MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Mar 17 00:34:01 2010
Length of input sequence	359 amino acids
Number of nanomers from input sequence	351
Number of nanomers with obligatory P1 anchor residue	144
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	35

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	FVLFCVVIV	165	3.0800	51.33
2	LFVLFCVVI	164	2.6000	43.33
3	ILIAVAVAV	3	2.5000	41.67
4	FWLLTAITC	333	2.4000	40.00
5	YVREIATVT	151	2.2900	38.17
6	LVLGLATAL	85	1.9900	33.17
7	VAILAGIWA	54	1.7000	28.33
8	FRNAAGLTP	136	1.6000	26.67

9	VVIVSAWSN	170	1.2700	21.17
10	IVSAWSNAV	172	1.1000	18.33
11	IRRSRNLGL	105	0.9000	15.00
12	WWNAAPAKI	246	0.9000	15.00
13	MAMVTAAYV	194	0.6500	10.83
14	FVAEITSVV	288	0.6000	10.00
15	YRNACVTAP	209	0.5900	9.83
16	YVLITFWQY	201	0.5200	8.67
17	IAVAVAVTV	5	0.5000	8.33
18	LVLQFRNAA	132	0.5000	8.33
19	VREIATVTL	152	0.5000	8.33
20	MVTAAYVLI	196	0.5000	8.33
21	LALIAAATA	230	0.5000	8.33
22	FRMAPFHHH	310	0.5000	8.33
23	VSILLTPVL	13	0.4700	7.83
24	LQILTFRTT	297	0.3900	6.50
25	MFRMAPFHH	309	0.3000	5.00
26	WNAAPAKIF	247	0.2000	3.33
27	IRLFTKQGF	22	0.0800	1.33
28	VGQITSAVL	120	-0.1000	0
29	MRQILIAVA	0	-0.2000	0
30	YNVRDPLDL	222	-0.2000	0
31	VAVAVTVSI	7	-0.3000	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	LFVLFCVVI	164	3.6000	60.00
2	ILIAVAVAV	3	3.5000	58.33
3	FVLFCVVIV	165	3.0800	51.33
4	LVLGLATAL	85	2.9900	49.83
5	VAILAGIWA	54	2.7000	45.00
6	FWLLTAITC	333	2.4000	40.00

7	VVIVSAWSN	170	2.2700	37.83
8	IVSAWSNAV	172	2.1000	35.00
9	IRRSRNLGL	105	1.9000	31.67
10	MAMVTAAYV	194	1.6500	27.50
11	FRNAAGLTP	136	1.6000	26.67
12	IAVAVAVTV	5	1.5000	25.00
13	LVLQFRNAA	132	1.5000	25.00
14	VREIATVTL	152	1.5000	25.00
15	MVTAAYVLI	196	1.5000	25.00
16	LALIAAATA	230	1.5000	25.00
17	VSILLTPVL	13	1.4700	24.50
18	LQILTFRTT	297	1.3900	23.17
19	MFRMAPFHH	309	1.3000	21.67
20	YVREIATVT	151	1.2900	21.50
21	IRLFTKQGF	22	1.0800	18.00
22	LGLATALGG	87	1.0000	16.67
23	VLFCVVIVS	166	1.0000	16.67
24	LGALFVAEI	284	1.0000	16.67
25	VGQITSAVL	120	0.9000	15.00
26	MRQILIAVA	0	0.8000	13.33
27	VAVAVTVSI	7	0.7000	11.67
28	VVLGALFVA	282	0.7000	11.67
29	VALFYGEWL	345	0.6800	11.33
30	FVAEITSVV	288	0.6000	10.00
31	LIRLFTKQG	21	0.5000	8.33
32	VTLAPVLFV	158	0.5000	8.33
33	FRMAPFHHH	310	0.5000	8.33
34	IKIRRSRNL	103	0.4900	8.17
35	LLVLGLATA	84	0.4000	6.67

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	VLFCVVIVS	166	4.5000	47.37
2	IRLFTKQGF	22	4.3000	45.26
3	VVLGALFVA	282	4.3000	45.26
4	LVLQFRNAA	132	4.0100	42.21
5	IREDGPPSH	34	4.0000	42.11
6	VVLQILTFR	295	3.7000	38.95
7	IFMGDTGSL	254	3.5600	37.47
8	LALGGVIAG	262	3.5000	36.84
9	LVLGLATAL	85	3.4600	36.42
10	MRQILIAVA	0	3.4000	35.79
11	LFGVLVLQF	128	3.3000	34.74
12	IRRSRNLGL	105	3.1600	33.26
13	ILIAVAVAV	3	3.0000	31.58
14	ILLTPVLIR	15	2.9000	30.53
15	FVLFCVVIV	165	2.8000	29.47
16	VIAGLSVTS	267	2.8000	29.47
17	VTLAPVLFV	158	2.7000	28.42
18	IRFWLLTAI	331	2.7000	28.42
19	VSILLTPVL	13	2.6600	28.00
20	VLFGVLVLQ	127	2.5000	26.32
21	YRNACVTAP	209	2.5000	26.32
22	VREIATVTL	152	2.4600	25.89
23	IVSAWSNAV	172	2.4100	25.37
24	VLGLATALG	86	2.4000	25.26
25	VVIVSAWSN	170	2.4000	25.26
26	LGALFVAEI	284	2.3000	24.21
27	VLQILTFRT	296	2.3000	24.21
28	LAFDGEGIG	72	2.2000	23.16
29	LFVAEITSV	287	2.2000	23.16
30	VAVAVTVSI	7	2.1000	22.11
31	LIRLFTKQG	21	2.1000	22.11
32	LGLATALGG	87	2.1000	22.11
33	LFVLFCVVI	164	2.1000	22.11
34	LIKIRRSRN	102	2.0700	21.79

35	MGGVAILAG	51	2.0000	21.05

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	IREDGPPSH	34	3.5800	39.34
2	VVLGALFVA	282	3.3000	36.26
3	VLFCVVIVS	166	3.1000	34.07
4	LVLQFRNAA	132	3.0100	33.08
5	FMGDTGSLA	255	2.9700	32.64
6	FVLFCVVIV	165	2.8000	30.77
7	YRNACVTAP	209	2.5000	27.47
8	MRQILIAVA	0	2.4000	26.37
9	VLFGVLVLQ	127	2.2000	24.18
10	IFMGDTGSL	254	1.6000	17.58
11	MFRMAPFHH	309	1.5800	17.36
12	LVLGLATAL	85	1.5000	16.48
13	FRMAPFHHH	310	1.4800	16.26
14	IRLFTKQGF	22	1.4000	15.38
15	VIAGLSVTS	267	1.4000	15.38
16	FWLLTAITC	333	1.3000	14.29
17	FVAEITSVV	288	1.2700	13.96
18	IRRSRNLGL	105	1.2000	13.19
19	VVLQILTFR	295	1.2000	13.19
20	LALGGVIAG	262	1.1000	12.09
21	ILIAVAVAV	3	1.0000	10.99
22	FIDDLIKIR	98	0.9000	9.89
23	FRNAAGLTP	136	0.9000	9.89
24	LIAAATAGA	232	0.9000	9.89
25	IRFWLLTAI	331	0.8000	8.79
26	FCVVIVSAW	168	0.7700	8.46
27	VSILLTPVL	13	0.7000	7.69
28	LLVLGLATA	84	0.7000	7.69

29	VTLAPVLFV	158	0.7000	7.69
30	LFCVVIVSA	167	0.7000	7.69
31	VVIVSAWSN	170	0.6000	6.59
32	YVLITFWQY	201	0.6000	6.59
33	WWNAAPAKI	246	0.6000	6.59
34	VLQILTFRT	296	0.6000	6.59
35	WLLTAITCG	334	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	LVLQFRNAA	132	4.7000	53.41
2	VLFCVVIVS	166	3.7800	42.95
3	MRQILIAVA	0	3.4000	38.64
4	IREDGPPSH	34	3.1800	36.14
5	VLFGVLVLQ	127	3.0800	35.00
6	VVLGALFVA	282	2.8000	31.82
7	IRRSRNLGL	105	2.7000	30.68
8	IRLFTKQGF	22	2.5000	28.41
9	LVLGLATAL	85	2.5000	28.41
10	VIAGLSVTS	267	2.2800	25.91
11	VTLAPVLFV	158	2.2000	25.00
12	VVLQILTFR	295	2.2000	25.00
13	IVSAWSNAV	172	2.1000	23.86
14	ILLTPVLIR	15	1.9000	21.59
15	LFGVLVLQF	128	1.9000	21.59
16	LIAAATAGA	232	1.9000	21.59
17	ILIAVAVAV	3	1.8800	21.36
18	IRFWLLTAI	331	1.8000	20.45
19	LALGGVIAG	262	1.7800	20.23
20	LLVLGLATA	84	1.7000	19.32
21	FMGDTGSLA	255	1.7000	19.32
22	IIRFWLLTA	330	1.7000	19.32

23	FVLFCVVIV	165	1.6800	19.09
24	LFCVVIVSA	167	1.5800	17.95
25	YRNACVTAP	209	1.5000	17.05
26	LALIAAATA	230	1.5000	17.05
27	LGALFVAEI	284	1.4000	15.91
28	LFYGEWLAA	347	1.4000	15.91
29	VREIATVTL	152	1.3800	15.68
30	LIRLFTKQG	21	1.3000	14.77
31	LGLNKTAKT	111	1.3000	14.77
32	FRMAPFHHH	310	1.2800	14.55
33	LGLATALGG	87	1.2000	13.64
34	LTPGSADLS	142	1.2000	13.64
35	IFMGDTGSL	254	1.2000	13.64

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	LVLQFRNAA	132	4.7000	53.41
2	VLFCVVIVS	166	3.7800	42.95
3	MRQILIAVA	0	3.4000	38.64
4	IREDGPPSH	34	3.1800	36.14
5	VLFGVLVLQ	127	3.0800	35.00
6	VVLGALFVA	282	2.8000	31.82
7	IRRSRNLGL	105	2.7000	30.68
8	IRLFTKQGF	22	2.5000	28.41
9	LVLGLATAL	85	2.5000	28.41
10	VIAGLSVTS	267	2.2800	25.91
11	VTLAPVLFV	158	2.2000	25.00
12	VVLQILTFR	295	2.2000	25.00
13	IVSAWSNAV	172	2.1000	23.86
14	ILLTPVLIR	15	1.9000	21.59
15	LFGVLVLQF	128	1.9000	21.59
16	LIAAATAGA	232	1.9000	21.59

17	ILIAVAVAV	3	1.8800	21.36
18	IRFWLLTAI	331	1.8000	20.45
19	LALGGVIAG	262	1.7800	20.23
20	LLVLGLATA	84	1.7000	19.32
21	FMGDTGSLA	255	1.7000	19.32
22	IIRFWLLTA	330	1.7000	19.32
23	FVLFCVVIV	165	1.6800	19.09
24	LFCVVIVSA	167	1.5800	17.95
25	YRNACVTAP	209	1.5000	17.05
26	LALIAAATA	230	1.5000	17.05
27	LGALFVAEI	284	1.4000	15.91
28	LFYGEWLAA	347	1.4000	15.91
29	VREIATVTL	152	1.3800	15.68
30	LIRLFTKQG	21	1.3000	14.77
31	LGLNKTAKT	111	1.3000	14.77
32	FRMAPFHHH	310	1.2800	14.55
33	LGLATALGG	87	1.2000	13.64
34	LTPGSADLS	142	1.2000	13.64
35	IFMGDTGSL	254	1.2000	13.64

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	LVLQFRNAA	132	4.7000	53.41
2	VLFCVVIVS	166	3.7800	42.95
3	MRQILIAVA	0	3.4000	38.64
4	IREDGPPSH	34	3.1800	36.14
5	VLFGVLVLQ	127	3.0800	35.00
6	VVLGALFVA	282	2.8000	31.82
7	IRRSRNLGL	105	2.7000	30.68
8	IRLFTKQGF	22	2.5000	28.41
9	LVLGLATAL	85	2.5000	28.41
10	VIAGLSVTS	267	2.2800	25.91

