MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Feb 19 20:04:59 2010
Length of input sequence	288 amino acids
Number of nanomers from input sequence	280
Number of nanomers with obligatory P1 anchor residue	103
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	28

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	YYPLTTLMM	34	1.2800	21.33
2	FQSISGGAI	122	1.2000	20.00
3	FVIGANHIG	89	1.1000	18.33
4	WVANPSAYG	134	0.7400	12.33
5	VYLNQGRLA	201	0.7300	12.17
6	IILAGGSGT	3	0.4000	6.67
7	YLNQGRLAV	202	0.4000	6.67
8	LMMAGIRDI	40	0.3900	6.50

9	YGPGLGTSL	111	0.3900	6.50
10	FHRLLGDGA	60	0.1000	1.67
11	LKRFQSISG	119	0.0800	1.33
12	YEITEVNQV	193	-0.1000	0
13	VKSGYGNYL	272	-0.1000	0
14	FYDNDVIEI	173	-0.1600	0
15	LGVNISYAT	70	-0.2600	0
16	IFYGPGLGT	109	-0.3000	0
17	VRTLERRQG	235	-0.4100	0
18	VQRARALVK	265	-0.5000	0
19	VVEFGAEGM	143	-0.5400	0
20	ITMGISKQL	16	-0.6000	0
21	LKVSIPEEV	244	-0.6000	0
22	MRGIILAGG	0	-0.9000	0
23	YWVANPSAY	133	-0.9000	0
24	IEIARGLKK	179	-1.1000	0
25	LTTLMMAGI	37	-1.2000	0
26	IRDIQLITT	45	-1.2000	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	VYLNQGRLA	201	1.7300	28.83
2	IILAGGSGT	3	1.4000	23.33
3	LMMAGIRDI	40	1.3900	23.17
4	FQSISGGAI	122	1.2000	20.00
5	FVIGANHIG	89	1.1000	18.33
6	LKRFQSISG	119	1.0800	18.00
7	LVLGDNIFY	103	1.0000	16.67
8	VKSGYGNYL	272	0.9000	15.00
9	LGVNISYAT	70	0.7400	12.33
10	IFYGPGLGT	109	0.7000	11.67
11	VRTLERRQG	235	0.5900	9.83

12	VQRARALVK	265	0.5000	8.33
13	VVEFGAEGM	143	0.4600	7.67
14	ITMGISKQL	16	0.4000	6.67
15	LKVSIPEEV	244	0.4000	6.67
16	YYPLTTLMM	34	0.2800	4.67
17	MRGIILAGG	0	0.1000	1.67
18	FHRLLGDGA	60	0.1000	1.67
19	IEIARGLKK	179	-0.1000	0
20	FYDNDVIEI	173	-0.1600	0
21	LTTLMMAGI	37	-0.2000	0
22	IRDIQLITT	45	-0.2000	0
23	LAGGSGTRL	5	-0.2100	0
24	VNISYATQD	72	-0.2100	0
25	WVANPSAYG	134	-0.2600	0
26	VIGANHIGA	90	-0.3000	0
27	IQLITTPHD	48	-0.3300	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	VLGDNIFYG	104	5.1000	53.68
2	IGADSVALV	96	4.3000	45.26
3	LVLGDNIFY	103	3.7000	38.95
4	IQLITTPHD	48	3.6000	37.89
5	MRGIILAGG	0	3.5000	36.84
6	LKKSARGEY	185	3.2000	33.68
7	LLGDGAHLG	63	3.1000	32.63
8	LMMAGIRDI	40	2.9000	30.53
9	LKVSIPEEV	244	2.9000	30.53
10	WRMGWIDDE	254	2.9000	30.53
11	VRTLERRQG	235	2.7000	28.42
12	IYYPLTTLM	33	2.5000	26.32
13	LVQRARALV	264	2.4000	25.26

14	MGISKQLLP	18	2.3000	24.21
15	YYPLTTLMM	34	2.3000	24.21
16	VNISYATQD	72	2.3000	24.21
17	FVIGANHIG	89	2.1000	22.11
18	ILAGGSGTR	4	2.0000	21.05
19	LYPITMGIS	13	2.0000	21.05
20	YLNQGRLAV	202	2.0000	21.05
21	ISGGAIFAY	125	1.9000	20.00
22	VQRARALVK	265	1.9000	20.00
23	MMAGIRDIQ	41	1.8000	18.95
24	LVKSGYGNY	271	1.8000	18.95
25	VEVLARGTA	210	1.7000	17.89
26	LPVYDKPMI	25	1.6000	16.84
27	LAQAFVIGA	85	1.6000	16.84
28	VIGANHIGA	90	1.6000	16.84

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	VLGDNIFYG	104	2.7000	29.67
2	WRMGWIDDE	254	2.5000	27.47
3	WIDDEQLVQ	258	2.5000	27.47
4	IGADSVALV	96	2.3000	25.27
5	YDNDVIEIA	174	2.0000	21.98
6	YLNQGRLAV	202	2.0000	21.98
7	YYPLTTLMM	34	1.8000	19.78
8	FVIGANHIG	89	1.7000	18.68
9	MMAGIRDIQ	41	1.5000	16.48
10	IQLITTPHD	48	1.5000	16.48
11	LVLGDNIFY	103	1.4000	15.38
12	WVANPSAYG	134	1.2000	13.19
13	MRGIILAGG	0	1.1000	12.09
14	FYGPGLGTS	110	1.1000	12.09

15	LGTSLKRFQ	115	1.1000	12.09
16	FYDNDVIEI	173	1.1000	12.09
17	YEITEVNQV	193	1.0100	11.10
18	LMMAGIRDI	40	1.0000	10.99
19	FQSISGGAI	122	1.0000	10.99
20	LKKSARGEY	185	0.9000	9.89
21	LKVSIPEEV	244	0.9000	9.89
22	YPLTTLMMA	35	0.8000	8.79
23	VQRARALVK	265	0.8000	8.79
24	LLGDGAHLG	63	0.7000	7.69
25	VEVLARGTA	210	0.7000	7.69
26	WLDTGTFDS	219	0.7000	7.69
27	LYPITMGIS	13	0.6000	6.59
28	LAQAFVIGA	85	0.6000	6.59

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	IGADSVALV	96	3.3000	37.50
2	MMAGIRDIQ	41	2.8000	31.82
3	LLGDGAHLG	63	2.5000	28.41
4	LKVSIPEEV	244	2.3000	26.14
5	VQRARALVK	265	2.3000	26.14
6	VLGDNIFYG	104	2.2000	25.00
7	IARGLKKSA	181	2.2000	25.00
8	MRGIILAGG	0	2.1000	23.86
9	LVLGDNIFY	103	2.0800	23.64
10	WIDDEQLVQ	258	2.0000	22.73
11	MGISKQLLP	18	1.8000	20.45
12	LGTSLKRFQ	115	1.8000	20.45
13	WRMGWIDDE	254	1.8000	20.45
14	LMMAGIRDI	40	1.7000	19.32
15	FVIGANHIG	89	1.5000	17.05

16	YLNQGRLAV	202	1.5000	17.05
17	YDNDVIEIA	174	1.4000	15.91
18	LVQRARALV	264	1.4000	15.91
19	YYPLTTLMM	34	1.3000	14.77
20	IEIARGLKK	179	1.3000	14.77
21	LAQAFVIGA	85	1.2800	14.55
22	VIGANHIGA	90	1.2800	14.55
23	VNISYATQD	72	1.2000	13.64
24	IQLITTPHD	48	1.1000	12.50
25	IYYPLTTLM	33	1.0000	11.36
26	VRTLERRQG	235	1.0000	11.36
27	IFYGPGLGT	109	0.9000	10.23
28	YEITEVNQV	193	0.7000	7.95

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	IGADSVALV	96	3.3000	37.50
2	MMAGIRDIQ	41	2.8000	31.82
3	LLGDGAHLG	63	2.5000	28.41
4	LKVSIPEEV	244	2.3000	26.14
5	VQRARALVK	265	2.3000	26.14
6	VLGDNIFYG	104	2.2000	25.00
7	IARGLKKSA	181	2.2000	25.00
8	MRGIILAGG	0	2.1000	23.86
9	LVLGDNIFY	103	2.0800	23.64
10	WIDDEQLVQ	258	2.0000	22.73
11	MGISKQLLP	18	1.8000	20.45
12	LGTSLKRFQ	115	1.8000	20.45
13	WRMGWIDDE	254	1.8000	20.45
14	LMMAGIRDI	40	1.7000	19.32
15	FVIGANHIG	89	1.5000	17.05
16	YLNQGRLAV	202	1.5000	17.05

17	YDNDVIEIA	174	1.4000	15.91
18	LVQRARALV	264	1.4000	15.91
19	YYPLTTLMM	34	1.3000	14.77
20	IEIARGLKK	179	1.3000	14.77
21	LAQAFVIGA	85	1.2800	14.55
22	VIGANHIGA	90	1.2800	14.55
23	VNISYATQD	72	1.2000	13.64
24	IQLITTPHD	48	1.1000	12.50
25	IYYPLTTLM	33	1.0000	11.36
26	VRTLERRQG	235	1.0000	11.36
27	IFYGPGLGT	109	0.9000	10.23
28	YEITEVNQV	193	0.7000	7.95

