	86	3.2000	40.00
2	VLEYRKLSA	202	3.0000	37.50
3	LEYRKLSAQ	203	2.6000	32.50
4	MAQLLVLES	56	2.3000	28.75
5	MYINSPGGG	73	1.4000	17.50
6	VLIHQPSLS	131	1.4000	17.50
7	IQTVCLGQA	99	1.2000	15.00
8	IERMRTLME	156	1.0000	12.50
9	LPNARVLIH	126	0.9800	12.25
10	IIFLGVQVD	40	0.9000	11.25
11	VIRKDTDRD	177	0.8000	10.00
12	ITMYINSPG	71	0.7000	8.75
13	YRKLSAQTA	205	0.7000	8.75
14	YVRADIQTV	94	0.6000	7.50
15	LLVLESLDP	59	0.5000	6.25
16	MQYVRADIQ	92	0.4000	5.00
17	LGQAASAAA	104	0.4000	5.00
18	LLAAGTPGK	114	0.3000	3.75
19	FGVKESNPY	24	-0.1000	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	MAIYDTMQY	86	4.3000	50.00
2	IERMRTLME	156	4.0000	46.51
3	IIFLGVQVD	40	3.6000	41.86
4	VIRKDTDRD	177	3.5000	40.70
5	LEYRKLSAQ	203	3.4000	39.53
6	VLEYRKLSA	202	3.0000	34.88
7	MYINSPGGG	73	2.7000	31.40
8	MAQLLVLES	56	2.3000	26.74
9	YGIIDTVLE	196	2.3000	26.74
10	LPNARVLIH	126	2.2000	25.58
11	ITMYINSPG	71	2.0000	23.26
12	VLIHQPSLS	131	1.4000	16.28
13	MQYVRADIQ	92	1.2000	13.95
14	IQTVCLGQA	99	1.2000	13.95
15	FGVKESNPY	24	1.0000	11.63
16	LLVLESLDP	59	0.9000	10.47
17	LVLESLDPD	60	0.9000	10.47
18	YVRADIQTV	94	0.9000	10.47
19	YRKLSAQTA	205	0.7000	8.14
20	ILTAEEAKD	187	0.6000	6.98
21	IMAQLLVLE	55	0.5000	5.81

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	LEYRKLSAQ	203	3.4000	39.08
2	MAIYDTMQY	86	3.2000	36.78
3	FGVKESNPY	24	2.9000	33.33

4	YRKLSAQTA	205	2.7000	31.03
5	YVRADIQTV	94	2.6000	29.89
6	VLEYRKLSA	202	2.6000	29.89
7	VLIHQPSLS	131	2.2000	25.29
8	MAQLLVLES	56	1.9000	21.84
9	FLGVQVDDA	42	1.5000	17.24
10	ITMYINSPG	71	1.5000	17.24
11	YGIIDTVLE	196	1.3000	14.94
12	VIRKDTDRD	177	1.0000	11.49
13	IIFLGVQVD	40	0.9000	10.34
14	FEERIIFLG	36	0.8500	9.77
15	MQYVRADIQ	92	0.6000	6.90
16	IERMRTLME	156	0.6000	6.90
17	LPNARVLIH	126	0.5800	6.67
18	VRADIQTVC	95	0.3000	3.45
19	LLVLESLDP	59	0.1000	1.15

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	MAIYDTMQY	86	4.9000	48.51
2	IERMRTLME	156	4.8000	47.52
3	YGIIDTVLE	196	3.8000	37.62
4	VLEYRKLSA	202	3.8000	37.62
5	MAQLLVLES	56	3.1000	30.69
6	LPNARVLIH	126	3.0000	29.70
7	IIFLGVQVD	40	2.7000	26.73
8	FTSLMAIYD	82	2.7000	26.73
9	LEYRKLSAQ	203	2.4000	23.76
10	FGVKESNPY	24	2.3000	22.77
11	VIRKDTDRD	177	2.2000	21.78
12	YVRADIQTV	94	2.0000	19.80
13	YILPSFIEH	13	1.8000	17.82