11	VTLAPVLFV	158	2.2000	25.00
12	VVLQILTFR	295	2.2000	25.00
13	IVSAWSNAV	172	2.1000	23.86
14	ILLTPVLIR	15	1.9000	21.59
15	LFGVLVLQF	128	1.9000	21.59
16	LIAAATAGA	232	1.9000	21.59
17	ILIAVAVAV	3	1.8800	21.36
18	IRFWLLTAI	331	1.8000	20.45
19	LALGGVIAG	262	1.7800	20.23
20	LLVLGLATA	84	1.7000	19.32
21	FMGDTGSLA	255	1.7000	19.32
22	IIRFWLLTA	330	1.7000	19.32
23	FVLFCVVIV	165	1.6800	19.09
24	LFCVVIVSA	167	1.5800	17.95
25	YRNACVTAP	209	1.5000	17.05
26	LALIAAATA	230	1.5000	17.05
27	LGALFVAEI	284	1.4000	15.91
28	LFYGEWLAA	347	1.4000	15.91
29	VREIATVTL	152	1.3800	15.68
30	LIRLFTKQG	21	1.3000	14.77
31	LGLNKTAKT	111	1.3000	14.77
32	FRMAPFHHH	310	1.2800	14.55
33	LGLATALGG	87	1.2000	13.64
34	LTPGSADLS	142	1.2000	13.64
35	IFMGDTGSL	254	1.2000	13.64

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	FVLFCVVIV	165	3.8000	40.00
2	VLFCVVIVS	166	3.5000	36.84
3	YRNACVTAP	209	3.5000	36.84
4	IRLFTKQGF	22	3.3000	34.74

5	VVLGALFVA	282	3.3000	34.74
6	LVLQFRNAA	132	3.0100	31.68
7	IREDGPPSH	34	3.0000	31.58
8	FMGDTGSLA	255	2.9700	31.26
9	VVLQILTFR	295	2.7000	28.42
10	IFMGDTGSL	254	2.5600	26.95
11	LALGGVIAG	262	2.5000	26.32
12	LVLGLATAL	85	2.4600	25.89
13	MRQILIAVA	0	2.4000	25.26
14	FIDDLIKIR	98	2.4000	25.26
15	LFGVLVLQF	128	2.3000	24.21
16	FVAEITSVV	288	2.2700	23.89
17	FRTTGRRMF	302	2.2000	23.16
18	IRRSRNLGL	105	2.1600	22.74
19	ILIAVAVAV	3	2.0000	21.05
20	WLLTAITCG	334	2.0000	21.05
21	ILLTPVLIR	15	1.9000	20.00
22	FGHQIREDG	30	1.9000	20.00
23	FRNAAGLTP	136	1.9000	20.00
24	YVLITFWQY	201	1.9000	20.00
25	VIAGLSVTS	267	1.8000	18.95
26	VTLAPVLFV	158	1.7000	17.89
27	IRFWLLTAI	331	1.7000	17.89
28	VSILLTPVL	13	1.6600	17.47
29	FGVLVLQFR	129	1.6000	16.84
30	VLFGVLVLQ	127	1.5000	15.79
31	WWNAAPAKI	246	1.5000	15.79
32	VREIATVTL	152	1.4600	15.37
33	IVSAWSNAV	172	1.4100	14.84
34	VLGLATALG	86	1.4000	14.74
35	VVIVSAWSN	170	1.4000	14.74

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

	2.08	8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVLQFRNAA	132	4.7000	53.41
2	VLFCVVIVS	166	3.7800	42.95
3	MRQILIAVA	0	3.4000	38.64
4	IREDGPPSH	34	3.1800	36.14
5	VLFGVLVLQ	127	3.0800	35.00
6	VVLGALFVA	282	2.8000	31.82
7	IRRSRNLGL	105	2.7000	30.68
8	IRLFTKQGF	22	2.5000	28.41
9	LVLGLATAL	85	2.5000	28.41
10	VIAGLSVTS	267	2.2800	25.91
11	VTLAPVLFV	158	2.2000	25.00
12	VVLQILTFR	295	2.2000	25.00
13	IVSAWSNAV	172	2.1000	23.86
14	ILLTPVLIR	15	1.9000	21.59
15	LFGVLVLQF	128	1.9000	21.59
16	LIAAATAGA	232	1.9000	21.59
17	ILIAVAVAV	3	1.8800	21.36
18	IRFWLLTAI	331	1.8000	20.45
19	LALGGVIAG	262	1.7800	20.23
20	LLVLGLATA	84	1.7000	19.32
21	FMGDTGSLA	255	1.7000	19.32
22	IIRFWLLTA	330	1.7000	19.32
23	FVLFCVVIV	165	1.6800	19.09
24	LFCVVIVSA	167	1.5800	17.95
25	YRNACVTAP	209	1.5000	17.05
26	LALIAAATA	230	1.5000	17.05
27	LGALFVAEI	284	1.4000	15.91
28	LFYGEWLAA	347	1.4000	15.91
29	VREIATVTL	152	1.3800	15.68
30	LIRLFTKQG	21	1.3000	14.77
31	LGLNKTAKT	111	1.3000	14.77
32	FRMAPFHHH	310	1.2800	14.55

33	LGLATALGG	87	1.2000	13.64
34	LTPGSADLS	142	1.2000	13.64
35	IFMGDTGSL	254	1.2000	13.64

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	FVAEITSVV	288	4.6000	53.49
2	IRRSRNLGL	105	3.7000	43.02
3	YVREIATVT	151	3.0000	34.88
4	FRMAPFHHH	310	2.5800	30.00
5	FVLFCVVIV	165	2.4800	28.84
6	VLFCVVIVS	166	2.4800	28.84
7	ILLTPVLIR	15	2.3000	26.74
8	LIRLFTKQG	21	2.2000	25.58
9	IVSAWSNAV	172	2.2000	25.58
10	YRNACVTAP	209	2.2000	25.58
11	LGLNKTAKT	111	2.1000	24.42
12	LIAAATAGA	232	2.0000	23.26
13	MRQILIAVA	0	1.9000	22.09
14	VLGLATALG	86	1.9000	22.09
15	VREIATVTL	152	1.7800	20.70
16	FWLLTAITC	333	1.7800	20.70
17	WLLTAITCG	334	1.5000	17.44
18	VSILLTPVL	13	1.2000	13.95
19	VAVAVTVSI	7	1.1800	13.72
20	LVLQFRNAA	132	1.1000	12.79
21	FMGDTGSLA	255	1.0000	11.63
22	VGWAETTVI	322	1.0000	11.63
23	VTLAPVLFV	158	0.9000	10.47
24	LGALFVAEI	284	0.9000	10.47
25	LLTAITCGL	335	0.9000	10.47
26	ILIAVAVAV	3	0.8800	10.23

27	LFVLFCVVI	164	0.8800	10.23
28	LALIAAATA	230	0.8000	9.30
29	FYGEWLAAV	348	0.8000	9.30
30	IREDGPPSH	34	0.7800	9.07
31	IGFLWWNAA	242	0.7000	8.14
32	VVLQILTFR	295	0.7000	8.14
33	FRNAAGLTP	136	0.6000	6.98
34	VLQILTFRT	296	0.5000	5.81
35	MFRMAPFHH	309	0.4800	5.58

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	IKIRRSRNL	103	5.3000	55.21
2	VLFCVVIVS	166	3.9000	40.62
3	IRFWLLTAI	331	3.3000	34.38
4	IRRSRNLGL	105	3.2000	33.33
5	IVSAWSNAV	172	3.2000	33.33
6	VLIRLFTKQ	20	3.0000	31.25
7	LIAAATAGA	232	3.0000	31.25
8	VVIVSAWSN	170	2.9000	30.21
9	FVLFCVVIV	165	2.8000	29.17
10	MFRMAPFHH	309	2.6800	27.92
11	ITFWQYRNA	204	2.6000	27.08
12	ILLTPVLIR	15	2.4000	25.00
13	VIIRFWLLT	329	2.4000	25.00
14	VAVAVTVSI	7	2.3000	23.96
15	VIAGLSVTS	267	2.3000	23.96
16	ILTFRTTGR	299	2.3000	23.96
17	VLQILTFRT	296	2.2800	23.75
18	VTLAPVLFV	158	2.2000	22.92
19	VGWAETTVI	322	2.2000	22.92
20	MRQILIAVA	0	2.1800	22.71

21	VREIATVTL	152	2.1800	22.71
22	LIRLFTKQG	21	2.1000	21.88
23	FRMAPFHHH	310	2.0800	21.67
24	ILIAVAVAV	3	2.0000	20.83
25	LQFRNAAGL	134	2.0000	20.83
26	IIRFWLLTA	330	2.0000	20.83
27	LLTAITCGL	335	1.9000	19.79
28	LGLNKTAKT	111	1.8000	18.75
29	VVLGALFVA	282	1.8000	18.75
30	VLQFRNAAG	133	1.6000	16.67
31	FLWWNAAPA	244	1.6000	16.67
32	LVLGLATAL	85	1.5000	15.62
33	VLGLATALG	86	1.5000	15.62
34	LGLATALGG	87	1.5000	15.62
35	VLVLQFRNA	131	1.5000	15.62

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	VLFCVVIVS	166	3.4800	39.55
2	MFRMAPFHH	309	3.3300	37.84
3	IVSAWSNAV	172	3.3000	37.50
4	ILTFRTTGR	299	3.3000	37.50
5	MRQILIAVA	0	3.2000	36.36
6	FVLFCVVIV	165	3.2000	36.36
7	VLGLATALG	86	3.1000	35.23
8	LIAAATAGA	232	3.0000	34.09
9	VREIATVTL	152	2.9000	32.95
10	IRRSRNLGL	105	2.8000	31.82
11	VLQILTFRT	296	2.7500	31.25
12	VGWAETTVI	322	2.5000	28.41
13	LIRLFTKQG	21	2.4000	27.27
14	VLQFRNAAG	133	2.3000	26.14

15	VSILLTPVL	13	2.1000	23.86
16	LALIAAATA	230	2.1000	23.86
17	LGALFVAEI	284	2.1000	23.86
18	VAVAVTVSI	7	2.0000	22.73
19	VVIVSAWSN	170	2.0000	22.73
20	IGFLWWNAA	242	2.0000	22.73
21	IIRFWLLTA	330	2.0000	22.73
22	IRFWLLTAI	331	1.9500	22.16
23	LFVLFCVVI	164	1.9000	21.59
24	LLTAITCGL	335	1.9000	21.59
25	ILIAVAVAV	3	1.7000	19.32
26	LFGVLVLQF	128	1.7000	19.32
27	YRNACVTAP	209	1.7000	19.32
28	FVAEITSVV	288	1.7000	19.32
29	VGQITSAVL	120	1.6000	18.18
30	LGLNKTAKT	111	1.5000	17.05
31	VTLAPVLFV	158	1.5000	17.05
32	IAGLSVTSR	268	1.5000	17.05
33	LLVLGLATA	84	1.4000	15.91
34	LVLQFRNAA	132	1.4000	15.91
35	VVLQILTFR	295	1.4000	15.91

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	FVLFCVVIV	165	4.5000	47.87
2	MFRMAPFHH	309	3.5500	37.77
3	VLGLATALG	86	3.4000	36.17
4	FRMAPFHHH	310	3.4000	36.17
5	YRNACVTAP	209	3.1000	32.98
6	VVIVSAWSN	170	3.0000	31.91
7	FVAEITSVV	288	3.0000	31.91
8	VREIATVTL	152	2.9000	30.85

9	IRRSRNLGL	105	2.8000	29.79
10	LIRLFTKQG	21	2.7000	28.72
11	VLQILTFRT	296	2.6500	28.19
12	VLQFRNAAG	133	2.6000	27.66
13	IVSAWSNAV	172	2.6000	27.66
14	YVLITFWQY	201	2.5000	26.60
15	VLFCVVIVS	166	2.4800	26.38
16	WSNAVNFTD	176	2.4500	26.06
17	FCVVIVSAW	168	2.3000	24.47
18	ILTFRTTGR	299	2.3000	24.47
19	MRQILIAVA	0	2.2000	23.40
20	VSILLTPVL	13	2.1000	22.34
21	LIAAATAGA	232	2.0000	21.28
22	FWLLTAITC	333	1.9800	21.06
23	LLTAITCGL	335	1.9000	20.21
24	YVREIATVT	151	1.8000	19.15
25	VGWAETTVI	322	1.7000	18.09
26	WLLTAITCG	334	1.7000	18.09
27	VGQITSAVL	120	1.6000	17.02
28	LFGVLVLQF	128	1.6000	17.02
29	LGLNKTAKT	111	1.4000	14.89
30	LGALFVAEI	284	1.3000	13.83
31	LIAVAVAVT	4	1.2000	12.77
32	VAVAVTVSI	7	1.2000	12.77
33	IRFWLLTAI	331	1.1500	12.23
34	LGLATALGG	87	1.1000	11.70
35	LFVLFCVVI	164	1.1000	11.70