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	IGADSVALV	96	3.3000	37.50
2	MMAGIRDIQ	41	2.8000	31.82
3	LLGDGAHLG	63	2.5000	28.41
4	LKVSIPEEV	244	2.3000	26.14
5	VQRARALVK	265	2.3000	26.14
6	VLGDNIFYG	104	2.2000	25.00
7	IARGLKKSA	181	2.2000	25.00
8	MRGIILAGG	0	2.1000	23.86
9	LVLGDNIFY	103	2.0800	23.64
10	WIDDEQLVQ	258	2.0000	22.73
11	MGISKQLLP	18	1.8000	20.45
12	LGTSLKRFQ	115	1.8000	20.45
13	WRMGWIDDE	254	1.8000	20.45
14	LMMAGIRDI	40	1.7000	19.32
15	FVIGANHIG	89	1.5000	17.05
16	YLNQGRLAV	202	1.5000	17.05
17	YDNDVIEIA	174	1.4000	15.91

18	LVQRARALV	264	1.4000	15.91
19	YYPLTTLMM	34	1.3000	14.77
20	IEIARGLKK	179	1.3000	14.77
21	LAQAFVIGA	85	1.2800	14.55
22	VIGANHIGA	90	1.2800	14.55
23	VNISYATQD	72	1.2000	13.64
24	IQLITTPHD	48	1.1000	12.50
25	IYYPLTTLM	33	1.0000	11.36
26	VRTLERRQG	235	1.0000	11.36
27	IFYGPGLGT	109	0.9000	10.23
28	YEITEVNQV	193	0.7000	7.95

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	VLGDNIFYG	104	4.1000	43.16
2	WRMGWIDDE	254	3.9000	41.05
3	YYPLTTLMM	34	3.3000	34.74
4	IGADSVALV	96	3.3000	34.74
5	FVIGANHIG	89	3.1000	32.63
6	YLNQGRLAV	202	3.0000	31.58
7	LVLGDNIFY	103	2.7000	28.42
8	IQLITTPHD	48	2.6000	27.37
9	WVANPSAYG	134	2.6000	27.37
10	MRGIILAGG	0	2.5000	26.32
11	LKKSARGEY	185	2.2000	23.16
12	LLGDGAHLG	63	2.1000	22.11
13	YEITEVNQV	193	2.0100	21.16
14	FYDNDVIEI	173	2.0000	21.05
15	YDNDVIEIA	174	2.0000	21.05
16	LMMAGIRDI	40	1.9000	20.00
17	FQSISGGAI	122	1.9000	20.00
18	LKVSIPEEV	244	1.9000	20.00

19	WIDDEQLVQ	258	1.8000	18.95
20	VRTLERRQG	235	1.7000	17.89
21	IYYPLTTLM	33	1.5000	15.79
22	FYGPGLGTS	110	1.5000	15.79
23	YFYDNDVIE	172	1.4000	14.74
24	LVQRARALV	264	1.4000	14.74
25	MGISKQLLP	18	1.3000	13.68
26	VNISYATQD	72	1.3000	13.68
27	YWVANPSAY	133	1.2700	13.37
28	WLDTGTFDS	219	1.1000	11.58

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	IGADSVALV	96	3.3000	37.50
2	MMAGIRDIQ	41	2.8000	31.82
3	LLGDGAHLG	63	2.5000	28.41
4	LKVSIPEEV	244	2.3000	26.14
5	VQRARALVK	265	2.3000	26.14
6	VLGDNIFYG	104	2.2000	25.00
7	IARGLKKSA	181	2.2000	25.00
8	MRGIILAGG	0	2.1000	23.86
9	LVLGDNIFY	103	2.0800	23.64
10	WIDDEQLVQ	258	2.0000	22.73
11	MGISKQLLP	18	1.8000	20.45
12	LGTSLKRFQ	115	1.8000	20.45
13	WRMGWIDDE	254	1.8000	20.45
14	LMMAGIRDI	40	1.7000	19.32
15	FVIGANHIG	89	1.5000	17.05
16	YLNQGRLAV	202	1.5000	17.05
17	YDNDVIEIA	174	1.4000	15.91
18	LVQRARALV	264	1.4000	15.91
19	YYPLTTLMM	34	1.3000	14.77

20	IEIARGLKK	179	1.3000	14.77
21	LAQAFVIGA	85	1.2800	14.55
22	VIGANHIGA	90	1.2800	14.55
23	VNISYATQD	72	1.2000	13.64
24	IQLITTPHD	48	1.1000	12.50
25	IYYPLTTLM	33	1.0000	11.36
26	VRTLERRQG	235	1.0000	11.36
27	IFYGPGLGT	109	0.9000	10.23
28	YEITEVNQV	193	0.7000	7.95

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	YYPLTTLMM	34	4.2000	48.84
2	YEITEVNQV	193	3.1000	36.05
3	WVANPSAYG	134	3.0000	34.88
4	FVIGANHIG	89	2.3000	26.74
5	WLDTGTFDS	219	2.0000	23.26
6	FGAEGMALS	146	1.6000	18.60
7	IQLITTPHD	48	1.5000	17.44
8	VQRARALVK	265	1.3000	15.12
9	YLLELLERN	279	1.2000	13.95
10	FYDNDVIEI	173	1.1800	13.72
11	IGADSVALV	96	1.1000	12.79
12	YPLTTLMMA	35	0.9000	10.47
13	FAYWVANPS	131	0.9000	10.47
14	LKVSIPEEV	244	0.9000	10.47
15	WIDDEQLVQ	258	0.9000	10.47
16	LVLGDNIFY	103	0.8800	10.23
17	YDNDVIEIA	174	0.7000	8.14
18	LLGDGAHLG	63	0.6000	6.98
19	IYYPLTTLM	33	0.5000	5.81
20	FHRLLGDGA	60	0.5000	5.81

21	FVRTLERRQ	234	0.4000	4.65
22	VNISYATQD	72	0.3000	3.49
23	YFYDNDVIE	172	0.2800	3.26
24	MRGIILAGG	0	0.1000	1.16
25	YPITMGISK	14	-0.0200	0
26	LAQAFVIGA	85	-0.0200	0
27	LKRFQSISG	119	-0.0200	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	LMMAGIRDI	40	3.8000	39.58
2	LVLGDNIFY	103	3.2000	33.33
3	VLARGTAWL	212	2.9000	30.21
4	FVIGANHIG	89	2.7000	28.13
5	FAYWVANPS	131	2.7000	28.13
6	LKRFQSISG	119	2.6000	27.08
7	VQRARALVK	265	2.6000	27.08
8	YYPLTTLMM	34	2.1000	21.88
9	IYYPLTTLM	33	2.0000	20.83
10	VTPKSNYAV	160	1.9000	19.79
11	VYLNQGRLA	201	1.7000	17.71
12	IQLITTPHD	48	1.4800	15.42
13	LAQAFVIGA	85	1.4000	14.58
14	LGVNISYAT	70	1.3000	13.54
15	WLDTGTFDS	219	1.3000	13.54
16	FVRTLERRQ	234	1.1000	11.46
17	YEITEVNQV	193	0.9000	9.38
18	IEIARGLKK	179	0.8000	8.33
19	ITMGISKQL	16	0.7000	7.29
20	WVANPSAYG	134	0.7000	7.29
21	LERRQGLKV	238	0.6000	6.25
22	VIGANHIGA	90	0.4000	4.17

