MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Mar 24 00:04:51 2010
Length of input sequence	410 amino acids
Number of nanomers from input sequence	402
Number of nanomers with obligatory P1 anchor residue	119
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	41

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	YVALPAYLA	136	3.5000	58.33
2	LVPQRGYHL	80	2.2000	36.67
3	LRRAEVVGV	192	1.8000	30.00
4	VVGFGGYVA	130	1.5800	26.33
5	LVICRAGAM	301	1.5800	26.33
6	YLAARGLPL	142	1.5000	25.00
7	LRGLETRLV	73	1.4900	24.83
8	MVVADAALT	347	1.4000	23.33

9	LELITAVPM	88	1.3800	23.00
10	VVIHEANAR	160	1.0000	16.67
11	LVALDPRVR	58	0.8900	14.83
12	LVFGGSQGA	232	0.8000	13.33
13	VVLAGGGTA	37	0.7000	11.67
14	VVNAGGGMV	340	0.5000	8.33
15	LNALPVVNA	335	0.3000	5.00
16	LGTLRGLET	70	0.2000	3.33
17	ICRAGAMTV	303	0.0900	1.50
18	VVGVPVRAS	197	-0.0600	0
19	FGGYVALPA	133	-0.1000	0
20	YHLELITAV	86	-0.1100	0
21	MAVADALVA	52	-0.2000	0
22	VVVGFGGYV	129	-0.2000	0
23	LAAMTAAAA	373	-0.2000	0
24	VLRAEARAH	213	-0.3100	0
25	VSLNRAVSG	241	-0.3600	0
26	YVPLPIGNG	323	-0.5000	0
27	FGGSQGAVS	234	-0.6000	0
28	VCVLHAHGP	259	-0.6000	0
29	LHAHGPQNV	262	-0.6000	0
30	YVAVPYLDR	283	-0.6500	0
31	LLVFGGSQG	231	-0.7200	0
32	VARQVAGLL	359	-0.8000	0
33	LAVATGAGA	397	-0.8000	0
34	VNAGGGMVV	341	-0.8100	0
35	VRITALGTL	65	-0.9000	0
36	LITAVPMPR	90	-1.0100	0
37	VPYLDRMEL	286	-1.0100	0
38	VAEVSAVGL	311	-1.0500	0
39	VGFGGYVAL	131	-1.2000	0
40	VIHEANARA	161	-1.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVPQRGYHL	80	3.2000	53.33
2	LRRAEVVGV	192	2.8000	46.67
3	VVGFGGYVA	130	2.5800	43.00
4	LVICRAGAM	301	2.5800	43.00
5	YVALPAYLA	136	2.5000	41.67
6	LRGLETRLV	73	2.4900	41.50
7	MVVADAALT	347	2.4000	40.00
8	LELITAVPM	88	2.3800	39.67
9	VVIHEANAR	160	2.0000	33.33
10	LVALDPRVR	58	1.8900	31.50
11	LVFGGSQGA	232	1.8000	30.00
12	VVLAGGGTA	37	1.7000	28.33
13	VVNAGGGMV	340	1.5000	25.00
14	LNALPVVNA	335	1.3000	21.67
15	LGTLRGLET	70	1.2000	20.00
16	ICRAGAMTV	303	1.0900	18.17
17	VVGVPVRAS	197	0.9400	15.67
18	MAVADALVA	52	0.8000	13.33
19	VVVGFGGYV	129	0.8000	13.33
20	LAAMTAAAA	373	0.8000	13.33
21	VLRAEARAH	213	0.6900	11.50
22	VSLNRAVSG	241	0.6400	10.67
23	YLAARGLPL	142	0.5000	8.33
24	VCVLHAHGP	259	0.4000	6.67
25	LHAHGPQNV	262	0.4000	6.67
26	LLVFGGSQG	231	0.2800	4.67
27	VARQVAGLL	359	0.2000	3.33
28	LAVATGAGA	397	0.2000	3.33
29	VNAGGGMVV	341	0.1900	3.17
30	VRITALGTL	65	0.1000	1.67
31	LITAVPMPR	90	-0.0100	0

32	VPYLDRMEL	286	-0.0100	0
33	VAEVSAVGL	311	-0.0500	0
34	FGGYVALPA	133	-0.1000	0
35	VGFGGYVAL	131	-0.2000	0
36	VIHEANARA	161	-0.2000	0
37	LNRAVSGAA	243	-0.2000	0
38	VLHAHGPQN	261	-0.2300	0
39	LARLPSRVW	104	-0.3100	0
40	VRASIAALD	202	-0.4000	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	VALDPRVRI	59	5.1000	53.68
2	LVICRAGAM	301	4.8000	50.53
3	LRRAEVVGV	192	4.6000	48.42
4	VVADAALTP	348	4.3000	45.26
5	VVIHEANAR	160	4.0100	42.21
6	VVGVPVRAS	197	3.7000	38.95
7	VDADVVVGF	125	3.3000	34.74
8	LITAVPMPR	90	3.2000	33.68
9	LVFGGSQGA	232	3.2000	33.68
10	LRAEARAHF	214	3.1000	32.63
11	VRITALGTL	65	2.9600	31.16
12	LELITAVPM	88	2.9000	30.53
13	VVVGFGGYV	129	2.8000	29.47
14	LRGLETRLV	73	2.6000	27.37
15	YVPLPIGNG	323	2.6000	27.37
16	VVLAGGGTA	37	2.5000	26.32
17	LLTDPARLA	366	2.4000	25.26
18	VPYLDRMEL	286	2.3600	24.84
19	VPMPRKPGG	94	2.3000	24.21
20	VRASIAALD	202	2.3000	24.21

21	VVNAGGGMV	340	2.3000	24.21
22	LVARQVAGL	358	2.2600	23.79
23	LVALDPRVR	58	2.2000	23.16
24	LNALPVVNA	335	2.2000	23.16
25	ICRAGAMTV	303	2.1000	22.11
26	MVVADAALT	347	2.1000	22.11
27	MTVAEVSAV	309	2.0700	21.79
28	VNAGGGMVV	341	2.0000	21.05
29	VWRAVREAR	111	1.9000	20.00
30	LVPQRGYHL	80	1.6100	16.95
31	VGVPVRASI	198	1.6000	16.84
32	VFGGSQGAV	233	1.6000	16.84
33	LPAIYVPLP	319	1.6000	16.84
34	LETRLVPQR	76	1.5000	15.79
35	VLSAVPDSG	183	1.5000	15.79
36	VSLNRAVSG	241	1.5000	15.79
37	LNRAVSGAA	243	1.5000	15.79
38	LHAHGPQNV	262	1.5000	15.79
39	LELRRRAQG	271	1.5000	15.79
40	ITALGTLRG	67	1.4000	14.74
41	LRRRAQGDP	273	1.4000	14.74

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	VALDPRVRI	59	3.2000	35.16
2	LRRAEVVGV	192	2.6000	28.57
3	VVGVPVRAS	197	2.3000	25.27
4	LVICRAGAM	301	2.3000	25.27
5	VVADAALTP	348	2.3000	25.27
6	LVFGGSQGA	232	2.2000	24.18
7	YVPLPIGNG	323	2.2000	24.18
8	YVALPAYLA	136	2.0500	22.53

9	VVIHEANAR	160	1.5100	16.59
10	VVLAGGGTA	37	1.5000	16.48
11	FGGSQGAVS	234	1.4000	15.38
12	LLTDPARLA	366	1.4000	15.38
13	LNALPVVNA	335	1.2000	13.19
14	VRITALGTL	65	1.0000	10.99
15	VLLVFGGSQ	230	0.9000	9.89
16	VVVGFGGYV	129	0.8000	8.79
17	YHLELITAV	86	0.7000	7.69
18	LITAVPMPR	90	0.7000	7.69
19	FPDDARVLL	224	0.7000	7.69
20	LRGLETRLV	73	0.6000	6.59
21	LAGGGTAGH	39	0.5800	6.37
22	LNRAVSGAA	243	0.5000	5.49
23	LELITAVPM	88	0.4000	4.40
24	VDADVVVGF	125	0.4000	4.40
25	VPYLDRMEL	286	0.4000	4.40
26	YAAADLVIC	296	0.4000	4.40
27	MVVADAALT	347	0.4000	4.40
28	VVNAGGGMV	340	0.3000	3.30
29	LVARQVAGL	358	0.3000	3.30
30	VRASIAALD	202	0.2000	2.20
31	LRAEARAHF	214	0.2000	2.20
32	ICRAGAMTV	303	0.1000	1.10
33	MTVAEVSAV	309	0.0700	0.77
34	VPMPRKPGG	94	-0.1000	0
35	FGGYVALPA	133	-0.1000	0
36	YVAVPYLDR	283	-0.1000	0
37	VARAALAVA	392	-0.1000	0
38	VLRAEARAH	213	-0.1200	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VALDPRVRI	59	4.0800	46.36
2	VVADAALTP	348	3.8000	43.18
3	LRRAEVVGV	192	3.4800	39.55
4	LVFGGSQGA	232	3.3000	37.50
5	VVIHEANAR	160	3.2000	36.36
6	VVGVPVRAS	197	3.0000	34.09
7	LLTDPARLA	366	2.1000	23.86
8	LNALPVVNA	335	2.0800	23.64
9	LVICRAGAM	301	1.9000	21.59
10	LAGGGTAGH	39	1.5800	17.95
11	LITAVPMPR	90	1.4000	15.91
12	MVVADAALT	347	1.4000	15.91
13	LRGLETRLV	73	1.3000	14.77
14	LVARQVAGL	358	1.3000	14.77
15	LELITAVPM	88	1.2800	14.55
16	VDADVVVGF	125	1.2800	14.55
17	MAVADALVA	52	1.2000	13.64
18	VRASIAALD	202	1.2000	13.64
19	LRAEARAHF	214	1.2000	13.64
20	VVLAGGGTA	37	1.1000	12.50
21	VPYLDRMEL	286	1.1000	12.50
22	LTPELVARQ	354	1.0000	11.36
23	VARAALAVA	392	0.9000	10.23
24	VWRAVREAR	111	0.8000	9.09
25	ICRAGAMTV	303	0.8000	9.09
26	MTVAEVSAV	309	0.8000	9.09
27	VGVPVRASI	198	0.7000	7.95
28	VNAGGGMVV	341	0.7000	7.95
29	VAGLLTDPA	363	0.7000	7.95
30	VRITALGTL	65	0.6000	6.82
31	LHAHGPQNV	262	0.6000	6.82
32	VLRAEARAH	213	0.5800	6.59
33	ITALGTLRG	67	0.5000	5.68

34	VLLVFGGSQ	230	0.5000	5.68
35	LVALDPRVR	58	0.4000	4.55
36	VVVGFGGYV	129	0.4000	4.55
37	VLSAVPDSG	183	0.4000	4.55
38	FGGSQGAVS	234	0.4000	4.55
39	LAAAGVCVL	254	0.2000	2.27
40	VGHRDAAGQ	383	0.2000	2.27
41	LNRAVSGAA	243	0.1000	1.14

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	VALDPRVRI	59	4.0800	46.36
2	VVADAALTP	348	3.8000	43.18
3	LRRAEVVGV	192	3.4800	39.55
4	LVFGGSQGA	232	3.3000	37.50
5	VVIHEANAR	160	3.2000	36.36
6	VVGVPVRAS	197	3.0000	34.09
7	LLTDPARLA	366	2.1000	23.86
8	LNALPVVNA	335	2.0800	23.64
9	LVICRAGAM	301	1.9000	21.59
10	LAGGGTAGH	39	1.5800	17.95
11	LITAVPMPR	90	1.4000	15.91
12	MVVADAALT	347	1.4000	15.91
13	LRGLETRLV	73	1.3000	14.77
14	LVARQVAGL	358	1.3000	14.77
15	LELITAVPM	88	1.2800	14.55
16	VDADVVVGF	125	1.2800	14.55
17	MAVADALVA	52	1.2000	13.64
18	VRASIAALD	202	1.2000	13.64
19	LRAEARAHF	214	1.2000	13.64
20	VVLAGGGTA	37	1.1000	12.50
21	VPYLDRMEL	286	1.1000	12.50

22	LTPELVARQ	354	1.0000	11.36
23	VARAALAVA	392	0.9000	10.23
24	VWRAVREAR	111	0.8000	9.09
25	ICRAGAMTV	303	0.8000	9.09
26	MTVAEVSAV	309	0.8000	9.09
27	VGVPVRASI	198	0.7000	7.95
28	VNAGGGMVV	341	0.7000	7.95
29	VAGLLTDPA	363	0.7000	7.95
30	VRITALGTL	65	0.6000	6.82
31	LHAHGPQNV	262	0.6000	6.82
32	VLRAEARAH	213	0.5800	6.59
33	ITALGTLRG	67	0.5000	5.68
34	VLLVFGGSQ	230	0.5000	5.68
35	LVALDPRVR	58	0.4000	4.55
36	VVVGFGGYV	129	0.4000	4.55
37	VLSAVPDSG	183	0.4000	4.55
38	FGGSQGAVS	234	0.4000	4.55
39	LAAAGVCVL	254	0.2000	2.27
40	VGHRDAAGQ	383	0.2000	2.27
41	LNRAVSGAA	243	0.1000	1.14

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	VALDPRVRI	59	4.0800	46.36
2	VVADAALTP	348	3.8000	43.18
3	LRRAEVVGV	192	3.4800	39.55
4	LVFGGSQGA	232	3.3000	37.50
5	VVIHEANAR	160	3.2000	36.36
6	VVGVPVRAS	197	3.0000	34.09
7	LLTDPARLA	366	2.1000	23.86
8	LNALPVVNA	335	2.0800	23.64
9	LVICRAGAM	301	1.9000	21.59