14	FEERIIFLG	36	1.8000	17.82
15	MYINSPGGG	73	1.8000	17.82
16	YRKLSAQTA	205	1.8000	17.82
17	LLVLESLDP	59	1.7000	16.83
18	ITMYINSPG	71	1.0000	9.90
19	LIHQPSLSG	132	1.0000	9.90
20	VLIHQPSLS	131	0.4000	3.96
21	IQTVCLGQA	99	0.3000	2.97

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	MAQLLVLES	56	3.5000	42.17
2	YRKLSAQTA	205	2.2000	26.51
3	LPNARVLIH	126	1.7800	21.45
4	LLVLESLDP	59	1.7000	20.48
5	YVRADIQTV	94	1.7000	20.48
6	IERMRTLME	156	1.4000	16.87
7	YGIIDTVLE	196	1.4000	16.87
8	MAIYDTMQY	86	0.9000	10.84
9	VLEYRKLSA	202	0.9000	10.84
10	VLIHQPSLS	131	0.8000	9.64
11	MYINSPGGG	73	0.5000	6.02
12	LLAAGTPGK	114	0.4500	5.42
13	IIFLGVQVD	40	0.4000	4.82
14	FTSLMAIYD	82	0.4000	4.82
15	IQTVCLGQA	99	0.4000	4.82
16	LIHQPSLSG	132	0.3000	3.61
17	FLGVQVDDA	42	0.1000	1.20
18	YILPSFIEH	13	-0.1200	0
19	IQPQARYIL	7	-0.3000	0
20	ILPSFIEHS	14	-0.3000	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	VLIHQPSLS	131	4.3000	51.19
2	MAQLLVLES	56	2.7000	32.14
3	IQPQARYIL	7	1.9000	22.62
4	VLEYRKLSA	202	1.9000	22.62
5	MAIYDTMQY	86	1.7000	20.24
6	LPNARVLIH	126	1.6800	20.00
7	MNSQNSQIQ	0	1.6000	19.05
8	LARHTGKDA	167	1.5000	17.86
9	IIFLGVQVD	40	1.4000	16.67
10	YVRADIQTV	94	1.4000	16.67
11	LIHQPSLSG	132	1.2000	14.29
12	YRKLSAQTA	205	1.2000	14.29
13	ILPSFIEHS	14	1.1000	13.10
14	IERMRTLME	156	1.1000	13.10
15	LLAAGTPGK	114	1.0000	11.90
16	LLVLESLDP	59	0.9000	10.71
17	LEYRKLSAQ	203	0.9000	10.71
18	MYINSPGGG	73	0.5000	5.95
19	IQAAEIERM	151	0.5000	5.95
20	LGQAASAAA	104	0.4000	4.76
21	FIEHSSFGV	18	0.2000	2.38

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	MAQLLVLES	56	4.5000	54.22
2	LPNARVLIH	126	2.7800	33.49
3	LLVLESLDP	59	2.7000	32.53

4	IERMRTLME	156	2.4000	28.92
5	MAIYDTMQY	86	1.9000	22.89
6	VLEYRKLSA	202	1.9000	22.89
7	VLIHQPSLS	131	1.8000	21.69
8	MYINSPGGG	73	1.5000	18.07
9	LLAAGTPGK	114	1.4500	17.47
10	IIFLGVQVD	40	1.4000	16.87
11	IQTVCLGQA	99	1.4000	16.87
12	LIHQPSLSG	132	1.3000	15.66
13	YRKLSAQTA	205	1.2000	14.46
14	IQPQARYIL	7	0.7000	8.43
15	ILPSFIEHS	14	0.7000	8.43
16	YVRADIQTV	94	0.7000	8.43
17	LGQAASAAA	104	0.4000	4.82
18	YGIIDTVLE	196	0.4000	4.82
19	MQYVRADIQ	92	0.2000	2.41
20	IQAAEIERM	151	0.2000	2.41

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	MAQLLVLES	56	4.5000	54.22
2	LPNARVLIH	126	2.7800	33.49
3	LLVLESLDP	59	2.7000	32.53
4	IERMRTLME	156	2.4000	28.92
5	MAIYDTMQY	86	1.9000	22.89
6	VLEYRKLSA	202	1.9000	22.89
7	VLIHQPSLS	131	1.8000	21.69
8	MYINSPGGG	73	1.5000	18.07
9	LLAAGTPGK	114	1.4500	17.47
10	IIFLGVQVD	40	1.4000	16.87
11	IQTVCLGQA	99	1.4000	16.87
12	LIHQPSLSG	132	1.3000	15.66

