MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Feb 19 23:46:32 2010
Length of input sequence	263 amino acids
Number of nanomers from input sequence	255
Number of nanomers with obligatory P1 anchor residue	78
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	26

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YRRGLAQLL	108	2.9000	48.33
2	IRLILGNAV	129	2.8000	46.67
3	LILGNAVDV	131	1.4000	23.33
4	LQHLIAPDS	140	1.0700	17.83
5	VVLEIGSGS	78	0.9000	15.00
6	MHAQPGVGL	6	0.8000	13.33
7	WERLWPELG	45	0.1000	1.67
8	LVPSGVLHA	183	-0.1000	0

9	FGRDAPVVL	72	-0.2000	0
10	LQPATMALI	171	-0.6000	0
11	LRPDTPVAS	14	-0.7000	0
12	LLPISVVRP	221	-0.7000	0
13	WFGRDAPVV	71	-0.7300	0
14	LEIGSGSGT	80	-0.8000	0
15	WKKHGCSER	249	-0.8000	0
16	LGLLALPQS	52	-0.8300	0
17	VRPATKYER	227	-1.0000	0
18	LGGGAVIEL	239	-1.0000	0
19	MVHHGQMHA	0	-1.1100	0
20	LWPELGLLA	48	-1.2000	0
21	LAMAKAEPH	91	-1.3000	0
22	IGSGSGTST	82	-1.4100	0
23	VIAVDVYRR	102	-1.5500	0
24	LPISVVRPA	222	-1.7100	0
25	MALIADRLV	176	-1.8100	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	IRLILGNAV	129	3.8000	63.33
2	LILGNAVDV	131	2.4000	40.00
3	LQHLIAPDS	140	2.0700	34.50
4	VVLEIGSGS	78	1.9000	31.67
5	YRRGLAQLL	108	1.9000	31.67
6	MHAQPGVGL	6	1.8000	30.00
7	LVPSGVLHA	183	0.9000	15.00
8	LQPATMALI	171	0.4000	6.67
9	LRPDTPVAS	14	0.3000	5.00
10	LLPISVVRP	221	0.3000	5.00
11	LEIGSGSGT	80	0.2000	3.33
12	LGLLALPQS	52	0.1700	2.83

13	MVHHGQMHA	0	-0.1100	0
14	LWPELGLLA	48	-0.2000	0
15	FGRDAPVVL	72	-0.2000	0
16	LAMAKAEPH	91	-0.3000	0
17	IGSGSGTST	82	-0.4100	0
18	VIAVDVYRR	102	-0.5500	0
19	LPISVVRPA	222	-0.7100	0
20	MALIADRLV	176	-0.8100	0
21	VRVFFPDPW	152	-0.8200	0
22	WERLWPELG	45	-0.9000	0
23	LAQLLCAID	112	-1.0000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRPDTPVAS	14	6.6000	69.47
2	LIADRLVPS	178	4.9000	51.58
3	LVPSGVLHA	183	4.5000	47.37
4	VRPATKYER	227	4.2500	44.74
5	VGSDGINIR	122	4.1100	43.26
6	LGLLALPQS	52	3.5000	36.84
7	IRLILGNAV	129	3.2100	33.79
8	LQHLIAPDS	140	3.2000	33.68
9	FGRDAPVVL	72	3.1600	33.26
10	MVHHGQMHA	0	3.1000	32.63
11	LCAIDKVGS	116	3.1000	32.63
12	LILGNAVDV	131	3.1000	32.63
13	IAPDSLCGV	144	3.1000	32.63
14	LLPISVVRP	221	2.9000	30.53
15	LGGGAVIEL	239	2.7600	29.05
16	VIAVDVYRR	102	2.7500	28.95
17	VVLEIGSGS	78	2.5700	27.05
18	IRSRRSGIS	30	2.5000	26.32

19	VRVDPDTEL	213	2.4600	25.89
20	LVRVDPDTE	212	2.4000	25.26
21	YRRGLAQLL	108	2.2600	23.79
22	LPISVVRPA	222	2.0000	21.05
23	ILGNAVDVL	132	1.9600	20.63
24	IELLWKKHG	245	1.9000	20.00
25	LLQPATMAL	170	1.8600	19.58
26	FFPDPWPKA	155	1.7000	17.89

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	LRPDTPVAS	14	5.2000	57.14
2	LIADRLVPS	178	3.5000	38.46
3	LVPSGVLHA	183	3.5000	38.46
4	FGRDAPVVL	72	3.2000	35.16
5	FFPDPWPKA	155	2.7000	29.67
6	YRRGLAQLL	108	2.3000	25.27
7	MVHHGQMHA	0	2.1000	23.08
8	LGLLALPQS	52	2.1000	23.08
9	LQHLIAPDS	140	1.8000	19.78
10	VRPATKYER	227	1.7500	19.23
11	LCAIDKVGS	116	1.7000	18.68
12	VGSDGINIR	122	1.6100	17.69
13	IRLILGNAV	129	1.2100	13.30
14	VVLEIGSGS	78	1.1700	12.86
15	IRSRRSGIS	30	1.1000	12.09
16	LILGNAVDV	131	1.1000	12.09
17	IAPDSLCGV	144	1.1000	12.09
18	LPISVVRPA	222	1.0000	10.99
19	LLPISVVRP	221	0.9000	9.89
20	LGGGAVIEL	239	0.8000	8.79
21	VRVDPDTEL	213	0.5000	5.49

22	LAMAKAEPH	91	0.2800	3.08
23	VIAVDVYRR	102	0.2500	2.75
24	WKKHGCSER	249	0.1700	1.87
25	WERLWPELG	45	0.1000	1.10

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	LRPDTPVAS	14	6.0800	69.09
2	LVPSGVLHA	183	5.0000	56.82
3	LIADRLVPS	178	4.3800	49.77
4	VGSDGINIR	122	3.3000	37.50
5	IRLILGNAV	129	2.9000	32.95
6	MVHHGQMHA	0	2.8000	31.82
7	LCAIDKVGS	116	2.5800	29.32
8	IAPDSLCGV	144	2.1000	23.86
9	FGRDAPVVL	72	2.0800	23.64
10	LILGNAVDV	131	1.9800	22.50
11	VVLEIGSGS	78	1.9000	21.59
12	LLPISVVRP	221	1.7800	20.23
13	LGLLALPQS	52	1.7000	19.32
14	LPISVVRPA	222	1.7000	19.32
15	LAMAKAEPH	91	1.6800	19.09
16	VRPATKYER	227	1.6000	18.18
17	VRVDPDTEL	213	1.5000	17.05
18	LGGGAVIEL	239	1.4800	16.82
19	YRRGLAQLL	108	1.4000	15.91
20	LQHLIAPDS	140	1.4000	15.91
21	INIRLILGN	127	1.3000	14.77
22	ILGNAVDVL	132	1.3000	14.77
23	LVRVDPDTE	212	1.3000	14.77
24	VHHGQMHAQ	1	1.1000	12.50
25	IELLWKKHG	245	1.1000	12.50

26	VRVFFPDPW	152	0.9000	10.23

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	LRPDTPVAS	14	6.0800	69.09
2	LVPSGVLHA	183	5.0000	56.82
3	LIADRLVPS	178	4.3800	49.77
4	VGSDGINIR	122	3.3000	37.50
5	IRLILGNAV	129	2.9000	32.95
6	MVHHGQMHA	0	2.8000	31.82
7	LCAIDKVGS	116	2.5800	29.32
8	IAPDSLCGV	144	2.1000	23.86
9	FGRDAPVVL	72	2.0800	23.64
10	LILGNAVDV	131	1.9800	22.50
11	VVLEIGSGS	78	1.9000	21.59
12	LLPISVVRP	221	1.7800	20.23
13	LGLLALPQS	52	1.7000	19.32
14	LPISVVRPA	222	1.7000	19.32
15	LAMAKAEPH	91	1.6800	19.09
16	VRPATKYER	227	1.6000	18.18
17	VRVDPDTEL	213	1.5000	17.05
18	LGGGAVIEL	239	1.4800	16.82
19	YRRGLAQLL	108	1.4000	15.91
20	LQHLIAPDS	140	1.4000	15.91
21	INIRLILGN	127	1.3000	14.77
22	ILGNAVDVL	132	1.3000	14.77
23	LVRVDPDTE	212	1.3000	14.77
24	VHHGQMHAQ	1	1.1000	12.50
25	IELLWKKHG	245	1.1000	12.50
26	VRVFFPDPW	152	0.9000	10.23