10	LAGGGTAGH	39	1.5800	17.95
11	LITAVPMPR	90	1.4000	15.91
12	MVVADAALT	347	1.4000	15.91
13	LRGLETRLV	73	1.3000	14.77
14	LVARQVAGL	358	1.3000	14.77
15	LELITAVPM	88	1.2800	14.55
16	VDADVVVGF	125	1.2800	14.55
17	MAVADALVA	52	1.2000	13.64
18	VRASIAALD	202	1.2000	13.64
19	LRAEARAHF	214	1.2000	13.64
20	VVLAGGGTA	37	1.1000	12.50
21	VPYLDRMEL	286	1.1000	12.50
22	LTPELVARQ	354	1.0000	11.36
23	VARAALAVA	392	0.9000	10.23
24	VWRAVREAR	111	0.8000	9.09
25	ICRAGAMTV	303	0.8000	9.09
26	MTVAEVSAV	309	0.8000	9.09
27	VGVPVRASI	198	0.7000	7.95
28	VNAGGGMVV	341	0.7000	7.95
29	VAGLLTDPA	363	0.7000	7.95
30	VRITALGTL	65	0.6000	6.82
31	LHAHGPQNV	262	0.6000	6.82
32	VLRAEARAH	213	0.5800	6.59
33	ITALGTLRG	67	0.5000	5.68
34	VLLVFGGSQ	230	0.5000	5.68
35	LVALDPRVR	58	0.4000	4.55
36	VVVGFGGYV	129	0.4000	4.55
37	VLSAVPDSG	183	0.4000	4.55
38	FGGSQGAVS	234	0.4000	4.55
39	LAAAGVCVL	254	0.2000	2.27
40	VGHRDAAGQ	383	0.2000	2.27
41	LNRAVSGAA	243	0.1000	1.14

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	VALDPRVRI	59	4.1000	43.16
2	LVICRAGAM	301	3.8000	40.00
3	LRRAEVVGV	192	3.6000	37.89
4	YVPLPIGNG	323	3.6000	37.89
5	VVADAALTP	348	3.3000	34.74
6	VVIHEANAR	160	3.0100	31.68
7	VVGVPVRAS	197	2.7000	28.42
8	VDADVVVGF	125	2.3000	24.21
9	LITAVPMPR	90	2.2000	23.16
10	LVFGGSQGA	232	2.2000	23.16
11	LRAEARAHF	214	2.1000	22.11
12	YVALPAYLA	136	2.0500	21.58
13	VRITALGTL	65	1.9600	20.63
14	LELITAVPM	88	1.9000	20.00
15	VVVGFGGYV	129	1.8000	18.95
16	FGGSQGAVS	234	1.8000	18.95
17	YHLELITAV	86	1.7000	17.89
18	FPDDARVLL	224	1.6600	17.47
19	LRGLETRLV	73	1.6000	16.84
20	VVLAGGGTA	37	1.5000	15.79
21	YVAVPYLDR	283	1.4000	14.74
22	LLTDPARLA	366	1.4000	14.74
23	VPYLDRMEL	286	1.3600	14.32
24	VPMPRKPGG	94	1.3000	13.68
25	VRASIAALD	202	1.3000	13.68
26	VVNAGGGMV	340	1.3000	13.68
27	LVARQVAGL	358	1.2600	13.26
28	LVALDPRVR	58	1.2000	12.63
29	LNALPVVNA	335	1.2000	12.63
30	ICRAGAMTV	303	1.1000	11.58
31	MVVADAALT	347	1.1000	11.58

32	MTVAEVSAV	309	1.0700	11.26
33	VNAGGGMVV	341	1.0000	10.53
34	VWRAVREAR	111	0.9000	9.47
35	LVPQRGYHL	80	0.6100	6.42
36	VGVPVRASI	198	0.6000	6.32
37	VFGGSQGAV	233	0.6000	6.32
38	LPAIYVPLP	319	0.6000	6.32
39	LETRLVPQR	76	0.5000	5.26
40	VLSAVPDSG	183	0.5000	5.26
41	VSLNRAVSG	241	0.5000	5.26

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	VALDPRVRI	59	4.0800	46.36
2	VVADAALTP	348	3.8000	43.18
3	LRRAEVVGV	192	3.4800	39.55
4	LVFGGSQGA	232	3.3000	37.50
5	VVIHEANAR	160	3.2000	36.36
6	VVGVPVRAS	197	3.0000	34.09
7	LLTDPARLA	366	2.1000	23.86
8	LNALPVVNA	335	2.0800	23.64
9	LVICRAGAM	301	1.9000	21.59
10	LAGGGTAGH	39	1.5800	17.95
11	LITAVPMPR	90	1.4000	15.91
12	MVVADAALT	347	1.4000	15.91
13	LRGLETRLV	73	1.3000	14.77
14	LVARQVAGL	358	1.3000	14.77
15	LELITAVPM	88	1.2800	14.55
16	VDADVVVGF	125	1.2800	14.55
17	MAVADALVA	52	1.2000	13.64
18	VRASIAALD	202	1.2000	13.64
19	LRAEARAHF	214	1.2000	13.64

20	VVLAGGGTA	37	1.1000	12.50
21	VPYLDRMEL	286	1.1000	12.50
22	LTPELVARQ	354	1.0000	11.36
23	VARAALAVA	392	0.9000	10.23
24	VWRAVREAR	111	0.8000	9.09
25	ICRAGAMTV	303	0.8000	9.09
26	MTVAEVSAV	309	0.8000	9.09
27	VGVPVRASI	198	0.7000	7.95
28	VNAGGGMVV	341	0.7000	7.95
29	VAGLLTDPA	363	0.7000	7.95
30	VRITALGTL	65	0.6000	6.82
31	LHAHGPQNV	262	0.6000	6.82
32	VLRAEARAH	213	0.5800	6.59
33	ITALGTLRG	67	0.5000	5.68
34	VLLVFGGSQ	230	0.5000	5.68
35	LVALDPRVR	58	0.4000	4.55
36	VVVGFGGYV	129	0.4000	4.55
37	VLSAVPDSG	183	0.4000	4.55
38	FGGSQGAVS	234	0.4000	4.55
39	LAAAGVCVL	254	0.2000	2.27
40	VGHRDAAGQ	383	0.2000	2.27
41	LNRAVSGAA	243	0.1000	1.14

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	VVIHEANAR	160	3.3000	38.37
2	VIHEANARA	161	3.1000	36.05
3	YHLELITAV	86	2.4000	27.91
4	LRGLETRLV	73	2.2000	25.58
5	LTPELVARQ	354	2.2000	25.58
6	LRRAEVVGV	192	2.1800	25.35
7	VVADAALTP	348	1.9000	22.09

8	YVALPAYLA	136	1.7000	19.77
9	VAGLLTDPA	363	1.6000	18.60
10	LNALPVVNA	335	1.5800	18.37
11	ITALGTLRG	67	1.4000	16.28
12	LVFGGSQGA	232	1.3000	15.12
13	LVICRAGAM	301	0.9000	10.47
14	VVGVPVRAS	197	0.8000	9.30
15	YVPLPIGNG	323	0.8000	9.30
16	FGGSQGAVS	234	0.7000	8.14
17	LELITAVPM	88	0.5800	6.74
18	VKDTVSQPA	0	0.5000	5.81
19	MVVADAALT	347	0.4000	4.65
20	VRASIAALD	202	0.3000	3.49
21	MAVADALVA	52	0.2000	2.33
22	LNRAVSGAA	243	0.2000	2.33
23	LHAHGPQNV	262	0.2000	2.33
24	LLTDPARLA	366	0.2000	2.33
25	LITAVPMPR	90	-0.1000	0
26	LAAMTAAAA	373	-0.1000	0
27	FGGYVALPA	133	-0.2000	0
28	ICRAGAMTV	303	-0.2000	0
29	LVALDPRVR	58	-0.3000	0
30	VSLNRAVSG	241	-0.3200	0
31	VGAHTADRV	175	-0.4000	0
32	LAGGGTAGH	39	-0.4200	0
33	VLRAEARAH	213	-0.4200	0
34	MTVAEVSAV	309	-0.5000	0
35	YVAVPYLDR	283	-0.6000	0
36	VVLAGGGTA	37	-0.7000	0
37	LARLPSRVW	104	-0.7000	0
38	LRAEARAHF	214	-0.7000	0
39	YLAARGLPL	142	-0.8000	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	VVGVPVRAS	197	4.9000	51.04
2	LRGLETRLV	73	4.7000	48.96
3	VVIHEANAR	160	4.4000	45.83
4	LVFGGSQGA	232	4.3000	44.79
5	VLRAEARAH	213	3.4800	36.25
6	LRRAEVVGV	192	3.3000	34.38
7	LVARQVAGL	358	3.0000	31.25
8	VPVRASIAA	200	2.5000	26.04
9	LHAHGPQNV	262	2.4000	25.00
10	LVALDPRVR	58	2.2000	22.92
11	VGHRDAAGQ	383	2.2000	22.92
12	VVGFGGYVA	130	2.0000	20.83
13	LARLPSRVW	104	1.8000	18.75
14	MAVADALVA	52	1.5000	15.62
15	LAGGGTAGH	39	1.4800	15.42
16	VKDTVSQPA	0	1.4000	14.58
17	YVALPAYLA	136	1.4000	14.58
18	MVVADAALT	347	1.4000	14.58
19	ITALGTLRG	67	1.3000	13.54
20	LNALPVVNA	335	1.3000	13.54
21	LVICRAGAM	301	1.1000	11.46
22	LELITAVPM	88	0.9800	10.21
23	LITAVPMPR	90	0.9000	9.38
24	ICRAGAMTV	303	0.8000	8.33
25	LPSRVWRAV	107	0.7000	7.29
26	MTAAAARVG	376	0.7000	7.29
27	LAAMTAAAA	373	0.6000	6.25
28	LVPQRGYHL	80	0.4000	4.17
29	LNRAVSGAA	243	0.4000	4.17
30	LLTDPARLA	366	0.4000	4.17
31	FGGYVALPA	133	0.3000	3.12

32	VIHEANARA	161	0.3000	3.12
33	IHEANARAG	162	0.3000	3.12
34	MTVAEVSAV	309	0.3000	3.12
35	LAAAGVCVL	254	-0.1000	0
36	LPPRRRRRI	150	-0.2000	0
37	VGLPAIYVP	317	-0.3000	0
38	VARAALAVA	392	-0.4000	0
39	VVLAGGGTA	37	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRGLETRLV	73	3.7000	42.05
2	VVGVPVRAS	197	3.5000	39.77
3	LRRAEVVGV	192	3.0000	34.09
4	LNALPVVNA	335	2.6000	29.55
5	VVIHEANAR	160	2.3000	26.14
6	ITALGTLRG	67	2.2000	25.00
7	LVICRAGAM	301	2.0000	22.73
8	YVALPAYLA	136	1.9000	21.59
9	VAGLLTDPA	363	1.9000	21.59
10	LAAMTAAAA	373	1.8000	20.45
11	LELITAVPM	88	1.7000	19.32
12	VVGFGGYVA	130	1.6000	18.18
13	VIHEANARA	161	1.5000	17.05
14	MVVADAALT	347	1.4000	15.91
15	LVFGGSQGA	232	1.3000	14.77
16	LNRAVSGAA	243	1.3000	14.77
17	LVALDPRVR	58	1.2000	13.64
18	MTVAEVSAV	309	1.2000	13.64
19	VLRAEARAH	213	0.8800	10.00
20	MAVADALVA	52	0.8000	9.09
21	LITAVPMPR	90	0.8000	9.09

22	LARLPSRVW	104	0.8000	9.09
23	ICRAGAMTV	303	0.7000	7.95
24	LTPELVARQ	354	0.6000	6.82
25	LLVFGGSQG	231	0.5000	5.68
26	VVLAGGGTA	37	0.4000	4.55
27	VLLVFGGSQ	230	0.3000	3.41
28	LDRMELAYA	289	0.1000	1.14
29	YVPLPIGNG	323	0.1000	1.14
30	LAAAGVCVL	254	-0.1000	0
31	VRASIAALD	202	-0.2000	0
32	VCVLHAHGP	259	-0.2000	0
33	LAGGGTAGH	39	-0.2200	0
34	VKDTVSQPA	0	-0.3000	0
35	LVPQRGYHL	80	-0.3000	0
36	FGGYVALPA	133	-0.4000	0
37	LVARQVAGL	358	-0.4000	0
38	VARAALAVA	392	-0.4000	0
39	VRITALGTL	65	-0.5000	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	LRGLETRLV	73	3.0000	31.91
2	YVALPAYLA	136	2.9000	30.85
3	ITALGTLRG	67	2.5000	26.60
4	VVGVPVRAS	197	2.5000	26.60
5	YVPLPIGNG	323	2.4000	25.53
6	LRRAEVVGV	192	2.3000	24.47
7	LVICRAGAM	301	2.1000	22.34
8	LELITAVPM	88	1.8000	19.15
9	LNALPVVNA	335	1.6000	17.02
10	VRASIAALD	202	1.5000	15.96
11	WRAVREARD	112	1.3000	13.83