13	YRKLSAQTA	205	1.2000	14.46
14	IQPQARYIL	7	0.7000	8.43
15	ILPSFIEHS	14	0.7000	8.43
16	YVRADIQTV	94	0.7000	8.43
17	LGQAASAAA	104	0.4000	4.82
18	YGIIDTVLE	196	0.4000	4.82
19	MQYVRADIQ	92	0.2000	2.41
20	IQAAEIERM	151	0.2000	2.41

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	VRADIQTVC	95	4.1000	45.05
2	VLIHQPSLS	131	3.7700	41.43
3	ILPSFIEHS	14	3.2000	35.16
4	VQVDDASAN	45	2.6700	29.34
5	MYINSPGGG	73	2.2000	24.18
6	LLAAGTPGK	114	2.2000	24.18
7	MAQLLVLES	56	2.1000	23.08
8	MQYVRADIQ	92	1.9000	20.88
9	YVRADIQTV	94	1.7000	18.68
10	IQTVCLGQA	99	1.5000	16.48
11	VCLGQAASA	102	1.5000	16.48
12	LPNARVLIH	126	1.4800	16.26
13	IQPQARYIL	7	1.4500	15.93
14	MAIYDTMQY	86	1.4000	15.38
15	MNSQNSQIQ	0	1.3000	14.29
16	IIFLGVQVD	40	1.3000	14.29
17	IQAAEIERM	151	1.3000	14.29
18	YRKLSAQTA	205	1.1000	12.09
19	IRKDTDRDK	178	0.9000	9.89
20	FLGVQVDDA	42	0.8000	8.79
21	YGIIDTVLE	196	0.8000	8.79

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	VLIHQPSLS	131	3.3000	39.29
2	YVRADIQTV	94	2.4000	28.57
3	YRKLSAQTA	205	2.2000	26.19
4	MAQLLVLES	56	1.7000	20.24
5	FIEHSSFGV	18	1.2000	14.29
6	IQPQARYIL	7	0.9000	10.71
7	VLEYRKLSA	202	0.9000	10.71
8	FGVKESNPY	24	0.8000	9.52
9	MAIYDTMQY	86	0.7000	8.33
10	LPNARVLIH	126	0.6800	8.10
11	MNSQNSQIQ	0	0.6000	7.14
12	LARHTGKDA	167	0.5000	5.95
13	IIFLGVQVD	40	0.4000	4.76
14	YGIIDTVLE	196	0.4000	4.76
15	LIHQPSLSG	132	0.2000	2.38
16	ILPSFIEHS	14	0.1000	1.19
17	IERMRTLME	156	0.1000	1.19
18	LLVLESLDP	59	-0.1000	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	VLIHQPSLS	131	3.7000	42.05
2	YVRADIQTV	94	3.4000	38.64
3	FIEHSSFGV	18	2.2000	25.00
4	YRKLSAQTA	205	2.2000	25.00
5	FGVKESNPY	24	2.1000	23.86
6	MAQLLVLES	56	2.1000	23.86

7	MAIYDTMQY	86	2.0000	22.73
8	IQPQARYIL	7	1.8600	21.14
9	YGIIDTVLE	196	1.8000	20.45
10	LIHQPSLSG	132	1.6000	18.18
11	IIFLGVQVD	40	1.5000	17.05
12	IERMRTLME	156	1.5000	17.05
13	IQAAEIERM	151	1.0000	11.36
14	LLVLESLDP	59	0.9000	10.23
15	MYINSPGGG	73	0.9000	10.23
16	VLEYRKLSA	202	0.9000	10.23
17	FEERIIFLG	36	0.8000	9.09
18	ILPSFIEHS	14	0.5000	5.68
19	IMAQLLVLE	55	0.5000	5.68
20	LARHTGKDA	167	0.5000	5.68
21	VIRKDTDRD	177	0.3000	3.41