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	FVLFCVVIV	165	4.2000	47.73
2	YRNACVTAP	209	2.7000	30.68

3	FVAEITSVV	288	2.7000	30.68
4	VLFCVVIVS	166	2.4800	28.18
5	MFRMAPFHH	309	2.3300	26.48
6	IVSAWSNAV	172	2.3000	26.14
7	ILTFRTTGR	299	2.3000	26.14
8	MRQILIAVA	0	2.2000	25.00
9	FRMAPFHHH	310	2.1800	24.77
10	VLGLATALG	86	2.1000	23.86
11	LIAAATAGA	232	2.0000	22.73
12	FWLLTAITC	333	1.9800	22.50
13	VREIATVTL	152	1.9000	21.59
14	IRRSRNLGL	105	1.8000	20.45
15	VLQILTFRT	296	1.7500	19.89
16	VGWAETTVI	322	1.5000	17.05
17	LIRLFTKQG	21	1.4000	15.91
18	FCVVIVSAW	168	1.4000	15.91
19	YVLITFWQY	201	1.4000	15.91
20	VLQFRNAAG	133	1.3000	14.77
21	VSILLTPVL	13	1.1000	12.50
22	LALIAAATA	230	1.1000	12.50
23	LGALFVAEI	284	1.1000	12.50
24	VAVAVTVSI	7	1.0000	11.36
25	VVIVSAWSN	170	1.0000	11.36
26	IGFLWWNAA	242	1.0000	11.36
27	IIRFWLLTA	330	1.0000	11.36
28	FLWWNAAPA	244	0.9500	10.80
29	IRFWLLTAI	331	0.9500	10.80
30	YVREIATVT	151	0.9000	10.23
31	LFVLFCVVI	164	0.9000	10.23
32	LLTAITCGL	335	0.9000	10.23
33	ILIAVAVAV	3	0.7000	7.95
34	LFGVLVLQF	128	0.7000	7.95
35	VGQITSAVL	120	0.6000	6.82

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	MFRMAPFHH	309	4.5500	48.40
2	VLGLATALG	86	4.4000	46.81
3	VVIVSAWSN	170	4.0000	42.55
4	VREIATVTL	152	3.9000	41.49
5	IRRSRNLGL	105	3.8000	40.43
6	LIRLFTKQG	21	3.7000	39.36
7	VLQILTFRT	296	3.6500	38.83
8	VLQFRNAAG	133	3.6000	38.30
9	IVSAWSNAV	172	3.6000	38.30
10	FVLFCVVIV	165	3.5000	37.23
11	VLFCVVIVS	166	3.4800	37.02
12	ILTFRTTGR	299	3.3000	35.11
13	MRQILIAVA	0	3.2000	34.04
14	VSILLTPVL	13	3.1000	32.98
15	LIAAATAGA	232	3.0000	31.91
16	LLTAITCGL	335	2.9000	30.85
17	VGWAETTVI	322	2.7000	28.72
18	VGQITSAVL	120	2.6000	27.66
19	LFGVLVLQF	128	2.6000	27.66
20	LGLNKTAKT	111	2.4000	25.53
21	FRMAPFHHH	310	2.4000	25.53
22	LGALFVAEI	284	2.3000	24.47
23	LIAVAVAVT	4	2.2000	23.40
24	VAVAVTVSI	7	2.2000	23.40
25	IRFWLLTAI	331	2.1500	22.87
26	LGLATALGG	87	2.1000	22.34
27	LFVLFCVVI	164	2.1000	22.34
28	YRNACVTAP	209	2.1000	22.34
29	LALIAAATA	230	2.1000	22.34
30	ILIAVAVAV	3	2.0000	21.28

31	IGFLWWNAA	242	2.0000	21.28
32	FVAEITSVV	288	2.0000	21.28
33	IIRFWLLTA	330	2.0000	21.28
34	VTLAPVLFV	158	1.8000	19.15
35	MGGVAILAG	51	1.7000	18.09

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	FVAEITSVV	288	5.6000	62.22
2	IRRSRNLGL	105	4.6600	51.78
3	ILLTPVLIR	15	3.8000	42.22
4	YVREIATVT	151	3.7000	41.11
5	LIRLFTKQG	21	3.6000	40.00
6	FVLFCVVIV	165	3.4800	38.67
7	VLGLATALG	86	3.3000	36.67
8	IVSAWSNAV	172	3.2000	35.56
9	YRNACVTAP	209	3.2000	35.56
10	WLLTAITCG	334	2.9000	32.22
11	VLFCVVIVS	166	2.8800	32.00
12	LGLNKTAKT	111	2.8000	31.11
13	VREIATVTL	152	2.7400	30.44
14	VVLQILTFR	295	2.2000	24.44
15	VSILLTPVL	13	2.1600	24.00
16	VAVAVTVSI	7	2.0800	23.11
17	LIAAATAGA	232	2.0000	22.22
18	FRMAPFHHH	310	2.0000	22.22
19	MRQILIAVA	0	1.9000	21.11
20	VTLAPVLFV	158	1.9000	21.11
21	VGWAETTVI	322	1.9000	21.11
22	ILIAVAVAV	3	1.8800	20.89
23	LLTAITCGL	335	1.8600	20.67
24	LGALFVAEI	284	1.8000	20.00

25	FYGEWLAAV	348	1.8000	20.00
26	LFVLFCVVI	164	1.7800	19.78
27	FWLLTAITC	333	1.7800	19.78
28	YVLITFWQY	201	1.7000	18.89
29	VLITFWQYR	202	1.7000	18.89
30	LGLATALGG	87	1.6000	17.78
31	LFGVLVLQF	128	1.6000	17.78
32	FRNAAGLTP	136	1.6000	17.78
33	WNAAPAKIF	247	1.4000	15.56
34	ILTFRTTGR	299	1.4000	15.56
35	FIDDLIKIR	98	1.3000	14.44

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	VLFCVVIVS	166	3.4800	39.55
2	MFRMAPFHH	309	3.3300	37.84
3	IVSAWSNAV	172	3.3000	37.50
4	ILTFRTTGR	299	3.3000	37.50
5	MRQILIAVA	0	3.2000	36.36
6	FVLFCVVIV	165	3.2000	36.36
7	VLGLATALG	86	3.1000	35.23
8	LIAAATAGA	232	3.0000	34.09
9	VREIATVTL	152	2.9000	32.95
10	IRRSRNLGL	105	2.8000	31.82
11	VLQILTFRT	296	2.7500	31.25
12	VGWAETTVI	322	2.5000	28.41
13	LIRLFTKQG	21	2.4000	27.27
14	VLQFRNAAG	133	2.3000	26.14
15	VSILLTPVL	13	2.1000	23.86
16	LALIAAATA	230	2.1000	23.86
17	LGALFVAEI	284	2.1000	23.86
18	VAVAVTVSI	7	2.0000	22.73

19	VVIVSAWSN	170	2.0000	22.73
20	IGFLWWNAA	242	2.0000	22.73
21	IIRFWLLTA	330	2.0000	22.73
22	IRFWLLTAI	331	1.9500	22.16
23	LFVLFCVVI	164	1.9000	21.59
24	LLTAITCGL	335	1.9000	21.59
25	ILIAVAVAV	3	1.7000	19.32
26	LFGVLVLQF	128	1.7000	19.32
27	YRNACVTAP	209	1.7000	19.32
28	FVAEITSVV	288	1.7000	19.32
29	VGQITSAVL	120	1.6000	18.18
30	LGLNKTAKT	111	1.5000	17.05
31	VTLAPVLFV	158	1.5000	17.05
32	IAGLSVTSR	268	1.5000	17.05
33	LLVLGLATA	84	1.4000	15.91
34	LVLQFRNAA	132	1.4000	15.91
35	VVLQILTFR	295	1.4000	15.91

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	FVAEITSVV	288	4.6000	53.49
2	IRRSRNLGL	105	3.7000	43.02
3	YVREIATVT	151	3.0000	34.88
4	FRMAPFHHH	310	2.5800	30.00
5	FVLFCVVIV	165	2.4800	28.84
6	VLFCVVIVS	166	2.4800	28.84
7	ILLTPVLIR	15	2.3000	26.74
8	LIRLFTKQG	21	2.2000	25.58
9	IVSAWSNAV	172	2.2000	25.58
10	YRNACVTAP	209	2.2000	25.58
11	LGLNKTAKT	111	2.1000	24.42
12	LIAAATAGA	232	2.0000	23.26

13	MRQILIAVA	0	1.9000	22.09
14	VLGLATALG	86	1.9000	22.09
15	VREIATVTL	152	1.7800	20.70
16	FWLLTAITC	333	1.7800	20.70
17	WLLTAITCG	334	1.5000	17.44
18	VSILLTPVL	13	1.2000	13.95
19	VAVAVTVSI	7	1.1800	13.72
20	LVLQFRNAA	132	1.1000	12.79
21	FMGDTGSLA	255	1.0000	11.63
22	VGWAETTVI	322	1.0000	11.63
23	VTLAPVLFV	158	0.9000	10.47
24	LGALFVAEI	284	0.9000	10.47
25	LLTAITCGL	335	0.9000	10.47
26	ILIAVAVAV	3	0.8800	10.23
27	LFVLFCVVI	164	0.8800	10.23
28	LALIAAATA	230	0.8000	9.30
29	FYGEWLAAV	348	0.8000	9.30
30	IREDGPPSH	34	0.7800	9.07
31	IGFLWWNAA	242	0.7000	8.14
32	VVLQILTFR	295	0.7000	8.14
33	FRNAAGLTP	136	0.6000	6.98
34	VLQILTFRT	296	0.5000	5.81
35	MFRMAPFHH	309	0.4800	5.58

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	IRRSRNLGL	105	8.4000	72.41
2	VAVTVSILL	9	7.3000	62.93
3	FVLFCVVIV	165	7.0000	60.34
4	VREIATVTL	152	6.0200	51.90
5	YVLITFWQY	201	5.9000	50.86
6	MGDTGSLAL	256	5.8000	50.00

7	IGASGLLVL	79	5.7000	49.14
8	LVLGLATAL	85	5.3000	45.69
9	LFGVLVLQF	128	5.3000	45.69
10	IVSAWSNAV	172	5.3000	45.69
11	YNVRDPLDL	222	5.3000	45.69
12	FRTTGRRMF	302	5.3000	45.69
13	IKIRRSRNL	103	5.2000	44.83
14	ILIAVAVAV	3	5.1000	43.97
15	MVTAAYVLI	196	5.1000	43.97
16	VGQITSAVL	120	4.6000	39.66
17	IRLFTKQGF	22	4.5000	38.79
18	LFVLFCVVI	164	4.5000	38.79
19	VAEITSVVL	289	4.5000	38.79
20	VAVAVTVSI	7	4.4200	38.10
21	VVIVSAWSN	170	4.4000	37.93
22	VTLAPVLFV	158	4.3000	37.07
23	IRFWLLTAI	331	4.3000	37.07
24	ILLTPVLIR	15	3.9000	33.62
25	VALFYGEWL	345	3.9000	33.62
26	LSVTSRTEI	271	3.8000	32.76
27	VGWAETTVI	322	3.7200	32.07
28	LLTPVLIRL	16	3.7000	31.90
29	LAGIWAGYL	57	3.7000	31.90
30	YLGAHLAGL	64	3.7000	31.90
31	FRNAAGLTP	136	3.7000	31.90
32	ITSVVLQIL	292	3.7000	31.90
33	VLQILTFRT	296	3.5200	30.34
34	FRMAPFHHH	310	3.5000	30.17
35	IFMGDTGSL	254	3.4200	29.48