23	MRGIILAGG	0	0.3800	3.96
24	LYFYDNDVI	171	0.2000	2.08
25	VRTLERRQG	235	-0.1000	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	YYPLTTLMM	34	3.0000	34.09
2	LKRFQSISG	119	2.8800	32.73
3	IQLITTPHD	48	2.5000	28.41
4	IYYPLTTLM	33	2.3000	26.14
5	VQRARALVK	265	1.9000	21.59
6	MRGIILAGG	0	1.4000	15.91
7	LMMAGIRDI	40	1.2000	13.64
8	FAYWVANPS	131	1.1500	13.07
9	LYFYDNDVI	171	1.1000	12.50
10	LVLGDNIFY	103	1.0800	12.27
11	LAQAFVIGA	85	0.9800	11.14
12	VVEFGAEGM	143	0.8000	9.09
13	LYPITMGIS	13	0.7000	7.95
14	YEITEVNQV	193	0.6000	6.82
15	WVANPSAYG	134	0.4000	4.55
16	WLDTGTFDS	219	0.3500	3.98
17	VNISYATQD	72	0.3000	3.41
18	FVIGANHIG	89	0.1000	1.14
19	IEIARGLKK	179	0.1000	1.14
20	VIGANHIGA	90	-0.0200	0
21	IILAGGSGT	3	-0.1000	0
22	LGVNISYAT	70	-0.1000	0
23	VNQVYLNQG	198	-0.1000	0
24	MIYYPLTTL	32	-0.2000	0
25	IRDIQLITT	45	-0.2200	0
26	LTTLMMAGI	37	-0.4000	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	YYPLTTLMM	34	5.1000	54.26
2	IQLITTPHD	48	4.2000	44.68
3	LKRFQSISG	119	3.1800	33.83
4	WVANPSAYG	134	2.7000	28.72
5	IYYPLTTLM	33	2.4000	25.53
6	FVIGANHIG	89	2.4000	25.53
7	FAYWVANPS	131	2.1500	22.87
8	VNISYATQD	72	2.0000	21.28
9	YEITEVNQV	193	1.9000	20.21
10	MRGIILAGG	0	1.7000	18.09
11	WLDTGTFDS	219	1.3500	14.36
12	WRMGWIDDE	254	1.2000	12.77
13	LVLGDNIFY	103	1.1800	12.55
14	YWVANPSAY	133	1.0000	10.64
15	VVEFGAEGM	143	0.9000	9.57
16	YFYDNDVIE	172	0.6000	6.38
17	YGVVEFGAE	141	0.5000	5.32
18	LMMAGIRDI	40	0.4000	4.26
19	LYFYDNDVI	171	0.3000	3.19
20	VNQVYLNQG	198	0.2000	2.13
21	VQRARALVK	265	0.2000	2.13
22	LAQAFVIGA	85	-0.0200	0
23	FVRTLERRQ	234	-0.1000	0
24	IILAGGSGT	3	-0.2000	0
25	MIYYPLTTL	32	-0.2000	0
26	FHRLLGDGA	60	-0.2000	0
27	LGVNISYAT	70	-0.2000	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	YYPLTTLMM	34	4.0000	45.45
2	FAYWVANPS	131	2.1500	24.43
3	LKRFQSISG	119	1.8800	21.36
4	YEITEVNQV	193	1.6000	18.18
5	IQLITTPHD	48	1.5000	17.05
6	WVANPSAYG	134	1.4000	15.91
7	WLDTGTFDS	219	1.3500	15.34
8	IYYPLTTLM	33	1.3000	14.77
9	FVIGANHIG	89	1.1000	12.50
10	VQRARALVK	265	0.9000	10.23
11	MRGIILAGG	0	0.4000	4.55
12	LMMAGIRDI	40	0.2000	2.27
13	LYFYDNDVI	171	0.1000	1.14
14	LVLGDNIFY	103	0.0800	0.91
15	LAQAFVIGA	85	-0.0200	0
16	YWVANPSAY	133	-0.1000	0
17	FHRLLGDGA	60	-0.2000	0
18	VVEFGAEGM	143	-0.2000	0
19	LYPITMGIS	13	-0.3000	0
20	FYDNDVIEI	173	-0.4200	0
21	FQSISGGAI	122	-0.5000	0
22	VNISYATQD	72	-0.7000	0
23	YPLTTLMMA	35	-0.8000	0
24	IEIARGLKK	179	-0.9000	0
25	FVRTLERRQ	234	-0.9000	0
26	IFAYWVANP	130	-1.0000	0
27	FGAEGMALS	146	-1.0000	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	IQLITTPHD	48	5.2000	55.32
2	LKRFQSISG	119	4.1800	44.47
3	YYPLTTLMM	34	4.1000	43.62
4	IYYPLTTLM	33	3.4000	36.17
5	VNISYATQD	72	3.0000	31.91
6	MRGIILAGG	0	2.7000	28.72
7	LVLGDNIFY	103	2.1800	23.19
8	VVEFGAEGM	143	1.9000	20.21
9	WVANPSAYG	134	1.7000	18.09
10	LMMAGIRDI	40	1.4000	14.89
11	FVIGANHIG	89	1.4000	14.89
12	LYFYDNDVI	171	1.3000	13.83
13	VNQVYLNQG	198	1.2000	12.77
14	VQRARALVK	265	1.2000	12.77
15	FAYWVANPS	131	1.1500	12.23
16	LAQAFVIGA	85	0.9800	10.43
17	YEITEVNQV	193	0.9000	9.57
18	IILAGGSGT	3	0.8000	8.51
19	MIYYPLTTL	32	0.8000	8.51
20	LGVNISYAT	70	0.8000	8.51
21	LYPITMGIS	13	0.7000	7.45
22	IRDIQLITT	45	0.6800	7.23
23	VLARGTAWL	212	0.5000	5.32
24	IFAYWVANP	130	0.4000	4.26
25	WLDTGTFDS	219	0.3500	3.72
26	MAGIRDIQL	42	0.2800	2.98
27	VLGDNIFYG	104	0.2500	2.66
28	VRTLERRQG	235	0.2000	2.13

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	YYPLTTLMM	34	5.7000	63.33
2	WVANPSAYG	134	4.4000	48.89
3	YEITEVNQV	193	4.1000	45.56
4	FVIGANHIG	89	3.7000	41.11
5	IQLITTPHD	48	2.6000	28.89
6	WLDTGTFDS	219	2.4000	26.67
7	LVLGDNIFY	103	2.1800	24.22
8	IGADSVALV	96	2.1000	23.33
9	FYDNDVIEI	173	2.0800	23.11
10	IYYPLTTLM	33	2.0000	22.22
11	LLGDGAHLG	63	2.0000	22.22
12	FGAEGMALS	146	2.0000	22.22
13	YLLELLERN	279	2.0000	22.22
14	LKVSIPEEV	244	1.9000	21.11
15	YFYDNDVIE	172	1.6800	18.67
16	MRGIILAGG	0	1.5000	16.67
17	VNISYATQD	72	1.4000	15.56
18	VQRARALVK	265	1.4000	15.56
19	LKRFQSISG	119	1.3800	15.33
20	FAYWVANPS	131	1.3000	14.44
21	WRMGWIDDE	254	1.3000	14.44
22	YPLTTLMMA	35	0.9000	10.00
23	VLGDNIFYG	104	0.9000	10.00
24	YLNQGRLAV	202	0.9000	10.00
25	LMMAGIRDI	40	0.8000	8.89
26	MGISKQLLP	18	0.7000	7.78
27	LYFYDNDVI	171	0.7000	7.78
28	YDNDVIEIA	174	0.7000	7.78

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	YYPLTTLMM	34	3.0000	34.09

2	LKRFQSISG	119	2.8800	32.73
3	IQLITTPHD	48	2.5000	28.41
4	IYYPLTTLM	33	2.3000	26.14
5	VQRARALVK	265	1.9000	21.59
6	MRGIILAGG	0	1.4000	15.91
7	LMMAGIRDI	40	1.2000	13.64
8	FAYWVANPS	131	1.1500	13.07
9	LYFYDNDVI	171	1.1000	12.50
10	LVLGDNIFY	103	1.0800	12.27
11	LAQAFVIGA	85	0.9800	11.14
12	VVEFGAEGM	143	0.8000	9.09
13	LYPITMGIS	13	0.7000	7.95
14	YEITEVNQV	193	0.6000	6.82
15	WVANPSAYG	134	0.4000	4.55
16	WLDTGTFDS	219	0.3500	3.98
17	VNISYATQD	72	0.3000	3.41
18	FVIGANHIG	89	0.1000	1.14
19	IEIARGLKK	179	0.1000	1.14
20	VIGANHIGA	90	-0.0200	0
21	IILAGGSGT	3	-0.1000	0
22	LGVNISYAT	70	-0.1000	0
23	VNQVYLNQG	198	-0.1000	0
24	MIYYPLTTL	32	-0.2000	0
25	IRDIQLITT	45	-0.2200	0
26	LTTLMMAGI	37	-0.4000	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	YYPLTTLMM	34	4.2000	48.84
2	YEITEVNQV	193	3.1000	36.05
3	WVANPSAYG	134	3.0000	34.88
4	FVIGANHIG	89	2.3000	26.74

5	WLDTGTFDS	219	2.0000	23.26
6	FGAEGMALS	146	1.6000	18.60
7	IQLITTPHD	48	1.5000	17.44
8	VQRARALVK	265	1.3000	15.12
9	YLLELLERN	279	1.2000	13.95
10	FYDNDVIEI	173	1.1800	13.72
11	IGADSVALV	96	1.1000	12.79
12	YPLTTLMMA	35	0.9000	10.47
13	FAYWVANPS	131	0.9000	10.47
14	LKVSIPEEV	244	0.9000	10.47
15	WIDDEQLVQ	258	0.9000	10.47
16	LVLGDNIFY	103	0.8800	10.23
17	YDNDVIEIA	174	0.7000	8.14
18	LLGDGAHLG	63	0.6000	6.98
19	IYYPLTTLM	33	0.5000	5.81
20	FHRLLGDGA	60	0.5000	5.81
21	FVRTLERRQ	234	0.4000	4.65
22	VNISYATQD	72	0.3000	3.49
23	YFYDNDVIE	172	0.2800	3.26
24	MRGIILAGG	0	0.1000	1.16
25	YPITMGISK	14	-0.0200	0
26	LAQAFVIGA	85	-0.0200	0
27	LKRFQSISG	119	-0.0200	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	YEITEVNQV	193	6.5000	56.03
2	FQSISGGAI	122	5.3000	45.69
3	LMMAGIRDI	40	5.1000	43.97
4	YYPLTTLMM	34	4.5200	38.97
5	LKVSIPEEV	244	4.5000	38.79
6	FYDNDVIEI	173	4.4000	37.93

7	LVLGDNIFY	103	3.9000	33.62
8	ITMGISKQL	16	3.8000	32.76
9	MAGIRDIQL	42	3.6000	31.03
10	YGNYLLELL	276	3.5000	30.17
11	MIYYPLTTL	32	3.4000	29.31
12	YGPGLGTSL	111	3.4000	29.31
13	LKRFQSISG	119	3.4000	29.31
14	VKSGYGNYL	272	3.4000	29.31
15	YPITMGISK	14	3.1000	26.72
16	YLNQGRLAV	202	3.1000	26.72
17	MGISKQLLP	18	3.0000	25.86
18	VVEFGAEGM	143	3.0000	25.86
19	IRDIQLITT	45	2.9000	25.00
20	WLDTGTFDS	219	2.8200	24.31
21	YPLTTLMMA	35	2.8000	24.14
22	LVKSGYGNY	271	2.7000	23.28
23	ITEVNQVYL	195	2.6000	22.41
24	VNISYATQD	72	2.5000	21.55
25	VALVLGDNI	101	2.4000	20.69
26	MGWIDDEQL	256	2.4000	20.69
27	IYYPLTTLM	33	2.3200	20.00
28	LERRQGLKV	238	2.3000	19.83