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	VLIHQPSLS	131	4.3000	51.19
2	MAQLLVLES	56	2.7000	32.14
3	IQPQARYIL	7	1.9000	22.62
4	VLEYRKLSA	202	1.9000	22.62
5	MAIYDTMQY	86	1.7000	20.24
6	LPNARVLIH	126	1.6800	20.00
7	MNSQNSQIQ	0	1.6000	19.05
8	LARHTGKDA	167	1.5000	17.86
9	IIFLGVQVD	40	1.4000	16.67
10	YVRADIQTV	94	1.4000	16.67
11	LIHQPSLSG	132	1.2000	14.29
12	YRKLSAQTA	205	1.2000	14.29
13	ILPSFIEHS	14	1.1000	13.10
14	IERMRTLME	156	1.1000	13.10

15	LLAAGTPGK	114	1.0000	11.90
16	LLVLESLDP	59	0.9000	10.71
17	LEYRKLSAQ	203	0.9000	10.71
18	MYINSPGGG	73	0.5000	5.95
19	IQAAEIERM	151	0.5000	5.95
20	LGQAASAAA	104	0.4000	4.76
21	FIEHSSFGV	18	0.2000	2.38

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	MAQLLVLES	56	3.9000	44.83
2	IERMRTLME	156	2.8000	32.18
3	YGIIDTVLE	196	2.8000	32.18
4	LLVLESLDP	59	2.7000	31.03
5	YVRADIQTV	94	2.7000	31.03
6	MAIYDTMQY	86	2.2000	25.29
7	YRKLSAQTA	205	2.2000	25.29
8	MYINSPGGG	73	1.9000	21.84
9	LIHQPSLSG	132	1.7000	19.54
10	IIFLGVQVD	40	1.5000	17.24
11	FTSLMAIYD	82	1.5000	17.24
12	LPNARVLIH	126	1.2000	13.79
13	VLIHQPSLS	131	1.2000	13.79
14	VLEYRKLSA	202	0.9000	10.34
15	YINSPGGGF	74	0.7000	8.05
16	IQAAEIERM	151	0.7000	8.05
17	IQPQARYIL	7	0.6600	7.59
18	LLAAGTPGK	114	0.5500	6.32
19	IQTVCLGQA	99	0.4000	4.60
20	ILPSFIEHS	14	0.1000	1.15
21	FLGVQVDDA	42	0.1000	1.15

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	VLIHQPSLS	131	4.7000	53.41
2	MAQLLVLES	56	3.1000	35.23
3	MAIYDTMQY	86	3.0000	34.09
4	IQPQARYIL	7	2.8600	32.50
5	LIHQPSLSG	132	2.6000	29.55
6	IIFLGVQVD	40	2.5000	28.41
7	IERMRTLME	156	2.5000	28.41
8	YVRADIQTV	94	2.4000	27.27
9	IQAAEIERM	151	2.0000	22.73
10	LLVLESLDP	59	1.9000	21.59
11	MYINSPGGG	73	1.9000	21.59
12	VLEYRKLSA	202	1.9000	21.59
13	ILPSFIEHS	14	1.5000	17.05
14	IMAQLLVLE	55	1.5000	17.05
15	LARHTGKDA	167	1.5000	17.05
16	VIRKDTDRD	177	1.3000	14.77
17	FIEHSSFGV	18	1.2000	13.64
18	YRKLSAQTA	205	1.2000	13.64
19	FGVKESNPY	24	1.1000	12.50
20	LLAAGTPGK	114	1.1000	12.50
21	LPNARVLIH	126	1.1000	12.50

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	VLIHQPSLS	131	3.7000	42.05
2	YVRADIQTV	94	3.4000	38.64
3	FIEHSSFGV	18	2.2000	25.00

4	YRKLSAQTA	205	2.2000	25.00
5	FGVKESNPY	24	2.1000	23.86
6	MAQLLVLES	56	2.1000	23.86
7	MAIYDTMQY	86	2.0000	22.73
8	IQPQARYIL	7	1.8600	21.14
9	YGIIDTVLE	196	1.8000	20.45
10	LIHQPSLSG	132	1.6000	18.18
11	IIFLGVQVD	40	1.5000	17.05
12	IERMRTLME	156	1.5000	17.05
13	IQAAEIERM	151	1.0000	11.36
14	LLVLESLDP	59	0.9000	10.23
15	MYINSPGGG	73	0.9000	10.23
16	VLEYRKLSA	202	0.9000	10.23
17	FEERIIFLG	36	0.8000	9.09
18	ILPSFIEHS	14	0.5000	5.68
19	IMAQLLVLE	55	0.5000	5.68
20	LARHTGKDA	167	0.5000	5.68
21	VIRKDTDRD	177	0.3000	3.41