12	VVIHEANAR	160	1.3000	13.83
13	MVVADAALT	347	1.3000	13.83
14	VLRAEARAH	213	1.1000	11.70
15	MELAYAAAD	292	1.1000	11.70
16	VAGLLTDPA	363	0.9000	9.57
17	LLVFGGSQG	231	0.8000	8.51
18	LAAMTAAAA	373	0.8000	8.51
19	LARLPSRVW	104	0.7000	7.45
20	YHLELITAV	86	0.6000	6.38
21	VVGFGGYVA	130	0.6000	6.38
22	FGGYVALPA	133	0.6000	6.38
23	VIHEANARA	161	0.5000	5.32
24	MTVAEVSAV	309	0.5000	5.32
25	YVAVPYLDR	283	0.4000	4.26
26	LTPELVARQ	354	0.4000	4.26
27	VEPAMAVAD	48	0.3000	3.19
28	LVFGGSQGA	232	0.3000	3.19
29	LNRAVSGAA	243	0.3000	3.19
30	LVALDPRVR	58	0.2000	2.13
31	VLLVFGGSQ	230	0.1000	1.06
32	LAAAGVCVL	254	-0.1000	0
33	MAVADALVA	52	-0.2000	0
34	LITAVPMPR	90	-0.2000	0
35	VREARDVLD	115	-0.2000	0
36	YLAARGLPL	142	-0.2000	0
37	IYVPLPIGN	322	-0.2200	0
38	LVPQRGYHL	80	-0.3000	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	YVALPAYLA	136	2.9000	32.95
2	LRGLETRLV	73	2.7000	30.68

3	VVGVPVRAS	197	2.5000	28.41
4	LRRAEVVGV	192	2.0000	22.73
5	LNALPVVNA	335	1.6000	18.18
6	VVIHEANAR	160	1.3000	14.77
7	ITALGTLRG	67	1.2000	13.64
8	YVPLPIGNG	323	1.1000	12.50
9	LVICRAGAM	301	1.0000	11.36
10	VAGLLTDPA	363	0.9000	10.23
11	LAAMTAAAA	373	0.8000	9.09
12	LELITAVPM	88	0.7000	7.95
13	VVGFGGYVA	130	0.6000	6.82
14	FGGYVALPA	133	0.6000	6.82
15	VIHEANARA	161	0.5000	5.68
16	YVAVPYLDR	283	0.4000	4.55
17	MVVADAALT	347	0.4000	4.55
18	YHLELITAV	86	0.3000	3.41
19	LVFGGSQGA	232	0.3000	3.41
20	LNRAVSGAA	243	0.3000	3.41
21	LVALDPRVR	58	0.2000	2.27
22	MTVAEVSAV	309	0.2000	2.27
23	VLRAEARAH	213	-0.1200	0
24	MAVADALVA	52	-0.2000	0
25	LITAVPMPR	90	-0.2000	0
26	LARLPSRVW	104	-0.2000	0
27	ICRAGAMTV	303	-0.3000	0
28	LTPELVARQ	354	-0.4000	0
29	LLVFGGSQG	231	-0.5000	0
30	VVLAGGGTA	37	-0.6000	0
31	VLLVFGGSQ	230	-0.7000	0
32	FGGSQGAVS	234	-0.8000	0
33	LDRMELAYA	289	-0.9000	0
34	VVADAALTP	348	-1.0000	0
35	LAAAGVCVL	254	-1.1000	0
36	YLAARGLPL	142	-1.2000	0

37	VRASIAALD	202	-1.2000	0
38	VCVLHAHGP	259	-1.2000	0
39	YAAADLVIC	296	-1.2000	0
40	LAGGGTAGH	39	-1.2200	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	LRGLETRLV	73	4.0000	42.55
2	ITALGTLRG	67	3.5000	37.23
3	VVGVPVRAS	197	3.5000	37.23
4	LRRAEVVGV	192	3.3000	35.11
5	LVICRAGAM	301	3.1000	32.98
6	LELITAVPM	88	2.8000	29.79
7	LNALPVVNA	335	2.6000	27.66
8	VRASIAALD	202	2.5000	26.60
9	VVIHEANAR	160	2.3000	24.47
10	MVVADAALT	347	2.3000	24.47
11	VLRAEARAH	213	2.1000	22.34
12	MELAYAAAD	292	2.1000	22.34
13	YVALPAYLA	136	1.9000	20.21
14	VAGLLTDPA	363	1.9000	20.21
15	LLVFGGSQG	231	1.8000	19.15
16	LAAMTAAAA	373	1.8000	19.15
17	LARLPSRVW	104	1.7000	18.09
18	VVGFGGYVA	130	1.6000	17.02
19	VIHEANARA	161	1.5000	15.96
20	MTVAEVSAV	309	1.5000	15.96
21	YVPLPIGNG	323	1.4000	14.89
22	LTPELVARQ	354	1.4000	14.89
23	VEPAMAVAD	48	1.3000	13.83
24	LVFGGSQGA	232	1.3000	13.83
25	LNRAVSGAA	243	1.3000	13.83

26	LVALDPRVR	58	1.2000	12.77
27	VLLVFGGSQ	230	1.1000	11.70
28	LAGGGTAGH	39	1.0000	10.64
29	ICRAGAMTV	303	1.0000	10.64
30	LAAAGVCVL	254	0.9000	9.57
31	MAVADALVA	52	0.8000	8.51
32	LITAVPMPR	90	0.8000	8.51
33	VREARDVLD	115	0.8000	8.51
34	IYVPLPIGN	322	0.7800	8.30
35	LVPQRGYHL	80	0.7000	7.45
36	VADALVALD	54	0.6000	6.38
37	LVARQVAGL	358	0.6000	6.38
38	VRITALGTL	65	0.5000	5.32
39	VVLAGGGTA	37	0.4000	4.26
40	VVADAALTP	348	0.4000	4.26
41	WRAVREARD	112	0.3000	3.19

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	VVIHEANAR	160	4.8000	53.33
2	YHLELITAV	86	3.4000	37.78
3	LRGLETRLV	73	3.2000	35.56
4	LRRAEVVGV	192	3.1800	35.33
5	VIHEANARA	161	3.1000	34.44
6	VVADAALTP	348	2.9000	32.22
7	ITALGTLRG	67	2.8000	31.11
8	LVICRAGAM	301	2.4000	26.67
9	YVPLPIGNG	323	2.2000	24.44
10	LELITAVPM	88	2.0800	23.11
11	YVALPAYLA	136	1.7000	18.89
12	VAGLLTDPA	363	1.6000	17.78
13	LNALPVVNA	335	1.5800	17.56

14	LTPELVARQ	354	1.5000	16.67
15	LITAVPMPR	90	1.4000	15.56
16	VRASIAALD	202	1.4000	15.56
17	LVFGGSQGA	232	1.3000	14.44
18	LVALDPRVR	58	1.2000	13.33
19	VVGVPVRAS	197	1.2000	13.33
20	LRAEARAHF	214	1.2000	13.33
21	LHAHGPQNV	262	1.2000	13.33
22	FGGSQGAVS	234	1.1000	12.22
23	MVVADAALT	347	1.1000	12.22
24	VSLNRAVSG	241	1.0800	12.00
25	VDADVVVGF	125	0.9800	10.89
26	VRITALGTL	65	0.9600	10.67
27	YVAVPYLDR	283	0.9000	10.00
28	ICRAGAMTV	303	0.8000	8.89
29	VGAHTADRV	175	0.6000	6.67
30	VKDTVSQPA	0	0.5000	5.56
31	MTVAEVSAV	309	0.5000	5.56
32	VLSAVPDSG	183	0.3000	3.33
33	MAVADALVA	52	0.2000	2.22
34	LNRAVSGAA	243	0.2000	2.22
35	LLTDPARLA	366	0.2000	2.22
36	YLAARGLPL	142	0.1600	1.78
37	LVARQVAGL	358	0.0600	0.67
38	LAAMTAAAA	373	-0.1000	0
39	LAAAGVCVL	254	-0.1400	0

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	LRGLETRLV	73	3.7000	42.05
2	VVGVPVRAS	197	3.5000	39.77
3	LRRAEVVGV	192	3.0000	34.09

4	LNALPVVNA	335	2.6000	29.55
5	VVIHEANAR	160	2.3000	26.14
6	ITALGTLRG	67	2.2000	25.00
7	LVICRAGAM	301	2.0000	22.73
8	YVALPAYLA	136	1.9000	21.59
9	VAGLLTDPA	363	1.9000	21.59
10	LAAMTAAAA	373	1.8000	20.45
11	LELITAVPM	88	1.7000	19.32
12	VVGFGGYVA	130	1.6000	18.18
13	VIHEANARA	161	1.5000	17.05
14	MVVADAALT	347	1.4000	15.91
15	LVFGGSQGA	232	1.3000	14.77
16	LNRAVSGAA	243	1.3000	14.77
17	LVALDPRVR	58	1.2000	13.64
18	MTVAEVSAV	309	1.2000	13.64
19	VLRAEARAH	213	0.8800	10.00
20	MAVADALVA	52	0.8000	9.09
21	LITAVPMPR	90	0.8000	9.09
22	LARLPSRVW	104	0.8000	9.09
23	ICRAGAMTV	303	0.7000	7.95
24	LTPELVARQ	354	0.6000	6.82
25	LLVFGGSQG	231	0.5000	5.68
26	VVLAGGGTA	37	0.4000	4.55
27	VLLVFGGSQ	230	0.3000	3.41
28	LDRMELAYA	289	0.1000	1.14
29	YVPLPIGNG	323	0.1000	1.14
30	LAAAGVCVL	254	-0.1000	0
31	VRASIAALD	202	-0.2000	0
32	VCVLHAHGP	259	-0.2000	0
33	LAGGGTAGH	39	-0.2200	0
34	VKDTVSQPA	0	-0.3000	0
35	LVPQRGYHL	80	-0.3000	0
36	FGGYVALPA	133	-0.4000	0
37	LVARQVAGL	358	-0.4000	0

38	VARAALAVA	392	-0.4000	0
39	VRITALGTL	65	-0.5000	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	VVIHEANAR	160	3.3000	38.37
2	VIHEANARA	161	3.1000	36.05
3	YHLELITAV	86	2.4000	27.91
4	LRGLETRLV	73	2.2000	25.58
5	LTPELVARQ	354	2.2000	25.58
6	LRRAEVVGV	192	2.1800	25.35
7	VVADAALTP	348	1.9000	22.09
8	YVALPAYLA	136	1.7000	19.77
9	VAGLLTDPA	363	1.6000	18.60
10	LNALPVVNA	335	1.5800	18.37
11	ITALGTLRG	67	1.4000	16.28
12	LVFGGSQGA	232	1.3000	15.12
13	LVICRAGAM	301	0.9000	10.47
14	VVGVPVRAS	197	0.8000	9.30
15	YVPLPIGNG	323	0.8000	9.30
16	FGGSQGAVS	234	0.7000	8.14
17	LELITAVPM	88	0.5800	6.74
18	VKDTVSQPA	0	0.5000	5.81
19	MVVADAALT	347	0.4000	4.65
20	VRASIAALD	202	0.3000	3.49
21	MAVADALVA	52	0.2000	2.33
22	LNRAVSGAA	243	0.2000	2.33
23	LHAHGPQNV	262	0.2000	2.33
24	LLTDPARLA	366	0.2000	2.33
25	LITAVPMPR	90	-0.1000	0
26	LAAMTAAAA	373	-0.1000	0
27	FGGYVALPA	133	-0.2000	0

28	ICRAGAMTV	303	-0.2000	0
29	LVALDPRVR	58	-0.3000	0
30	VSLNRAVSG	241	-0.3200	0
31	VGAHTADRV	175	-0.4000	0
32	LAGGGTAGH	39	-0.4200	0
33	VLRAEARAH	213	-0.4200	0
34	MTVAEVSAV	309	-0.5000	0
35	YVAVPYLDR	283	-0.6000	0
36	VVLAGGGTA	37	-0.7000	0
37	LARLPSRVW	104	-0.7000	0
38	LRAEARAHF	214	-0.7000	0
39	YLAARGLPL	142	-0.8000	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	VRITALGTL	65	6.6000	56.90
2	YLAARGLPL	142	6.0000	51.72
3	LRRAEVVGV	192	5.6000	48.28
4	LELITAVPM	88	4.8000	41.38
5	LVICRAGAM	301	4.6000	39.66
6	LVPQRGYHL	80	4.4000	37.93
7	VAEVSAVGL	311	3.7000	31.90
8	ICRAGAMTV	303	3.5000	30.17
9	LVARQVAGL	358	3.5000	30.17
10	YVAVPYLDR	283	3.4000	29.31
11	VVIHEANAR	160	3.3000	28.45
12	LRGLETRLV	73	3.2200	27.76
13	VGFGGYVAL	131	3.2000	27.59
14	YVALPAYLA	136	3.0000	25.86
15	VVNAGGGMV	340	3.0000	25.86
16	YHLELITAV	86	2.8000	24.14
17	VVGVPVRAS	197	2.7000	23.28