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	LRPDTPVAS	14	6.0800	69.09
2	LVPSGVLHA	183	5.0000	56.82
3	LIADRLVPS	178	4.3800	49.77
4	VGSDGINIR	122	3.3000	37.50
5	IRLILGNAV	129	2.9000	32.95
6	MVHHGQMHA	0	2.8000	31.82
7	LCAIDKVGS	116	2.5800	29.32
8	IAPDSLCGV	144	2.1000	23.86
9	FGRDAPVVL	72	2.0800	23.64
10	LILGNAVDV	131	1.9800	22.50
11	VVLEIGSGS	78	1.9000	21.59
12	LLPISVVRP	221	1.7800	20.23
13	LGLLALPQS	52	1.7000	19.32
14	LPISVVRPA	222	1.7000	19.32
15	LAMAKAEPH	91	1.6800	19.09
16	VRPATKYER	227	1.6000	18.18
17	VRVDPDTEL	213	1.5000	17.05
18	LGGGAVIEL	239	1.4800	16.82
19	YRRGLAQLL	108	1.4000	15.91
20	LQHLIAPDS	140	1.4000	15.91
21	INIRLILGN	127	1.3000	14.77
22	ILGNAVDVL	132	1.3000	14.77
23	LVRVDPDTE	212	1.3000	14.77
24	VHHGQMHAQ	1	1.1000	12.50
25	IELLWKKHG	245	1.1000	12.50
26	VRVFFPDPW	152	0.9000	10.23

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	LRPDTPVAS	14	5.6000	58.95
2	FGRDAPVVL	72	4.1600	43.79
3	LIADRLVPS	178	3.9000	41.05
4	LVPSGVLHA	183	3.5000	36.84
5	YRRGLAQLL	108	3.2600	34.32
6	VRPATKYER	227	3.2500	34.21
7	VGSDGINIR	122	3.1100	32.74
8	FFPDPWPKA	155	2.7000	28.42
9	LGLLALPQS	52	2.5000	26.32
10	IRLILGNAV	129	2.2100	23.26
11	LQHLIAPDS	140	2.2000	23.16
12	MVHHGQMHA	0	2.1000	22.11
13	LCAIDKVGS	116	2.1000	22.11
14	LILGNAVDV	131	2.1000	22.11
15	IAPDSLCGV	144	2.1000	22.11
16	LLPISVVRP	221	1.9000	20.00
17	LGGGAVIEL	239	1.7600	18.53
18	VIAVDVYRR	102	1.7500	18.42
19	WKKHGCSER	249	1.6700	17.58
20	VVLEIGSGS	78	1.5700	16.53
21	IRSRRSGIS	30	1.5000	15.79
22	WERLWPELG	45	1.5000	15.79
23	VRVDPDTEL	213	1.4600	15.37
24	LVRVDPDTE	212	1.4000	14.74
25	WFGRDAPVV	71	1.0000	10.53
26	LPISVVRPA	222	1.0000	10.53

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	LRPDTPVAS	14	6.0800	69.09
2	LVPSGVLHA	183	5.0000	56.82

3	LIADRLVPS	178	4.3800	49.77
4	VGSDGINIR	122	3.3000	37.50
5	IRLILGNAV	129	2.9000	32.95
6	MVHHGQMHA	0	2.8000	31.82
7	LCAIDKVGS	116	2.5800	29.32
8	IAPDSLCGV	144	2.1000	23.86
9	FGRDAPVVL	72	2.0800	23.64
10	LILGNAVDV	131	1.9800	22.50
11	VVLEIGSGS	78	1.9000	21.59
12	LLPISVVRP	221	1.7800	20.23
13	LGLLALPQS	52	1.7000	19.32
14	LPISVVRPA	222	1.7000	19.32
15	LAMAKAEPH	91	1.6800	19.09
16	VRPATKYER	227	1.6000	18.18
17	VRVDPDTEL	213	1.5000	17.05
18	LGGGAVIEL	239	1.4800	16.82
19	YRRGLAQLL	108	1.4000	15.91
20	LQHLIAPDS	140	1.4000	15.91
21	INIRLILGN	127	1.3000	14.77
22	ILGNAVDVL	132	1.3000	14.77
23	LVRVDPDTE	212	1.3000	14.77
24	VHHGQMHAQ	1	1.1000	12.50
25	IELLWKKHG	245	1.1000	12.50
26	VRVFFPDPW	152	0.9000	10.23

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	LVPSGVLHA	183	3.8000	44.19
2	LRPDTPVAS	14	3.6800	42.79
3	VVLEIGSGS	78	2.6000	30.23
4	MVHHGQMHA	0	1.7000	19.77
5	FGRDAPVVL	72	1.6800	19.53

6	IRLILGNAV	129	1.4000	16.28
7	LQHLIAPDS	140	1.2000	13.95
8	LIADRLVPS	178	1.1800	13.72
9	WKKHGCSER	249	1.0000	11.63
10	VRVDPDTEL	213	0.9000	10.47
11	WERLWPELG	45	0.8000	9.30
12	FFPDPWPKA	155	0.8000	9.30
13	LLPISVVRP	221	0.7800	9.07
14	ILGNAVDVL	132	0.7000	8.14
15	LAMAKAEPH	91	0.6800	7.91
16	VGSDGINIR	122	0.6000	6.98
17	VLHAATDHP	188	0.5000	5.81
18	LPISVVRPA	222	0.5000	5.81
19	YRRGLAQLL	108	0.3000	3.49
20	LGLLALPQS	52	0.2000	2.33
21	LLQPATMAL	170	0.1000	1.16
22	VVRPATKYE	226	0.1000	1.16
23	IRSRRSGIS	30	-0.1000	0
24	LWPELGLLA	48	-0.1000	0
25	VRVFFPDPW	152	-0.5000	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	LVPSGVLHA	183	3.3000	34.38
2	IRSRRSGIS	30	3.0000	31.25
3	MVHHGQMHA	0	2.8000	29.17
4	INIRLILGN	127	2.8000	29.17
5	LPISVVRPA	222	2.6000	27.08
6	VVRPATKYE	226	1.7000	17.71
7	IRLILGNAV	129	1.6800	17.50
8	VFFPDPWPK	154	1.4000	14.58
9	LLQPATMAL	170	1.4000	14.58

10	YRRGLAQLL	108	1.3000	13.54
11	VIAVDVYRR	102	1.2000	12.50
12	LLPISVVRP	221	1.1800	12.29
13	LRPDTPVAS	14	1.1000	11.46
14	MALIADRLV	176	0.9800	10.21
15	LILGNAVDV	131	0.9000	9.38
16	VGLRPDTPV	12	0.8000	8.33
17	LIAPDSLCG	143	0.8000	8.33
18	LGNAVDVLQ	133	0.6000	6.25
19	VYRRGLAQL	107	0.5000	5.21
20	LQHLIAPDS	140	0.5000	5.21
21	VLQHLIAPD	139	0.4000	4.17
22	LGGGAVIEL	239	0.4000	4.17
23	LAMAKAEPH	91	0.2800	2.92
24	VHHGQMHAQ	1	0.2000	2.08
25	LQPATMALI	171	0.1000	1.04

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	LVPSGVLHA	183	2.9000	32.95
2	IRLILGNAV	129	2.8000	31.82
3	LQHLIAPDS	140	2.1000	23.86
4	LRPDTPVAS	14	2.0000	22.73
5	LLPISVVRP	221	1.9000	21.59
6	VVLEIGSGS	78	1.7000	19.32
7	VRVFFPDPW	152	1.5000	17.05
8	VIAVDVYRR	102	1.3000	14.77
9	LLQPATMAL	170	1.3000	14.77
10	LGLLALPQS	52	1.1000	12.50
11	LAMAKAEPH	91	0.7800	8.86
12	VLHAATDHP	188	0.6000	6.82
13	MVHHGQMHA	0	0.5000	5.68

14	IRSRRSGIS	30	0.5000	5.68
15	LVRVDPDTE	212	0.4000	4.55
16	ISVVRPATK	224	0.4000	4.55
17	VVRPATKYE	226	0.4000	4.55
18	LGNAVDVLQ	133	0.3000	3.41
19	LPISVVRPA	222	0.3000	3.41
20	LCGVRVFFP	149	0.2500	2.84
21	LIAPDSLCG	143	0.1000	1.14
22	LQPATMALI	171	0.1000	1.14
23	VRVDPDTEL	213	-0.1000	0
24	VLEIGSGSG	79	-0.3000	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	LVRVDPDTE	212	2.4000	25.53
2	VVRPATKYE	226	2.4000	25.53
3	IRLILGNAV	129	2.1000	22.34
4	LVPSGVLHA	183	1.9000	20.21
5	WERLWPELG	45	1.4000	14.89
6	VRVFFPDPW	152	1.4000	14.89
7	LLQPATMAL	170	1.3000	13.83
8	LLPISVVRP	221	1.3000	13.83
9	LQHLIAPDS	140	1.1000	11.70
10	LRPDTPVAS	14	1.0000	10.64
11	LAMAKAEPH	91	1.0000	10.64
12	LAQLLCAID	112	1.0000	10.64
13	VVLEIGSGS	78	0.7000	7.45
14	LIAPDSLCG	143	0.4000	4.26
15	VIAVDVYRR	102	0.3000	3.19
16	YRRGLAQLL	108	0.3000	3.19
17	LGLLALPQS	52	0.1000	1.06
18	LGNAVDVLQ	133	0.1000	1.06