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	VLIHQPSLS	131	4.3000	47.78
2	IIFLGVQVD	40	4.1000	45.56
3	IERMRTLME	156	4.1000	45.56
4	IMAQLLVLE	55	3.1000	34.44
5	IQPQARYIL	7	2.9000	32.22
6	LPNARVLIH	126	2.9000	32.22
7	VIRKDTDRD	177	2.9000	32.22
8	MAIYDTMQY	86	2.8000	31.11
9	MAQLLVLES	56	2.7000	30.00
10	LIHQPSLSG	132	2.5000	27.78
11	LEIQAAEIE	149	2.5000	27.78

12	MNSQNSQIQ	0	2.4000	26.67
13	YGIIDTVLE	196	2.4000	26.67
14	VLEYRKLSA	202	1.9000	21.11
15	MYINSPGGG	73	1.8000	20.00
16	LVLESLDPD	60	1.7000	18.89
17	YVRADIQTV	94	1.7000	18.89
18	IQGQFSDLE	142	1.7000	18.89
19	LEYRKLSAQ	203	1.7000	18.89
20	IQAAEIERM	151	1.6000	17.78
21	LARHTGKDA	167	1.5000	16.67

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	MAQLLVLES	56	3.9000	44.83
2	IERMRTLME	156	2.8000	32.18
3	YGIIDTVLE	196	2.8000	32.18
4	LLVLESLDP	59	2.7000	31.03
5	YVRADIQTV	94	2.7000	31.03
6	MAIYDTMQY	86	2.2000	25.29
7	YRKLSAQTA	205	2.2000	25.29
8	MYINSPGGG	73	1.9000	21.84
9	LIHQPSLSG	132	1.7000	19.54
10	IIFLGVQVD	40	1.5000	17.24
11	FTSLMAIYD	82	1.5000	17.24
12	LPNARVLIH	126	1.2000	13.79
13	VLIHQPSLS	131	1.2000	13.79
14	VLEYRKLSA	202	0.9000	10.34
15	YINSPGGGF	74	0.7000	8.05
16	IQAAEIERM	151	0.7000	8.05
17	IQPQARYIL	7	0.6600	7.59
18	LLAAGTPGK	114	0.5500	6.32
19	IQTVCLGQA	99	0.4000	4.60

20	ILPSFIEHS	14	0.1000	1.15
21	FLGVQVDDA	42	0.1000	1.15

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	YRKLSAQTA	205	2.1000	30.88
2	MAQLLVLES	56	1.7000	25.00
3	YVRADIQTV	94	1.6000	23.53
4	YGIIDTVLE	196	0.9000	13.24
5	VLIHQPSLS	131	0.8000	11.76
6	FLGVQVDDA	42	0.4000	5.88
7	MYINSPGGG	73	0.4000	5.88
8	IIFLGVQVD	40	0.3000	4.41
9	IQTVCLGQA	99	0.3000	4.41
10	LPNARVLIH	126	-0.0200	0
11	LLVLESLDP	59	-0.1000	0
12	IERMRTLME	156	-0.4000	0
13	MQYVRADIQ	92	-0.5000	0
14	LGQAASAAA	104	-0.6000	0
15	MAIYDTMQY	86	-0.7000	0
16	LLAAGTPGK	114	-0.7000	0
17	VLEYRKLSA	202	-0.9000	0
18	IQPQARYIL	7	-1.0000	0
19	FSDLEIQAA	146	-1.0000	0
20	MNSQNSQIQ	0	-1.2000	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	MAQLLVLES	56	4.5000	54.22