18	VVGFGGYVA	130	2.6000	22.41
19	VPYLDRMEL	286	2.6000	22.41
20	LVFGGSQGA	232	2.5000	21.55
21	LAAAGVCVL	254	2.5000	21.55
22	LHAHGPQNV	262	2.5000	21.55
23	VALDPRVRI	59	2.3000	19.83
24	FGGYVALPA	133	2.0000	17.24
25	MTVAEVSAV	309	2.0000	17.24
26	MVVADAALT	347	2.0000	17.24
27	VKDTVSQPA	0	1.9000	16.38
28	VVVGFGGYV	129	1.9000	16.38
29	VSAVGLPAI	314	1.9000	16.38
30	VNAGGGMVV	341	1.9000	16.38
31	MAVADALVA	52	1.7000	14.66
32	VARQVAGLL	359	1.6000	13.79
33	VVLAGGGTA	37	1.5000	12.93
34	VRASIAALD	202	1.5000	12.93
35	FGGSQGAVS	234	1.3000	11.21
36	VLRAEARAH	213	1.2000	10.34
37	VGVPVRASI	198	1.1000	9.48
38	LNRAVSGAA	243	1.1000	9.48
39	VVADAALTP	348	1.1000	9.48
40	LARLPSRVW	104	1.0000	8.62
41	LSAVPDSGL	184	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	VRITALGTL	65	6.6000	56.90
2	YLAARGLPL	142	6.0000	51.72
3	LRRAEVVGV	192	5.6000	48.28
4	LELITAVPM	88	4.8000	41.38
5	LVICRAGAM	301	4.6000	39.66

6	LVPQRGYHL	80	4.4000	37.93
7	VAEVSAVGL	311	3.7000	31.90
8	ICRAGAMTV	303	3.5000	30.17
9	LVARQVAGL	358	3.5000	30.17
10	YVAVPYLDR	283	3.4000	29.31
11	VVIHEANAR	160	3.3000	28.45
12	LRGLETRLV	73	3.2200	27.76
13	VGFGGYVAL	131	3.2000	27.59
14	YVALPAYLA	136	3.0000	25.86
15	VVNAGGGMV	340	3.0000	25.86
16	YHLELITAV	86	2.8000	24.14
17	VVGVPVRAS	197	2.7000	23.28
18	VVGFGGYVA	130	2.6000	22.41
19	VPYLDRMEL	286	2.6000	22.41
20	LVFGGSQGA	232	2.5000	21.55
21	LAAAGVCVL	254	2.5000	21.55
22	LHAHGPQNV	262	2.5000	21.55
23	VALDPRVRI	59	2.3000	19.83
24	FGGYVALPA	133	2.0000	17.24
25	MTVAEVSAV	309	2.0000	17.24
26	MVVADAALT	347	2.0000	17.24
27	VKDTVSQPA	0	1.9000	16.38
28	VVVGFGGYV	129	1.9000	16.38
29	VSAVGLPAI	314	1.9000	16.38
30	VNAGGGMVV	341	1.9000	16.38
31	MAVADALVA	52	1.7000	14.66
32	VARQVAGLL	359	1.6000	13.79
33	VVLAGGGTA	37	1.5000	12.93
34	VRASIAALD	202	1.5000	12.93
35	FGGSQGAVS	234	1.3000	11.21
36	VLRAEARAH	213	1.2000	10.34
37	VGVPVRASI	198	1.1000	9.48
38	LNRAVSGAA	243	1.1000	9.48
39	VVADAALTP	348	1.1000	9.48

40	LARLPSRVW	104	1.0000	8.62
41	LSAVPDSGL	184	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	LVARQVAGL	358	4.6000	53.49
2	LELRRRAQG	271	3.7000	43.02
3	YVPLPIGNG	323	3.6000	41.86
4	VGHRDAAGQ	383	3.3000	38.37
5	VVGVPVRAS	197	2.9000	33.72
6	LVICRAGAM	301	2.8000	32.56
7	FGGYVALPA	133	2.6000	30.23
8	LRRRAQGDP	273	2.5000	29.07
9	WRAVREARD	112	2.1000	24.42
10	LRGLETRLV	73	1.9000	22.09
11	YVALPAYLA	136	1.7000	19.77
12	LRRAEVVGV	192	1.6000	18.60
13	VRITALGTL	65	1.4000	16.28
14	LPPRRRRRI	150	1.4000	16.28
15	VLRAEARAH	213	1.4000	16.28
16	VLLVFGGSQ	230	1.4000	16.28
17	VICRAGAMT	302	1.4000	16.28
18	MVVADAALT	347	1.3000	15.12
19	VRASIAALD	202	1.2000	13.95
20	VLELRRRAQ	270	1.2000	13.95
21	LRAEARAHF	214	1.1000	12.79
22	MELAYAAAD	292	1.1000	12.79
23	LPAYLAARG	139	1.0000	11.63
24	VVLAGGGTA	37	0.9000	10.47
25	LANRVGAHT	171	0.8000	9.30
26	LTPELVARQ	354	0.8000	9.30
27	LVALDPRVR	58	0.7000	8.14

28	IAALDRAVL	206	0.7000	8.14
29	VPYLDRMEL	286	0.7000	8.14
30	LNALPVVNA	335	0.6000	6.98
31	LDPRVRITA	61	0.5000	5.81
32	ITALGTLRG	67	0.5000	5.81
33	LETRLVPQR	76	0.4000	4.65
34	VPVRASIAA	200	0.4000	4.65
35	YLDRMELAY	288	0.4000	4.65
36	LAAMTAAAA	373	0.4000	4.65
37	LAGGGTAGH	39	0.3000	3.49
38	MPRKPGGDL	96	0.3000	3.49
39	LAAAGVCVL	254	0.2000	2.33

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVARQVAGL	358	3.6000	45.00
2	VVGVPVRAS	197	2.9000	36.25
3	FGGYVALPA	133	2.6000	32.50
4	VGHRDAAGQ	383	2.5000	31.25
5	LELRRRAQG	271	2.4000	30.00
6	YVPLPIGNG	323	2.3000	28.75
7	LRRRAQGDP	273	2.1000	26.25
8	YVALPAYLA	136	1.7000	21.25
9	LVICRAGAM	301	1.7000	21.25
10	LRGLETRLV	73	1.6000	20.00
11	LRRAEVVGV	192	1.3000	16.25
12	LPPRRRRRI	150	1.2000	15.00
13	VVLAGGGTA	37	0.9000	11.25
14	LVALDPRVR	58	0.7000	8.75
15	VLLVFGGSQ	230	0.6000	7.50
16	LNALPVVNA	335	0.6000	7.50
17	LDPRVRITA	61	0.5000	6.25

18	VICRAGAMT	302	0.5000	6.25
19	VRITALGTL	65	0.4000	5.00
20	LETRLVPQR	76	0.4000	5.00
21	VPVRASIAA	200	0.4000	5.00
22	VLELRRRAQ	270	0.4000	5.00
23	MVVADAALT	347	0.4000	5.00
24	LAAMTAAAA	373	0.4000	5.00
25	LRAEARAHF	214	0.2000	2.50
26	VLRAEARAH	213	0.1800	2.25
27	LANRVGAHT	171	-0.1000	0
28	LNRAVSGAA	243	-0.1000	0
29	VARAALAVA	392	-0.1000	0
30	LPAYLAARG	139	-0.3000	0
31	VGVPVRASI	198	-0.3000	0
32	IAALDRAVL	206	-0.3000	0
33	FGGSQGAVS	234	-0.3000	0
34	YVAVPYLDR	283	-0.3000	0
35	VPYLDRMEL	286	-0.3000	0
36	VVNAGGGMV	340	-0.3000	0
37	LVFGGSQGA	232	-0.4000	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	LVARQVAGL	358	4.6000	57.50
2	VVGVPVRAS	197	3.9000	48.75
3	VGHRDAAGQ	383	3.5000	43.75
4	LELRRRAQG	271	3.4000	42.50
5	LRRRAQGDP	273	3.1000	38.75
6	LVICRAGAM	301	2.7000	33.75
7	LRGLETRLV	73	2.6000	32.50
8	LRRAEVVGV	192	2.3000	28.75
9	LPPRRRRRI	150	2.2000	27.50

10	VVLAGGGTA	37	1.9000	23.75
11	LVALDPRVR	58	1.7000	21.25
12	FGGYVALPA	133	1.6000	20.00
13	VLLVFGGSQ	230	1.6000	20.00
14	LNALPVVNA	335	1.6000	20.00
15	LDPRVRITA	61	1.5000	18.75
16	VICRAGAMT	302	1.5000	18.75
17	VRITALGTL	65	1.4000	17.50
18	LETRLVPQR	76	1.4000	17.50
19	VPVRASIAA	200	1.4000	17.50
20	VLELRRRAQ	270	1.4000	17.50
21	MVVADAALT	347	1.4000	17.50
22	LAAMTAAAA	373	1.4000	17.50
23	YVPLPIGNG	323	1.3000	16.25
24	LRAEARAHF	214	1.2000	15.00
25	VLRAEARAH	213	1.1800	14.75
26	VVGFGGYVA	130	1.0000	12.50
27	LDRMELAYA	289	1.0000	12.50
28	LTPELVARQ	354	1.0000	12.50
29	LANRVGAHT	171	0.9000	11.25
30	LNRAVSGAA	243	0.9000	11.25
31	VARAALAVA	392	0.9000	11.25
32	YVALPAYLA	136	0.7000	8.75
33	LPAYLAARG	139	0.7000	8.75
34	VGVPVRASI	198	0.7000	8.75
35	IAALDRAVL	206	0.7000	8.75
36	VPYLDRMEL	286	0.7000	8.75
37	VVNAGGGMV	340	0.7000	8.75
38	LVFGGSQGA	232	0.6000	7.50
39	LITAVPMPR	90	0.3000	3.75
40	MPRKPGGDL	96	0.3000	3.75
41	VVIHEANAR	160	0.3000	3.75

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	LVARQVAGL	358	5.6000	65.12
2	LELRRRAQG	271	4.7000	54.65
3	VGHRDAAGQ	383	4.3000	50.00
4	VVGVPVRAS	197	3.9000	45.35
5	LVICRAGAM	301	3.8000	44.19
6	LRRRAQGDP	273	3.5000	40.70
7	LRGLETRLV	73	2.9000	33.72
8	LRRAEVVGV	192	2.6000	30.23
9	YVPLPIGNG	323	2.6000	30.23
10	VRITALGTL	65	2.4000	27.91
11	LPPRRRRRI	150	2.4000	27.91
12	VLRAEARAH	213	2.4000	27.91
13	VLLVFGGSQ	230	2.4000	27.91
14	VICRAGAMT	302	2.4000	27.91
15	MVVADAALT	347	2.3000	26.74
16	VRASIAALD	202	2.2000	25.58
17	VLELRRRAQ	270	2.2000	25.58
18	LRAEARAHF	214	2.1000	24.42
19	MELAYAAAD	292	2.1000	24.42
20	LPAYLAARG	139	2.0000	23.26
21	VVLAGGGTA	37	1.9000	22.09
22	LANRVGAHT	171	1.8000	20.93
23	LTPELVARQ	354	1.8000	20.93
24	LVALDPRVR	58	1.7000	19.77
25	IAALDRAVL	206	1.7000	19.77
26	VPYLDRMEL	286	1.7000	19.77
27	FGGYVALPA	133	1.6000	18.60
28	LNALPVVNA	335	1.6000	18.60
29	LDPRVRITA	61	1.5000	17.44
30	ITALGTLRG	67	1.5000	17.44
31	LETRLVPQR	76	1.4000	16.28

32	VPVRASIAA	200	1.4000	16.28
33	LAAMTAAAA	373	1.4000	16.28
34	LAGGGTAGH	39	1.3000	15.12
35	MPRKPGGDL	96	1.3000	15.12
36	LAAAGVCVL	254	1.2000	13.95
37	WRAVREARD	112	1.1000	12.79
38	LELITAVPM	88	1.0000	11.63
39	VVGFGGYVA	130	1.0000	11.63
40	LDRMELAYA	289	1.0000	11.63
41	VVNAGGGMV	340	1.0000	11.63

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	LVARQVAGL	358	3.6000	41.38
2	FGGYVALPA	133	3.2000	36.78
3	YVALPAYLA	136	2.6000	29.89
4	VVGVPVRAS	197	2.6000	29.89
5	VGHRDAAGQ	383	2.5000	28.74
6	LELRRRAQG	271	2.4000	27.59
7	LRRAEVVGV	192	2.3000	26.44
8	YVPLPIGNG	323	1.6000	18.39
9	LNALPVVNA	335	1.6000	18.39
10	LRRRAQGDP	273	1.4000	16.09
11	LDPRVRITA	61	1.3800	15.86
12	LRGLETRLV	73	1.3000	14.94
13	VVIHEANAR	160	1.3000	14.94
14	VPVRASIAA	200	1.2800	14.71
15	YHLELITAV	86	1.2000	13.79
16	LVICRAGAM	301	1.0000	11.49
17	VVGFGGYVA	130	0.9000	10.34
18	LPPRRRRRI	150	0.9000	10.34
19	VPYLDRMEL	286	0.7000	8.05

20	LETRLVPQR	76	0.6000	6.90
21	LVFGGSQGA	232	0.6000	6.90
22	VICRAGAMT	302	0.5000	5.75
23	MTVAEVSAV	309	0.5000	5.75
24	LVALDPRVR	58	0.4000	4.60
25	MVVADAALT	347	0.4000	4.60
26	LAAMTAAAA	373	0.4000	4.60
27	LITAVPMPR	90	0.3000	3.45
28	YVAVPYLDR	283	0.3000	3.45
29	VVLAGGGTA	37	0.2000	2.30
30	LRAEARAHF	214	0.2000	2.30
31	VLELRRRAQ	270	0.1000	1.15
32	YAAADLVIC	296	0.1000	1.15
33	LELITAVPM	88	-0.1000	0
34	LANRVGAHT	171	-0.1000	0
35	VLLVFGGSQ	230	-0.1000	0
36	YLDRMELAY	288	-0.1000	0
37	VARAALAVA	392	-0.1000	0
38	VLRAEARAH	213	-0.1200	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	LVARQVAGL	358	4.6000	45.54
2	FGGYVALPA	133	4.4000	43.56
3	LELRRRAQG	271	3.7000	36.63
4	YVPLPIGNG	323	3.7000	36.63
5	VGHRDAAGQ	383	3.3000	32.67
6	VVGVPVRAS	197	3.1000	30.69
7	LVICRAGAM	301	2.9000	28.71
8	LRRRAQGDP	273	2.6000	25.74
9	YVALPAYLA	136	2.4000	23.76
10	ITALGTLRG	67	2.3000	22.77