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	YEITEVNQV	193	6.5000	56.03
2	FQSISGGAI	122	5.3000	45.69
3	LMMAGIRDI	40	5.1000	43.97
4	YYPLTTLMM	34	4.5200	38.97
5	LKVSIPEEV	244	4.5000	38.79
6	FYDNDVIEI	173	4.4000	37.93
7	LVLGDNIFY	103	3.9000	33.62

8	ITMGISKQL	16	3.8000	32.76
9	MAGIRDIQL	42	3.6000	31.03
10	YGNYLLELL	276	3.5000	30.17
11	MIYYPLTTL	32	3.4000	29.31
12	YGPGLGTSL	111	3.4000	29.31
13	LKRFQSISG	119	3.4000	29.31
14	VKSGYGNYL	272	3.4000	29.31
15	YPITMGISK	14	3.1000	26.72
16	YLNQGRLAV	202	3.1000	26.72
17	MGISKQLLP	18	3.0000	25.86
18	VVEFGAEGM	143	3.0000	25.86
19	IRDIQLITT	45	2.9000	25.00
20	WLDTGTFDS	219	2.8200	24.31
21	YPLTTLMMA	35	2.8000	24.14
22	LVKSGYGNY	271	2.7000	23.28
23	ITEVNQVYL	195	2.6000	22.41
24	VNISYATQD	72	2.5000	21.55
25	VALVLGDNI	101	2.4000	20.69
26	MGWIDDEQL	256	2.4000	20.69
27	IYYPLTTLM	33	2.3200	20.00
28	LERRQGLKV	238	2.3000	19.83

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	LVQRARALV	264	4.0000	46.51
2	YYPLTTLMM	34	3.1000	36.05
3	VLARGTAWL	212	3.1000	36.05
4	VRTLERRQG	235	2.6000	30.23
5	IFAYWVANP	130	2.3000	26.74
6	WVANPSAYG	134	2.3000	26.74
7	MRGIILAGG	0	2.2000	25.58
8	WRMGWIDDE	254	2.2000	25.58

9	IQLITTPHD	48	2.1000	24.42
10	LMMAGIRDI	40	1.5000	17.44
11	FVIGANHIG	89	1.4000	16.28
12	LPVYDKPMI	25	1.2000	13.95
13	FVRTLERRQ	234	1.1000	12.79
14	YGNYLLELL	276	1.0000	11.63
15	MIYYPLTTL	32	0.9000	10.47
16	YLNQGRLAV	202	0.8000	9.30
17	VEVLARGTA	210	0.8000	9.30
18	IGANHIGAD	91	0.7000	8.14
19	LKRFQSISG	119	0.7000	8.14
20	YGVVEFGAE	141	0.7000	8.14
21	LERRQGLKV	238	0.7000	8.14
22	FYGPGLGTS	110	0.5000	5.81
23	LGTSLKRFQ	115	0.5000	5.81
24	FQSISGGAI	122	0.4000	4.65
25	VAWRMGWID	252	0.4000	4.65
26	LNQGRLAVE	203	0.3000	3.49
27	FAYWVANPS	131	0.2000	2.33
28	YEITEVNQV	193	0.1000	1.16

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	LVQRARALV	264	3.7000	46.25
2	VLARGTAWL	212	2.1000	26.25
3	YYPLTTLMM	34	2.0000	25.00
4	IFAYWVANP	130	1.9000	23.75
5	LMMAGIRDI	40	1.3000	16.25
6	VRTLERRQG	235	1.3000	16.25
7	LPVYDKPMI	25	1.0000	12.50
8	WVANPSAYG	134	1.0000	12.50
9	MRGIILAGG	0	0.9000	11.25

10	VEVLARGTA	210	0.8000	10.00
11	FYGPGLGTS	110	0.5000	6.25
12	YLNQGRLAV	202	0.5000	6.25
13	LERRQGLKV	238	0.4000	5.00
14	FVRTLERRQ	234	0.3000	3.75
15	VQRARALVK	265	0.3000	3.75
16	FQSISGGAI	122	0.2000	2.50
17	FAYWVANPS	131	0.2000	2.50
18	FVIGANHIG	89	0.1000	1.25
19	MIYYPLTTL	32	-0.1000	0
20	LYPITMGIS	13	-0.2000	0
21	YEITEVNQV	193	-0.2000	0
22	LGTSLKRFQ	115	-0.3000	0
23	FYDNDVIEI	173	-0.3000	0
24	LYFYDNDVI	171	-0.4000	0
25	VYLNQGRLA	201	-0.4000	0
26	YPLTTLMMA	35	-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	LVQRARALV	264	4.7000	58.75
2	VLARGTAWL	212	3.1000	38.75
3	IFAYWVANP	130	2.9000	36.25
4	LMMAGIRDI	40	2.3000	28.75
5	VRTLERRQG	235	2.3000	28.75
6	LPVYDKPMI	25	2.0000	25.00
7	MRGIILAGG	0	1.9000	23.75
8	VEVLARGTA	210	1.8000	22.50
9	LERRQGLKV	238	1.4000	17.50
10	VQRARALVK	265	1.3000	16.25
11	YYPLTTLMM	34	1.0000	12.50
12	MIYYPLTTL	32	0.9000	11.25

13	LYPITMGIS	13	0.8000	10.00
14	LGTSLKRFQ	115	0.7000	8.75
15	LYFYDNDVI	171	0.6000	7.50
16	VYLNQGRLA	201	0.6000	7.50
17	IQLITTPHD	48	0.4000	5.00
18	LAQAFVIGA	85	0.4000	5.00
19	VIGANHIGA	90	0.4000	5.00
20	LKRFQSISG	119	0.4000	5.00
21	VIEIARGLK	178	0.4000	5.00
22	IEIARGLKK	179	0.3000	3.75
23	VTPKSNYAV	160	0.2000	2.50
24	IARGLKKSA	181	0.2000	2.50
25	LVLGDNIFY	103	-0.3000	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	LVQRARALV	264	5.0000	58.14
2	VLARGTAWL	212	4.1000	47.67
3	VRTLERRQG	235	3.6000	41.86
4	IFAYWVANP	130	3.3000	38.37
5	MRGIILAGG	0	3.2000	37.21
6	IQLITTPHD	48	3.1000	36.05
7	LMMAGIRDI	40	2.5000	29.07
8	LPVYDKPMI	25	2.2000	25.58
9	YYPLTTLMM	34	2.1000	24.42
10	MIYYPLTTL	32	1.9000	22.09
11	VEVLARGTA	210	1.8000	20.93
12	IGANHIGAD	91	1.7000	19.77
13	LKRFQSISG	119	1.7000	19.77
14	LERRQGLKV	238	1.7000	19.77
15	LGTSLKRFQ	115	1.5000	17.44
16	VAWRMGWID	252	1.4000	16.28

17	WVANPSAYG	134	1.3000	15.12
18	LNQGRLAVE	203	1.3000	15.12
19	WRMGWIDDE	254	1.2000	13.95
20	LYPITMGIS	13	0.8000	9.30
21	LVLGDNIFY	103	0.8000	9.30
22	LYFYDNDVI	171	0.8000	9.30
23	LKKSARGEY	185	0.7000	8.14
24	VYLNQGRLA	201	0.6000	6.98
25	VQRARALVK	265	0.6000	6.98
26	VTPKSNYAV	160	0.5000	5.81
27	LAQAFVIGA	85	0.4000	4.65
28	FVIGANHIG	89	0.4000	4.65

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	LVQRARALV	264	3.7000	42.53
2	MIYYPLTTL	32	2.7000	31.03
3	YYPLTTLMM	34	2.6000	29.89
4	FAYWVANPS	131	2.2000	25.29
5	VLARGTAWL	212	2.1000	24.14
6	IFAYWVANP	130	1.9000	21.84
7	YEITEVNQV	193	1.8000	20.69
8	YGNYLLELL	276	1.7000	19.54
9	LEEKPVTPK	155	1.5000	17.24
10	LPVYDKPMI	25	1.2000	13.79
11	YLNQGRLAV	202	1.1000	12.64
12	LMMAGIRDI	40	1.0000	11.49
13	WVANPSAYG	134	1.0000	11.49
14	VRTLERRQG	235	1.0000	11.49
15	LERRQGLKV	238	1.0000	11.49
16	MRGIILAGG	0	0.9000	10.34
17	VQRARALVK	265	0.9000	10.34

18	LYFYDNDVI	171	0.8000	9.20
19	FVIGANHIG	89	0.6000	6.90
20	FYDNDVIEI	173	0.5800	6.67
21	IYYPLTTLM	33	0.5000	5.75
22	YPLTTLMMA	35	0.4000	4.60
23	YWVANPSAY	133	0.4000	4.60
24	WRMGWIDDE	254	0.4000	4.60
25	FHRLLGDGA	60	0.3000	3.45
26	LAQAFVIGA	85	0.2800	3.22
27	VIGANHIGA	90	0.2800	3.22
28	LKRFQSISG	119	0.2800	3.22

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	YYPLTTLMM	34	4.9000	48.51
2	LVQRARALV	264	4.0000	39.60
3	IQLITTPHD	48	3.2500	32.18
4	VLARGTAWL	212	3.1000	30.69
5	VRTLERRQG	235	2.8000	27.72
6	YLNQGRLAV	202	2.6000	25.74
7	LERRQGLKV	238	2.5000	24.75
8	LPVYDKPMI	25	2.3500	23.27
9	LKRFQSISG	119	2.3000	22.77
10	IFAYWVANP	130	2.3000	22.77
11	WVANPSAYG	134	2.3000	22.77
12	MRGIILAGG	0	2.2000	21.78
13	FVIGANHIG	89	2.1000	20.79
14	YGNYLLELL	276	2.1000	20.79
15	MIYYPLTTL	32	2.0000	19.80
16	WRMGWIDDE	254	1.9000	18.81
17	LMMAGIRDI	40	1.7000	16.83
18	FYDNDVIEI	173	1.5000	14.85