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	IRRSRNLGL	105	8.4000	72.41
2	VAVTVSILL	9	7.3000	62.93
3	FVLFCVVIV	165	7.0000	60.34
4	VREIATVTL	152	6.0200	51.90
5	YVLITFWQY	201	5.9000	50.86
6	MGDTGSLAL	256	5.8000	50.00
7	IGASGLLVL	79	5.7000	49.14
8	LVLGLATAL	85	5.3000	45.69
9	LFGVLVLQF	128	5.3000	45.69
10	IVSAWSNAV	172	5.3000	45.69
11	YNVRDPLDL	222	5.3000	45.69
12	FRTTGRRMF	302	5.3000	45.69
13	IKIRRSRNL	103	5.2000	44.83
14	ILIAVAVAV	3	5.1000	43.97
15	MVTAAYVLI	196	5.1000	43.97
16	VGQITSAVL	120	4.6000	39.66
17	IRLFTKQGF	22	4.5000	38.79
18	LFVLFCVVI	164	4.5000	38.79
19	VAEITSVVL	289	4.5000	38.79
20	VAVAVTVSI	7	4.4200	38.10
21	VVIVSAWSN	170	4.4000	37.93
22	VTLAPVLFV	158	4.3000	37.07
23	IRFWLLTAI	331	4.3000	37.07
24	ILLTPVLIR	15	3.9000	33.62
25	VALFYGEWL	345	3.9000	33.62
26	LSVTSRTEI	271	3.8000	32.76
27	VGWAETTVI	322	3.7200	32.07
28	LLTPVLIRL	16	3.7000	31.90
29	LAGIWAGYL	57	3.7000	31.90
30	YLGAHLAGL	64	3.7000	31.90
31	FRNAAGLTP	136	3.7000	31.90
32	ITSVVLQIL	292	3.7000	31.90
33	VLQILTFRT	296	3.5200	30.34
34	FRMAPFHHH	310	3.5000	30.17

35	IFMGDTGSL	254	3.4200	29.48

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	WQYRNACVT	207	4.0000	46.51
2	YNVRDPLDL	222	3.8000	44.19
3	LQFRNAAGL	134	3.3000	38.37
4	FVLFCVVIV	165	3.3000	38.37
5	IKIRRSRNL	103	3.2000	37.21
6	MFRMAPFHH	309	2.8000	32.56
7	IRLFTKQGF	22	2.7000	31.40
8	FRMAPFHHH	310	2.6000	30.23
9	VVIVSAWSN	170	2.3000	26.74
10	MRQILIAVA	0	2.2000	25.58
11	VLGLATALG	86	2.0000	23.26
12	VLFCVVIVS	166	1.9000	22.09
13	VIIRFWLLT	329	1.9000	22.09
14	LIRLFTKQG	21	1.8000	20.93
15	LFTKQGFGH	24	1.8000	20.93
16	WAGYLGAHL	61	1.7000	19.77
17	FRTTGRRMF	302	1.5000	17.44
18	YLGAHLAGL	64	1.4000	16.28
19	LLVLGLATA	84	1.4000	16.28
20	LGCYNVRDP	219	1.4000	16.28
21	LTFRTTGRR	300	1.4000	16.28
22	LIAVAVAVT	4	1.3000	15.12
23	VLIRLFTKQ	20	1.3000	15.12
24	LGALFVAEI	284	1.3000	15.12
25	IIRFWLLTA	330	1.2000	13.95
26	LFGVLVLQF	128	1.1000	12.79
27	FWQYRNACV	206	1.1000	12.79
28	LGLNKTAKT	111	1.0000	11.63

29	FLWWNAAPA	244	1.0000	11.63
30	YVLITFWQY	201	0.9000	10.47
31	LIAAATAGA	232	0.9000	10.47
32	LVLQFRNAA	132	0.8000	9.30
33	FRNAAGLTP	136	0.8000	9.30
34	WWNAAPAKI	246	0.8000	9.30
35	FWLLTAITC	333	0.8000	9.30

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	WQYRNACVT	207	3.1000	38.75
2	FVLFCVVIV	165	3.0000	37.50
3	YNVRDPLDL	222	2.8000	35.00
4	LQFRNAAGL	134	2.3000	28.75
5	MRQILIAVA	0	2.2000	27.50
6	IKIRRSRNL	103	2.2000	27.50
7	VLFCVVIVS	166	1.9000	23.75
8	IRLFTKQGF	22	1.8000	22.50
9	MFRMAPFHH	309	1.5800	19.75
10	LLVLGLATA	84	1.4000	17.50
11	LTFRTTGRR	300	1.4000	17.50
12	FRMAPFHHH	310	1.3800	17.25
13	IIRFWLLTA	330	1.2000	15.00
14	LGALFVAEI	284	1.1000	13.75
15	LGCYNVRDP	219	1.0000	12.50
16	FLWWNAAPA	244	1.0000	12.50
17	VIIRFWLLT	329	1.0000	12.50
18	LIAAATAGA	232	0.9000	11.25
19	LVLQFRNAA	132	0.8000	10.00
20	FWQYRNACV	206	0.8000	10.00
21	FWLLTAITC	333	0.8000	10.00
22	WAGYLGAHL	61	0.7000	8.75

23	VLGLATALG	86	0.7000	8.75
24	WWNAAPAKI	246	0.6000	7.50
25	FRTTGRRMF	302	0.6000	7.50
26	LFTKQGFGH	24	0.5800	7.25
27	VLIRLFTKQ	20	0.5000	6.25
28	LIRLFTKQG	21	0.5000	6.25
29	LIAVAVAVT	4	0.4000	5.00
30	YLGAHLAGL	64	0.4000	5.00
31	FRNAAGLTP	136	0.4000	5.00
32	VVLGALFVA	282	0.4000	5.00
33	VVIVSAWSN	170	0.3000	3.75
34	LALIAAATA	230	0.3000	3.75
35	LFGVLVLQF	128	0.2000	2.50

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	LQFRNAAGL	134	3.3000	41.25
2	MRQILIAVA	0	3.2000	40.00
3	IKIRRSRNL	103	3.2000	40.00
4	VLFCVVIVS	166	2.9000	36.25
5	IRLFTKQGF	22	2.8000	35.00
6	MFRMAPFHH	309	2.5800	32.25
7	LLVLGLATA	84	2.4000	30.00
8	LTFRTTGRR	300	2.4000	30.00
9	IIRFWLLTA	330	2.2000	27.50
10	WQYRNACVT	207	2.1000	26.25
11	LGALFVAEI	284	2.1000	26.25
12	FVLFCVVIV	165	2.0000	25.00
13	LGCYNVRDP	219	2.0000	25.00
14	VIIRFWLLT	329	2.0000	25.00
15	LIAAATAGA	232	1.9000	23.75
16	LVLQFRNAA	132	1.8000	22.50

17	YNVRDPLDL	222	1.8000	22.50
18	VLGLATALG	86	1.7000	21.25
19	LFTKQGFGH	24	1.5800	19.75
20	VLIRLFTKQ	20	1.5000	18.75
21	LIRLFTKQG	21	1.5000	18.75
22	LIAVAVAVT	4	1.4000	17.50
23	VVLGALFVA	282	1.4000	17.50
24	VVIVSAWSN	170	1.3000	16.25
25	LALIAAATA	230	1.3000	16.25
26	LFGVLVLQF	128	1.2000	15.00
27	VTLAPVLFV	158	1.2000	15.00
28	LGGVIAGLS	264	1.2000	15.00
29	LGLNKTAKT	111	1.1000	13.75
30	MAMVTAAYV	194	1.0000	12.50
31	ILLTPVLIR	15	0.9000	11.25
32	LLTAITCGL	335	0.8000	10.00
33	ILIAVAVAV	3	0.7000	8.75
34	VAILAGIWA	54	0.7000	8.75
35	LFCVVIVSA	167	0.7000	8.75

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	LQFRNAAGL	134	4.3000	50.00
2	IKIRRSRNL	103	4.2000	48.84
3	MFRMAPFHH	309	3.8000	44.19
4	IRLFTKQGF	22	3.7000	43.02
5	VVIVSAWSN	170	3.3000	38.37
6	MRQILIAVA	0	3.2000	37.21
7	VLGLATALG	86	3.0000	34.88
8	WQYRNACVT	207	3.0000	34.88
9	VLFCVVIVS	166	2.9000	33.72
10	VIIRFWLLT	329	2.9000	33.72

11	LIRLFTKQG	21	2.8000	32.56
12	LFTKQGFGH	24	2.8000	32.56
13	YNVRDPLDL	222	2.8000	32.56
14	LLVLGLATA	84	2.4000	27.91
15	LGCYNVRDP	219	2.4000	27.91
16	LTFRTTGRR	300	2.4000	27.91
17	LIAVAVAVT	4	2.3000	26.74
18	VLIRLFTKQ	20	2.3000	26.74
19	FVLFCVVIV	165	2.3000	26.74
20	LGALFVAEI	284	2.3000	26.74
21	IIRFWLLTA	330	2.2000	25.58
22	LFGVLVLQF	128	2.1000	24.42
23	LGLNKTAKT	111	2.0000	23.26
24	LIAAATAGA	232	1.9000	22.09
25	LVLQFRNAA	132	1.8000	20.93
26	LLTAITCGL	335	1.8000	20.93
27	MGGVAILAG	51	1.7000	19.77
28	LIKIRRSRN	102	1.7000	19.77
29	FRMAPFHHH	310	1.6000	18.60
30	VSILLTPVL	13	1.5000	17.44
31	LGLATALGG	87	1.5000	17.44
32	VTLAPVLFV	158	1.5000	17.44
33	IFMGDTGSL	254	1.5000	17.44
34	VVLGALFVA	282	1.4000	16.28
35	MAMVTAAYV	194	1.3000	15.12

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	FVLFCVVIV	165	4.0000	45.98
2	YNVRDPLDL	222	3.4000	39.08
3	VLIRLFTKQ	20	3.3000	37.93
4	WQYRNACVT	207	3.1000	35.63

5	YRNACVTAP	209	3.0000	34.48
6	IRLFTKQGF	22	2.8000	32.18
7	LVLQFRNAA	132	2.8000	32.18
8	VLFCVVIVS	166	2.7800	31.95
9	MFRMAPFHH	309	2.4300	27.93
10	LQFRNAAGL	134	2.3000	26.44
11	IRFWLLTAI	331	2.3000	26.44
12	MRQILIAVA	0	2.2000	25.29
13	IKIRRSRNL	103	1.9000	21.84
14	FRMAPFHHH	310	1.8800	21.61
15	IIRFWLLTA	330	1.8000	20.69
16	FVAEITSVV	288	1.7000	19.54
17	FWLLTAITC	333	1.6800	19.31
18	VIIRFWLLT	329	1.6000	18.39
19	FCVVIVSAW	168	1.5000	17.24
20	LFTKQGFGH	24	1.4300	16.44
21	LLVLGLATA	84	1.4000	16.09
22	VVLGALFVA	282	1.2500	14.37
23	IVSAWSNAV	172	1.2000	13.79
24	LGALFVAEI	284	1.1000	12.64
25	WLLTAITCG	334	1.1000	12.64
26	FRNAAGLTP	136	1.0000	11.49
27	YVREIATVT	151	1.0000	11.49
28	FLWWNAAPA	244	1.0000	11.49
29	LIAAATAGA	232	0.9000	10.34
30	LFGVLVLQF	128	0.8000	9.20
31	VTLAPVLFV	158	0.8000	9.20
32	VVIVSAWSN	170	0.8000	9.20
33	FWQYRNACV	206	0.8000	9.20
34	ILIAVAVAV	3	0.7000	8.05
35	WAGYLGAHL	61	0.7000	8.05

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

	2.8	10.1

Rank	Sequence	At Position	Score	% of Highest Score
1	YNVRDPLDL	222	5.6000	55.45
2	WQYRNACVT	207	4.0000	39.60
3	FVLFCVVIV	165	3.8000	37.62
4	VIIRFWLLT	329	3.7000	36.63
5	VLFCVVIVS	166	3.5000	34.65
6	IKIRRSRNL	103	3.4000	33.66
7	LQFRNAAGL	134	3.3000	32.67
8	MFRMAPFHH	309	3.3000	32.67
9	FRMAPFHHH	310	3.3000	32.67
10	VVIVSAWSN	170	3.1000	30.69
11	IIRFWLLTA	330	3.0000	29.70
12	LFGVLVLQF	128	2.9000	28.71
13	IRLFTKQGF	22	2.8000	27.72
14	FRNAAGLTP	136	2.6000	25.74
15	MGGVAILAG	51	2.5000	24.75
16	VLIRLFTKQ	20	2.4000	23.76
17	LIRLFTKQG	21	2.4000	23.76
18	FWLLTAITC	333	2.4000	23.76
19	LFTKQGFGH	24	2.3000	22.77
20	LGLATALGG	87	2.3000	22.77
21	VTLAPVLFV	158	2.3000	22.77
22	MRQILIAVA	0	2.2000	21.78
23	VLGLATALG	86	2.0000	19.80
24	IRRSRNLGL	105	1.8000	17.82
25	ILLTPVLIR	15	1.7000	16.83
26	WAGYLGAHL	61	1.7000	16.83
27	YVLITFWQY	201	1.7000	16.83
28	YRNACVTAP	209	1.7000	16.83
29	FRTTGRRMF	302	1.7000	16.83
30	VSILLTPVL	13	1.6500	16.34
31	LGCYNVRDP	219	1.6000	15.84
32	LTFRTTGRR	300	1.5000	14.85