11	VPYLDRMEL	286	2.3000	22.77
12	YLDRMELAY	288	2.2000	21.78
13	LDPRVRITA	61	2.1000	20.79
14	LRGLETRLV	73	2.1000	20.79
15	WRAVREARD	112	2.1000	20.79
16	LRRAEVVGV	192	2.1000	20.79
17	VPVRASIAA	200	2.0000	19.80
18	YLAARGLPL	142	1.8000	17.82
19	LPPRRRRRI	150	1.6000	15.84
20	VLRAEARAH	213	1.6000	15.84
21	LETRLVPQR	76	1.5500	15.35
22	VRITALGTL	65	1.5000	14.85
23	VLLVFGGSQ	230	1.5000	14.85
24	YVAVPYLDR	283	1.5000	14.85
25	VLELRRRAQ	270	1.4000	13.86
26	VICRAGAMT	302	1.4000	13.86
27	IYVPLPIGN	322	1.3000	12.87
28	MVVADAALT	347	1.3000	12.87
29	VRASIAALD	202	1.2000	11.88
30	LRAEARAHF	214	1.1000	10.89
31	MELAYAAAD	292	1.1000	10.89
32	LNALPVVNA	335	1.1000	10.89
33	VVLAGGGTA	37	1.0000	9.90
34	MAVADALVA	52	1.0000	9.90
35	LPAYLAARG	139	1.0000	9.90
36	LVALDPRVR	58	0.9000	8.91
37	LITAVPMPR	90	0.9000	8.91
38	LANRVGAHT	171	0.8000	7.92
39	LTPELVARQ	354	0.8000	7.92
40	LGTLRGLET	70	0.7000	6.93
41	VVGFGGYVA	130	0.7000	6.93

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

	1.1	

Rank	Sequence	At Position	Score	% of Highest Score
1	VVGVPVRAS	197	3.2000	38.55
2	YVALPAYLA	136	2.8000	33.73
3	YVPLPIGNG	323	2.8000	33.73
4	LRGLETRLV	73	2.2000	26.51
5	LRRAEVVGV	192	1.8000	21.69
6	LVICRAGAM	301	1.8000	21.69
7	VPYLDRMEL	286	1.7000	20.48
8	YVAVPYLDR	283	1.6000	19.28
9	FGGYVALPA	133	1.5000	18.07
10	LNALPVVNA	335	1.5000	18.07
11	ITALGTLRG	67	1.4000	16.87
12	LVALDPRVR	58	1.3000	15.66
13	VVLAGGGTA	37	1.0000	12.05
14	MAVADALVA	52	1.0000	12.05
15	VLELRRRAQ	270	1.0000	12.05
16	VRITALGTL	65	0.9000	10.84
17	LITAVPMPR	90	0.9000	10.84
18	YLAARGLPL	142	0.8000	9.64
19	VLLVFGGSQ	230	0.8000	9.64
20	VVGFGGYVA	130	0.6000	7.23
21	LVARQVAGL	358	0.6000	7.23
22	MVVADAALT	347	0.4000	4.82
23	VLRAEARAH	213	0.3800	4.58
24	ICRAGAMTV	303	0.3000	3.61
25	LGTLRGLET	70	0.2000	2.41
26	IAALDRAVL	206	0.1000	1.20
27	VARAALAVA	392	-0.1000	0
28	VVNAGGGMV	340	-0.2000	0
29	LDRMELAYA	289	-0.4000	0
30	YAAADLVIC	296	-0.4000	0
31	VVADAALTP	348	-0.4000	0
32	WRAVREARD	112	-0.5000	0

33	LRAEARAHF	214	-0.5000	0
34	VGHRDAAGQ	383	-0.5000	0
35	LELRRRAQG	271	-0.6000	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	VVGVPVRAS	197	4.5000	53.57
2	VVIHEANAR	160	4.2000	50.00
3	LRGLETRLV	73	4.1000	48.81
4	LRRAEVVGV	192	3.3000	39.29
5	LVALDPRVR	58	3.2000	38.10
6	VLRAEARAH	213	2.9800	35.48
7	VLELRRRAQ	270	2.9000	34.52
8	LVARQVAGL	358	2.5000	29.76
9	LNALPVVNA	335	2.3000	27.38
10	VVGFGGYVA	130	2.2000	26.19
11	LPPRRRRRI	150	1.9000	22.62
12	LHAHGPQNV	262	1.7000	20.24
13	LVICRAGAM	301	1.7000	20.24
14	MVVADAALT	347	1.4000	16.67
15	VGHRDAAGQ	383	1.4000	16.67
16	YVALPAYLA	136	1.3000	15.48
17	LELRRRAQG	271	1.3000	15.48
18	LARLPSRVW	104	1.2000	14.29
19	LVPQRGYHL	80	1.1000	13.10
20	LRAEARAHF	214	1.1000	13.10
21	VVLAGGGTA	37	0.9000	10.71
22	MAVADALVA	52	0.9000	10.71
23	LVFGGSQGA	232	0.9000	10.71
24	LTPELVARQ	354	0.9000	10.71
25	VARAALAVA	392	0.9000	10.71
26	LLTDPARLA	366	0.8000	9.52

27	LAAMTAAAA	373	0.8000	9.52
28	VPYLDRMEL	286	0.7000	8.33
29	ITALGTLRG	67	0.6000	7.14
30	LITAVPMPR	90	0.6000	7.14
31	FGGYVALPA	133	0.5000	5.95
32	IAALDRAVL	206	0.4000	4.76
33	LDRMELAYA	289	0.4000	4.76
34	VRITALGTL	65	0.3000	3.57
35	VALDPRVRI	59	0.2000	2.38
36	LPLPPRRRR	148	0.2000	2.38
37	VGVPVRASI	198	0.2000	2.38
38	LAAAGVCVL	254	0.2000	2.38
39	MTAAAARVG	376	0.2000	2.38
40	MTVAEVSAV	309	0.1000	1.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVGVPVRAS	197	4.2000	50.60
2	LRGLETRLV	73	3.2000	38.55
3	LRRAEVVGV	192	2.8000	33.73
4	LVICRAGAM	301	2.8000	33.73
5	VPYLDRMEL	286	2.7000	32.53
6	LNALPVVNA	335	2.5000	30.12
7	ITALGTLRG	67	2.4000	28.92
8	LVALDPRVR	58	2.3000	27.71
9	VVLAGGGTA	37	2.0000	24.10
10	MAVADALVA	52	2.0000	24.10
11	VLELRRRAQ	270	2.0000	24.10
12	VRITALGTL	65	1.9000	22.89
13	LITAVPMPR	90	1.9000	22.89
14	YVALPAYLA	136	1.8000	21.69
15	VLLVFGGSQ	230	1.8000	21.69

16	YVPLPIGNG	323	1.8000	21.69
17	VVGFGGYVA	130	1.6000	19.28
18	LVARQVAGL	358	1.6000	19.28
19	MVVADAALT	347	1.4000	16.87
20	VLRAEARAH	213	1.3800	16.63
21	ICRAGAMTV	303	1.3000	15.66
22	LGTLRGLET	70	1.2000	14.46
23	IAALDRAVL	206	1.1000	13.25
24	LELITAVPM	88	1.0000	12.05
25	VVIHEANAR	160	1.0000	12.05
26	LNRAVSGAA	243	1.0000	12.05
27	LAAMTAAAA	373	1.0000	12.05
28	VARAALAVA	392	0.9000	10.84
29	VVNAGGGMV	340	0.8000	9.64
30	YVAVPYLDR	283	0.6000	7.23
31	LDRMELAYA	289	0.6000	7.23
32	VVADAALTP	348	0.6000	7.23
33	FGGYVALPA	133	0.5000	6.02
34	LRAEARAHF	214	0.5000	6.02
35	VGHRDAAGQ	383	0.5000	6.02
36	LELRRRAQG	271	0.4000	4.82
37	LARLPSRVW	104	0.3000	3.61
38	LTPELVARQ	354	0.3000	3.61
39	LPAIYVPLP	319	0.2500	3.01
40	LAAAGVCVL	254	0.2000	2.41
41	LRRRAQGDP	273	0.2000	2.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVGVPVRAS	197	4.2000	50.60
2	LRGLETRLV	73	3.2000	38.55
3	LRRAEVVGV	192	2.8000	33.73

4	LVICRAGAM	301	2.8000	33.73
5	VPYLDRMEL	286	2.7000	32.53
6	LNALPVVNA	335	2.5000	30.12
7	ITALGTLRG	67	2.4000	28.92
8	LVALDPRVR	58	2.3000	27.71
9	VVLAGGGTA	37	2.0000	24.10
10	MAVADALVA	52	2.0000	24.10
11	VLELRRRAQ	270	2.0000	24.10
12	VRITALGTL	65	1.9000	22.89
13	LITAVPMPR	90	1.9000	22.89
14	YVALPAYLA	136	1.8000	21.69
15	VLLVFGGSQ	230	1.8000	21.69
16	YVPLPIGNG	323	1.8000	21.69
17	VVGFGGYVA	130	1.6000	19.28
18	LVARQVAGL	358	1.6000	19.28
19	MVVADAALT	347	1.4000	16.87
20	VLRAEARAH	213	1.3800	16.63
21	ICRAGAMTV	303	1.3000	15.66
22	LGTLRGLET	70	1.2000	14.46
23	IAALDRAVL	206	1.1000	13.25
24	LELITAVPM	88	1.0000	12.05
25	VVIHEANAR	160	1.0000	12.05
26	LNRAVSGAA	243	1.0000	12.05
27	LAAMTAAAA	373	1.0000	12.05
28	VARAALAVA	392	0.9000	10.84
29	VVNAGGGMV	340	0.8000	9.64
30	YVAVPYLDR	283	0.6000	7.23
31	LDRMELAYA	289	0.6000	7.23
32	VVADAALTP	348	0.6000	7.23
33	FGGYVALPA	133	0.5000	6.02
34	LRAEARAHF	214	0.5000	6.02
35	VGHRDAAGQ	383	0.5000	6.02
36	LELRRRAQG	271	0.4000	4.82
37	LARLPSRVW	104	0.3000	3.61

38	LTPELVARQ	354	0.3000	3.61
39	LPAIYVPLP	319	0.2500	3.01
40	LAAAGVCVL	254	0.2000	2.41
41	LRRRAQGDP	273	0.2000	2.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VALDPRVRI	59	4.2000	46.15
2	LRRAEVVGV	192	3.6000	39.56
3	VVGVPVRAS	197	3.3000	36.26
4	LVICRAGAM	301	3.3000	36.26
5	VVADAALTP	348	3.3000	36.26
6	LVFGGSQGA	232	3.2000	35.16
7	VVIHEANAR	160	2.5100	27.58
8	VVLAGGGTA	37	2.5000	27.47
9	LLTDPARLA	366	2.4000	26.37
10	LNALPVVNA	335	2.2000	24.18
11	VRITALGTL	65	2.0000	21.98
12	VLLVFGGSQ	230	1.9000	20.88
13	VVVGFGGYV	129	1.8000	19.78
14	LITAVPMPR	90	1.7000	18.68
15	LRGLETRLV	73	1.6000	17.58
16	LAGGGTAGH	39	1.5800	17.36
17	LNRAVSGAA	243	1.5000	16.48
18	LELITAVPM	88	1.4000	15.38
19	VDADVVVGF	125	1.4000	15.38
20	VPYLDRMEL	286	1.4000	15.38
21	MVVADAALT	347	1.4000	15.38
22	VVNAGGGMV	340	1.3000	14.29
23	LVARQVAGL	358	1.3000	14.29
24	VRASIAALD	202	1.2000	13.19
25	LRAEARAHF	214	1.2000	13.19

26	YVPLPIGNG	323	1.2000	13.19
27	ICRAGAMTV	303	1.1000	12.09
28	MTVAEVSAV	309	1.0700	11.76
29	YVALPAYLA	136	1.0500	11.54
30	VNAGGGMVV	341	1.0000	10.99
31	LTPELVARQ	354	1.0000	10.99
32	VPMPRKPGG	94	0.9000	9.89
33	VARAALAVA	392	0.9000	9.89
34	VLRAEARAH	213	0.8800	9.67
35	MAVADALVA	52	0.7000	7.69
36	LVALDPRVR	58	0.7000	7.69
37	VGVPVRASI	198	0.7000	7.69
38	LVPQRGYHL	80	0.6500	7.14
39	VFGGSQGAV	233	0.6000	6.59
40	LPAIYVPLP	319	0.6000	6.59
41	VVGFGGYVA	130	0.5500	6.04

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	VVGVPVRAS	197	3.5000	41.67
2	VVIHEANAR	160	3.2000	38.10
3	LRGLETRLV	73	3.1000	36.90
4	YVALPAYLA	136	2.3000	27.38
5	LRRAEVVGV	192	2.3000	27.38
6	LVALDPRVR	58	2.2000	26.19
7	VLRAEARAH	213	1.9800	23.57
8	VLELRRRAQ	270	1.9000	22.62
9	FGGYVALPA	133	1.5000	17.86
10	LVARQVAGL	358	1.5000	17.86
11	LNALPVVNA	335	1.3000	15.48
12	VVGFGGYVA	130	1.2000	14.29
13	YVPLPIGNG	323	1.0000	11.90