19	VLQHLIAPD	139	-0.1000	0
20	VRVDPDTEL	213	-0.1000	0
21	INIRLILGN	127	-0.3000	0
22	LCGVRVFFP	149	-0.3500	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	LVPSGVLHA	183	1.9000	21.59
2	IRLILGNAV	129	1.8000	20.45
3	LQHLIAPDS	140	1.1000	12.50
4	LRPDTPVAS	14	1.0000	11.36
5	LLPISVVRP	221	0.9000	10.23
6	VVLEIGSGS	78	0.7000	7.95
7	VRVFFPDPW	152	0.5000	5.68
8	VIAVDVYRR	102	0.3000	3.41
9	LLQPATMAL	170	0.3000	3.41
10	WERLWPELG	45	0.1000	1.14
11	LGLLALPQS	52	0.1000	1.14
12	LAMAKAEPH	91	-0.2200	0
13	VLHAATDHP	188	-0.4000	0
14	WKKHGCSER	249	-0.4000	0
15	MVHHGQMHA	0	-0.5000	0
16	IRSRRSGIS	30	-0.5000	0
17	LVRVDPDTE	212	-0.6000	0
18	ISVVRPATK	224	-0.6000	0
19	VVRPATKYE	226	-0.6000	0
20	YRRGLAQLL	108	-0.7000	0
21	LGNAVDVLQ	133	-0.7000	0
22	LPISVVRPA	222	-0.7000	0
23	LCGVRVFFP	149	-0.7500	0
24	LIAPDSLCG	143	-0.9000	0
25	LQPATMALI	171	-0.9000	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	LVRVDPDTE	212	3.4000	36.17
2	VVRPATKYE	226	3.4000	36.17
3	IRLILGNAV	129	3.1000	32.98
4	LVPSGVLHA	183	2.9000	30.85
5	VRVFFPDPW	152	2.4000	25.53
6	LLQPATMAL	170	2.3000	24.47
7	LLPISVVRP	221	2.3000	24.47
8	LQHLIAPDS	140	2.1000	22.34
9	LRPDTPVAS	14	2.0000	21.28
10	LAMAKAEPH	91	2.0000	21.28
11	LAQLLCAID	112	2.0000	21.28
12	VVLEIGSGS	78	1.7000	18.09
13	LIAPDSLCG	143	1.4000	14.89
14	VIAVDVYRR	102	1.3000	13.83
15	LGLLALPQS	52	1.1000	11.70
16	LGNAVDVLQ	133	1.1000	11.70
17	VLEIGSGSG	79	1.0000	10.64
18	VLHAATDHP	188	1.0000	10.64
19	VLQHLIAPD	139	0.9000	9.57
20	VRVDPDTEL	213	0.9000	9.57
21	INIRLILGN	127	0.7000	7.45
22	LCGVRVFFP	149	0.6500	6.91
23	MAKAEPHVD	93	0.6000	6.38
24	MVHHGQMHA	0	0.5000	5.32
25	IRSRRSGIS	30	0.5000	5.32
26	WERLWPELG	45	0.4000	4.26

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

	2.3	

Rank	Sequence	At Position	Score	% of Highest Score
1	LRPDTPVAS	14	4.0800	45.33
2	LVPSGVLHA	183	3.8000	42.22
3	VVLEIGSGS	78	3.0000	33.33
4	FGRDAPVVL	72	2.6400	29.33
5	WKKHGCSER	249	2.5000	27.78
6	IRLILGNAV	129	2.4000	26.67
7	WERLWPELG	45	2.2000	24.44
8	VGSDGINIR	122	2.1000	23.33
9	VRVDPDTEL	213	1.8600	20.67
10	LLPISVVRP	221	1.7800	19.78
11	MVHHGQMHA	0	1.7000	18.89
12	ILGNAVDVL	132	1.6600	18.44
13	LQHLIAPDS	140	1.6000	17.78
14	LIADRLVPS	178	1.5800	17.56
15	VLHAATDHP	188	1.5000	16.67
16	VVRPATKYE	226	1.5000	16.67
17	YRRGLAQLL	108	1.2600	14.00
18	LLQPATMAL	170	1.0600	11.78
19	FFPDPWPKA	155	0.8000	8.89
20	LGLLALPQS	52	0.6000	6.67
21	LIAPDSLCG	143	0.6000	6.67
22	LPISVVRPA	222	0.5000	5.56
23	VLQHLIAPD	139	0.4000	4.44
24	IRSRRSGIS	30	0.3000	3.33
25	YAEHIAAAG	198	0.3000	3.33
26	LVRVDPDTE	212	0.3000	3.33

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	LVPSGVLHA	183	2.9000	32.95
2	IRLILGNAV	129	2.8000	31.82
3	LQHLIAPDS	140	2.1000	23.86
4	LRPDTPVAS	14	2.0000	22.73
5	LLPISVVRP	221	1.9000	21.59
6	VVLEIGSGS	78	1.7000	19.32
7	VRVFFPDPW	152	1.5000	17.05
8	VIAVDVYRR	102	1.3000	14.77
9	LLQPATMAL	170	1.3000	14.77
10	LGLLALPQS	52	1.1000	12.50
11	LAMAKAEPH	91	0.7800	8.86
12	VLHAATDHP	188	0.6000	6.82
13	MVHHGQMHA	0	0.5000	5.68
14	IRSRRSGIS	30	0.5000	5.68
15	LVRVDPDTE	212	0.4000	4.55
16	ISVVRPATK	224	0.4000	4.55
17	VVRPATKYE	226	0.4000	4.55
18	LGNAVDVLQ	133	0.3000	3.41
19	LPISVVRPA	222	0.3000	3.41
20	LCGVRVFFP	149	0.2500	2.84
21	LIAPDSLCG	143	0.1000	1.14
22	LQPATMALI	171	0.1000	1.14
23	VRVDPDTEL	213	-0.1000	0
24	VLEIGSGSG	79	-0.3000	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	LVPSGVLHA	183	3.8000	44.19
2	LRPDTPVAS	14	3.6800	42.79
3	VVLEIGSGS	78	2.6000	30.23
4	MVHHGQMHA	0	1.7000	19.77
5	FGRDAPVVL	72	1.6800	19.53

6	IRLILGNAV	129	1.4000	16.28
7	LQHLIAPDS	140	1.2000	13.95
8	LIADRLVPS	178	1.1800	13.72
9	WKKHGCSER	249	1.0000	11.63
10	VRVDPDTEL	213	0.9000	10.47
11	WERLWPELG	45	0.8000	9.30
12	FFPDPWPKA	155	0.8000	9.30
13	LLPISVVRP	221	0.7800	9.07
14	ILGNAVDVL	132	0.7000	8.14
15	LAMAKAEPH	91	0.6800	7.91
16	VGSDGINIR	122	0.6000	6.98
17	VLHAATDHP	188	0.5000	5.81
18	LPISVVRPA	222	0.5000	5.81
19	YRRGLAQLL	108	0.3000	3.49
20	LGLLALPQS	52	0.2000	2.33
21	LLQPATMAL	170	0.1000	1.16
22	VVRPATKYE	226	0.1000	1.16
23	IRSRRSGIS	30	-0.1000	0
24	LWPELGLLA	48	-0.1000	0
25	VRVFFPDPW	152	-0.5000	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	YRRGLAQLL	108	6.3000	54.31
2	IRLILGNAV	129	6.1000	52.59
3	LVPSGVLHA	183	5.2000	44.83
4	LGGGAVIEL	239	4.5000	38.79
5	FGRDAPVVL	72	4.1000	35.34
6	LLQPATMAL	170	3.9200	33.79
7	LILGNAVDV	131	3.6000	31.03
8	LQPATMALI	171	3.1000	26.72
9	MHAQPGVGL	6	2.7000	23.28

10	LLPISVVRP	221	2.5000	21.55
11	LPISVVRPA	222	2.3000	19.83
12	WPELGLLAL	49	2.2000	18.97
13	MVHHGQMHA	0	2.1000	18.10
14	VIAVDVYRR	102	2.0000	17.24
15	VYRRGLAQL	107	2.0000	17.24
16	VRVDPDTEL	213	1.9000	16.38
17	WFGRDAPVV	71	1.7000	14.66
18	LCGVRVFFP	149	1.7000	14.66
19	INIRLILGN	127	1.4000	12.07
20	IDKVGSDGI	119	1.3000	11.21
21	ILGNAVDVL	132	1.3000	11.21
22	MALIADRLV	176	1.3000	11.21
23	VRPATKYER	227	1.3000	11.21
24	LAMAKAEPH	91	1.1000	9.48
25	LIAPDSLCG	143	1.1000	9.48
26	VRVFFPDPW	152	0.9000	7.76