2	LPNARVLIH	126	2.7800	33.49
3	LLVLESLDP	59	2.7000	32.53
4	IERMRTLME	156	2.4000	28.92
5	MAIYDTMQY	86	1.9000	22.89
6	VLEYRKLSA	202	1.9000	22.89
7	VLIHQPSLS	131	1.8000	21.69
8	MYINSPGGG	73	1.5000	18.07
9	LLAAGTPGK	114	1.4500	17.47
10	IIFLGVQVD	40	1.4000	16.87
11	IQTVCLGQA	99	1.4000	16.87
12	LIHQPSLSG	132	1.3000	15.66
13	YRKLSAQTA	205	1.2000	14.46
14	IQPQARYIL	7	0.7000	8.43
15	ILPSFIEHS	14	0.7000	8.43
16	YVRADIQTV	94	0.7000	8.43
17	LGQAASAAA	104	0.4000	4.82
18	YGIIDTVLE	196	0.4000	4.82
19	MQYVRADIQ	92	0.2000	2.41
20	IQAAEIERM	151	0.2000	2.41

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	IERMRTLME	156	4.4000	49.44
2	YGIIDTVLE	196	4.4000	49.44
3	MAQLLVLES	56	3.5000	39.33
4	IIFLGVQVD	40	3.1000	34.83
5	FTSLMAIYD	82	3.1000	34.83
6	LPNARVLIH	126	3.0000	33.71
7	YRKLSAQTA	205	2.2000	24.72
8	LLVLESLDP	59	2.1000	23.60
9	MAIYDTMQY	86	2.0000	22.47
10	YVRADIQTV	94	2.0000	22.47

11	MYINSPGGG	73	1.8000	20.22
12	LIHQPSLSG	132	1.6000	17.98
13	YILPSFIEH	13	1.1000	12.36
14	VLEYRKLSA	202	0.9000	10.11
15	VLIHQPSLS	131	0.8000	8.99
16	IQPQARYIL	7	0.7000	7.87
17	IMAQLLVLE	55	0.6000	6.74
18	IQTVCLGQA	99	0.4000	4.49
19	IQAAEIERM	151	0.3000	3.37
20	LEIQAAEIE	149	0.2000	2.25
21	FLGVQVDDA	42	0.1000	1.12

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	VLIHQPSLS	131	4.3000	51.19
2	MAQLLVLES	56	2.7000	32.14
3	IQPQARYIL	7	1.9000	22.62
4	VLEYRKLSA	202	1.9000	22.62
5	MAIYDTMQY	86	1.7000	20.24
6	LPNARVLIH	126	1.6800	20.00
7	MNSQNSQIQ	0	1.6000	19.05
8	LARHTGKDA	167	1.5000	17.86
9	IIFLGVQVD	40	1.4000	16.67
10	YVRADIQTV	94	1.4000	16.67
11	LIHQPSLSG	132	1.2000	14.29
12	YRKLSAQTA	205	1.2000	14.29
13	ILPSFIEHS	14	1.1000	13.10
14	IERMRTLME	156	1.1000	13.10
15	LLAAGTPGK	114	1.0000	11.90
16	LLVLESLDP	59	0.9000	10.71
17	LEYRKLSAQ	203	0.9000	10.71
18	MYINSPGGG	73	0.5000	5.95

19	IQAAEIERM	151	0.5000	5.95
20	LGQAASAAA	104	0.4000	4.76
21	FIEHSSFGV	18	0.2000	2.38

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	VLIHQPSLS	131	3.3000	39.29
2	YVRADIQTV	94	2.4000	28.57
3	YRKLSAQTA	205	2.2000	26.19
4	MAQLLVLES	56	1.7000	20.24
5	FIEHSSFGV	18	1.2000	14.29
6	IQPQARYIL	7	0.9000	10.71
7	VLEYRKLSA	202	0.9000	10.71
8	FGVKESNPY	24	0.8000	9.52
9	MAIYDTMQY	86	0.7000	8.33
10	LPNARVLIH	126	0.6800	8.10
11	MNSQNSQIQ	0	0.6000	7.14
12	LARHTGKDA	167	0.5000	5.95
13	IIFLGVQVD	40	0.4000	4.76
14	YGIIDTVLE	196	0.4000	4.76
15	LIHQPSLSG	132	0.2000	2.38
16	ILPSFIEHS	14	0.1000	1.19
17	IERMRTLME	156	0.1000	1.19
18	LLVLESLDP	59	-0.1000	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	VLIHQPSLS	131	4.7000	53.41
2	MAQLLVLES	56	3.1000	35.23