19	LVLGDNIFY	103	1.4000	13.86
20	VQRARALVK	265	1.4000	13.86
21	FVRTLERRQ	234	1.3000	12.87
22	WIDDEQLVQ	258	1.3000	12.87
23	VAWRMGWID	252	1.2000	11.88
24	YPLTTLMMA	35	1.0000	9.90
25	LAQAFVIGA	85	1.0000	9.90
26	VIGANHIGA	90	1.0000	9.90
27	VYDKPMIYY	27	0.9000	8.91
28	IRDIQLITT	45	0.9000	8.91

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	YYPLTTLMM	34	4.2000	50.60
2	YLNQGRLAV	202	2.9000	34.94
3	VQRARALVK	265	2.1000	25.30
4	VRTLERRQG	235	1.9000	22.89
5	MRGIILAGG	0	1.5000	18.07
6	LMMAGIRDI	40	1.5000	18.07
7	YPLTTLMMA	35	1.4000	16.87
8	FYDNDVIEI	173	1.3000	15.66
9	VEVLARGTA	210	1.3000	15.66
10	IQLITTPHD	48	1.1500	13.86
11	IEIARGLKK	179	1.1000	13.25
12	LAQAFVIGA	85	1.0000	12.05
13	VIGANHIGA	90	1.0000	12.05
14	WVANPSAYG	134	1.0000	12.05
15	LKRFQSISG	119	0.9000	10.84
16	FQSISGGAI	122	0.9000	10.84
17	FVRTLERRQ	234	0.9000	10.84
18	LVQRARALV	264	0.7000	8.43
19	IRDIQLITT	45	0.6000	7.23

20	LYPITMGIS	13	0.5000	6.02
21	YEITEVNQV	193	0.5000	6.02
22	FAYWVANPS	131	0.4000	4.82
23	YPITMGISK	14	0.2000	2.41
24	MGISKQLLP	18	0.2000	2.41
25	LGTSLKRFQ	115	0.2000	2.41
26	WLDTGTFDS	219	0.2000	2.41
27	FVIGANHIG	89	0.1000	1.20
28	VIEIARGLK	178	0.1000	1.20

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	LMMAGIRDI	40	4.1000	48.81
2	VRTLERRQG	235	3.8000	45.24
3	LGTSLKRFQ	115	2.9000	34.52
4	LVQRARALV	264	2.6000	30.95
5	VYLNQGRLA	201	2.5000	29.76
6	VQRARALVK	265	2.0000	23.81
7	YLNQGRLAV	202	1.8000	21.43
8	YYPLTTLMM	34	1.4000	16.67
9	FAYWVANPS	131	1.3000	15.48
10	IFAYWVANP	130	1.1000	13.10
11	MRGIILAGG	0	1.0000	11.90
12	LKRFQSISG	119	1.0000	11.90
13	IEIARGLKK	179	1.0000	11.90
14	VLARGTAWL	212	1.0000	11.90
15	FVRTLERRQ	234	1.0000	11.90
16	LPVYDKPMI	25	0.9000	10.71
17	LAQAFVIGA	85	0.7000	8.33
18	VIGANHIGA	90	0.7000	8.33
19	MIYYPLTTL	32	0.6000	7.14
20	IARGLKKSA	181	0.5000	5.95

21	VEVLARGTA	210	0.5000	5.95
22	VVEFGAEGM	143	0.3000	3.57
23	MGISKQLLP	18	0.2000	2.38
24	IQLITTPHD	48	0.2000	2.38
25	VLGDNIFYG	104	0.1000	1.19
26	WVANPSAYG	134	0.1000	1.19
27	YEITEVNQV	193	0.1000	1.19

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	YYPLTTLMM	34	3.2000	38.55
2	VQRARALVK	265	3.1000	37.35
3	VRTLERRQG	235	2.9000	34.94
4	MRGIILAGG	0	2.5000	30.12
5	LMMAGIRDI	40	2.5000	30.12
6	VEVLARGTA	210	2.3000	27.71
7	IQLITTPHD	48	2.1500	25.90
8	IEIARGLKK	179	2.1000	25.30
9	LAQAFVIGA	85	2.0000	24.10
10	VIGANHIGA	90	2.0000	24.10
11	LKRFQSISG	119	1.9000	22.89
12	YLNQGRLAV	202	1.9000	22.89
13	LVQRARALV	264	1.7000	20.48
14	IRDIQLITT	45	1.6000	19.28
15	LYPITMGIS	13	1.5000	18.07
16	MGISKQLLP	18	1.2000	14.46
17	LGTSLKRFQ	115	1.2000	14.46
18	VIEIARGLK	178	1.1000	13.25
19	VYLNQGRLA	201	0.8000	9.64
20	LVLGDNIFY	103	0.6000	7.23
21	YPLTTLMMA	35	0.4000	4.82
22	FYDNDVIEI	173	0.3000	3.61

23	LPVYDKPMI	25	0.2500	3.01
24	LERRQGLKV	238	0.2000	2.41
25	IARGLKKSA	181	0.1000	1.20
26	VLARGTAWL	212	0.1000	1.20

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	YYPLTTLMM	34	3.2000	38.55
2	VQRARALVK	265	3.1000	37.35
3	VRTLERRQG	235	2.9000	34.94
4	MRGIILAGG	0	2.5000	30.12
5	LMMAGIRDI	40	2.5000	30.12
6	VEVLARGTA	210	2.3000	27.71
7	IQLITTPHD	48	2.1500	25.90
8	IEIARGLKK	179	2.1000	25.30
9	LAQAFVIGA	85	2.0000	24.10
10	VIGANHIGA	90	2.0000	24.10
11	LKRFQSISG	119	1.9000	22.89
12	YLNQGRLAV	202	1.9000	22.89
13	LVQRARALV	264	1.7000	20.48
14	IRDIQLITT	45	1.6000	19.28
15	LYPITMGIS	13	1.5000	18.07
16	MGISKQLLP	18	1.2000	14.46
17	LGTSLKRFQ	115	1.2000	14.46
18	VIEIARGLK	178	1.1000	13.25
19	VYLNQGRLA	201	0.8000	9.64
20	LVLGDNIFY	103	0.6000	7.23
21	YPLTTLMMA	35	0.4000	4.82
22	FYDNDVIEI	173	0.3000	3.61
23	LPVYDKPMI	25	0.2500	3.01
24	LERRQGLKV	238	0.2000	2.41
25	IARGLKKSA	181	0.1000	1.20

26	VLARGTAWL	212	0.1000	1.20

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	VLGDNIFYG	104	3.7000	40.66
2	IGADSVALV	96	3.3000	36.26
3	MMAGIRDIQ	41	2.5000	27.47
4	IQLITTPHD	48	2.5000	27.47
5	LVLGDNIFY	103	2.4000	26.37
6	MRGIILAGG	0	2.1000	23.08
7	LGTSLKRFQ	115	2.1000	23.08
8	LMMAGIRDI	40	2.0000	21.98
9	LKKSARGEY	185	1.9000	20.88
10	LKVSIPEEV	244	1.9000	20.88
11	VQRARALVK	265	1.8000	19.78
12	LLGDGAHLG	63	1.7000	18.68
13	VEVLARGTA	210	1.7000	18.68
14	LYPITMGIS	13	1.6000	17.58
15	LAQAFVIGA	85	1.6000	17.58
16	VIGANHIGA	90	1.6000	17.58
17	IARGLKKSA	181	1.6000	17.58
18	WRMGWIDDE	254	1.5000	16.48
19	WIDDEQLVQ	258	1.5000	16.48
20	LVQRARALV	264	1.4000	15.38
21	MGISKQLLP	18	1.3000	14.29
22	VRTLERRQG	235	1.3000	14.29
23	VNISYATQD	72	1.2000	13.19
24	VIEIARGLK	178	1.2000	13.19
25	IYYPLTTLM	33	1.0000	10.99
26	YDNDVIEIA	174	1.0000	10.99
27	YLNQGRLAV	202	1.0000	10.99
28	YYPLTTLMM	34	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	LMMAGIRDI	40	3.1000	36.90
2	YLNQGRLAV	202	2.8000	33.33
3	VRTLERRQG	235	2.8000	33.33
4	YYPLTTLMM	34	2.4000	28.57
5	FAYWVANPS	131	2.3000	27.38
6	FVRTLERRQ	234	2.0000	23.81
7	LGTSLKRFQ	115	1.9000	22.62
8	LVQRARALV	264	1.6000	19.05
9	VYLNQGRLA	201	1.5000	17.86
10	WVANPSAYG	134	1.1000	13.10
11	YEITEVNQV	193	1.1000	13.10
12	VQRARALVK	265	1.0000	11.90
13	FVIGANHIG	89	0.8000	9.52
14	WLDTGTFDS	219	0.7000	8.33
15	IFAYWVANP	130	0.1000	1.19
16	FYDNDVIEI	173	0.1000	1.19
17	LPVYDKPMI	25	-0.1000	0
18	FHRLLGDGA	60	-0.3000	0
19	LAQAFVIGA	85	-0.3000	0
20	VIGANHIGA	90	-0.3000	0
21	MIYYPLTTL	32	-0.4000	0
22	YPLTTLMMA	35	-0.4000	0
23	WRMGWIDDE	254	-0.4000	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	VRTLERRQG	235	4.2000	47.73