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	YRRGLAQLL	108	6.3000	54.31
2	IRLILGNAV	129	6.1000	52.59
3	LVPSGVLHA	183	5.2000	44.83
4	LGGGAVIEL	239	4.5000	38.79
5	FGRDAPVVL	72	4.1000	35.34
6	LLQPATMAL	170	3.9200	33.79
7	LILGNAVDV	131	3.6000	31.03
8	LQPATMALI	171	3.1000	26.72
9	MHAQPGVGL	6	2.7000	23.28
10	LLPISVVRP	221	2.5000	21.55
11	LPISVVRPA	222	2.3000	19.83
12	WPELGLLAL	49	2.2000	18.97

13	MVHHGQMHA	0	2.1000	18.10
14	VIAVDVYRR	102	2.0000	17.24
15	VYRRGLAQL	107	2.0000	17.24
16	VRVDPDTEL	213	1.9000	16.38
17	WFGRDAPVV	71	1.7000	14.66
18	LCGVRVFFP	149	1.7000	14.66
19	INIRLILGN	127	1.4000	12.07
20	IDKVGSDGI	119	1.3000	11.21
21	ILGNAVDVL	132	1.3000	11.21
22	MALIADRLV	176	1.3000	11.21
23	VRPATKYER	227	1.3000	11.21
24	LAMAKAEPH	91	1.1000	9.48
25	LIAPDSLCG	143	1.1000	9.48
26	VRVFFPDPW	152	0.9000	7.76

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	INIRLILGN	127	4.6000	53.49
2	IRSRRSGIS	30	3.8000	44.19
3	VYRRGLAQL	107	3.1000	36.05
4	YERKAQLGG	233	2.8000	32.56
5	LLWKKHGCS	247	2.4000	27.91
6	VVRPATKYE	226	2.1000	24.42
7	LWKKHGCSE	248	1.8000	20.93
8	WFGRDAPVV	71	1.7000	19.77
9	IELLWKKHG	245	1.6000	18.60
10	LVRVDPDTE	212	1.5000	17.44
11	LVPSGVLHA	183	1.3000	15.12
12	LGLLALPQS	52	0.9000	10.47
13	VDVYRRGLA	105	0.9000	10.47
14	YRRGLAQLL	108	0.7000	8.14
15	LAQLLCAID	112	0.7000	8.14

16	VLQHLIAPD	139	0.7000	8.14
17	VRPATKYER	227	0.7000	8.14
18	LRPDTPVAS	14	0.6000	6.98
19	LQHLIAPDS	140	0.6000	6.98
20	IADRLVPSG	179	0.3000	3.49
21	LCAIDKVGS	116	0.2000	2.33
22	VRVFFPDPW	152	0.2000	2.33
23	IRLILGNAV	129	0.1000	1.16
24	WERLWPELG	45	-0.1000	0
25	VVLEIGSGS	78	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRSRRSGIS	30	3.8000	47.50
2	INIRLILGN	127	2.6000	32.50
3	LLWKKHGCS	247	2.4000	30.00
4	VYRRGLAQL	107	2.1000	26.25
5	YERKAQLGG	233	1.5000	18.75
6	WFGRDAPVV	71	1.4000	17.50
7	LVPSGVLHA	183	1.3000	16.25
8	LGLLALPQS	52	0.9000	11.25
9	VDVYRRGLA	105	0.9000	11.25
10	VRPATKYER	227	0.7000	8.75
11	LRPDTPVAS	14	0.6000	7.50
12	LQHLIAPDS	140	0.6000	7.50
13	IELLWKKHG	245	0.3000	3.75
14	LCAIDKVGS	116	0.2000	2.50
15	VVLEIGSGS	78	-0.2000	0
16	IRLILGNAV	129	-0.2000	0
17	MVHHGQMHA	0	-0.3000	0
18	YRRGLAQLL	108	-0.3000	0
19	ISVVRPATK	224	-0.3000	0

20	LPISVVRPA	222	-0.4000	0
21	VIAVDVYRR	102	-0.5000	0
22	LLPISVVRP	221	-0.6000	0
23	VRVFFPDPW	152	-0.7000	0
24	LQPATMALI	171	-0.7000	0
25	VVRPATKYE	226	-0.9000	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	IRSRRSGIS	30	4.8000	60.00
2	INIRLILGN	127	3.6000	45.00
3	LLWKKHGCS	247	3.4000	42.50
4	VYRRGLAQL	107	3.1000	38.75
5	LVPSGVLHA	183	2.3000	28.75
6	LGLLALPQS	52	1.9000	23.75
7	VDVYRRGLA	105	1.9000	23.75
8	VRPATKYER	227	1.7000	21.25
9	LRPDTPVAS	14	1.6000	20.00
10	LQHLIAPDS	140	1.6000	20.00
11	IELLWKKHG	245	1.3000	16.25
12	LCAIDKVGS	116	1.2000	15.00
13	VVLEIGSGS	78	0.8000	10.00
14	IRLILGNAV	129	0.8000	10.00
15	MVHHGQMHA	0	0.7000	8.75
16	ISVVRPATK	224	0.7000	8.75
17	LPISVVRPA	222	0.6000	7.50
18	VIAVDVYRR	102	0.5000	6.25
19	YERKAQLGG	233	0.5000	6.25
20	WFGRDAPVV	71	0.4000	5.00
21	LLPISVVRP	221	0.4000	5.00
22	VRVFFPDPW	152	0.3000	3.75
23	LQPATMALI	171	0.3000	3.75

24	VVRPATKYE	226	0.1000	1.25

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	INIRLILGN	127	5.6000	65.12
2	IRSRRSGIS	30	4.8000	55.81
3	VYRRGLAQL	107	4.1000	47.67
4	LLWKKHGCS	247	3.4000	39.53
5	VVRPATKYE	226	3.1000	36.05
6	LWKKHGCSE	248	2.8000	32.56
7	IELLWKKHG	245	2.6000	30.23
8	LVRVDPDTE	212	2.5000	29.07
9	LVPSGVLHA	183	2.3000	26.74
10	LGLLALPQS	52	1.9000	22.09
11	VDVYRRGLA	105	1.9000	22.09
12	YERKAQLGG	233	1.8000	20.93
13	LAQLLCAID	112	1.7000	19.77
14	VLQHLIAPD	139	1.7000	19.77
15	VRPATKYER	227	1.7000	19.77
16	LRPDTPVAS	14	1.6000	18.60
17	LQHLIAPDS	140	1.6000	18.60
18	IADRLVPSG	179	1.3000	15.12
19	LCAIDKVGS	116	1.2000	13.95
20	VRVFFPDPW	152	1.2000	13.95
21	IRLILGNAV	129	1.1000	12.79
22	VVLEIGSGS	78	0.8000	9.30
23	LLPISVVRP	221	0.8000	9.30
24	MVHHGQMHA	0	0.7000	8.14
25	WFGRDAPVV	71	0.7000	8.14
26	MAKAEPHVD	93	0.6000	6.98

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	INIRLILGN	127	3.2000	36.78
2	IRSRRSGIS	30	3.1000	35.63
3	VYRRGLAQL	107	2.1000	24.14
4	YERKAQLGG	233	2.1000	24.14
5	LVPSGVLHA	183	1.9000	21.84
6	IRLILGNAV	129	1.8000	20.69
7	LLWKKHGCS	247	1.7000	19.54
8	LRPDTPVAS	14	1.6000	18.39
9	WFGRDAPVV	71	1.6000	18.39
10	VVLEIGSGS	78	1.6000	18.39
11	VRPATKYER	227	1.6000	18.39
12	LCAIDKVGS	116	1.2000	13.79
13	LGLLALPQS	52	1.1000	12.64
14	LQHLIAPDS	140	0.8000	9.20
15	MVHHGQMHA	0	0.7000	8.05
16	YRRGLAQLL	108	0.7000	8.05
17	VRVFFPDPW	152	0.5000	5.75
18	VIAVDVYRR	102	0.4000	4.60
19	LLPISVVRP	221	0.4000	4.60
20	WERLWPELG	45	0.3000	3.45
21	VDVYRRGLA	105	0.2000	2.30
22	VGLRPDTPV	12	0.1000	1.15
23	LLALPQSPR	54	-0.1000	0
24	LIADRLVPS	178	-0.1000	0
25	IELLWKKHG	245	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score