3	MAIYDTMQY	86	3.0000	34.09
4	IQPQARYIL	7	2.8600	32.50
5	LIHQPSLSG	132	2.6000	29.55
6	IIFLGVQVD	40	2.5000	28.41
7	IERMRTLME	156	2.5000	28.41
8	YVRADIQTV	94	2.4000	27.27
9	IQAAEIERM	151	2.0000	22.73
10	LLVLESLDP	59	1.9000	21.59
11	MYINSPGGG	73	1.9000	21.59
12	VLEYRKLSA	202	1.9000	21.59
13	ILPSFIEHS	14	1.5000	17.05
14	IMAQLLVLE	55	1.5000	17.05
15	LARHTGKDA	167	1.5000	17.05
16	VIRKDTDRD	177	1.3000	14.77
17	FIEHSSFGV	18	1.2000	13.64
18	YRKLSAQTA	205	1.2000	13.64
19	FGVKESNPY	24	1.1000	12.50
20	LLAAGTPGK	114	1.1000	12.50
21	LPNARVLIH	126	1.1000	12.50

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	VLIHQPSLS	131	4.7000	53.41
2	MAQLLVLES	56	3.1000	35.23
3	MAIYDTMQY	86	3.0000	34.09
4	IQPQARYIL	7	2.8600	32.50
5	LIHQPSLSG	132	2.6000	29.55
6	IIFLGVQVD	40	2.5000	28.41
7	IERMRTLME	156	2.5000	28.41
8	YVRADIQTV	94	2.4000	27.27
9	IQAAEIERM	151	2.0000	22.73
10	LLVLESLDP	59	1.9000	21.59

11	MYINSPGGG	73	1.9000	21.59
12	VLEYRKLSA	202	1.9000	21.59
13	ILPSFIEHS	14	1.5000	17.05
14	IMAQLLVLE	55	1.5000	17.05
15	LARHTGKDA	167	1.5000	17.05
16	VIRKDTDRD	177	1.3000	14.77
17	FIEHSSFGV	18	1.2000	13.64
18	YRKLSAQTA	205	1.2000	13.64
19	FGVKESNPY	24	1.1000	12.50
20	LLAAGTPGK	114	1.1000	12.50
21	LPNARVLIH	126	1.1000	12.50

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	MAIYDTMQY	86	4.7600	48.57
2	ITMYINSPG	71	4.1000	41.84
3	VLEYRKLSA	202	3.9000	39.80
4	LLVLESLDP	59	3.4000	34.69
5	VLIHQPSLS	131	3.4000	34.69
6	IQPQARYIL	7	2.9000	29.59
7	MRTLMETTL	159	2.4000	24.49
8	FIEHSSFGV	18	2.3000	23.47
9	LIHQPSLSG	132	2.2000	22.45
10	LARHTGKDA	167	2.0000	20.41
11	VLLAAGTPG	113	1.9000	19.39
12	YVRADIQTV	94	1.8500	18.88
13	MAQLLVLES	56	1.8000	18.37
14	IERMRTLME	156	1.7600	17.96
15	IQTVCLGQA	99	1.6000	16.33
16	VIQGQFSDL	141	1.6000	16.33
17	LPSFIEHSS	15	1.4000	14.29
18	YRKLSAQTA	205	1.4000	14.29