33	YLGAHLAGL	64	1.4000	13.86
34	LLVLGLATA	84	1.4000	13.86
35	VTAAYVLIT	197	1.4000	13.86

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	VLFCVVIVS	166	3.5000	42.17
2	FVLFCVVIV	165	3.4000	40.96
3	IIRFWLLTA	330	2.9000	34.94
4	MRQILIAVA	0	2.8000	33.73
5	FWLLTAITC	333	2.8000	33.73
6	FRNAAGLTP	136	2.2000	26.51
7	ILLTPVLIR	15	2.1000	25.30
8	LFGVLVLQF	128	2.1000	25.30
9	FRMAPFHHH	310	2.0800	25.06
10	VTLAPVLFV	158	2.0000	24.10
11	IRLFTKQGF	22	1.8000	21.69
12	LLVLGLATA	84	1.8000	21.69
13	VAILAGIWA	54	1.7000	20.48
14	LVLQFRNAA	132	1.7000	20.48
15	MFRMAPFHH	309	1.6800	20.24
16	YNVRDPLDL	222	1.6000	19.28
17	LIRLFTKQG	21	1.5000	18.07
18	LGALFVAEI	284	1.5000	18.07
19	MGGVAILAG	51	1.3000	15.66
20	YRNACVTAP	209	1.3000	15.66
21	VVIVSAWSN	170	1.2000	14.46
22	YVLITFWQY	201	1.2000	14.46
23	FRTTGRRMF	302	1.2000	14.46
24	VLGLATALG	86	1.1000	13.25
25	IRRSRNLGL	105	1.1000	13.25
26	VSILLTPVL	13	1.0500	12.65

27	LGLATALGG	87	1.0000	12.05
28	LALIAAATA	230	0.9000	10.84
29	LIAAATAGA	232	0.9000	10.84
30	FLWWNAAPA	244	0.9000	10.84
31	WWNAAPAKI	246	0.6000	7.23
32	LIAVAVAVT	4	0.5000	6.02
33	LFVLFCVVI	164	0.5000	6.02
34	VTAAYVLIT	197	0.5000	6.02
35	IRFWLLTAI	331	0.5000	6.02

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	LVLQFRNAA	132	4.8000	57.14
2	IRLFTKQGF	22	3.9000	46.43
3	MFRMAPFHH	309	3.4800	41.43
4	FVLFCVVIV	165	3.3000	39.29
5	VLFCVVIVS	166	3.2000	38.10
6	IIRFWLLTA	330	3.2000	38.10
7	IKIRRSRNL	103	2.9000	34.52
8	IRFWLLTAI	331	2.7000	32.14
9	VVLGALFVA	282	2.4000	28.57
10	MRQILIAVA	0	2.3000	27.38
11	LLVLGLATA	84	2.1000	25.00
12	LIRLFTKQG	21	2.0000	23.81
13	LGCYNVRDP	219	2.0000	23.81
14	VVLQILTFR	295	2.0000	23.81
15	VTLAPVLFV	158	1.9000	22.62
16	LIAAATAGA	232	1.9000	22.62
17	LGALFVAEI	284	1.8000	21.43
18	ILIAVAVAV	3	1.7000	20.24
19	VLVLQFRNA	131	1.7000	20.24
20	VVIVSAWSN	170	1.7000	20.24

21	LQILTFRTT	297	1.7000	20.24
22	IVSAWSNAV	172	1.6000	19.05
23	LFTKQGFGH	24	1.5800	18.81
24	FRMAPFHHH	310	1.5800	18.81
25	ILLTPVLIR	15	1.5000	17.86
26	VLGLATALG	86	1.4000	16.67
27	LFVLFCVVI	164	1.3000	15.48
28	ITFWQYRNA	204	1.3000	15.48
29	FRTTGRRMF	302	1.3000	15.48
30	LGLNKTAKT	111	1.2000	14.29
31	LQFRNAAGL	134	1.2000	14.29
32	IRRSRNLGL	105	1.1000	13.10
33	VAVAVTVSI	7	0.9000	10.71
34	VSILLTPVL	13	0.9000	10.71
35	VLIRLFTKQ	20	0.9000	10.71

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	VLFCVVIVS	166	4.5000	54.22
2	IIRFWLLTA	330	3.9000	46.99
3	MRQILIAVA	0	3.8000	45.78
4	ILLTPVLIR	15	3.1000	37.35
5	LFGVLVLQF	128	3.1000	37.35
6	VTLAPVLFV	158	3.0000	36.14
7	IRLFTKQGF	22	2.8000	33.73
8	LLVLGLATA	84	2.8000	33.73
9	VAILAGIWA	54	2.7000	32.53
10	LVLQFRNAA	132	2.7000	32.53
11	MFRMAPFHH	309	2.6800	32.29
12	LIRLFTKQG	21	2.5000	30.12
13	LGALFVAEI	284	2.5000	30.12
14	FVLFCVVIV	165	2.4000	28.92

15	MGGVAILAG	51	2.3000	27.71
16	VVIVSAWSN	170	2.2000	26.51
17	VLGLATALG	86	2.1000	25.30
18	IRRSRNLGL	105	2.1000	25.30
19	VSILLTPVL	13	2.0500	24.70
20	LGLATALGG	87	2.0000	24.10
21	LALIAAATA	230	1.9000	22.89
22	LIAAATAGA	232	1.9000	22.89
23	FWLLTAITC	333	1.8000	21.69
24	LIAVAVAVT	4	1.5000	18.07
25	LFVLFCVVI	164	1.5000	18.07
26	VTAAYVLIT	197	1.5000	18.07
27	IRFWLLTAI	331	1.5000	18.07
28	LGGVIAGLS	264	1.4000	16.87
29	LFCVVIVSA	167	1.3000	15.66
30	ILIAVAVAV	3	1.2000	14.46
31	FRNAAGLTP	136	1.2000	14.46
32	VVLGALFVA	282	1.2000	14.46
33	LGLNKTAKT	111	1.1000	13.25
34	VREIATVTL	152	1.1000	13.25
35	MAMVTAAYV	194	1.1000	13.25

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	VLFCVVIVS	166	4.5000	54.22
2	IIRFWLLTA	330	3.9000	46.99
3	MRQILIAVA	0	3.8000	45.78
4	ILLTPVLIR	15	3.1000	37.35
5	LFGVLVLQF	128	3.1000	37.35
6	VTLAPVLFV	158	3.0000	36.14
7	IRLFTKQGF	22	2.8000	33.73
8	LLVLGLATA	84	2.8000	33.73

9	VAILAGIWA	54	2.7000	32.53
10	LVLQFRNAA	132	2.7000	32.53
11	MFRMAPFHH	309	2.6800	32.29
12	LIRLFTKQG	21	2.5000	30.12
13	LGALFVAEI	284	2.5000	30.12
14	FVLFCVVIV	165	2.4000	28.92
15	MGGVAILAG	51	2.3000	27.71
16	VVIVSAWSN	170	2.2000	26.51
17	VLGLATALG	86	2.1000	25.30
18	IRRSRNLGL	105	2.1000	25.30
19	VSILLTPVL	13	2.0500	24.70
20	LGLATALGG	87	2.0000	24.10
21	LALIAAATA	230	1.9000	22.89
22	LIAAATAGA	232	1.9000	22.89
23	FWLLTAITC	333	1.8000	21.69
24	LIAVAVAVT	4	1.5000	18.07
25	LFVLFCVVI	164	1.5000	18.07
26	VTAAYVLIT	197	1.5000	18.07
27	IRFWLLTAI	331	1.5000	18.07
28	LGGVIAGLS	264	1.4000	16.87
29	LFCVVIVSA	167	1.3000	15.66
30	ILIAVAVAV	3	1.2000	14.46
31	FRNAAGLTP	136	1.2000	14.46
32	VVLGALFVA	282	1.2000	14.46
33	LGLNKTAKT	111	1.1000	13.25
34	VREIATVTL	152	1.1000	13.25
35	MAMVTAAYV	194	1.1000	13.25

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	IREDGPPSH	34	4.5800	50.33
2	VVLGALFVA	282	4.3000	47.25

3	VLFCVVIVS	166	4.1000	45.05
4	LVLQFRNAA	132	4.0100	44.07
5	MRQILIAVA	0	3.4000	37.36
6	VLFGVLVLQ	127	3.2000	35.16
7	IFMGDTGSL	254	2.6000	28.57
8	MFRMAPFHH	309	2.5800	28.35
9	LVLGLATAL	85	2.5000	27.47
10	IRLFTKQGF	22	2.4000	26.37
11	VIAGLSVTS	267	2.4000	26.37
12	IRRSRNLGL	105	2.2000	24.18
13	VVLQILTFR	295	2.2000	24.18
14	LALGGVIAG	262	2.1000	23.08
15	ILIAVAVAV	3	2.0000	21.98
16	FMGDTGSLA	255	1.9700	21.65
17	LIAAATAGA	232	1.9000	20.88
18	FVLFCVVIV	165	1.8000	19.78
19	IRFWLLTAI	331	1.8000	19.78
20	VSILLTPVL	13	1.7000	18.68
21	LLVLGLATA	84	1.7000	18.68
22	VTLAPVLFV	158	1.7000	18.68
23	LFCVVIVSA	167	1.7000	18.68
24	VVIVSAWSN	170	1.6000	17.58
25	VLQILTFRT	296	1.6000	17.58
26	VREIATVTL	152	1.5000	16.48
27	YRNACVTAP	209	1.5000	16.48
28	LALIAAATA	230	1.5000	16.48
29	LGGVIAGLS	264	1.5000	16.48
30	IVSAWSNAV	172	1.4100	15.49
31	ILLTPVLIR	15	1.4000	15.38
32	LFGVLVLQF	128	1.4000	15.38
33	LGALFVAEI	284	1.4000	15.38
34	LGLNKTAKT	111	1.3000	14.29
35	LIKIRRSRN	102	1.2700	13.96

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	FVLFCVVIV	165	4.3000	51.19
2	LVLQFRNAA	132	3.8000	45.24
3	IRLFTKQGF	22	2.9000	34.52
4	FRMAPFHHH	310	2.5800	30.71
5	MFRMAPFHH	309	2.4800	29.52
6	FRTTGRRMF	302	2.3000	27.38
7	VLFCVVIVS	166	2.2000	26.19
8	IIRFWLLTA	330	2.2000	26.19
9	IKIRRSRNL	103	1.9000	22.62
10	YRNACVTAP	209	1.7000	20.24
11	FLWWNAAPA	244	1.7000	20.24
12	IRFWLLTAI	331	1.7000	20.24
13	YNVRDPLDL	222	1.4000	16.67
14	VVLGALFVA	282	1.4000	16.67
15	MRQILIAVA	0	1.3000	15.48
16	LLVLGLATA	84	1.1000	13.10
17	FRNAAGLTP	136	1.1000	13.10
18	LIRLFTKQG	21	1.0000	11.90
19	WQYRNACVT	207	1.0000	11.90
20	LGCYNVRDP	219	1.0000	11.90
21	VVLQILTFR	295	1.0000	11.90
22	VTLAPVLFV	158	0.9000	10.71
23	LIAAATAGA	232	0.9000	10.71
24	LGALFVAEI	284	0.8000	9.52
25	FWLLTAITC	333	0.8000	9.52
26	ILIAVAVAV	3	0.7000	8.33
27	VLVLQFRNA	131	0.7000	8.33
28	VVIVSAWSN	170	0.7000	8.33
29	LQILTFRTT	297	0.7000	8.33
30	IVSAWSNAV	172	0.6000	7.14