1	INIRLILGN	127	6.4000	63.37
2	YERKAQLGG	233	4.6000	45.54
3	IRSRRSGIS	30	3.9000	38.61
4	VYRRGLAQL	107	3.1000	30.69
5	LVPSGVLHA	183	3.1000	30.69
6	WFGRDAPVV	71	2.8500	28.22
7	VVRPATKYE	226	2.7000	26.73
8	LLWKKHGCS	247	2.5000	24.75
9	IELLWKKHG	245	2.2000	21.78
10	LGLLALPQS	52	2.0500	20.30
11	LWKKHGCSE	248	1.8000	17.82
12	LQHLIAPDS	140	1.7500	17.33
13	IADRLVPSG	179	1.4500	14.36
14	VRPATKYER	227	1.4000	13.86
15	MVHHGQMHA	0	1.3000	12.87
16	LVRVDPDTE	212	1.2000	11.88
17	LRPDTPVAS	14	1.1000	10.89
18	LLQPATMAL	170	1.1000	10.89
19	WERLWPELG	45	1.0000	9.90
20	VDVYRRGLA	105	1.0000	9.90
21	YRRGLAQLL	108	0.8000	7.92
22	LIAPDSLCG	143	0.8000	7.92
23	WPELGLLAL	49	0.7000	6.93
24	LAQLLCAID	112	0.7000	6.93
25	LCAIDKVGS	116	0.7000	6.93
26	VLQHLIAPD	139	0.7000	6.93

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	LVPSGVLHA	183	3.4000	40.96
2	LGLLALPQS	52	2.4500	29.52
3	LQHLIAPDS	140	2.1500	25.90

4	MVHHGQMHA	0	1.7000	20.48
5	INIRLILGN	127	1.4000	16.87
6	VRPATKYER	227	1.4000	16.87
7	LCAIDKVGS	116	1.3000	15.66
8	IELLWKKHG	245	1.3000	15.66
9	IRSRRSGIS	30	0.9000	10.84
10	IRLILGNAV	129	0.7000	8.43
11	VDVLQHLIA	137	0.7000	8.43
12	LLPISVVRP	221	0.5000	6.02
13	YERKAQLGG	233	0.5000	6.02
14	LRPDTPVAS	14	0.4000	4.82
15	VIAVDVYRR	102	0.3000	3.61
16	WERLWPELG	45	0.1000	1.20
17	WPELGLLAL	49	0.1000	1.20
18	LPISVVRPA	222	0.1000	1.20
19	ISVVRPATK	224	-0.2000	0
20	LLWKKHGCS	247	-0.3000	0
21	WFGRDAPVV	71	-0.4500	0
22	LLQPATMAL	170	-0.6000	0
23	LQPATMALI	171	-0.7000	0
24	LAMAKAEPH	91	-0.8200	0
25	VVLEIGSGS	78	-0.9000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MVHHGQMHA	0	3.5000	41.67
2	LVPSGVLHA	183	3.4000	40.48
3	LPISVVRPA	222	2.8000	33.33
4	VRPATKYER	227	2.6000	30.95
5	LGLLALPQS	52	2.3000	27.38
6	LRPDTPVAS	14	2.2000	26.19
7	INIRLILGN	127	2.2000	26.19

8	LQHLIAPDS	140	2.0000	23.81
9	IELLWKKHG	245	1.8000	21.43
10	IRSRRSGIS	30	1.7000	20.24
11	VLQHLIAPD	139	1.5000	17.86
12	VRVFFPDPW	152	1.5000	17.86
13	LCAIDKVGS	116	1.3000	15.48
14	IRLILGNAV	129	1.3000	15.48
15	VVLEIGSGS	78	1.1000	13.10
16	VYRRGLAQL	107	1.0000	11.90
17	LLWKKHGCS	247	0.9000	10.71
18	VFFPDPWPK	154	0.7000	8.33
19	LIADRLVPS	178	0.5000	5.95
20	LLPISVVRP	221	0.5000	5.95
21	LAMAKAEPH	91	0.4800	5.71
22	VVRPATKYE	226	0.4000	4.76
23	LQPATMALI	171	0.3000	3.57
24	VIAVDVYRR	102	0.2000	2.38

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVPSGVLHA	183	4.4000	53.01
2	LGLLALPQS	52	3.4500	41.57
3	LQHLIAPDS	140	3.1500	37.95
4	MVHHGQMHA	0	2.7000	32.53
5	INIRLILGN	127	2.4000	28.92
6	VRPATKYER	227	2.4000	28.92
7	LCAIDKVGS	116	2.3000	27.71
8	IELLWKKHG	245	2.3000	27.71
9	IRSRRSGIS	30	1.9000	22.89
10	IRLILGNAV	129	1.7000	20.48
11	VDVLQHLIA	137	1.7000	20.48
12	LLPISVVRP	221	1.5000	18.07

13	LRPDTPVAS	14	1.4000	16.87
14	VIAVDVYRR	102	1.3000	15.66
15	LPISVVRPA	222	1.1000	13.25
16	ISVVRPATK	224	0.8000	9.64
17	LLWKKHGCS	247	0.7000	8.43
18	LLQPATMAL	170	0.4000	4.82
19	LQPATMALI	171	0.3000	3.61
20	LAMAKAEPH	91	0.1800	2.17
21	VVLEIGSGS	78	0.1000	1.20
22	VYRRGLAQL	107	0.1000	1.20
23	LCGVRVFFP	149	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	LVPSGVLHA	183	4.4000	53.01
2	LGLLALPQS	52	3.4500	41.57
3	LQHLIAPDS	140	3.1500	37.95
4	MVHHGQMHA	0	2.7000	32.53
5	INIRLILGN	127	2.4000	28.92
6	VRPATKYER	227	2.4000	28.92
7	LCAIDKVGS	116	2.3000	27.71
8	IELLWKKHG	245	2.3000	27.71
9	IRSRRSGIS	30	1.9000	22.89
10	IRLILGNAV	129	1.7000	20.48
11	VDVLQHLIA	137	1.7000	20.48
12	LLPISVVRP	221	1.5000	18.07
13	LRPDTPVAS	14	1.4000	16.87
14	VIAVDVYRR	102	1.3000	15.66
15	LPISVVRPA	222	1.1000	13.25
16	ISVVRPATK	224	0.8000	9.64
17	LLWKKHGCS	247	0.7000	8.43
18	LLQPATMAL	170	0.4000	4.82

19	LQPATMALI	171	0.3000	3.61
20	LAMAKAEPH	91	0.1800	2.17
21	VVLEIGSGS	78	0.1000	1.20
22	VYRRGLAQL	107	0.1000	1.20
23	LCGVRVFFP	149	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	LRPDTPVAS	14	6.2000	68.13
2	LIADRLVPS	178	4.5000	49.45
3	LVPSGVLHA	183	4.5000	49.45
4	MVHHGQMHA	0	3.1000	34.07
5	LGLLALPQS	52	3.1000	34.07
6	LQHLIAPDS	140	2.8000	30.77
7	VRPATKYER	227	2.7500	30.22
8	LCAIDKVGS	116	2.7000	29.67
9	VGSDGINIR	122	2.6100	28.68
10	IRLILGNAV	129	2.2100	24.29
11	FGRDAPVVL	72	2.2000	24.18
12	VVLEIGSGS	78	2.1700	23.85
13	IRSRRSGIS	30	2.1000	23.08
14	LILGNAVDV	131	2.1000	23.08
15	IAPDSLCGV	144	2.1000	23.08
16	LPISVVRPA	222	2.0000	21.98
17	LLPISVVRP	221	1.9000	20.88
18	LGGGAVIEL	239	1.8000	19.78
19	FFPDPWPKA	155	1.7000	18.68
20	VRVDPDTEL	213	1.5000	16.48
21	YRRGLAQLL	108	1.3000	14.29
22	LAMAKAEPH	91	1.2800	14.07
23	VIAVDVYRR	102	1.2500	13.74
24	ILGNAVDVL	132	1.0000	10.99