14	LPPRRRRRI	150	0.9000	10.71
15	LHAHGPQNV	262	0.7000	8.33
16	LVICRAGAM	301	0.7000	8.33
17	MVVADAALT	347	0.4000	4.76
18	VGHRDAAGQ	383	0.4000	4.76
19	LELRRRAQG	271	0.3000	3.57
20	LARLPSRVW	104	0.2000	2.38
21	LVPQRGYHL	80	0.1000	1.19
22	LRAEARAHF	214	0.1000	1.19
23	FGGSQGAVS	234	0.1000	1.19
24	YAAADLVIC	296	0.1000	1.19
25	VVLAGGGTA	37	-0.1000	0
26	MAVADALVA	52	-0.1000	0
27	LVFGGSQGA	232	-0.1000	0
28	LTPELVARQ	354	-0.1000	0
29	VARAALAVA	392	-0.1000	0
30	YHLELITAV	86	-0.2000	0
31	LLTDPARLA	366	-0.2000	0
32	LAAMTAAAA	373	-0.2000	0
33	YLAARGLPL	142	-0.3000	0
34	VPYLDRMEL	286	-0.3000	0
35	ITALGTLRG	67	-0.4000	0
36	LITAVPMPR	90	-0.4000	0
37	IAALDRAVL	206	-0.6000	0
38	LDRMELAYA	289	-0.6000	0
39	VRITALGTL	65	-0.7000	0
40	VALDPRVRI	59	-0.8000	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	VVIHEANAR	160	4.7000	53.41
2	LRGLETRLV	73	4.1000	46.59

3	VVGVPVRAS	197	3.9000	44.32
4	LVALDPRVR	58	3.7000	42.05
5	LRRAEVVGV	192	3.3000	37.50
6	LVARQVAGL	358	2.4600	27.95
7	YVPLPIGNG	323	2.4000	27.27
8	YVALPAYLA	136	2.3000	26.14
9	LVICRAGAM	301	2.2000	25.00
10	LRAEARAHF	214	2.0000	22.73
11	LPPRRRRRI	150	1.8000	20.45
12	LHAHGPQNV	262	1.7000	19.32
13	LELRRRAQG	271	1.7000	19.32
14	FGGYVALPA	133	1.5000	17.05
15	VLRAEARAH	213	1.4000	15.91
16	LNALPVVNA	335	1.3000	14.77
17	VVGFGGYVA	130	1.2000	13.64
18	VLELRRRAQ	270	1.2000	13.64
19	LITAVPMPR	90	1.1000	12.50
20	MVVADAALT	347	1.1000	12.50
21	LVPQRGYHL	80	1.0600	12.05
22	ITALGTLRG	67	1.0000	11.36
23	YHLELITAV	86	0.8000	9.09
24	LPLPPRRRR	148	0.7000	7.95
25	YVAVPYLDR	283	0.7000	7.95
26	YLAARGLPL	142	0.6600	7.50
27	VPYLDRMEL	286	0.6600	7.50
28	MTAAAARVG	376	0.6000	6.82
29	LETRLVPQR	76	0.5000	5.68
30	LELITAVPM	88	0.5000	5.68
31	FGGSQGAVS	234	0.5000	5.68
32	IAALDRAVL	206	0.3600	4.09
33	VRITALGTL	65	0.2600	2.95
34	LARLPSRVW	104	0.2000	2.27
35	IHEANARAG	162	0.2000	2.27
36	LAAAGVCVL	254	0.1600	1.82

37	VALDPRVRI	59	0.1000	1.14
38	VWRAVREAR	111	0.1000	1.14
39	VGVPVRASI	198	0.1000	1.14
40	LLVFGGSQG	231	0.1000	1.14
41	VSLNRAVSG	241	0.1000	1.14

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	VVGVPVRAS	197	4.5000	53.57
2	VVIHEANAR	160	4.2000	50.00
3	LRGLETRLV	73	4.1000	48.81
4	LRRAEVVGV	192	3.3000	39.29
5	LVALDPRVR	58	3.2000	38.10
6	VLRAEARAH	213	2.9800	35.48
7	VLELRRRAQ	270	2.9000	34.52
8	LVARQVAGL	358	2.5000	29.76
9	LNALPVVNA	335	2.3000	27.38
10	VVGFGGYVA	130	2.2000	26.19
11	LPPRRRRRI	150	1.9000	22.62
12	LHAHGPQNV	262	1.7000	20.24
13	LVICRAGAM	301	1.7000	20.24
14	MVVADAALT	347	1.4000	16.67
15	VGHRDAAGQ	383	1.4000	16.67
16	YVALPAYLA	136	1.3000	15.48
17	LELRRRAQG	271	1.3000	15.48
18	LARLPSRVW	104	1.2000	14.29
19	LVPQRGYHL	80	1.1000	13.10
20	LRAEARAHF	214	1.1000	13.10
21	VVLAGGGTA	37	0.9000	10.71
22	MAVADALVA	52	0.9000	10.71
23	LVFGGSQGA	232	0.9000	10.71
24	LTPELVARQ	354	0.9000	10.71

25	VARAALAVA	392	0.9000	10.71
26	LLTDPARLA	366	0.8000	9.52
27	LAAMTAAAA	373	0.8000	9.52
28	VPYLDRMEL	286	0.7000	8.33
29	ITALGTLRG	67	0.6000	7.14
30	LITAVPMPR	90	0.6000	7.14
31	FGGYVALPA	133	0.5000	5.95
32	IAALDRAVL	206	0.4000	4.76
33	LDRMELAYA	289	0.4000	4.76
34	VRITALGTL	65	0.3000	3.57
35	VALDPRVRI	59	0.2000	2.38
36	LPLPPRRRR	148	0.2000	2.38
37	VGVPVRASI	198	0.2000	2.38
38	LAAAGVCVL	254	0.2000	2.38
39	MTAAAARVG	376	0.2000	2.38
40	MTVAEVSAV	309	0.1000	1.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVPLPIGNG	323	4.2000	48.28
2	VVGVPVRAS	197	3.6000	41.38
3	LVICRAGAM	301	3.3000	37.93
4	LRGLETRLV	73	3.2000	36.78
5	YVAVPYLDR	283	3.1000	35.63
6	LVALDPRVR	58	2.8000	32.18
7	ITALGTLRG	67	2.8000	32.18
8	YVALPAYLA	136	2.8000	32.18
9	LRRAEVVGV	192	2.8000	32.18
10	VPYLDRMEL	286	2.6600	30.57
11	LITAVPMPR	90	2.4000	27.59
12	VRITALGTL	65	1.8600	21.38
13	YLAARGLPL	142	1.7600	20.23

14	LVARQVAGL	358	1.5600	17.93
15	LELITAVPM	88	1.5000	17.24
16	FGGYVALPA	133	1.5000	17.24
17	VVIHEANAR	160	1.5000	17.24
18	LNALPVVNA	335	1.5000	17.24
19	LRAEARAHF	214	1.4000	16.09
20	ICRAGAMTV	303	1.3000	14.94
21	MVVADAALT	347	1.1000	12.64
22	IAALDRAVL	206	1.0600	12.18
23	VVLAGGGTA	37	1.0000	11.49
24	MAVADALVA	52	1.0000	11.49
25	LGTLRGLET	70	0.9000	10.34
26	LELRRRAQG	271	0.8000	9.20
27	VVNAGGGMV	340	0.8000	9.20
28	WRAVREARD	112	0.6000	6.90
29	VVGFGGYVA	130	0.6000	6.90
30	VVADAALTP	348	0.6000	6.90
31	FGGSQGAVS	234	0.4000	4.60
32	VLELRRRAQ	270	0.3000	3.45
33	LPAIYVPLP	319	0.2500	2.87
34	LRRRAQGDP	273	0.2000	2.30
35	LAAAGVCVL	254	0.1600	1.84
36	VLLVFGGSQ	230	0.1000	1.15
37	VCVLHAHGP	259	0.1000	1.15
38	LETRLVPQR	76	0.0500	0.57

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	VVIHEANAR	160	5.7000	64.77
2	LRGLETRLV	73	5.1000	57.95
3	VVGVPVRAS	197	4.9000	55.68
4	LVALDPRVR	58	4.7000	53.41

5	LRRAEVVGV	192	4.3000	48.86
6	LVARQVAGL	358	3.4600	39.32
7	LVICRAGAM	301	3.2000	36.36
8	LRAEARAHF	214	3.0000	34.09
9	LPPRRRRRI	150	2.8000	31.82
10	LHAHGPQNV	262	2.7000	30.68
11	LELRRRAQG	271	2.7000	30.68
12	VLRAEARAH	213	2.4000	27.27
13	LNALPVVNA	335	2.3000	26.14
14	VVGFGGYVA	130	2.2000	25.00
15	VLELRRRAQ	270	2.2000	25.00
16	LITAVPMPR	90	2.1000	23.86
17	MVVADAALT	347	2.1000	23.86
18	LVPQRGYHL	80	2.0600	23.41
19	ITALGTLRG	67	2.0000	22.73
20	LPLPPRRRR	148	1.7000	19.32
21	VPYLDRMEL	286	1.6600	18.86
22	MTAAAARVG	376	1.6000	18.18
23	LETRLVPQR	76	1.5000	17.05
24	LELITAVPM	88	1.5000	17.05
25	YVPLPIGNG	323	1.4000	15.91
26	IAALDRAVL	206	1.3600	15.45
27	YVALPAYLA	136	1.3000	14.77
28	VRITALGTL	65	1.2600	14.32
29	LARLPSRVW	104	1.2000	13.64
30	IHEANARAG	162	1.2000	13.64
31	LAAAGVCVL	254	1.1600	13.18
32	VALDPRVRI	59	1.1000	12.50
33	VWRAVREAR	111	1.1000	12.50
34	VGVPVRASI	198	1.1000	12.50
35	LLVFGGSQG	231	1.1000	12.50
36	VSLNRAVSG	241	1.1000	12.50
37	MTVAEVSAV	309	1.1000	12.50
38	VRASIAALD	202	1.0000	11.36

39	LRRRAQGDP	273	1.0000	11.36
40	ICRAGAMTV	303	1.0000	11.36
41	VVLAGGGTA	37	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	VVIHEANAR	160	4.7000	53.41
2	LRGLETRLV	73	4.1000	46.59
3	VVGVPVRAS	197	3.9000	44.32
4	LVALDPRVR	58	3.7000	42.05
5	LRRAEVVGV	192	3.3000	37.50
6	LVARQVAGL	358	2.4600	27.95
7	YVPLPIGNG	323	2.4000	27.27
8	YVALPAYLA	136	2.3000	26.14
9	LVICRAGAM	301	2.2000	25.00
10	LRAEARAHF	214	2.0000	22.73
11	LPPRRRRRI	150	1.8000	20.45
12	LHAHGPQNV	262	1.7000	19.32
13	LELRRRAQG	271	1.7000	19.32
14	FGGYVALPA	133	1.5000	17.05
15	VLRAEARAH	213	1.4000	15.91
16	LNALPVVNA	335	1.3000	14.77
17	VVGFGGYVA	130	1.2000	13.64
18	VLELRRRAQ	270	1.2000	13.64
19	LITAVPMPR	90	1.1000	12.50
20	MVVADAALT	347	1.1000	12.50
21	LVPQRGYHL	80	1.0600	12.05
22	ITALGTLRG	67	1.0000	11.36
23	YHLELITAV	86	0.8000	9.09
24	LPLPPRRRR	148	0.7000	7.95
25	YVAVPYLDR	283	0.7000	7.95
26	YLAARGLPL	142	0.6600	7.50

27	VPYLDRMEL	286	0.6600	7.50
28	MTAAAARVG	376	0.6000	6.82
29	LETRLVPQR	76	0.5000	5.68
30	LELITAVPM	88	0.5000	5.68
31	FGGSQGAVS	234	0.5000	5.68
32	IAALDRAVL	206	0.3600	4.09
33	VRITALGTL	65	0.2600	2.95
34	LARLPSRVW	104	0.2000	2.27
35	IHEANARAG	162	0.2000	2.27
36	LAAAGVCVL	254	0.1600	1.82
37	VALDPRVRI	59	0.1000	1.14
38	VWRAVREAR	111	0.1000	1.14
39	VGVPVRASI	198	0.1000	1.14
40	LLVFGGSQG	231	0.1000	1.14
41	VSLNRAVSG	241	0.1000	1.14

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	VVGVPVRAS	197	4.5000	50.00
2	LRGLETRLV	73	4.4000	48.89
3	VVIHEANAR	160	4.2000	46.67
4	VLRAEARAH	213	4.2000	46.67
5	VLELRRRAQ	270	3.7000	41.11
6	LRRAEVVGV	192	3.6000	40.00
7	LVARQVAGL	358	3.5000	38.89
8	LVALDPRVR	58	3.2000	35.56
9	LVICRAGAM	301	2.8000	31.11
10	VRASIAALD	202	2.6000	28.89
11	LELRRRAQG	271	2.6000	28.89
12	LNALPVVNA	335	2.3000	25.56
13	MVVADAALT	347	2.3000	25.56
14	VVGFGGYVA	130	2.2000	24.44