2	LMMAGIRDI	40	4.0000	45.45
3	YYPLTTLMM	34	3.9000	44.32
4	YLNQGRLAV	202	3.8000	43.18
5	FAYWVANPS	131	2.7000	30.68
6	LVQRARALV	264	2.6000	29.55
7	WVANPSAYG	134	2.5000	28.41
8	FVIGANHIG	89	2.2000	25.00
9	YEITEVNQV	193	2.1000	23.86
10	VYLNQGRLA	201	1.5000	17.05
11	MRGIILAGG	0	1.4000	15.91
12	LKRFQSISG	119	1.4000	15.91
13	FVRTLERRQ	234	1.3000	14.77
14	LGTSLKRFQ	115	1.2000	13.64
15	IFAYWVANP	130	1.1000	12.50
16	WLDTGTFDS	219	1.1000	12.50
17	VQRARALVK	265	1.1000	12.50
18	FYDNDVIEI	173	1.0000	11.36
19	WRMGWIDDE	254	1.0000	11.36
20	VLARGTAWL	212	0.9600	10.91
21	LPVYDKPMI	25	0.8000	9.09
22	VVEFGAEGM	143	0.8000	9.09
23	MIYYPLTTL	32	0.5600	6.36
24	YGNYLLELL	276	0.5600	6.36
25	VLGDNIFYG	104	0.5000	5.68
26	IQLITTPHD	48	0.3000	3.41
27	YWVANPSAY	133	0.3000	3.41
28	MGISKQLLP	18	0.2000	2.27

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	LMMAGIRDI	40	4.1000	48.81
2	VRTLERRQG	235	3.8000	45.24

3	LGTSLKRFQ	115	2.9000	34.52
4	LVQRARALV	264	2.6000	30.95
5	VYLNQGRLA	201	2.5000	29.76
6	VQRARALVK	265	2.0000	23.81
7	YLNQGRLAV	202	1.8000	21.43
8	YYPLTTLMM	34	1.4000	16.67
9	FAYWVANPS	131	1.3000	15.48
10	IFAYWVANP	130	1.1000	13.10
11	MRGIILAGG	0	1.0000	11.90
12	LKRFQSISG	119	1.0000	11.90
13	IEIARGLKK	179	1.0000	11.90
14	VLARGTAWL	212	1.0000	11.90
15	FVRTLERRQ	234	1.0000	11.90
16	LPVYDKPMI	25	0.9000	10.71
17	LAQAFVIGA	85	0.7000	8.33
18	VIGANHIGA	90	0.7000	8.33
19	MIYYPLTTL	32	0.6000	7.14
20	IARGLKKSA	181	0.5000	5.95
21	VEVLARGTA	210	0.5000	5.95
22	VVEFGAEGM	143	0.3000	3.57
23	MGISKQLLP	18	0.2000	2.38
24	IQLITTPHD	48	0.2000	2.38
25	VLGDNIFYG	104	0.1000	1.19
26	WVANPSAYG	134	0.1000	1.19
27	YEITEVNQV	193	0.1000	1.19

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	YYPLTTLMM	34	5.7000	65.52
2	YLNQGRLAV	202	3.9000	44.83
3	VRTLERRQG	235	3.3000	37.93
4	MRGIILAGG	0	2.9000	33.33

5	LMMAGIRDI	40	2.4000	27.59
6	WVANPSAYG	134	2.4000	27.59
7	LKRFQSISG	119	2.3000	26.44
8	IQLITTPHD	48	2.2500	25.86
9	FYDNDVIEI	173	2.2000	25.29
10	VQRARALVK	265	2.2000	25.29
11	FQSISGGAI	122	1.8000	20.69
12	LVQRARALV	264	1.7000	19.54
13	FVIGANHIG	89	1.5000	17.24
14	YEITEVNQV	193	1.5000	17.24
15	YPLTTLMMA	35	1.4000	16.09
16	IRDIQLITT	45	1.3000	14.94
17	VEVLARGTA	210	1.3000	14.94
18	MGISKQLLP	18	1.2000	13.79
19	IEIARGLKK	179	1.2000	13.79
20	LAQAFVIGA	85	1.0000	11.49
21	VIGANHIGA	90	1.0000	11.49
22	LYPITMGIS	13	0.9000	10.34
23	LVLGDNIFY	103	0.9000	10.34
24	FAYWVANPS	131	0.8000	9.20
25	WLDTGTFDS	219	0.6000	6.90
26	YPITMGISK	14	0.3000	3.45
27	FYGPGLGTS	110	0.3000	3.45
28	LKKSARGEY	185	0.3000	3.45

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	VRTLERRQG	235	5.2000	59.09
2	LMMAGIRDI	40	5.0000	56.82
3	LVQRARALV	264	3.6000	40.91
4	YYPLTTLMM	34	2.9000	32.95
5	YLNQGRLAV	202	2.8000	31.82

6	VYLNQGRLA	201	2.5000	28.41
7	MRGIILAGG	0	2.4000	27.27
8	LKRFQSISG	119	2.4000	27.27
9	LGTSLKRFQ	115	2.2000	25.00
10	IFAYWVANP	130	2.1000	23.86
11	VQRARALVK	265	2.1000	23.86
12	VLARGTAWL	212	1.9600	22.27
13	LPVYDKPMI	25	1.8000	20.45
14	VVEFGAEGM	143	1.8000	20.45
15	FAYWVANPS	131	1.7000	19.32
16	MIYYPLTTL	32	1.5600	17.73
17	VLGDNIFYG	104	1.5000	17.05
18	WVANPSAYG	134	1.5000	17.05
19	IQLITTPHD	48	1.3000	14.77
20	MGISKQLLP	18	1.2000	13.64
21	IYYPLTTLM	33	1.2000	13.64
22	FVIGANHIG	89	1.2000	13.64
23	IEIARGLKK	179	1.1000	12.50
24	YEITEVNQV	193	1.1000	12.50
25	LERRQGLKV	238	1.0000	11.36
26	LVLGDNIFY	103	0.8000	9.09
27	LKVSIPEEV	244	0.8000	9.09
28	LAQAFVIGA	85	0.7000	7.95

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	VRTLERRQG	235	4.2000	47.73
2	LMMAGIRDI	40	4.0000	45.45
3	YYPLTTLMM	34	3.9000	44.32
4	YLNQGRLAV	202	3.8000	43.18
5	FAYWVANPS	131	2.7000	30.68
6	LVQRARALV	264	2.6000	29.55

7	WVANPSAYG	134	2.5000	28.41
8	FVIGANHIG	89	2.2000	25.00
9	YEITEVNQV	193	2.1000	23.86
10	VYLNQGRLA	201	1.5000	17.05
11	MRGIILAGG	0	1.4000	15.91
12	LKRFQSISG	119	1.4000	15.91
13	FVRTLERRQ	234	1.3000	14.77
14	LGTSLKRFQ	115	1.2000	13.64
15	IFAYWVANP	130	1.1000	12.50
16	WLDTGTFDS	219	1.1000	12.50
17	VQRARALVK	265	1.1000	12.50
18	FYDNDVIEI	173	1.0000	11.36
19	WRMGWIDDE	254	1.0000	11.36
20	VLARGTAWL	212	0.9600	10.91
21	LPVYDKPMI	25	0.8000	9.09
22	VVEFGAEGM	143	0.8000	9.09
23	MIYYPLTTL	32	0.5600	6.36
24	YGNYLLELL	276	0.5600	6.36
25	VLGDNIFYG	104	0.5000	5.68
26	IQLITTPHD	48	0.3000	3.41
27	YWVANPSAY	133	0.3000	3.41
28	MGISKQLLP	18	0.2000	2.27

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	VRTLERRQG	235	5.1000	56.67
2	LMMAGIRDI	40	4.3000	47.78
3	LGTSLKRFQ	115	3.7000	41.11
4	IQLITTPHD	48	2.9000	32.22
5	LVQRARALV	264	2.9000	32.22
6	YYPLTTLMM	34	2.5000	27.78
7	VYLNQGRLA	201	2.5000	27.78

8	MRGIILAGG	0	2.3000	25.56
9	LKRFQSISG	119	2.3000	25.56
10	YLNQGRLAV	202	2.1000	23.33
11	VLARGTAWL	212	2.0000	22.22
12	VNISYATQD	72	1.8000	20.00
13	FVRTLERRQ	234	1.8000	20.00
14	MIYYPLTTL	32	1.6000	17.78
15	WRMGWIDDE	254	1.6000	17.78
16	IFAYWVANP	130	1.5000	16.67
17	VLGDNIFYG	104	1.4000	15.56
18	WVANPSAYG	134	1.4000	15.56
19	VVEFGAEGM	143	1.4000	15.56
20	FAYWVANPS	131	1.3000	14.44
21	VQRARALVK	265	1.3000	14.44
22	LPVYDKPMI	25	1.1000	12.22
23	FVIGANHIG	89	1.1000	12.22
24	VAWRMGWID	252	0.9000	10.00
25	IYYPLTTLM	33	0.8000	8.89
26	IGANHIGAD	91	0.8000	8.89
27	LNQGRLAVE	203	0.8000	8.89
28	LAQAFVIGA	85	0.7000	7.78

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	YYPLTTLMM	34	5.7000	65.52
2	YLNQGRLAV	202	3.9000	44.83
3	VRTLERRQG	235	3.3000	37.93
4	MRGIILAGG	0	2.9000	33.33
5	LMMAGIRDI	40	2.4000	27.59
6	WVANPSAYG	134	2.4000	27.59
7	LKRFQSISG	119	2.3000	26.44
8	IQLITTPHD	48	2.2500	25.86