25	LVRVDPDTE	212	1.0000	10.99
26	LLQPATMAL	170	0.9000	9.89

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	MVHHGQMHA	0	2.5000	29.76
2	LVPSGVLHA	183	2.4000	28.57
3	LPISVVRPA	222	1.8000	21.43
4	VRPATKYER	227	1.6000	19.05
5	LGLLALPQS	52	1.3000	15.48
6	LRPDTPVAS	14	1.2000	14.29
7	INIRLILGN	127	1.2000	14.29
8	LQHLIAPDS	140	1.0000	11.90
9	IELLWKKHG	245	0.8000	9.52
10	IRSRRSGIS	30	0.7000	8.33
11	YERKAQLGG	233	0.7000	8.33
12	WKKHGCSER	249	0.7000	8.33
13	VLQHLIAPD	139	0.5000	5.95
14	VRVFFPDPW	152	0.5000	5.95
15	LCAIDKVGS	116	0.3000	3.57
16	IRLILGNAV	129	0.3000	3.57
17	VVLEIGSGS	78	0.1000	1.19
18	LLWKKHGCS	247	-0.1000	0
19	WERLWPELG	45	-0.3000	0
20	VFFPDPWPK	154	-0.3000	0
21	LIADRLVPS	178	-0.5000	0
22	LLPISVVRP	221	-0.5000	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	VRPATKYER	227	3.1000	35.23
2	MVHHGQMHA	0	2.5000	28.41
3	LVPSGVLHA	183	2.4000	27.27
4	IELLWKKHG	245	2.2000	25.00
5	WKKHGCSER	249	2.2000	25.00
6	YERKAQLGG	233	2.1000	23.86
7	INIRLILGN	127	2.0000	22.73
8	LPISVVRPA	222	1.8000	20.45
9	LGLLALPQS	52	1.7000	19.32
10	LRPDTPVAS	14	1.6000	18.18
11	VLQHLIAPD	139	1.6000	18.18
12	LQHLIAPDS	140	1.4000	15.91
13	IRLILGNAV	129	1.3000	14.77
14	IRSRRSGIS	30	1.1000	12.50
15	WERLWPELG	45	1.1000	12.50
16	WFGRDAPVV	71	1.0000	11.36
17	VYRRGLAQL	107	0.9600	10.91
18	YRRGLAQLL	108	0.9600	10.91
19	VVRPATKYE	226	0.8000	9.09
20	VIAVDVYRR	102	0.7000	7.95
21	LCAIDKVGS	116	0.7000	7.95
22	YAEHIAAAG	198	0.7000	7.95
23	VVLEIGSGS	78	0.5000	5.68
24	VRVFFPDPW	152	0.5000	5.68
25	LLPISVVRP	221	0.5000	5.68
26	LLWKKHGCS	247	0.3000	3.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MVHHGQMHA	0	3.5000	41.67
2	LVPSGVLHA	183	3.4000	40.48

3	LPISVVRPA	222	2.8000	33.33
4	VRPATKYER	227	2.6000	30.95
5	LGLLALPQS	52	2.3000	27.38
6	LRPDTPVAS	14	2.2000	26.19
7	INIRLILGN	127	2.2000	26.19
8	LQHLIAPDS	140	2.0000	23.81
9	IELLWKKHG	245	1.8000	21.43
10	IRSRRSGIS	30	1.7000	20.24
11	VLQHLIAPD	139	1.5000	17.86
12	VRVFFPDPW	152	1.5000	17.86
13	LCAIDKVGS	116	1.3000	15.48
14	IRLILGNAV	129	1.3000	15.48
15	VVLEIGSGS	78	1.1000	13.10
16	VYRRGLAQL	107	1.0000	11.90
17	LLWKKHGCS	247	0.9000	10.71
18	VFFPDPWPK	154	0.7000	8.33
19	LIADRLVPS	178	0.5000	5.95
20	LLPISVVRP	221	0.5000	5.95
21	LAMAKAEPH	91	0.4800	5.71
22	VVRPATKYE	226	0.4000	4.76
23	LQPATMALI	171	0.3000	3.57
24	VIAVDVYRR	102	0.2000	2.38

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVPSGVLHA	183	3.4000	39.08
2	VRPATKYER	227	2.9000	33.33
3	LGLLALPQS	52	2.8500	32.76
4	IELLWKKHG	245	2.7000	31.03
5	LQHLIAPDS	140	2.5500	29.31
6	INIRLILGN	127	2.2000	25.29
7	YERKAQLGG	233	1.9000	21.84

8	VIAVDVYRR	102	1.8000	20.69
9	MVHHGQMHA	0	1.7000	19.54
10	LCAIDKVGS	116	1.7000	19.54
11	IRLILGNAV	129	1.7000	19.54
12	WERLWPELG	45	1.5000	17.24
13	LLPISVVRP	221	1.5000	17.24
14	IRSRRSGIS	30	1.3000	14.94
15	WPELGLLAL	49	1.0600	12.18
16	LRPDTPVAS	14	0.8000	9.20
17	VDVLQHLIA	137	0.7000	8.05
18	WFGRDAPVV	71	0.5500	6.32
19	VVRPATKYE	226	0.4000	4.60
20	LLQPATMAL	170	0.3600	4.14
21	LIAPDSLCG	143	0.2000	2.30
22	LQPATMALI	171	0.2000	2.30
23	LCGVRVFFP	149	0.1000	1.15
24	LPISVVRPA	222	0.1000	1.15
25	LLWKKHGCS	247	0.1000	1.15
26	VYRRGLAQL	107	0.0600	0.69

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	VRPATKYER	227	4.1000	46.59
2	MVHHGQMHA	0	3.5000	39.77
3	LVPSGVLHA	183	3.4000	38.64
4	IELLWKKHG	245	3.2000	36.36
5	INIRLILGN	127	3.0000	34.09
6	LPISVVRPA	222	2.8000	31.82
7	LGLLALPQS	52	2.7000	30.68
8	LRPDTPVAS	14	2.6000	29.55
9	VLQHLIAPD	139	2.6000	29.55
10	LQHLIAPDS	140	2.4000	27.27

11	IRLILGNAV	129	2.3000	26.14
12	IRSRRSGIS	30	2.1000	23.86
13	VYRRGLAQL	107	1.9600	22.27
14	VVRPATKYE	226	1.8000	20.45
15	VIAVDVYRR	102	1.7000	19.32
16	LCAIDKVGS	116	1.7000	19.32
17	VVLEIGSGS	78	1.5000	17.05
18	VRVFFPDPW	152	1.5000	17.05
19	LLPISVVRP	221	1.5000	17.05
20	LLWKKHGCS	247	1.3000	14.77
21	LQPATMALI	171	1.2000	13.64
22	WKKHGCSER	249	1.2000	13.64
23	YERKAQLGG	233	1.1000	12.50
24	LPSTSIRSR	25	1.0000	11.36
25	ILGNAVDVL	132	0.9600	10.91
26	LIADRLVPS	178	0.9000	10.23

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	VRPATKYER	227	3.1000	35.23
2	MVHHGQMHA	0	2.5000	28.41
3	LVPSGVLHA	183	2.4000	27.27
4	IELLWKKHG	245	2.2000	25.00
5	WKKHGCSER	249	2.2000	25.00
6	YERKAQLGG	233	2.1000	23.86
7	INIRLILGN	127	2.0000	22.73
8	LPISVVRPA	222	1.8000	20.45
9	LGLLALPQS	52	1.7000	19.32
10	LRPDTPVAS	14	1.6000	18.18
11	VLQHLIAPD	139	1.6000	18.18
12	LQHLIAPDS	140	1.4000	15.91
13	IRLILGNAV	129	1.3000	14.77

14	IRSRRSGIS	30	1.1000	12.50
15	WERLWPELG	45	1.1000	12.50
16	WFGRDAPVV	71	1.0000	11.36
17	VYRRGLAQL	107	0.9600	10.91
18	YRRGLAQLL	108	0.9600	10.91
19	VVRPATKYE	226	0.8000	9.09
20	VIAVDVYRR	102	0.7000	7.95
21	LCAIDKVGS	116	0.7000	7.95
22	YAEHIAAAG	198	0.7000	7.95
23	VVLEIGSGS	78	0.5000	5.68
24	VRVFFPDPW	152	0.5000	5.68
25	LLPISVVRP	221	0.5000	5.68
26	LLWKKHGCS	247	0.3000	3.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	INIRLILGN	127	4.2000	46.67
2	VLQHLIAPD	139	4.2000	46.67
3	MVHHGQMHA	0	3.5000	38.89
4	LVPSGVLHA	183	3.4000	37.78
5	VVRPATKYE	226	3.4000	37.78
6	IELLWKKHG	245	3.1000	34.44
7	LPISVVRPA	222	2.8000	31.11
8	VRPATKYER	227	2.6000	28.89
9	VRVFFPDPW	152	2.4000	26.67
10	LGLLALPQS	52	2.3000	25.56
11	LRPDTPVAS	14	2.2000	24.44
12	LVRVDPDTE	212	2.2000	24.44
13	VYRRGLAQL	107	2.0000	22.22
14	LQHLIAPDS	140	2.0000	22.22
15	MAKAEPHVD	93	1.8000	20.00
16	IRSRRSGIS	30	1.7000	18.89

17	LAMAKAEPH	91	1.7000	18.89
18	IRLILGNAV	129	1.6000	17.78
19	LAQLLCAID	112	1.4000	15.56
20	LCAIDKVGS	116	1.3000	14.44
21	LWKKHGCSE	248	1.3000	14.44
22	VVLEIGSGS	78	1.1000	12.22
23	ILGNAVDVL	132	1.0000	11.11
24	YERKAQLGG	233	1.0000	11.11
25	LLPISVVRP	221	0.9000	10.00
26	LLWKKHGCS	247	0.9000	10.00