15	VGHRDAAGQ	383	2.2000	24.44
16	LVPQRGYHL	80	2.1000	23.33
17	LARLPSRVW	104	2.1000	23.33
18	LPPRRRRRI	150	2.1000	23.33
19	LDRAVLRAE	209	2.1000	23.33
20	MELAYAAAD	292	2.1000	23.33
21	LRAEARAHF	214	2.0000	22.22
22	LHAHGPQNV	262	2.0000	22.22
23	ITALGTLRG	67	1.9000	21.11
24	VPYLDRMEL	286	1.7000	18.89
25	LTPELVARQ	354	1.7000	18.89
26	MTAAAARVG	376	1.5000	16.67
27	IAALDRAVL	206	1.4000	15.56
28	VEPAMAVAD	48	1.3000	14.44
29	VRITALGTL	65	1.3000	14.44
30	YVALPAYLA	136	1.3000	14.44
31	YVPLPIGNG	323	1.3000	14.44
32	LAAAGVCVL	254	1.2000	13.33
33	LELITAVPM	88	1.1000	12.22
34	IHEANARAG	162	1.1000	12.22
35	LLVFGGSQG	231	1.0000	11.11
36	VSLNRAVSG	241	1.0000	11.11
37	IGNGEQRLN	328	1.0000	11.11
38	VVLAGGGTA	37	0.9000	10.00
39	MAVADALVA	52	0.9000	10.00
40	VADALVALD	54	0.9000	10.00
41	LVFGGSQGA	232	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	YVPLPIGNG	323	4.2000	48.28
2	VVGVPVRAS	197	3.6000	41.38

3	LVICRAGAM	301	3.3000	37.93
4	LRGLETRLV	73	3.2000	36.78
5	YVAVPYLDR	283	3.1000	35.63
6	LVALDPRVR	58	2.8000	32.18
7	ITALGTLRG	67	2.8000	32.18
8	YVALPAYLA	136	2.8000	32.18
9	LRRAEVVGV	192	2.8000	32.18
10	VPYLDRMEL	286	2.6600	30.57
11	LITAVPMPR	90	2.4000	27.59
12	VRITALGTL	65	1.8600	21.38
13	YLAARGLPL	142	1.7600	20.23
14	LVARQVAGL	358	1.5600	17.93
15	LELITAVPM	88	1.5000	17.24
16	FGGYVALPA	133	1.5000	17.24
17	VVIHEANAR	160	1.5000	17.24
18	LNALPVVNA	335	1.5000	17.24
19	LRAEARAHF	214	1.4000	16.09
20	ICRAGAMTV	303	1.3000	14.94
21	MVVADAALT	347	1.1000	12.64
22	IAALDRAVL	206	1.0600	12.18
23	VVLAGGGTA	37	1.0000	11.49
24	MAVADALVA	52	1.0000	11.49
25	LGTLRGLET	70	0.9000	10.34
26	LELRRRAQG	271	0.8000	9.20
27	VVNAGGGMV	340	0.8000	9.20
28	WRAVREARD	112	0.6000	6.90
29	VVGFGGYVA	130	0.6000	6.90
30	VVADAALTP	348	0.6000	6.90
31	FGGSQGAVS	234	0.4000	4.60
32	VLELRRRAQ	270	0.3000	3.45
33	LPAIYVPLP	319	0.2500	2.87
34	LRRRAQGDP	273	0.2000	2.30
35	LAAAGVCVL	254	0.1600	1.84
36	VLLVFGGSQ	230	0.1000	1.15

37	VCVLHAHGP	259	0.1000	1.15
38	LETRLVPQR	76	0.0500	0.57

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	VVGVPVRAS	197	3.0000	44.12
2	YVPLPIGNG	323	2.7000	39.71
3	YVALPAYLA	136	2.1000	30.88
4	LRGLETRLV	73	2.0000	29.41
5	LVICRAGAM	301	1.7000	25.00
6	LRRAEVVGV	192	1.3000	19.12
7	LVALDPRVR	58	1.1000	16.18
8	LNALPVVNA	335	1.0000	14.71
9	VVLAGGGTA	37	0.9000	13.24
10	VRITALGTL	65	0.8000	11.76
11	VLELRRRAQ	270	0.8000	11.76
12	VLLVFGGSQ	230	0.7000	10.29
13	LVARQVAGL	358	0.6000	8.82
14	MVVADAALT	347	0.4000	5.88
15	VLRAEARAH	213	0.1800	2.65
16	IAALDRAVL	206	0.1000	1.47
17	VPYLDRMEL	286	0.1000	1.47
18	VVGFGGYVA	130	-0.1000	0
19	LNRAVSGAA	243	-0.1000	0
20	VARAALAVA	392	-0.1000	0
21	YVAVPYLDR	283	-0.2000	0
22	FGGYVALPA	133	-0.3000	0
23	VVIHEANAR	160	-0.3000	0
24	VVNAGGGMV	340	-0.3000	0
25	ITALGTLRG	67	-0.4000	0
26	LDRMELAYA	289	-0.4000	0
27	LELITAVPM	88	-0.5000	0

28	WRAVREARD	112	-0.5000	0
29	LRAEARAHF	214	-0.5000	0
30	VGHRDAAGQ	383	-0.5000	0
31	LELRRRAQG	271	-0.6000	0
32	LITAVPMPR	90	-0.7000	0
33	LTPELVARQ	354	-0.7000	0
34	MAVADALVA	52	-0.8000	0
35	LAAAGVCVL	254	-0.8000	0
36	LARLPSRVW	104	-0.9000	0
37	LRRRAQGDP	273	-0.9000	0
38	YAAADLVIC	296	-0.9000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVGVPVRAS	197	4.2000	50.60
2	LRGLETRLV	73	3.2000	38.55
3	LRRAEVVGV	192	2.8000	33.73
4	LVICRAGAM	301	2.8000	33.73
5	VPYLDRMEL	286	2.7000	32.53
6	LNALPVVNA	335	2.5000	30.12
7	ITALGTLRG	67	2.4000	28.92
8	LVALDPRVR	58	2.3000	27.71
9	VVLAGGGTA	37	2.0000	24.10
10	MAVADALVA	52	2.0000	24.10
11	VLELRRRAQ	270	2.0000	24.10
12	VRITALGTL	65	1.9000	22.89
13	LITAVPMPR	90	1.9000	22.89
14	YVALPAYLA	136	1.8000	21.69
15	VLLVFGGSQ	230	1.8000	21.69
16	YVPLPIGNG	323	1.8000	21.69
17	VVGFGGYVA	130	1.6000	19.28
18	LVARQVAGL	358	1.6000	19.28

19	MVVADAALT	347	1.4000	16.87
20	VLRAEARAH	213	1.3800	16.63
21	ICRAGAMTV	303	1.3000	15.66
22	LGTLRGLET	70	1.2000	14.46
23	IAALDRAVL	206	1.1000	13.25
24	LELITAVPM	88	1.0000	12.05
25	VVIHEANAR	160	1.0000	12.05
26	LNRAVSGAA	243	1.0000	12.05
27	LAAMTAAAA	373	1.0000	12.05
28	VARAALAVA	392	0.9000	10.84
29	VVNAGGGMV	340	0.8000	9.64
30	YVAVPYLDR	283	0.6000	7.23
31	LDRMELAYA	289	0.6000	7.23
32	VVADAALTP	348	0.6000	7.23
33	FGGYVALPA	133	0.5000	6.02
34	LRAEARAHF	214	0.5000	6.02
35	VGHRDAAGQ	383	0.5000	6.02
36	LELRRRAQG	271	0.4000	4.82
37	LARLPSRVW	104	0.3000	3.61
38	LTPELVARQ	354	0.3000	3.61
39	LPAIYVPLP	319	0.2500	3.01
40	LAAAGVCVL	254	0.2000	2.41
41	LRRRAQGDP	273	0.2000	2.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVPLPIGNG	323	4.1000	46.07
2	VVGVPVRAS	197	3.2000	35.96
3	LVICRAGAM	301	2.9000	32.58
4	YVALPAYLA	136	2.8000	31.46
5	ITALGTLRG	67	2.7000	30.34
6	VPYLDRMEL	286	2.7000	30.34

7	LRGLETRLV	73	2.5000	28.09
8	WRAVREARD	112	2.2000	24.72
9	LRRAEVVGV	192	2.1000	23.60
10	VRITALGTL	65	1.9000	21.35
11	YLAARGLPL	142	1.8000	20.22
12	VLELRRRAQ	270	1.8000	20.22
13	VLRAEARAH	213	1.6000	17.98
14	VLLVFGGSQ	230	1.6000	17.98
15	YVAVPYLDR	283	1.6000	17.98
16	LVARQVAGL	358	1.6000	17.98
17	FGGYVALPA	133	1.5000	16.85
18	VRASIAALD	202	1.5000	16.85
19	LNALPVVNA	335	1.5000	16.85
20	LVALDPRVR	58	1.3000	14.61
21	MVVADAALT	347	1.3000	14.61
22	LGTLRGLET	70	1.1000	12.36
23	LELITAVPM	88	1.1000	12.36
24	IAALDRAVL	206	1.1000	12.36
25	MELAYAAAD	292	1.1000	12.36
26	VVLAGGGTA	37	1.0000	11.24
27	MAVADALVA	52	1.0000	11.24
28	LITAVPMPR	90	0.9000	10.11
29	LELRRRAQG	271	0.7000	7.87
30	VVGFGGYVA	130	0.6000	6.74
31	ICRAGAMTV	303	0.6000	6.74
32	IYVPLPIGN	322	0.6000	6.74
33	LRAEARAHF	214	0.4000	4.49
34	VGHRDAAGQ	383	0.3000	3.37
35	LARLPSRVW	104	0.2000	2.25
36	LAAAGVCVL	254	0.2000	2.25
37	VVNAGGGMV	340	0.1000	1.12
38	LTPELVARQ	354	0.1000	1.12
39	VLHAHGPQN	261	0.0500	0.56

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	VVGVPVRAS	197	4.5000	53.57
2	VVIHEANAR	160	4.2000	50.00
3	LRGLETRLV	73	4.1000	48.81
4	LRRAEVVGV	192	3.3000	39.29
5	LVALDPRVR	58	3.2000	38.10
6	VLRAEARAH	213	2.9800	35.48
7	VLELRRRAQ	270	2.9000	34.52
8	LVARQVAGL	358	2.5000	29.76
9	LNALPVVNA	335	2.3000	27.38
10	VVGFGGYVA	130	2.2000	26.19
11	LPPRRRRRI	150	1.9000	22.62
12	LHAHGPQNV	262	1.7000	20.24
13	LVICRAGAM	301	1.7000	20.24
14	MVVADAALT	347	1.4000	16.67
15	VGHRDAAGQ	383	1.4000	16.67
16	YVALPAYLA	136	1.3000	15.48
17	LELRRRAQG	271	1.3000	15.48
18	LARLPSRVW	104	1.2000	14.29
19	LVPQRGYHL	80	1.1000	13.10
20	LRAEARAHF	214	1.1000	13.10
21	VVLAGGGTA	37	0.9000	10.71
22	MAVADALVA	52	0.9000	10.71
23	LVFGGSQGA	232	0.9000	10.71
24	LTPELVARQ	354	0.9000	10.71
25	VARAALAVA	392	0.9000	10.71
26	LLTDPARLA	366	0.8000	9.52
27	LAAMTAAAA	373	0.8000	9.52
28	VPYLDRMEL	286	0.7000	8.33
29	ITALGTLRG	67	0.6000	7.14
30	LITAVPMPR	90	0.6000	7.14

31	FGGYVALPA	133	0.5000	5.95
32	IAALDRAVL	206	0.4000	4.76
33	LDRMELAYA	289	0.4000	4.76
34	VRITALGTL	65	0.3000	3.57
35	VALDPRVRI	59	0.2000	2.38
36	LPLPPRRRR	148	0.2000	2.38
37	VGVPVRASI	198	0.2000	2.38
38	LAAAGVCVL	254	0.2000	2.38
39	MTAAAARVG	376	0.2000	2.38
40	MTVAEVSAV	309	0.1000	1.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVGVPVRAS	197	3.5000	41.67
2	VVIHEANAR	160	3.2000	38.10
3	LRGLETRLV	73	3.1000	36.90
4	YVALPAYLA	136	2.3000	27.38
5	LRRAEVVGV	192	2.3000	27.38
6	LVALDPRVR	58	2.2000	26.19
7	VLRAEARAH	213	1.9800	23.57
8	VLELRRRAQ	270	1.9000	22.62
9	FGGYVALPA	133	1.5000	17.86
10	LVARQVAGL	358	1.5000	17.86
11	LNALPVVNA	335	1.3000	15.48
12	VVGFGGYVA	130	1.2000	14.29
13	YVPLPIGNG	323	1.0000	11.90
14	LPPRRRRRI	150	0.9000	10.71
15	LHAHGPQNV	262	0.7000	8.33
16	LVICRAGAM	301	0.7000	8.33
17	MVVADAALT	347	0.4000	4.76
18	VGHRDAAGQ	383	0.4000	4.76
19	LELRRRAQG	271	0.3000	3.57