31	WWNAAPAKI	246	0.6000	7.14
32	LFTKQGFGH	24	0.5800	6.90
33	ILLTPVLIR	15	0.5000	5.95
34	YVLITFWQY	201	0.5000	5.95
35	FHHHFELVG	315	0.5000	5.95

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	FVLFCVVIV	165	5.3000	60.23
2	IRLFTKQGF	22	4.8000	54.55
3	FRTTGRRMF	302	4.2000	47.73
4	LVLQFRNAA	132	3.8000	43.18
5	IKIRRSRNL	103	2.8600	32.50
6	YRNACVTAP	209	2.7000	30.68
7	VLFCVVIVS	166	2.6000	29.55
8	IRFWLLTAI	331	2.6000	29.55
9	VVLQILTFR	295	2.5000	28.41
10	LIRLFTKQG	21	2.4000	27.27
11	YNVRDPLDL	222	2.3600	26.82
12	IIRFWLLTA	330	2.2000	25.00
13	FRNAAGLTP	136	2.1000	23.86
14	ILLTPVLIR	15	2.0000	22.73
15	LGCYNVRDP	219	2.0000	22.73
16	FRMAPFHHH	310	2.0000	22.73
17	VTLAPVLFV	158	1.9000	21.59
18	MFRMAPFHH	309	1.9000	21.59
19	FHHHFELVG	315	1.9000	21.59
20	VLGLATALG	86	1.8000	20.45
21	YVLITFWQY	201	1.8000	20.45
22	ILIAVAVAV	3	1.7000	19.32
23	FGHQIREDG	30	1.7000	19.32
24	FGVLVLQFR	129	1.7000	19.32

25	WQYRNACVT	207	1.7000	19.32
26	FLWWNAAPA	244	1.7000	19.32
27	WNAAPAKIF	247	1.7000	19.32
28	LGALFVAEI	284	1.7000	19.32
29	LFGVLVLQF	128	1.6000	18.18
30	IVSAWSNAV	172	1.6000	18.18
31	VVIVSAWSN	170	1.5000	17.05
32	WWNAAPAKI	246	1.5000	17.05
33	VVLGALFVA	282	1.4000	15.91
34	LQILTFRTT	297	1.4000	15.91
35	YLGAHLAGL	64	1.3600	15.45

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	LVLQFRNAA	132	4.8000	57.14
2	IRLFTKQGF	22	3.9000	46.43
3	MFRMAPFHH	309	3.4800	41.43
4	FVLFCVVIV	165	3.3000	39.29
5	VLFCVVIVS	166	3.2000	38.10
6	IIRFWLLTA	330	3.2000	38.10
7	IKIRRSRNL	103	2.9000	34.52
8	IRFWLLTAI	331	2.7000	32.14
9	VVLGALFVA	282	2.4000	28.57
10	MRQILIAVA	0	2.3000	27.38
11	LLVLGLATA	84	2.1000	25.00
12	LIRLFTKQG	21	2.0000	23.81
13	LGCYNVRDP	219	2.0000	23.81
14	VVLQILTFR	295	2.0000	23.81
15	VTLAPVLFV	158	1.9000	22.62
16	LIAAATAGA	232	1.9000	22.62
17	LGALFVAEI	284	1.8000	21.43
18	ILIAVAVAV	3	1.7000	20.24

19	VLVLQFRNA	131	1.7000	20.24
20	VVIVSAWSN	170	1.7000	20.24
21	LQILTFRTT	297	1.7000	20.24
22	IVSAWSNAV	172	1.6000	19.05
23	LFTKQGFGH	24	1.5800	18.81
24	FRMAPFHHH	310	1.5800	18.81
25	ILLTPVLIR	15	1.5000	17.86
26	VLGLATALG	86	1.4000	16.67
27	LFVLFCVVI	164	1.3000	15.48
28	ITFWQYRNA	204	1.3000	15.48
29	FRTTGRRMF	302	1.3000	15.48
30	LGLNKTAKT	111	1.2000	14.29
31	LQFRNAAGL	134	1.2000	14.29
32	IRRSRNLGL	105	1.1000	13.10
33	VAVAVTVSI	7	0.9000	10.71
34	VSILLTPVL	13	0.9000	10.71
35	VLIRLFTKQ	20	0.9000	10.71

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	FVLFCVVIV	165	4.4000	50.57
2	LFGVLVLQF	128	4.0000	45.98
3	VLFCVVIVS	166	3.9000	44.83
4	IRLFTKQGF	22	3.7000	42.53
5	ILLTPVLIR	15	3.6000	41.38
6	FRNAAGLTP	136	3.2000	36.78
7	FRTTGRRMF	302	3.1000	35.63
8	VTLAPVLFV	158	3.0000	34.48
9	LIRLFTKQG	21	2.9000	33.33
10	IIRFWLLTA	330	2.9000	33.33
11	MRQILIAVA	0	2.8000	32.18
12	FWLLTAITC	333	2.8000	32.18

13	MGGVAILAG	51	2.7000	31.03
14	YNVRDPLDL	222	2.5600	29.43
15	VLGLATALG	86	2.5000	28.74
16	YVLITFWQY	201	2.5000	28.74
17	LGLATALGG	87	2.4000	27.59
18	LGALFVAEI	284	2.4000	27.59
19	YRNACVTAP	209	2.3000	26.44
20	IRRSRNLGL	105	2.0600	23.68
21	VSILLTPVL	13	2.0100	23.10
22	VVIVSAWSN	170	2.0000	22.99
23	LLVLGLATA	84	1.8000	20.69
24	VAILAGIWA	54	1.7000	19.54
25	FGVLVLQFR	129	1.7000	19.54
26	LVLQFRNAA	132	1.7000	19.54
27	WWNAAPAKI	246	1.5000	17.24
28	WNAAPAKIF	247	1.5000	17.24
29	FRMAPFHHH	310	1.5000	17.24
30	LFVLFCVVI	164	1.4000	16.09
31	IRFWLLTAI	331	1.4000	16.09
32	YLGAHLAGL	64	1.3600	15.63
33	ILIAVAVAV	3	1.2000	13.79
34	LIAVAVAVT	4	1.2000	13.79
35	VNFTDGLDG	180	1.2000	13.79

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	IRLFTKQGF	22	5.8000	65.91
2	LVLQFRNAA	132	4.8000	54.55
3	FVLFCVVIV	165	4.3000	48.86
4	IKIRRSRNL	103	3.8600	43.86
5	VLFCVVIVS	166	3.6000	40.91
6	IRFWLLTAI	331	3.6000	40.91

7	VVLQILTFR	295	3.5000	39.77
8	LIRLFTKQG	21	3.4000	38.64
9	FRTTGRRMF	302	3.2000	36.36
10	IIRFWLLTA	330	3.2000	36.36
11	ILLTPVLIR	15	3.0000	34.09
12	LGCYNVRDP	219	3.0000	34.09
13	VTLAPVLFV	158	2.9000	32.95
14	MFRMAPFHH	309	2.9000	32.95
15	VLGLATALG	86	2.8000	31.82
16	ILIAVAVAV	3	2.7000	30.68
17	LGALFVAEI	284	2.7000	30.68
18	LFGVLVLQF	128	2.6000	29.55
19	IVSAWSNAV	172	2.6000	29.55
20	VVIVSAWSN	170	2.5000	28.41
21	VVLGALFVA	282	2.4000	27.27
22	LQILTFRTT	297	2.4000	27.27
23	MRQILIAVA	0	2.3000	26.14
24	LGLATALGG	87	2.3000	26.14
25	LTPVLIRLF	17	2.2000	25.00
26	LFVLFCVVI	164	2.2000	25.00
27	ILTFRTTGR	299	2.2000	25.00
28	LQFRNAAGL	134	2.1600	24.55
29	LLVLGLATA	84	2.1000	23.86
30	IRRSRNLGL	105	2.0600	23.41
31	LGLNKTAKT	111	1.9000	21.59
32	LIAAATAGA	232	1.9000	21.59
33	VSILLTPVL	13	1.8600	21.14
34	VAVAVTVSI	7	1.8000	20.45
35	LLTAITCGL	335	1.7600	20.00

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	FVLFCVVIV	165	5.3000	60.23
2	IRLFTKQGF	22	4.8000	54.55
3	FRTTGRRMF	302	4.2000	47.73
4	LVLQFRNAA	132	3.8000	43.18
5	IKIRRSRNL	103	2.8600	32.50
6	YRNACVTAP	209	2.7000	30.68
7	VLFCVVIVS	166	2.6000	29.55
8	IRFWLLTAI	331	2.6000	29.55
9	VVLQILTFR	295	2.5000	28.41
10	LIRLFTKQG	21	2.4000	27.27
11	YNVRDPLDL	222	2.3600	26.82
12	IIRFWLLTA	330	2.2000	25.00
13	FRNAAGLTP	136	2.1000	23.86
14	ILLTPVLIR	15	2.0000	22.73
15	LGCYNVRDP	219	2.0000	22.73
16	FRMAPFHHH	310	2.0000	22.73
17	VTLAPVLFV	158	1.9000	21.59
18	MFRMAPFHH	309	1.9000	21.59
19	FHHHFELVG	315	1.9000	21.59
20	VLGLATALG	86	1.8000	20.45
21	YVLITFWQY	201	1.8000	20.45
22	ILIAVAVAV	3	1.7000	19.32
23	FGHQIREDG	30	1.7000	19.32
24	FGVLVLQFR	129	1.7000	19.32
25	WQYRNACVT	207	1.7000	19.32
26	FLWWNAAPA	244	1.7000	19.32
27	WNAAPAKIF	247	1.7000	19.32
28	LGALFVAEI	284	1.7000	19.32
29	LFGVLVLQF	128	1.6000	18.18
30	IVSAWSNAV	172	1.6000	18.18
31	VVIVSAWSN	170	1.5000	17.05
32	WWNAAPAKI	246	1.5000	17.05
33	VVLGALFVA	282	1.4000	15.91
34	LQILTFRTT	297	1.4000	15.91

35	YLGAHLAGL	64	1.3600	15.45

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	IRLFTKQGF	22	4.8000	53.33
2	LVLQFRNAA	132	4.8000	53.33
3	MFRMAPFHH	309	4.7000	52.22
4	IKIRRSRNL	103	3.9000	43.33
5	VVIVSAWSN	170	3.7000	41.11
6	FVLFCVVIV	165	3.6000	40.00
7	LIRLFTKQG	21	3.3000	36.67
8	VLFCVVIVS	166	3.2000	35.56
9	IIRFWLLTA	330	3.2000	35.56
10	IRFWLLTAI	331	2.9000	32.22
11	LFTKQGFGH	24	2.8000	31.11
12	FRMAPFHHH	310	2.8000	31.11
13	VLGLATALG	86	2.7000	30.00
14	LQILTFRTT	297	2.6000	28.89
15	MAPFHHHFE	312	2.6000	28.89
16	LGCYNVRDP	219	2.4000	26.67
17	VVLGALFVA	282	2.4000	26.67
18	MRQILIAVA	0	2.3000	25.56
19	LGLATALGG	87	2.2000	24.44
20	LQFRNAAGL	134	2.2000	24.44
21	VTLAPVLFV	158	2.2000	24.44
22	FRTTGRRMF	302	2.2000	24.44
23	LLVLGLATA	84	2.1000	23.33
24	IRRSRNLGL	105	2.1000	23.33
25	LGLNKTAKT	111	2.1000	23.33
26	ILIAVAVAV	3	2.0000	22.22
27	LITFWQYRN	203	2.0000	22.22
28	LGALFVAEI	284	2.0000	22.22

29	VVLQILTFR	295	2.0000	22.22
30	VSILLTPVL	13	1.9000	21.11
31	IVSAWSNAV	172	1.9000	21.11
32	LIAAATAGA	232	1.9000	21.11
33	LLTAITCGL	335	1.8000	20.00
34	VLIRLFTKQ	20	1.7000	18.89
35	VLFGVLVLQ	127	1.7000	18.89