9	FYDNDVIEI	173	2.2000	25.29
10	VQRARALVK	265	2.2000	25.29
11	FQSISGGAI	122	1.8000	20.69
12	LVQRARALV	264	1.7000	19.54
13	FVIGANHIG	89	1.5000	17.24
14	YEITEVNQV	193	1.5000	17.24
15	YPLTTLMMA	35	1.4000	16.09
16	IRDIQLITT	45	1.3000	14.94
17	VEVLARGTA	210	1.3000	14.94
18	MGISKQLLP	18	1.2000	13.79
19	IEIARGLKK	179	1.2000	13.79
20	LAQAFVIGA	85	1.0000	11.49
21	VIGANHIGA	90	1.0000	11.49
22	LYPITMGIS	13	0.9000	10.34
23	LVLGDNIFY	103	0.9000	10.34
24	FAYWVANPS	131	0.8000	9.20
25	WLDTGTFDS	219	0.6000	6.90
26	YPITMGISK	14	0.3000	3.45
27	FYGPGLGTS	110	0.3000	3.45
28	LKKSARGEY	185	0.3000	3.45

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	YYPLTTLMM	34	2.4000	35.29
2	VRTLERRQG	235	1.7000	25.00
3	MRGIILAGG	0	1.5000	22.06
4	LMMAGIRDI	40	1.3000	19.12
5	VEVLARGTA	210	1.2000	17.65
6	YLNQGRLAV	202	1.1000	16.18
7	WVANPSAYG	134	1.0000	14.71
8	FQSISGGAI	122	0.8000	11.76
9	FVRTLERRQ	234	0.7000	10.29

10	LVQRARALV	264	0.7000	10.29
11	LYPITMGIS	13	0.4000	5.88
12	VQRARALVK	265	0.3000	4.41
13	YEITEVNQV	193	0.2000	2.94
14	FAYWVANPS	131	0.1000	1.47
15	YPLTTLMMA	35	-0.2000	0
16	FYGPGLGTS	110	-0.2000	0
17	FYDNDVIEI	173	-0.3000	0
18	WLDTGTFDS	219	-0.3000	0
19	VYLNQGRLA	201	-0.4000	0
20	FHRLLGDGA	60	-0.5000	0
21	LAQAFVIGA	85	-0.6000	0
22	FVIGANHIG	89	-0.6000	0
23	VIGANHIGA	90	-0.6000	0
24	LKRFQSISG	119	-0.7000	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	YYPLTTLMM	34	3.2000	38.55
2	VQRARALVK	265	3.1000	37.35
3	VRTLERRQG	235	2.9000	34.94
4	MRGIILAGG	0	2.5000	30.12
5	LMMAGIRDI	40	2.5000	30.12
6	VEVLARGTA	210	2.3000	27.71
7	IQLITTPHD	48	2.1500	25.90
8	IEIARGLKK	179	2.1000	25.30
9	LAQAFVIGA	85	2.0000	24.10
10	VIGANHIGA	90	2.0000	24.10
11	LKRFQSISG	119	1.9000	22.89
12	YLNQGRLAV	202	1.9000	22.89
13	LVQRARALV	264	1.7000	20.48
14	IRDIQLITT	45	1.6000	19.28

15	LYPITMGIS	13	1.5000	18.07
16	MGISKQLLP	18	1.2000	14.46
17	LGTSLKRFQ	115	1.2000	14.46
18	VIEIARGLK	178	1.1000	13.25
19	VYLNQGRLA	201	0.8000	9.64
20	LVLGDNIFY	103	0.6000	7.23
21	YPLTTLMMA	35	0.4000	4.82
22	FYDNDVIEI	173	0.3000	3.61
23	LPVYDKPMI	25	0.2500	3.01
24	LERRQGLKV	238	0.2000	2.41
25	IARGLKKSA	181	0.1000	1.20
26	VLARGTAWL	212	0.1000	1.20

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	YYPLTTLMM	34	5.3000	59.55
2	IQLITTPHD	48	3.8500	43.26
3	YLNQGRLAV	202	3.2000	35.96
4	VRTLERRQG	235	3.2000	35.96
5	MRGIILAGG	0	2.8000	31.46
6	WVANPSAYG	134	2.3000	25.84
7	LKRFQSISG	119	2.2000	24.72
8	LMMAGIRDI	40	1.7000	19.10
9	FVRTLERRQ	234	1.7000	19.10
10	IRDIQLITT	45	1.5000	16.85
11	FYDNDVIEI	173	1.5000	16.85
12	YPLTTLMMA	35	1.4000	15.73
13	FVIGANHIG	89	1.4000	15.73
14	VQRARALVK	265	1.4000	15.73
15	VEVLARGTA	210	1.3000	14.61
16	WRMGWIDDE	254	1.2000	13.48
17	FQSISGGAI	122	1.1000	12.36

18	LAQAFVIGA	85	1.0000	11.24
19	VIGANHIGA	90	1.0000	11.24
20	LGTSLKRFQ	115	1.0000	11.24
21	LVQRARALV	264	1.0000	11.24
22	YGVVEFGAE	141	0.9000	10.11
23	IGANHIGAD	91	0.8000	8.99
24	YEITEVNQV	193	0.8000	8.99
25	LVLGDNIFY	103	0.7000	7.87
26	MGISKQLLP	18	0.6000	6.74
27	WIDDEQLVQ	258	0.6000	6.74
28	LYPITMGIS	13	0.5000	5.62

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	LMMAGIRDI	40	4.1000	48.81
2	VRTLERRQG	235	3.8000	45.24
3	LGTSLKRFQ	115	2.9000	34.52
4	LVQRARALV	264	2.6000	30.95
5	VYLNQGRLA	201	2.5000	29.76
6	VQRARALVK	265	2.0000	23.81
7	YLNQGRLAV	202	1.8000	21.43
8	YYPLTTLMM	34	1.4000	16.67
9	FAYWVANPS	131	1.3000	15.48
10	IFAYWVANP	130	1.1000	13.10
11	MRGIILAGG	0	1.0000	11.90
12	LKRFQSISG	119	1.0000	11.90
13	IEIARGLKK	179	1.0000	11.90
14	VLARGTAWL	212	1.0000	11.90
15	FVRTLERRQ	234	1.0000	11.90
16	LPVYDKPMI	25	0.9000	10.71
17	LAQAFVIGA	85	0.7000	8.33
18	VIGANHIGA	90	0.7000	8.33

19	MIYYPLTTL	32	0.6000	7.14
20	IARGLKKSA	181	0.5000	5.95
21	VEVLARGTA	210	0.5000	5.95
22	VVEFGAEGM	143	0.3000	3.57
23	MGISKQLLP	18	0.2000	2.38
24	IQLITTPHD	48	0.2000	2.38
25	VLGDNIFYG	104	0.1000	1.19
26	WVANPSAYG	134	0.1000	1.19
27	YEITEVNQV	193	0.1000	1.19

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	LMMAGIRDI	40	3.1000	36.90
2	YLNQGRLAV	202	2.8000	33.33
3	VRTLERRQG	235	2.8000	33.33
4	YYPLTTLMM	34	2.4000	28.57
5	FAYWVANPS	131	2.3000	27.38
6	FVRTLERRQ	234	2.0000	23.81
7	LGTSLKRFQ	115	1.9000	22.62
8	LVQRARALV	264	1.6000	19.05
9	VYLNQGRLA	201	1.5000	17.86
10	WVANPSAYG	134	1.1000	13.10
11	YEITEVNQV	193	1.1000	13.10
12	VQRARALVK	265	1.0000	11.90
13	FVIGANHIG	89	0.8000	9.52
14	WLDTGTFDS	219	0.7000	8.33
15	IFAYWVANP	130	0.1000	1.19
16	FYDNDVIEI	173	0.1000	1.19
17	LPVYDKPMI	25	-0.1000	0
18	FHRLLGDGA	60	-0.3000	0
19	LAQAFVIGA	85	-0.3000	0
20	VIGANHIGA	90	-0.3000	0

21	MIYYPLTTL	32	-0.4000	0
22	YPLTTLMMA	35	-0.4000	0
23	WRMGWIDDE	254	-0.4000	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	VRTLERRQG	235	5.2000	59.09
2	LMMAGIRDI	40	5.0000	56.82
3	LVQRARALV	264	3.6000	40.91
4	YYPLTTLMM	34	2.9000	32.95
5	YLNQGRLAV	202	2.8000	31.82
6	VYLNQGRLA	201	2.5000	28.41
7	MRGIILAGG	0	2.4000	27.27
8	LKRFQSISG	119	2.4000	27.27
9	LGTSLKRFQ	115	2.2000	25.00
10	IFAYWVANP	130	2.1000	23.86
11	VQRARALVK	265	2.1000	23.86
12	VLARGTAWL	212	1.9600	22.27
13	LPVYDKPMI	25	1.8000	20.45
14	VVEFGAEGM	143	1.8000	20.45
15	FAYWVANPS	131	1.7000	19.32
16	MIYYPLTTL	32	1.5600	17.73
17	VLGDNIFYG	104	1.5000	17.05
18	WVANPSAYG	134	1.5000	17.05
19	IQLITTPHD	48	1.3000	14.77
20	MGISKQLLP	18	1.2000	13.64
21	IYYPLTTLM	33	1.2000	13.64
22	FVIGANHIG	89	1.2000	13.64
23	IEIARGLKK	179	1.1000	12.50
24	YEITEVNQV	193	1.1000	12.50
25	LERRQGLKV	238	1.0000	11.36
26	LVLGDNIFY	103	0.8000	9.09