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	LVPSGVLHA	183	3.4000	39.08
2	VRPATKYER	227	2.9000	33.33
3	LGLLALPQS	52	2.8500	32.76
4	IELLWKKHG	245	2.7000	31.03
5	LQHLIAPDS	140	2.5500	29.31
6	INIRLILGN	127	2.2000	25.29
7	YERKAQLGG	233	1.9000	21.84
8	VIAVDVYRR	102	1.8000	20.69
9	MVHHGQMHA	0	1.7000	19.54
10	LCAIDKVGS	116	1.7000	19.54
11	IRLILGNAV	129	1.7000	19.54
12	WERLWPELG	45	1.5000	17.24
13	LLPISVVRP	221	1.5000	17.24
14	IRSRRSGIS	30	1.3000	14.94
15	WPELGLLAL	49	1.0600	12.18
16	LRPDTPVAS	14	0.8000	9.20
17	VDVLQHLIA	137	0.7000	8.05
18	WFGRDAPVV	71	0.5500	6.32
19	VVRPATKYE	226	0.4000	4.60

20	LLQPATMAL	170	0.3600	4.14
21	LIAPDSLCG	143	0.2000	2.30
22	LQPATMALI	171	0.2000	2.30
23	LCGVRVFFP	149	0.1000	1.15
24	LPISVVRPA	222	0.1000	1.15
25	LLWKKHGCS	247	0.1000	1.15
26	VYRRGLAQL	107	0.0600	0.69

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	LVPSGVLHA	183	1.6000	23.53
2	LGLLALPQS	52	1.3000	19.12
3	LQHLIAPDS	140	1.0000	14.71
4	IRSRRSGIS	30	0.8000	11.76
5	LCAIDKVGS	116	0.8000	11.76
6	VRPATKYER	227	0.7000	10.29
7	IELLWKKHG	245	0.7000	10.29
8	IRLILGNAV	129	0.4000	5.88
9	MVHHGQMHA	0	0.1000	1.47
10	LRPDTPVAS	14	-0.1000	0
11	LPISVVRPA	222	-0.1000	0
12	ISVVRPATK	224	-0.2000	0
13	VIAVDVYRR	102	-0.4000	0
14	INIRLILGN	127	-0.4000	0
15	LLWKKHGCS	247	-0.4000	0
16	LQPATMALI	171	-0.7000	0
17	VRVFFPDPW	152	-0.8000	0
18	VVLEIGSGS	78	-0.9000	0
19	VYRRGLAQL	107	-0.9000	0
20	WERLWPELG	45	-1.0000	0
21	YRRGLAQLL	108	-1.0000	0
22	VDVLQHLIA	137	-1.1000	0

23	YERKAQLGG	233	-1.3000	0
24	LCGVRVFFP	149	-1.4000	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	LVPSGVLHA	183	4.4000	53.01
2	LGLLALPQS	52	3.4500	41.57
3	LQHLIAPDS	140	3.1500	37.95
4	MVHHGQMHA	0	2.7000	32.53
5	INIRLILGN	127	2.4000	28.92
6	VRPATKYER	227	2.4000	28.92
7	LCAIDKVGS	116	2.3000	27.71
8	IELLWKKHG	245	2.3000	27.71
9	IRSRRSGIS	30	1.9000	22.89
10	IRLILGNAV	129	1.7000	20.48
11	VDVLQHLIA	137	1.7000	20.48
12	LLPISVVRP	221	1.5000	18.07
13	LRPDTPVAS	14	1.4000	16.87
14	VIAVDVYRR	102	1.3000	15.66
15	LPISVVRPA	222	1.1000	13.25
16	ISVVRPATK	224	0.8000	9.64
17	LLWKKHGCS	247	0.7000	8.43
18	LLQPATMAL	170	0.4000	4.82
19	LQPATMALI	171	0.3000	3.61
20	LAMAKAEPH	91	0.1800	2.17
21	VVLEIGSGS	78	0.1000	1.20
22	VYRRGLAQL	107	0.1000	1.20
23	LCGVRVFFP	149	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	INIRLILGN	127	3.4000	38.20
2	LVPSGVLHA	183	3.4000	38.20
3	IELLWKKHG	245	2.6000	29.21
4	LGLLALPQS	52	2.4500	27.53
5	LQHLIAPDS	140	2.1500	24.16
6	VVRPATKYE	226	2.0000	22.47
7	YERKAQLGG	233	1.8000	20.22
8	MVHHGQMHA	0	1.7000	19.10
9	WERLWPELG	45	1.4000	15.73
10	VRPATKYER	227	1.4000	15.73
11	LCAIDKVGS	116	1.3000	14.61
12	LVRVDPDTE	212	1.3000	14.61
13	WPELGLLAL	49	1.1000	12.36
14	LAQLLCAID	112	1.1000	12.36
15	VLQHLIAPD	139	1.1000	12.36
16	IRLILGNAV	129	1.0000	11.24
17	IRSRRSGIS	30	0.9000	10.11
18	LLPISVVRP	221	0.9000	10.11
19	VDVLQHLIA	137	0.7000	7.87
20	LRPDTPVAS	14	0.4000	4.49
21	LAMAKAEPH	91	0.4000	4.49
22	LLQPATMAL	170	0.4000	4.49
23	MAKAEPHVD	93	0.3000	3.37
24	VIAVDVYRR	102	0.3000	3.37
25	VYRRGLAQL	107	0.1000	1.12
26	YRRGLAQLL	108	0.1000	1.12

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MVHHGQMHA	0	3.5000	41.67
2	LVPSGVLHA	183	3.4000	40.48

3	LPISVVRPA	222	2.8000	33.33
4	VRPATKYER	227	2.6000	30.95
5	LGLLALPQS	52	2.3000	27.38
6	LRPDTPVAS	14	2.2000	26.19
7	INIRLILGN	127	2.2000	26.19
8	LQHLIAPDS	140	2.0000	23.81
9	IELLWKKHG	245	1.8000	21.43
10	IRSRRSGIS	30	1.7000	20.24
11	VLQHLIAPD	139	1.5000	17.86
12	VRVFFPDPW	152	1.5000	17.86
13	LCAIDKVGS	116	1.3000	15.48
14	IRLILGNAV	129	1.3000	15.48
15	VVLEIGSGS	78	1.1000	13.10
16	VYRRGLAQL	107	1.0000	11.90
17	LLWKKHGCS	247	0.9000	10.71
18	VFFPDPWPK	154	0.7000	8.33
19	LIADRLVPS	178	0.5000	5.95
20	LLPISVVRP	221	0.5000	5.95
21	LAMAKAEPH	91	0.4800	5.71
22	VVRPATKYE	226	0.4000	4.76
23	LQPATMALI	171	0.3000	3.57
24	VIAVDVYRR	102	0.2000	2.38

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MVHHGQMHA	0	2.5000	29.76
2	LVPSGVLHA	183	2.4000	28.57
3	LPISVVRPA	222	1.8000	21.43
4	VRPATKYER	227	1.6000	19.05
5	LGLLALPQS	52	1.3000	15.48
6	LRPDTPVAS	14	1.2000	14.29
7	INIRLILGN	127	1.2000	14.29

8	LQHLIAPDS	140	1.0000	11.90
9	IELLWKKHG	245	0.8000	9.52
10	IRSRRSGIS	30	0.7000	8.33
11	YERKAQLGG	233	0.7000	8.33
12	WKKHGCSER	249	0.7000	8.33
13	VLQHLIAPD	139	0.5000	5.95
14	VRVFFPDPW	152	0.5000	5.95
15	LCAIDKVGS	116	0.3000	3.57
16	IRLILGNAV	129	0.3000	3.57
17	VVLEIGSGS	78	0.1000	1.19
18	LLWKKHGCS	247	-0.1000	0
19	WERLWPELG	45	-0.3000	0
20	VFFPDPWPK	154	-0.3000	0
21	LIADRLVPS	178	-0.5000	0
22	LLPISVVRP	221	-0.5000	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	VRPATKYER	227	4.1000	46.59
2	MVHHGQMHA	0	3.5000	39.77
3	LVPSGVLHA	183	3.4000	38.64
4	IELLWKKHG	245	3.2000	36.36
5	INIRLILGN	127	3.0000	34.09
6	LPISVVRPA	222	2.8000	31.82
7	LGLLALPQS	52	2.7000	30.68
8	LRPDTPVAS	14	2.6000	29.55
9	VLQHLIAPD	139	2.6000	29.55
10	LQHLIAPDS	140	2.4000	27.27
11	IRLILGNAV	129	2.3000	26.14
12	IRSRRSGIS	30	2.1000	23.86
13	VYRRGLAQL	107	1.9600	22.27
14	VVRPATKYE	226	1.8000	20.45

15	VIAVDVYRR	102	1.7000	19.32
16	LCAIDKVGS	116	1.7000	19.32
17	VVLEIGSGS	78	1.5000	17.05
18	VRVFFPDPW	152	1.5000	17.05
19	LLPISVVRP	221	1.5000	17.05
20	LLWKKHGCS	247	1.3000	14.77
21	LQPATMALI	171	1.2000	13.64
22	WKKHGCSER	249	1.2000	13.64
23	YERKAQLGG	233	1.1000	12.50
24	LPSTSIRSR	25	1.0000	11.36
25	ILGNAVDVL	132	0.9600	10.91
26	LIADRLVPS	178	0.9000	10.23