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	FVLFCVVIV	165	4.4000	50.57
2	LFGVLVLQF	128	4.0000	45.98
3	VLFCVVIVS	166	3.9000	44.83
4	IRLFTKQGF	22	3.7000	42.53
5	ILLTPVLIR	15	3.6000	41.38
6	FRNAAGLTP	136	3.2000	36.78
7	FRTTGRRMF	302	3.1000	35.63
8	VTLAPVLFV	158	3.0000	34.48
9	LIRLFTKQG	21	2.9000	33.33
10	IIRFWLLTA	330	2.9000	33.33
11	MRQILIAVA	0	2.8000	32.18
12	FWLLTAITC	333	2.8000	32.18
13	MGGVAILAG	51	2.7000	31.03
14	YNVRDPLDL	222	2.5600	29.43
15	VLGLATALG	86	2.5000	28.74
16	YVLITFWQY	201	2.5000	28.74
17	LGLATALGG	87	2.4000	27.59
18	LGALFVAEI	284	2.4000	27.59
19	YRNACVTAP	209	2.3000	26.44
20	IRRSRNLGL	105	2.0600	23.68
21	VSILLTPVL	13	2.0100	23.10
22	VVIVSAWSN	170	2.0000	22.99

23	LLVLGLATA	84	1.8000	20.69
24	VAILAGIWA	54	1.7000	19.54
25	FGVLVLQFR	129	1.7000	19.54
26	LVLQFRNAA	132	1.7000	19.54
27	WWNAAPAKI	246	1.5000	17.24
28	WNAAPAKIF	247	1.5000	17.24
29	FRMAPFHHH	310	1.5000	17.24
30	LFVLFCVVI	164	1.4000	16.09
31	IRFWLLTAI	331	1.4000	16.09
32	YLGAHLAGL	64	1.3600	15.63
33	ILIAVAVAV	3	1.2000	13.79
34	LIAVAVAVT	4	1.2000	13.79
35	VNFTDGLDG	180	1.2000	13.79

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	FVLFCVVIV	165	2.9000	42.65
2	MRQILIAVA	0	2.8000	41.18
3	VLFCVVIVS	166	1.9000	27.94
4	LLVLGLATA	84	1.8000	26.47
5	IRLFTKQGF	22	1.7000	25.00
6	LGALFVAEI	284	1.5000	22.06
7	LVLQFRNAA	132	1.4000	20.59
8	FRMAPFHHH	310	1.3800	20.29
9	FWLLTAITC	333	1.2000	17.65
10	MFRMAPFHH	309	1.1800	17.35
11	VLGLATALG	86	1.1000	16.18
12	IIRFWLLTA	330	1.1000	16.18
13	FRTTGRRMF	302	1.0000	14.71
14	LIRLFTKQG	21	0.9000	13.24
15	LALIAAATA	230	0.9000	13.24
16	LIAAATAGA	232	0.9000	13.24

17	FLWWNAAPA	244	0.9000	13.24
18	WWNAAPAKI	246	0.6000	8.82
19	LIAVAVAVT	4	0.5000	7.35
20	YLGAHLAGL	64	0.4000	5.88
21	FRNAAGLTP	136	0.4000	5.88
22	VVIVSAWSN	170	0.4000	5.88
23	YVLITFWQY	201	0.4000	5.88
24	ILLTPVLIR	15	0.3000	4.41
25	LFGVLVLQF	128	0.3000	4.41
26	LGGVIAGLS	264	0.3000	4.41
27	VTLAPVLFV	158	0.2000	2.94
28	YRNACVTAP	209	0.2000	2.94
29	VAILAGIWA	54	0.1000	1.47
30	LGLNKTAKT	111	0.1000	1.47
31	FGVLVLQFR	129	0.1000	1.47
32	MAMVTAAYV	194	0.1000	1.47
33	WQYRNACVT	207	0.1000	1.47

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	VLFCVVIVS	166	4.5000	54.22
2	IIRFWLLTA	330	3.9000	46.99
3	MRQILIAVA	0	3.8000	45.78
4	ILLTPVLIR	15	3.1000	37.35
5	LFGVLVLQF	128	3.1000	37.35
6	VTLAPVLFV	158	3.0000	36.14
7	IRLFTKQGF	22	2.8000	33.73
8	LLVLGLATA	84	2.8000	33.73
9	VAILAGIWA	54	2.7000	32.53
10	LVLQFRNAA	132	2.7000	32.53
11	MFRMAPFHH	309	2.6800	32.29
12	LIRLFTKQG	21	2.5000	30.12

13	LGALFVAEI	284	2.5000	30.12
14	FVLFCVVIV	165	2.4000	28.92
15	MGGVAILAG	51	2.3000	27.71
16	VVIVSAWSN	170	2.2000	26.51
17	VLGLATALG	86	2.1000	25.30
18	IRRSRNLGL	105	2.1000	25.30
19	VSILLTPVL	13	2.0500	24.70
20	LGLATALGG	87	2.0000	24.10
21	LALIAAATA	230	1.9000	22.89
22	LIAAATAGA	232	1.9000	22.89
23	FWLLTAITC	333	1.8000	21.69
24	LIAVAVAVT	4	1.5000	18.07
25	LFVLFCVVI	164	1.5000	18.07
26	VTAAYVLIT	197	1.5000	18.07
27	IRFWLLTAI	331	1.5000	18.07
28	LGGVIAGLS	264	1.4000	16.87
29	LFCVVIVSA	167	1.3000	15.66
30	ILIAVAVAV	3	1.2000	14.46
31	FRNAAGLTP	136	1.2000	14.46
32	VVLGALFVA	282	1.2000	14.46
33	LGLNKTAKT	111	1.1000	13.25
34	VREIATVTL	152	1.1000	13.25
35	MAMVTAAYV	194	1.1000	13.25

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	FVLFCVVIV	165	3.7000	41.57
2	VLFCVVIVS	166	3.5000	39.33
3	FRMAPFHHH	310	3.3000	37.08
4	VVIVSAWSN	170	3.2000	35.96
5	LFGVLVLQF	128	3.0000	33.71
6	MFRMAPFHH	309	2.9000	32.58

7	IIRFWLLTA	330	2.9000	32.58
8	MRQILIAVA	0	2.8000	31.46
9	LIRLFTKQG	21	2.8000	31.46
10	FWLLTAITC	333	2.8000	31.46
11	IRLFTKQGF	22	2.7000	30.34
12	MGGVAILAG	51	2.6000	29.21
13	FRNAAGLTP	136	2.6000	29.21
14	YNVRDPLDL	222	2.6000	29.21
15	VLGLATALG	86	2.4000	26.97
16	LGLATALGG	87	2.3000	25.84
17	VTLAPVLFV	158	2.3000	25.84
18	YVLITFWQY	201	2.3000	25.84
19	ILLTPVLIR	15	2.1000	23.60
20	IRRSRNLGL	105	2.1000	23.60
21	FRTTGRRMF	302	2.1000	23.60
22	VSILLTPVL	13	2.0500	23.03
23	LLVLGLATA	84	1.8000	20.22
24	VAILAGIWA	54	1.7000	19.10
25	LVLQFRNAA	132	1.7000	19.10
26	YRNACVTAP	209	1.7000	19.10
27	LGALFVAEI	284	1.7000	19.10
28	LIAVAVAVT	4	1.4000	15.73
29	YLGAHLAGL	64	1.4000	15.73
30	VTAAYVLIT	197	1.4000	15.73
31	LIKIRRSRN	102	1.3000	14.61
32	VREIATVTL	152	1.1000	12.36
33	VNFTDGLDG	180	1.1000	12.36
34	WLLTAITCG	334	1.1000	12.36
35	LGLNKTAKT	111	1.0000	11.24

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	LVLQFRNAA	132	4.8000	57.14
2	IRLFTKQGF	22	3.9000	46.43
3	MFRMAPFHH	309	3.4800	41.43
4	FVLFCVVIV	165	3.3000	39.29
5	VLFCVVIVS	166	3.2000	38.10
6	IIRFWLLTA	330	3.2000	38.10
7	IKIRRSRNL	103	2.9000	34.52
8	IRFWLLTAI	331	2.7000	32.14
9	VVLGALFVA	282	2.4000	28.57
10	MRQILIAVA	0	2.3000	27.38
11	LLVLGLATA	84	2.1000	25.00
12	LIRLFTKQG	21	2.0000	23.81
13	LGCYNVRDP	219	2.0000	23.81
14	VVLQILTFR	295	2.0000	23.81
15	VTLAPVLFV	158	1.9000	22.62
16	LIAAATAGA	232	1.9000	22.62
17	LGALFVAEI	284	1.8000	21.43
18	ILIAVAVAV	3	1.7000	20.24
19	VLVLQFRNA	131	1.7000	20.24
20	VVIVSAWSN	170	1.7000	20.24
21	LQILTFRTT	297	1.7000	20.24
22	IVSAWSNAV	172	1.6000	19.05
23	LFTKQGFGH	24	1.5800	18.81
24	FRMAPFHHH	310	1.5800	18.81
25	ILLTPVLIR	15	1.5000	17.86
26	VLGLATALG	86	1.4000	16.67
27	LFVLFCVVI	164	1.3000	15.48
28	ITFWQYRNA	204	1.3000	15.48
29	FRTTGRRMF	302	1.3000	15.48
30	LGLNKTAKT	111	1.2000	14.29
31	LQFRNAAGL	134	1.2000	14.29
32	IRRSRNLGL	105	1.1000	13.10
33	VAVAVTVSI	7	0.9000	10.71
34	VSILLTPVL	13	0.9000	10.71

35	VLIRLFTKQ	20	0.9000	10.71

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	FVLFCVVIV	165	4.3000	51.19
2	LVLQFRNAA	132	3.8000	45.24
3	IRLFTKQGF	22	2.9000	34.52
4	FRMAPFHHH	310	2.5800	30.71
5	MFRMAPFHH	309	2.4800	29.52
6	FRTTGRRMF	302	2.3000	27.38
7	VLFCVVIVS	166	2.2000	26.19
8	IIRFWLLTA	330	2.2000	26.19
9	IKIRRSRNL	103	1.9000	22.62
10	YRNACVTAP	209	1.7000	20.24
11	FLWWNAAPA	244	1.7000	20.24
12	IRFWLLTAI	331	1.7000	20.24
13	YNVRDPLDL	222	1.4000	16.67
14	VVLGALFVA	282	1.4000	16.67
15	MRQILIAVA	0	1.3000	15.48
16	LLVLGLATA	84	1.1000	13.10
17	FRNAAGLTP	136	1.1000	13.10
18	LIRLFTKQG	21	1.0000	11.90
19	WQYRNACVT	207	1.0000	11.90
20	LGCYNVRDP	219	1.0000	11.90
21	VVLQILTFR	295	1.0000	11.90
22	VTLAPVLFV	158	0.9000	10.71
23	LIAAATAGA	232	0.9000	10.71
24	LGALFVAEI	284	0.8000	9.52
25	FWLLTAITC	333	0.8000	9.52
26	ILIAVAVAV	3	0.7000	8.33
27	VLVLQFRNA	131	0.7000	8.33
28	VVIVSAWSN	170	0.7000	8.33

29	LQILTFRTT	297	0.7000	8.33
30	IVSAWSNAV	172	0.6000	7.14
31	WWNAAPAKI	246	0.6000	7.14
32	LFTKQGFGH	24	0.5800	6.90
33	ILLTPVLIR	15	0.5000	5.95
34	YVLITFWQY	201	0.5000	5.95
35	FHHHFELVG	315	0.5000	5.95

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	IRLFTKQGF	22	5.8000	65.91
2	LVLQFRNAA	132	4.8000	54.55
3	FVLFCVVIV	165	4.3000	48.86
4	IKIRRSRNL	103	3.8600	43.86
5	VLFCVVIVS	166	3.6000	40.91
6	IRFWLLTAI	331	3.6000	40.91
7	VVLQILTFR	295	3.5000	39.77
8	LIRLFTKQG	21	3.4000	38.64
9	FRTTGRRMF	302	3.2000	36.36
10	IIRFWLLTA	330	3.2000	36.36
11	ILLTPVLIR	15	3.0000	34.09
12	LGCYNVRDP	219	3.0000	34.09
13	VTLAPVLFV	158	2.9000	32.95
14	MFRMAPFHH	309	2.9000	32.95
15	VLGLATALG	86	2.8000	31.82
16	ILIAVAVAV	3	2.7000	30.68
17	LGALFVAEI	284	2.7000	30.68
18	LFGVLVLQF	128	2.6000	29.55
19	IVSAWSNAV	172	2.6000	29.55
20	VVIVSAWSN	170	2.5000	28.41
21	VVLGALFVA	282	2.4000	27.27
22	LQILTFRTT	297	2.4000	27.27