27	LKVSIPEEV	244	0.8000	9.09
28	LAQAFVIGA	85	0.7000	7.95

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	VRTLERRQG	235	5.2000	59.09
2	LMMAGIRDI	40	5.0000	56.82
3	LVQRARALV	264	3.6000	40.91
4	YYPLTTLMM	34	2.9000	32.95
5	YLNQGRLAV	202	2.8000	31.82
6	VYLNQGRLA	201	2.5000	28.41
7	MRGIILAGG	0	2.4000	27.27
8	LKRFQSISG	119	2.4000	27.27
9	LGTSLKRFQ	115	2.2000	25.00
10	IFAYWVANP	130	2.1000	23.86
11	VQRARALVK	265	2.1000	23.86
12	VLARGTAWL	212	1.9600	22.27
13	LPVYDKPMI	25	1.8000	20.45
14	VVEFGAEGM	143	1.8000	20.45
15	FAYWVANPS	131	1.7000	19.32
16	MIYYPLTTL	32	1.5600	17.73
17	VLGDNIFYG	104	1.5000	17.05
18	WVANPSAYG	134	1.5000	17.05
19	IQLITTPHD	48	1.3000	14.77
20	MGISKQLLP	18	1.2000	13.64
21	IYYPLTTLM	33	1.2000	13.64
22	FVIGANHIG	89	1.2000	13.64
23	IEIARGLKK	179	1.1000	12.50
24	YEITEVNQV	193	1.1000	12.50
25	LERRQGLKV	238	1.0000	11.36
26	LVLGDNIFY	103	0.8000	9.09
27	LKVSIPEEV	244	0.8000	9.09

28	LAQAFVIGA	85	0.7000	7.95

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	LKRFQSISG	119	5.5000	56.12
2	MIYYPLTTL	32	5.3000	54.08
3	LYFYDNDVI	171	4.9000	50.00
4	LVLGDNIFY	103	4.4000	44.90
5	IFYGPGLGT	109	3.8000	38.78
6	LERRQGLKV	238	3.7000	37.76
7	LVQRARALV	264	3.6000	36.73
8	LPVYDKPMI	25	3.2000	32.65
9	FVIGANHIG	89	3.1000	31.63
10	IRDIQLITT	45	3.0000	30.61
11	VKSGYGNYL	272	3.0000	30.61
12	YLNQGRLAV	202	2.9000	29.59
13	LMMAGIRDI	40	2.7500	28.06
14	IILAGGSGT	3	2.7000	27.55
15	VVEFGAEGM	143	2.6800	27.35
16	YYPLTTLMM	34	2.6400	26.94
17	YGNYLLELL	276	2.5000	25.51
18	MRGIILAGG	0	2.4000	24.49
19	MAGIRDIQL	42	2.4000	24.49
20	VRTLERRQG	235	2.4000	24.49
21	VIGANHIGA	90	2.3000	23.47
22	IEIARGLKK	179	2.3000	23.47
23	ITMGISKQL	16	2.2000	22.45
24	FQSISGGAI	122	2.2000	22.45
25	VEVLARGTA	210	2.1000	21.43
26	VQRARALVK	265	2.1000	21.43
27	LGVNISYAT	70	1.9000	19.39
28	IFAYWVANP	130	1.9000	19.39

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	LKRFQSISG	119	4.5000	45.92
2	MIYYPLTTL	32	4.3000	43.88
3	FVIGANHIG	89	4.1000	41.84
4	LYFYDNDVI	171	3.9000	39.80
5	YLNQGRLAV	202	3.9000	39.80
6	YYPLTTLMM	34	3.6400	37.14
7	YGNYLLELL	276	3.5000	35.71
8	LVLGDNIFY	103	3.4000	34.69
9	FQSISGGAI	122	3.2000	32.65
10	IFYGPGLGT	109	2.8000	28.57
11	LERRQGLKV	238	2.7000	27.55
12	LVQRARALV	264	2.6000	26.53
13	LPVYDKPMI	25	2.2000	22.45
14	YPLTTLMMA	35	2.1000	21.43
15	IRDIQLITT	45	2.0000	20.41
16	YGPGLGTSL	111	2.0000	20.41
17	YEITEVNQV	193	2.0000	20.41
18	VKSGYGNYL	272	2.0000	20.41
19	FHRLLGDGA	60	1.8000	18.37
20	LMMAGIRDI	40	1.7500	17.86
21	IILAGGSGT	3	1.7000	17.35
22	WVANPSAYG	134	1.7000	17.35
23	VVEFGAEGM	143	1.6800	17.14
24	FAYWVANPS	131	1.6000	16.33
25	MRGIILAGG	0	1.4000	14.29
26	MAGIRDIQL	42	1.4000	14.29
27	VRTLERRQG	235	1.4000	14.29
28	VIGANHIGA	90	1.3000	13.27

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	LKRFQSISG	119	5.5000	56.12
2	MIYYPLTTL	32	5.3000	54.08
3	LYFYDNDVI	171	4.9000	50.00
4	LVLGDNIFY	103	4.4000	44.90
5	IFYGPGLGT	109	3.8000	38.78
6	LERRQGLKV	238	3.7000	37.76
7	LVQRARALV	264	3.6000	36.73
8	LPVYDKPMI	25	3.2000	32.65
9	FVIGANHIG	89	3.1000	31.63
10	IRDIQLITT	45	3.0000	30.61
11	VKSGYGNYL	272	3.0000	30.61
12	YLNQGRLAV	202	2.9000	29.59
13	LMMAGIRDI	40	2.7500	28.06
14	IILAGGSGT	3	2.7000	27.55
15	VVEFGAEGM	143	2.6800	27.35
16	YYPLTTLMM	34	2.6400	26.94
17	YGNYLLELL	276	2.5000	25.51
18	MRGIILAGG	0	2.4000	24.49
19	MAGIRDIQL	42	2.4000	24.49
20	VRTLERRQG	235	2.4000	24.49
21	VIGANHIGA	90	2.3000	23.47
22	IEIARGLKK	179	2.3000	23.47
23	ITMGISKQL	16	2.2000	22.45
24	FQSISGGAI	122	2.2000	22.45
25	VEVLARGTA	210	2.1000	21.43
26	VQRARALVK	265	2.1000	21.43
27	LGVNISYAT	70	1.9000	19.39
28	IFAYWVANP	130	1.9000	19.39

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	YPITMGISK	14	4.9000	50.00
2	FQSISGGAI	122	4.2000	42.86
3	VQRARALVK	265	4.2000	42.86
4	IEIARGLKK	179	3.6000	36.73
5	FVRTLERRQ	234	3.1000	31.63
6	LMMAGIRDI	40	2.6000	26.53
7	FVIGANHIG	89	2.3000	23.47
8	VIEIARGLK	178	2.2000	22.45
9	VRTLERRQG	235	2.2000	22.45
10	MRGIILAGG	0	2.1000	21.43
11	YYPLTTLMM	34	2.1000	21.43
12	LVLGDNIFY	103	1.7000	17.35
13	YWVANPSAY	133	1.7000	17.35
14	LVKSGYGNY	271	1.5000	15.31
15	WLDTGTFDS	219	1.4000	14.29
16	LYPITMGIS	13	1.3000	13.27
17	LKRFQSISG	119	1.3000	13.27
18	IRDIQLITT	45	1.2000	12.24
19	ILAGGSGTR	4	1.0000	10.20
20	MAGIRDIQL	42	1.0000	10.20
21	MIYYPLTTL	32	0.9000	9.18
22	YEITEVNQV	193	0.9000	9.18
23	LLPVYDKPM	24	0.8000	8.16
24	VNQVYLNQG	198	0.8000	8.16
25	LLDAADFVR	228	0.7000	7.14
26	FAYWVANPS	131	0.6000	6.12
27	ITMGISKQL	16	0.5000	5.10
28	VALVLGDNI	101	0.5000	5.10

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	YPITMGISK	14	4.9000	50.00
2	FQSISGGAI	122	4.2000	42.86
3	VQRARALVK	265	4.2000	42.86
4	IEIARGLKK	179	3.6000	36.73
5	FVRTLERRQ	234	3.1000	31.63
6	LMMAGIRDI	40	2.6000	26.53
7	FVIGANHIG	89	2.3000	23.47
8	VIEIARGLK	178	2.2000	22.45
9	VRTLERRQG	235	2.2000	22.45
10	MRGIILAGG	0	2.1000	21.43
11	YYPLTTLMM	34	2.1000	21.43
12	LVLGDNIFY	103	1.7000	17.35
13	YWVANPSAY	133	1.7000	17.35
14	LVKSGYGNY	271	1.5000	15.31
15	WLDTGTFDS	219	1.4000	14.29
16	LYPITMGIS	13	1.3000	13.27
17	LKRFQSISG	119	1.3000	13.27
18	IRDIQLITT	45	1.2000	12.24
19	ILAGGSGTR	4	1.0000	10.20
20	MAGIRDIQL	42	1.0000	10.20
21	MIYYPLTTL	32	0.9000	9.18
22	YEITEVNQV	193	0.9000	9.18
23	LLPVYDKPM	24	0.8000	8.16
24	VNQVYLNQG	198	0.8000	8.16
25	LLDAADFVR	228	0.7000	7.14
26	FAYWVANPS	131	0.6000	6.12
27	ITMGISKQL	16	0.5000	5.10
28	VALVLGDNI	101	0.5000	5.10