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	VRPATKYER	227	4.1000	46.59
2	MVHHGQMHA	0	3.5000	39.77
3	LVPSGVLHA	183	3.4000	38.64
4	IELLWKKHG	245	3.2000	36.36
5	INIRLILGN	127	3.0000	34.09
6	LPISVVRPA	222	2.8000	31.82
7	LGLLALPQS	52	2.7000	30.68
8	LRPDTPVAS	14	2.6000	29.55
9	VLQHLIAPD	139	2.6000	29.55
10	LQHLIAPDS	140	2.4000	27.27
11	IRLILGNAV	129	2.3000	26.14
12	IRSRRSGIS	30	2.1000	23.86
13	VYRRGLAQL	107	1.9600	22.27
14	VVRPATKYE	226	1.8000	20.45
15	VIAVDVYRR	102	1.7000	19.32
16	LCAIDKVGS	116	1.7000	19.32
17	VVLEIGSGS	78	1.5000	17.05

18	VRVFFPDPW	152	1.5000	17.05
19	LLPISVVRP	221	1.5000	17.05
20	LLWKKHGCS	247	1.3000	14.77
21	LQPATMALI	171	1.2000	13.64
22	WKKHGCSER	249	1.2000	13.64
23	YERKAQLGG	233	1.1000	12.50
24	LPSTSIRSR	25	1.0000	11.36
25	ILGNAVDVL	132	0.9600	10.91
26	LIADRLVPS	178	0.9000	10.23

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	IRLILGNAV	129	5.3000	54.08
2	MVHHGQMHA	0	4.3000	43.88
3	LVPSGVLHA	183	3.7000	37.76
4	INIRLILGN	127	3.2500	33.16
5	VVLEIGSGS	78	3.0000	30.61
6	IRSRRSGIS	30	2.9000	29.59
7	LLQPATMAL	170	2.8600	29.18
8	VRVFFPDPW	152	2.8000	28.57
9	VDVYRRGLA	105	2.7000	27.55
10	LILGNAVDV	131	2.7000	27.55
11	VRVDPDTEL	213	2.6000	26.53
12	VYRRGLAQL	107	2.5000	25.51
13	LIAPDSLCG	143	2.5000	25.51
14	LGGGAVIEL	239	2.4000	24.49
15	LQPATMALI	171	2.3000	23.47
16	LGLLALPQS	52	2.2000	22.45
17	LEIGSGSGT	80	2.2000	22.45
18	YRRGLAQLL	108	2.1000	21.43
19	LWPELGLLA	48	2.0000	20.41
20	LRPDTPVAS	14	1.9000	19.39

21	LQHLIAPDS	140	1.9000	19.39
22	VRPATKYER	227	1.9000	19.39
23	VGLRPDTPV	12	1.8000	18.37
24	MHAQPGVGL	6	1.3000	13.27
25	IGSGSGTST	82	1.2000	12.24
26	VDVLQHLIA	137	1.1000	11.22

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	IRLILGNAV	129	4.3000	43.88
2	MVHHGQMHA	0	3.3000	33.67
3	YRRGLAQLL	108	3.1000	31.63
4	LVPSGVLHA	183	2.7000	27.55
5	INIRLILGN	127	2.2500	22.96
6	VVLEIGSGS	78	2.0000	20.41
7	IRSRRSGIS	30	1.9000	19.39
8	LLQPATMAL	170	1.8600	18.98
9	WFGRDAPVV	71	1.8000	18.37
10	VRVFFPDPW	152	1.8000	18.37
11	VDVYRRGLA	105	1.7000	17.35
12	LILGNAVDV	131	1.7000	17.35
13	VRVDPDTEL	213	1.6000	16.33
14	VYRRGLAQL	107	1.5000	15.31
15	LIAPDSLCG	143	1.5000	15.31
16	WKKHGCSER	249	1.5000	15.31
17	WPELGLLAL	49	1.4000	14.29
18	FGRDAPVVL	72	1.4000	14.29
19	LGGGAVIEL	239	1.4000	14.29
20	LQPATMALI	171	1.3000	13.27
21	LGLLALPQS	52	1.2000	12.24
22	LEIGSGSGT	80	1.2000	12.24
23	LWPELGLLA	48	1.0000	10.20

24	LRPDTPVAS	14	0.9000	9.18
25	LQHLIAPDS	140	0.9000	9.18
26	VRPATKYER	227	0.9000	9.18

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	IRLILGNAV	129	5.3000	54.08
2	MVHHGQMHA	0	4.3000	43.88
3	LVPSGVLHA	183	3.7000	37.76
4	INIRLILGN	127	3.2500	33.16
5	VVLEIGSGS	78	3.0000	30.61
6	IRSRRSGIS	30	2.9000	29.59
7	LLQPATMAL	170	2.8600	29.18
8	VRVFFPDPW	152	2.8000	28.57
9	VDVYRRGLA	105	2.7000	27.55
10	LILGNAVDV	131	2.7000	27.55
11	VRVDPDTEL	213	2.6000	26.53
12	VYRRGLAQL	107	2.5000	25.51
13	LIAPDSLCG	143	2.5000	25.51
14	LGGGAVIEL	239	2.4000	24.49
15	LQPATMALI	171	2.3000	23.47
16	LGLLALPQS	52	2.2000	22.45
17	LEIGSGSGT	80	2.2000	22.45
18	YRRGLAQLL	108	2.1000	21.43
19	LWPELGLLA	48	2.0000	20.41
20	LRPDTPVAS	14	1.9000	19.39
21	LQHLIAPDS	140	1.9000	19.39
22	VRPATKYER	227	1.9000	19.39
23	VGLRPDTPV	12	1.8000	18.37
24	MHAQPGVGL	6	1.3000	13.27
25	IGSGSGTST	82	1.2000	12.24
26	VDVLQHLIA	137	1.1000	11.22

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	VRPATKYER	227	3.7000	37.76
2	VIAVDVYRR	102	3.6000	36.73
3	IRLILGNAV	129	3.5000	35.71
4	YRRGLAQLL	108	3.3000	33.67
5	ISVVRPATK	224	3.2000	32.65
6	VFFPDPWPK	154	2.4000	24.49
7	WPKARHHKR	160	2.0000	20.41
8	WKKHGCSER	249	2.0000	20.41
9	LLALPQSPR	54	1.5000	15.31
10	LPSTSIRSR	25	1.4000	14.29
11	WERLWPELG	45	1.1000	11.22
12	LQHLIAPDS	140	1.1000	11.22
13	VVLEIGSGS	78	1.0000	10.20
14	LVRVDPDTE	212	1.0000	10.20
15	VLEIGSGSG	79	0.6000	6.12
16	IRSRRSGIS	30	0.5000	5.10
17	FGRDAPVVL	72	0.5000	5.10
18	LAMAKAEPH	91	0.5000	5.10
19	IELLWKKHG	245	0.5000	5.10
20	MALIADRLV	176	0.4000	4.08
21	FPDPWPKAR	156	0.3000	3.06
22	LRPDTPVAS	14	0.2000	2.04
23	LGLLALPQS	52	0.2000	2.04
24	LQPATMALI	171	0.2000	2.04
25	LVPSGVLHA	183	0.2000	2.04

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	VRPATKYER	227	3.7000	37.76
2	VIAVDVYRR	102	3.6000	36.73
3	IRLILGNAV	129	3.5000	35.71
4	YRRGLAQLL	108	3.3000	33.67
5	ISVVRPATK	224	3.2000	32.65
6	VFFPDPWPK	154	2.4000	24.49
7	WPKARHHKR	160	2.0000	20.41
8	WKKHGCSER	249	2.0000	20.41
9	LLALPQSPR	54	1.5000	15.31
10	LPSTSIRSR	25	1.4000	14.29
11	WERLWPELG	45	1.1000	11.22
12	LQHLIAPDS	140	1.1000	11.22
13	VVLEIGSGS	78	1.0000	10.20
14	LVRVDPDTE	212	1.0000	10.20
15	VLEIGSGSG	79	0.6000	6.12
16	IRSRRSGIS	30	0.5000	5.10
17	FGRDAPVVL	72	0.5000	5.10
18	LAMAKAEPH	91	0.5000	5.10
19	IELLWKKHG	245	0.5000	5.10
20	MALIADRLV	176	0.4000	4.08
21	FPDPWPKAR	156	0.3000	3.06
22	LRPDTPVAS	14	0.2000	2.04
23	LGLLALPQS	52	0.2000	2.04
24	LQPATMALI	171	0.2000	2.04
25	LVPSGVLHA	183	0.2000	2.04