23	MRQILIAVA	0	2.3000	26.14
24	LGLATALGG	87	2.3000	26.14
25	LTPVLIRLF	17	2.2000	25.00
26	LFVLFCVVI	164	2.2000	25.00
27	ILTFRTTGR	299	2.2000	25.00
28	LQFRNAAGL	134	2.1600	24.55
29	LLVLGLATA	84	2.1000	23.86
30	IRRSRNLGL	105	2.0600	23.41
31	LGLNKTAKT	111	1.9000	21.59
32	LIAAATAGA	232	1.9000	21.59
33	VSILLTPVL	13	1.8600	21.14
34	VAVAVTVSI	7	1.8000	20.45
35	LLTAITCGL	335	1.7600	20.00

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	IRLFTKQGF	22	5.8000	65.91
2	LVLQFRNAA	132	4.8000	54.55
3	FVLFCVVIV	165	4.3000	48.86
4	IKIRRSRNL	103	3.8600	43.86
5	VLFCVVIVS	166	3.6000	40.91
6	IRFWLLTAI	331	3.6000	40.91
7	VVLQILTFR	295	3.5000	39.77
8	LIRLFTKQG	21	3.4000	38.64
9	FRTTGRRMF	302	3.2000	36.36
10	IIRFWLLTA	330	3.2000	36.36
11	ILLTPVLIR	15	3.0000	34.09
12	LGCYNVRDP	219	3.0000	34.09
13	VTLAPVLFV	158	2.9000	32.95
14	MFRMAPFHH	309	2.9000	32.95
15	VLGLATALG	86	2.8000	31.82
16	ILIAVAVAV	3	2.7000	30.68

17	LGALFVAEI	284	2.7000	30.68
18	LFGVLVLQF	128	2.6000	29.55
19	IVSAWSNAV	172	2.6000	29.55
20	VVIVSAWSN	170	2.5000	28.41
21	VVLGALFVA	282	2.4000	27.27
22	LQILTFRTT	297	2.4000	27.27
23	MRQILIAVA	0	2.3000	26.14
24	LGLATALGG	87	2.3000	26.14
25	LTPVLIRLF	17	2.2000	25.00
26	LFVLFCVVI	164	2.2000	25.00
27	ILTFRTTGR	299	2.2000	25.00
28	LQFRNAAGL	134	2.1600	24.55
29	LLVLGLATA	84	2.1000	23.86
30	IRRSRNLGL	105	2.0600	23.41
31	LGLNKTAKT	111	1.9000	21.59
32	LIAAATAGA	232	1.9000	21.59
33	VSILLTPVL	13	1.8600	21.14
34	VAVAVTVSI	7	1.8000	20.45
35	LLTAITCGL	335	1.7600	20.00

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	IIRFWLLTA	330	6.3000	64.29
2	IRRSRNLGL	105	5.7000	58.16
3	FVLFCVVIV	165	4.8000	48.98
4	VVLGALFVA	282	4.7000	47.96
5	IRLFTKQGF	22	4.6000	46.94
6	IRFWLLTAI	331	4.5000	45.92
7	VIIRFWLLT	329	4.1000	41.84
8	VAILAGIWA	54	4.0000	40.82
9	LVLQFRNAA	132	4.0000	40.82
10	IVSAWSNAV	172	3.9000	39.80

11	LVLGLATAL	85	3.8000	38.78
12	VALFYGEWL	345	3.7000	37.76
13	MVTAAYVLI	196	3.5000	35.71
14	IKIRRSRNL	103	3.4000	34.69
15	VLQFRNAAG	133	3.3000	33.67
16	VVIVSAWSN	170	3.2000	32.65
17	ILIAVAVAV	3	3.1000	31.63
18	LFYGEWLAA	347	3.1000	31.63
19	FRNAAGLTP	136	3.0000	30.61
20	LLTPVLIRL	16	2.9000	29.59
21	VTLAPVLFV	158	2.9000	29.59
22	VNFTDGLDG	180	2.9000	29.59
23	MRQILIAVA	0	2.8500	29.08
24	VAVTVSILL	9	2.8000	28.57
25	IGASGLLVL	79	2.8000	28.57
26	LFVLFCVVI	164	2.8000	28.57
27	VLQILTFRT	296	2.7600	28.16
28	WAGYLGAHL	61	2.7000	27.55
29	LQFRNAAGL	134	2.7000	27.55
30	VLFCVVIVS	166	2.7000	27.55
31	YNVRDPLDL	222	2.7000	27.55
32	IFMGDTGSL	254	2.6600	27.14
33	LGLATALGG	87	2.6000	26.53
34	VRDPLDLAL	224	2.6000	26.53
35	MFRMAPFHH	309	2.6000	26.53

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	FVLFCVVIV	165	5.8000	59.18
2	IIRFWLLTA	330	5.3000	54.08
3	IRRSRNLGL	105	4.7000	47.96
4	FRNAAGLTP	136	4.0000	40.82

5	WAGYLGAHL	61	3.7000	37.76
6	YNVRDPLDL	222	3.7000	37.76
7	VVLGALFVA	282	3.7000	37.76
8	IRLFTKQGF	22	3.6000	36.73
9	IRFWLLTAI	331	3.5000	35.71
10	FWQYRNACV	206	3.4000	34.69
11	YVLITFWQY	201	3.1000	31.63
12	VIIRFWLLT	329	3.1000	31.63
13	VAILAGIWA	54	3.0000	30.61
14	LVLQFRNAA	132	3.0000	30.61
15	IVSAWSNAV	172	2.9000	29.59
16	FWLLTAITC	333	2.9000	29.59
17	LVLGLATAL	85	2.8000	28.57
18	FRMAPFHHH	310	2.8000	28.57
19	VALFYGEWL	345	2.7000	27.55
20	MVTAAYVLI	196	2.5000	25.51
21	IKIRRSRNL	103	2.4000	24.49
22	VLQFRNAAG	133	2.3000	23.47
23	YVREIATVT	151	2.2000	22.45
24	VVIVSAWSN	170	2.2000	22.45
25	FHHHFELVG	315	2.2000	22.45
26	ILIAVAVAV	3	2.1000	21.43
27	LFYGEWLAA	347	2.1000	21.43
28	FVAEITSVV	288	2.0600	21.02
29	WQYRNACVT	207	2.0000	20.41
30	FRTTGRRMF	302	2.0000	20.41
31	LLTPVLIRL	16	1.9000	19.39
32	YLGAHLAGL	64	1.9000	19.39
33	VTLAPVLFV	158	1.9000	19.39
34	VNFTDGLDG	180	1.9000	19.39
35	MRQILIAVA	0	1.8500	18.88

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

	3.1	9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IIRFWLLTA	330	6.3000	64.29
2	IRRSRNLGL	105	5.7000	58.16
3	FVLFCVVIV	165	4.8000	48.98
4	VVLGALFVA	282	4.7000	47.96
5	IRLFTKQGF	22	4.6000	46.94
6	IRFWLLTAI	331	4.5000	45.92
7	VIIRFWLLT	329	4.1000	41.84
8	VAILAGIWA	54	4.0000	40.82
9	LVLQFRNAA	132	4.0000	40.82
10	IVSAWSNAV	172	3.9000	39.80
11	LVLGLATAL	85	3.8000	38.78
12	VALFYGEWL	345	3.7000	37.76
13	MVTAAYVLI	196	3.5000	35.71
14	IKIRRSRNL	103	3.4000	34.69
15	VLQFRNAAG	133	3.3000	33.67
16	VVIVSAWSN	170	3.2000	32.65
17	ILIAVAVAV	3	3.1000	31.63
18	LFYGEWLAA	347	3.1000	31.63
19	FRNAAGLTP	136	3.0000	30.61
20	LLTPVLIRL	16	2.9000	29.59
21	VTLAPVLFV	158	2.9000	29.59
22	VNFTDGLDG	180	2.9000	29.59
23	MRQILIAVA	0	2.8500	29.08
24	VAVTVSILL	9	2.8000	28.57
25	IGASGLLVL	79	2.8000	28.57
26	LFVLFCVVI	164	2.8000	28.57
27	VLQILTFRT	296	2.7600	28.16
28	WAGYLGAHL	61	2.7000	27.55
29	LQFRNAAGL	134	2.7000	27.55
30	VLFCVVIVS	166	2.7000	27.55
31	YNVRDPLDL	222	2.7000	27.55
32	IFMGDTGSL	254	2.6600	27.14

33	LGLATALGG	87	2.6000	26.53
34	VRDPLDLAL	224	2.6000	26.53
35	MFRMAPFHH	309	2.6000	26.53

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	MFRMAPFHH	309	4.9000	50.00
2	YVLITFWQY	201	4.4000	44.90
3	VVIVSAWSN	170	4.1000	41.84
4	FRMAPFHHH	310	4.1000	41.84
5	FGVLVLQFR	129	3.8000	38.78
6	FRTTGRRMF	302	3.7000	37.76
7	VLITFWQYR	202	3.3000	33.67
8	VVLQILTFR	295	3.2000	32.65
9	ILLTPVLIR	15	3.1000	31.63
10	VGFIDDLIK	96	2.9000	29.59
11	WNAAPAKIF	247	2.9000	29.59
12	FWLLTAITC	333	2.7000	27.55
13	LAGIWAGYL	57	2.4000	24.49
14	FRNAAGLTP	136	2.2000	22.45
15	LVLGLATAL	85	2.1000	21.43
16	LGGVIAGLS	264	2.1000	21.43
17	IRLFTKQGF	22	2.0000	20.41
18	VAILAGIWA	54	2.0000	20.41
19	IKIRRSRNL	103	2.0000	20.41
20	IRRSRNLGL	105	2.0000	20.41
21	ILAVVLGAL	279	2.0000	20.41
22	LIRLFTKQG	21	1.9000	19.39
23	VAVTVSILL	9	1.8000	18.37
24	LFVLFCVVI	164	1.8000	18.37
25	WWNAAPAKI	246	1.8000	18.37
26	VLQILTFRT	296	1.8000	18.37

27	YNVRDPLDL	222	1.7000	17.35
28	LQILTFRTT	297	1.7000	17.35
29	VGQITSAVL	120	1.6000	16.33
30	LFGVLVLQF	128	1.6000	16.33
31	YVREIATVT	151	1.6000	16.33
32	VNFTDGLDG	180	1.6000	16.33
33	WLLTAITCG	334	1.6000	16.33
34	LTPVLIRLF	17	1.5000	15.31
35	YLGAHLAGL	64	1.5000	15.31

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	MFRMAPFHH	309	4.9000	50.00
2	YVLITFWQY	201	4.4000	44.90
3	VVIVSAWSN	170	4.1000	41.84
4	FRMAPFHHH	310	4.1000	41.84
5	FGVLVLQFR	129	3.8000	38.78
6	FRTTGRRMF	302	3.7000	37.76
7	VLITFWQYR	202	3.3000	33.67
8	VVLQILTFR	295	3.2000	32.65
9	ILLTPVLIR	15	3.1000	31.63
10	VGFIDDLIK	96	2.9000	29.59
11	WNAAPAKIF	247	2.9000	29.59
12	FWLLTAITC	333	2.7000	27.55
13	LAGIWAGYL	57	2.4000	24.49
14	FRNAAGLTP	136	2.2000	22.45
15	LVLGLATAL	85	2.1000	21.43
16	LGGVIAGLS	264	2.1000	21.43
17	IRLFTKQGF	22	2.0000	20.41
18	VAILAGIWA	54	2.0000	20.41
19	IKIRRSRNL	103	2.0000	20.41
20	IRRSRNLGL	105	2.0000	20.41

21	ILAVVLGAL	279	2.0000	20.41
22	LIRLFTKQG	21	1.9000	19.39
23	VAVTVSILL	9	1.8000	18.37
24	LFVLFCVVI	164	1.8000	18.37
25	WWNAAPAKI	246	1.8000	18.37
26	VLQILTFRT	296	1.8000	18.37
27	YNVRDPLDL	222	1.7000	17.35
28	LQILTFRTT	297	1.7000	17.35
29	VGQITSAVL	120	1.6000	16.33
30	LFGVLVLQF	128	1.6000	16.33
31	YVREIATVT	151	1.6000	16.33
32	VNFTDGLDG	180	1.6000	16.33
33	WLLTAITCG	334	1.6000	16.33
34	LTPVLIRLF	17	1.5000	15.31
35	YLGAHLAGL	64	1.5000	15.31