19	IHQPSLSGV	133	1.3000	13.27
20	MYINSPGGG	73	1.2000	12.24
21	VRADIQTVC	95	1.2000	12.24

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	MAIYDTMQY	86	3.7600	38.37
2	FIEHSSFGV	18	3.3000	33.67
3	ITMYINSPG	71	3.1000	31.63
4	VLEYRKLSA	202	2.9000	29.59
5	YVRADIQTV	94	2.8500	29.08
6	LLVLESLDP	59	2.4000	24.49
7	VLIHQPSLS	131	2.4000	24.49
8	YRKLSAQTA	205	2.4000	24.49
9	IQPQARYIL	7	1.9000	19.39
10	YILPSFIEH	13	1.9000	19.39
11	YINSPGGGF	74	1.4000	14.29
12	MRTLMETTL	159	1.4000	14.29
13	LIHQPSLSG	132	1.2000	12.24
14	LARHTGKDA	167	1.0000	10.20
15	YGIIDTVLE	196	0.9600	9.80
16	VLLAAGTPG	113	0.9000	9.18
17	MAQLLVLES	56	0.8000	8.16
18	IERMRTLME	156	0.7600	7.76
19	FGVKESNPY	24	0.7000	7.14
20	IQTVCLGQA	99	0.6000	6.12
21	VIQGQFSDL	141	0.6000	6.12

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	MAIYDTMQY	86	4.7600	48.57
2	ITMYINSPG	71	4.1000	41.84
3	VLEYRKLSA	202	3.9000	39.80
4	LLVLESLDP	59	3.4000	34.69
5	VLIHQPSLS	131	3.4000	34.69
6	IQPQARYIL	7	2.9000	29.59
7	MRTLMETTL	159	2.4000	24.49
8	FIEHSSFGV	18	2.3000	23.47
9	LIHQPSLSG	132	2.2000	22.45
10	LARHTGKDA	167	2.0000	20.41
11	VLLAAGTPG	113	1.9000	19.39
12	YVRADIQTV	94	1.8500	18.88
13	MAQLLVLES	56	1.8000	18.37
14	IERMRTLME	156	1.7600	17.96
15	IQTVCLGQA	99	1.6000	16.33
16	VIQGQFSDL	141	1.6000	16.33
17	LPSFIEHSS	15	1.4000	14.29
18	YRKLSAQTA	205	1.4000	14.29
19	IHQPSLSGV	133	1.3000	13.27
20	MYINSPGGG	73	1.2000	12.24
21	VRADIQTVC	95	1.2000	12.24

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	YRKLSAQTA	205	3.5000	35.71
2	YINSPGGGF	74	2.6000	26.53
3	VKESNPYNK	26	2.5000	25.51
4	YVRADIQTV	94	1.9000	19.39
5	YGIIDTVLE	196	1.6000	16.33
6	VLLAAGTPG	113	1.4000	14.29
7	MRTLMETTL	159	1.4000	14.29

8	MQYVRADIQ	92	1.3000	13.27
9	LLAAGTPGK	114	1.3000	13.27
10	IRKDTDRDK	178	1.3000	13.27
11	IYDTMQYVR	88	1.2000	12.24
12	YILPSFIEH	13	1.1000	11.22
13	MALPNARVL	124	1.1000	11.22
14	IQPQARYIL	7	1.0000	10.20
15	MYINSPGGG	73	0.9000	9.18
16	IQTVCLGQA	99	0.9000	9.18
17	MAIYDTMQY	86	0.8000	8.16
18	VLIHQPSLS	131	0.8000	8.16
19	LAAGTPGKR	115	0.7000	7.14
20	IERMRTLME	156	0.7000	7.14
21	IDTVLEYRK	199	0.7000	7.14

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	YRKLSAQTA	205	3.5000	35.71
2	YINSPGGGF	74	2.6000	26.53
3	VKESNPYNK	26	2.5000	25.51
4	YVRADIQTV	94	1.9000	19.39
5	YGIIDTVLE	196	1.6000	16.33
6	VLLAAGTPG	113	1.4000	14.29
7	MRTLMETTL	159	1.4000	14.29
8	MQYVRADIQ	92	1.3000	13.27
9	LLAAGTPGK	114	1.3000	13.27
10	IRKDTDRDK	178	1.3000	13.27
11	IYDTMQYVR	88	1.2000	12.24
12	YILPSFIEH	13	1.1000	11.22
13	MALPNARVL	124	1.1000	11.22
14	IQPQARYIL	7	1.0000	10.20
15	MYINSPGGG	73	0.9000	9.18

16	IQTVCLGQA	99	0.9000	9.18
17	MAIYDTMQY	86	0.8000	8.16
18	VLIHQPSLS	131	0.8000	8.16
19	LAAGTPGKR	115	0.7000	7.14
20	IERMRTLME	156	0.7000	7.14
21	IDTVLEYRK	199	0.7000	7.14