20	LARLPSRVW	104	0.2000	2.38
21	LVPQRGYHL	80	0.1000	1.19
22	LRAEARAHF	214	0.1000	1.19
23	FGGSQGAVS	234	0.1000	1.19
24	YAAADLVIC	296	0.1000	1.19
25	VVLAGGGTA	37	-0.1000	0
26	MAVADALVA	52	-0.1000	0
27	LVFGGSQGA	232	-0.1000	0
28	LTPELVARQ	354	-0.1000	0
29	VARAALAVA	392	-0.1000	0
30	YHLELITAV	86	-0.2000	0
31	LLTDPARLA	366	-0.2000	0
32	LAAMTAAAA	373	-0.2000	0
33	YLAARGLPL	142	-0.3000	0
34	VPYLDRMEL	286	-0.3000	0
35	ITALGTLRG	67	-0.4000	0
36	LITAVPMPR	90	-0.4000	0
37	IAALDRAVL	206	-0.6000	0
38	LDRMELAYA	289	-0.6000	0
39	VRITALGTL	65	-0.7000	0
40	VALDPRVRI	59	-0.8000	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	VVIHEANAR	160	5.7000	64.77
2	LRGLETRLV	73	5.1000	57.95
3	VVGVPVRAS	197	4.9000	55.68
4	LVALDPRVR	58	4.7000	53.41
5	LRRAEVVGV	192	4.3000	48.86
6	LVARQVAGL	358	3.4600	39.32
7	LVICRAGAM	301	3.2000	36.36
8	LRAEARAHF	214	3.0000	34.09

9	LPPRRRRRI	150	2.8000	31.82
10	LHAHGPQNV	262	2.7000	30.68
11	LELRRRAQG	271	2.7000	30.68
12	VLRAEARAH	213	2.4000	27.27
13	LNALPVVNA	335	2.3000	26.14
14	VVGFGGYVA	130	2.2000	25.00
15	VLELRRRAQ	270	2.2000	25.00
16	LITAVPMPR	90	2.1000	23.86
17	MVVADAALT	347	2.1000	23.86
18	LVPQRGYHL	80	2.0600	23.41
19	ITALGTLRG	67	2.0000	22.73
20	LPLPPRRRR	148	1.7000	19.32
21	VPYLDRMEL	286	1.6600	18.86
22	MTAAAARVG	376	1.6000	18.18
23	LETRLVPQR	76	1.5000	17.05
24	LELITAVPM	88	1.5000	17.05
25	YVPLPIGNG	323	1.4000	15.91
26	IAALDRAVL	206	1.3600	15.45
27	YVALPAYLA	136	1.3000	14.77
28	VRITALGTL	65	1.2600	14.32
29	LARLPSRVW	104	1.2000	13.64
30	IHEANARAG	162	1.2000	13.64
31	LAAAGVCVL	254	1.1600	13.18
32	VALDPRVRI	59	1.1000	12.50
33	VWRAVREAR	111	1.1000	12.50
34	VGVPVRASI	198	1.1000	12.50
35	LLVFGGSQG	231	1.1000	12.50
36	VSLNRAVSG	241	1.1000	12.50
37	MTVAEVSAV	309	1.1000	12.50
38	VRASIAALD	202	1.0000	11.36
39	LRRRAQGDP	273	1.0000	11.36
40	ICRAGAMTV	303	1.0000	11.36
41	VVLAGGGTA	37	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	VVIHEANAR	160	5.7000	64.77
2	LRGLETRLV	73	5.1000	57.95
3	VVGVPVRAS	197	4.9000	55.68
4	LVALDPRVR	58	4.7000	53.41
5	LRRAEVVGV	192	4.3000	48.86
6	LVARQVAGL	358	3.4600	39.32
7	LVICRAGAM	301	3.2000	36.36
8	LRAEARAHF	214	3.0000	34.09
9	LPPRRRRRI	150	2.8000	31.82
10	LHAHGPQNV	262	2.7000	30.68
11	LELRRRAQG	271	2.7000	30.68
12	VLRAEARAH	213	2.4000	27.27
13	LNALPVVNA	335	2.3000	26.14
14	VVGFGGYVA	130	2.2000	25.00
15	VLELRRRAQ	270	2.2000	25.00
16	LITAVPMPR	90	2.1000	23.86
17	MVVADAALT	347	2.1000	23.86
18	LVPQRGYHL	80	2.0600	23.41
19	ITALGTLRG	67	2.0000	22.73
20	LPLPPRRRR	148	1.7000	19.32
21	VPYLDRMEL	286	1.6600	18.86
22	MTAAAARVG	376	1.6000	18.18
23	LETRLVPQR	76	1.5000	17.05
24	LELITAVPM	88	1.5000	17.05
25	YVPLPIGNG	323	1.4000	15.91
26	IAALDRAVL	206	1.3600	15.45
27	YVALPAYLA	136	1.3000	14.77
28	VRITALGTL	65	1.2600	14.32
29	LARLPSRVW	104	1.2000	13.64
30	IHEANARAG	162	1.2000	13.64

31	LAAAGVCVL	254	1.1600	13.18
32	VALDPRVRI	59	1.1000	12.50
33	VWRAVREAR	111	1.1000	12.50
34	VGVPVRASI	198	1.1000	12.50
35	LLVFGGSQG	231	1.1000	12.50
36	VSLNRAVSG	241	1.1000	12.50
37	MTVAEVSAV	309	1.1000	12.50
38	VRASIAALD	202	1.0000	11.36
39	LRRRAQGDP	273	1.0000	11.36
40	ICRAGAMTV	303	1.0000	11.36
41	VVLAGGGTA	37	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	VVGFGGYVA	130	5.9000	60.20
2	VVIHEANAR	160	4.4000	44.90
3	VRITALGTL	65	4.1000	41.84
4	FGGYVALPA	133	4.1000	41.84
5	VPYLDRMEL	286	4.0000	40.82
6	LLVFGGSQG	231	3.9000	39.80
7	LVICRAGAM	301	3.6800	37.55
8	VVLAGGGTA	37	3.6000	36.73
9	VVVGFGGYV	129	3.4000	34.69
10	VVNAGGGMV	340	3.4000	34.69
11	LVPQRGYHL	80	3.3000	33.67
12	VNAGGGMVV	341	3.3000	33.67
13	LGTLRGLET	70	3.2000	32.65
14	LRRAEVVGV	192	3.2000	32.65
15	LVFGGSQGA	232	3.2000	32.65
16	VALPAYLAA	137	3.0000	30.61
17	YLAARGLPL	142	2.9000	29.59
18	ICRAGAMTV	303	2.7000	27.55

19	LRGLETRLV	73	2.6600	27.14
20	VALDPRVRI	59	2.6000	26.53
21	YVAVPYLDR	283	2.6000	26.53
22	VGFGGYVAL	131	2.5000	25.51
23	VVADAALTP	348	2.5000	25.51
24	LVARQVAGL	358	2.5000	25.51
25	MAVADALVA	52	2.4000	24.49
26	VGVPVRASI	198	2.4000	24.49
27	MVVADAALT	347	2.4000	24.49
28	YVALPAYLA	136	2.3000	23.47
29	VPVRASIAA	200	2.3000	23.47
30	LRAEARAHF	214	2.2000	22.45
31	LNRAVSGAA	243	2.1000	21.43
32	LELITAVPM	88	2.0800	21.22
33	IAALDRAVL	206	2.0000	20.41
34	LDPRVRITA	61	1.7000	17.35
35	LHAHGPQNV	262	1.7000	17.35
36	LITAVPMPR	90	1.6000	16.33
37	VICRAGAMT	302	1.6000	16.33
38	ITALGTLRG	67	1.5600	15.92
39	LELRRRAQG	271	1.5000	15.31
40	VIHEANARA	161	1.4000	14.29
41	VVGVPVRAS	197	1.4000	14.29

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	FGGYVALPA	133	5.1000	52.04
2	VVGFGGYVA	130	4.9000	50.00
3	YLAARGLPL	142	3.9000	39.80
4	YVAVPYLDR	283	3.6000	36.73
5	VVIHEANAR	160	3.4000	34.69
6	YVALPAYLA	136	3.3000	33.67

7	VRITALGTL	65	3.1000	31.63
8	VPYLDRMEL	286	3.0000	30.61
9	LLVFGGSQG	231	2.9000	29.59
10	LVICRAGAM	301	2.6800	27.35
11	VVLAGGGTA	37	2.6000	26.53
12	VVVGFGGYV	129	2.4000	24.49
13	VVNAGGGMV	340	2.4000	24.49
14	LVPQRGYHL	80	2.3000	23.47
15	VNAGGGMVV	341	2.3000	23.47
16	LGTLRGLET	70	2.2000	22.45
17	LRRAEVVGV	192	2.2000	22.45
18	LVFGGSQGA	232	2.2000	22.45
19	YVPLPIGNG	323	2.1500	21.94
20	VALPAYLAA	137	2.0000	20.41
21	YHLELITAV	86	1.7500	17.86
22	ICRAGAMTV	303	1.7000	17.35
23	LRGLETRLV	73	1.6600	16.94
24	VALDPRVRI	59	1.6000	16.33
25	VGFGGYVAL	131	1.5000	15.31
26	VVADAALTP	348	1.5000	15.31
27	LVARQVAGL	358	1.5000	15.31
28	MAVADALVA	52	1.4000	14.29
29	VGVPVRASI	198	1.4000	14.29
30	MVVADAALT	347	1.4000	14.29
31	VPVRASIAA	200	1.3000	13.27
32	LRAEARAHF	214	1.2000	12.24
33	LNRAVSGAA	243	1.1000	11.22
34	LELITAVPM	88	1.0800	11.02
35	IAALDRAVL	206	1.0000	10.20
36	FGFPDDARV	222	0.9000	9.18
37	LDPRVRITA	61	0.7000	7.14
38	LHAHGPQNV	262	0.7000	7.14
39	LITAVPMPR	90	0.6000	6.12
40	FGGSQGAVS	234	0.6000	6.12

41	VICRAGAMT	302	0.6000	6.12

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVGFGGYVA	130	5.9000	60.20
2	VVIHEANAR	160	4.4000	44.90
3	VRITALGTL	65	4.1000	41.84
4	FGGYVALPA	133	4.1000	41.84
5	VPYLDRMEL	286	4.0000	40.82
6	LLVFGGSQG	231	3.9000	39.80
7	LVICRAGAM	301	3.6800	37.55
8	VVLAGGGTA	37	3.6000	36.73
9	VVVGFGGYV	129	3.4000	34.69
10	VVNAGGGMV	340	3.4000	34.69
11	LVPQRGYHL	80	3.3000	33.67
12	VNAGGGMVV	341	3.3000	33.67
13	LGTLRGLET	70	3.2000	32.65
14	LRRAEVVGV	192	3.2000	32.65
15	LVFGGSQGA	232	3.2000	32.65
16	VALPAYLAA	137	3.0000	30.61
17	YLAARGLPL	142	2.9000	29.59
18	ICRAGAMTV	303	2.7000	27.55
19	LRGLETRLV	73	2.6600	27.14
20	VALDPRVRI	59	2.6000	26.53
21	YVAVPYLDR	283	2.6000	26.53
22	VGFGGYVAL	131	2.5000	25.51
23	VVADAALTP	348	2.5000	25.51
24	LVARQVAGL	358	2.5000	25.51
25	MAVADALVA	52	2.4000	24.49
26	VGVPVRASI	198	2.4000	24.49
27	MVVADAALT	347	2.4000	24.49
28	YVALPAYLA	136	2.3000	23.47

29	VPVRASIAA	200	2.3000	23.47
30	LRAEARAHF	214	2.2000	22.45
31	LNRAVSGAA	243	2.1000	21.43
32	LELITAVPM	88	2.0800	21.22
33	IAALDRAVL	206	2.0000	20.41
34	LDPRVRITA	61	1.7000	17.35
35	LHAHGPQNV	262	1.7000	17.35
36	LITAVPMPR	90	1.6000	16.33
37	VICRAGAMT	302	1.6000	16.33
38	ITALGTLRG	67	1.5600	15.92
39	LELRRRAQG	271	1.5000	15.31
40	VIHEANARA	161	1.4000	14.29
41	VVGVPVRAS	197	1.4000	14.29

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	LVALDPRVR	58	5.7000	58.16
2	YVAVPYLDR	283	5.3000	54.08
3	VVIHEANAR	160	4.2000	42.86
4	VRITALGTL	65	3.9000	39.80
5	YVALPAYLA	136	3.9000	39.80
6	LVICRAGAM	301	3.7000	37.76
7	LITAVPMPR	90	3.2000	32.65
8	VVGVPVRAS	197	3.1000	31.63
9	VLLVFGGSQ	230	3.1000	31.63
10	VLRAEARAH	213	3.0000	30.61
11	LVPQRGYHL	80	2.9000	29.59
12	YLAARGLPL	142	2.6000	26.53
13	YVPLPIGNG	323	2.6000	26.53
14	VVLAGGGTA	37	2.4000	24.49
15	LRGLETRLV	73	2.3000	23.47
16	VVNAGGGMV	340	1.7000	17.35

17	LELITAVPM	88	1.6000	16.33
18	VVGFGGYVA	130	1.6000	16.33
19	MVVADAALT	347	1.4000	14.29
20	VSVVLAGGG	35	1.3000	13.27
21	LPVVNAGGG	338	1.1000	11.22
22	VARQVAGLL	359	0.9000	9.18
23	ITAVPMPRK	91	0.7000	7.14
24	FGGYVALPA	133	0.7000	7.14
25	LAAMTAAAA	373	0.7000	7.14
26	MTAAAARVG	376	0.7000	7.14
27	FGGSQGAVS	234	0.6000	6.12
28	LNRAVSGAA	243	0.6000	6.12
29	LPLPPRRRR	148	0.5000	5.10
30	LVFGGSQGA	232	0.5000	5.10
31	VCVLHAHGP	259	0.5000	5.10
32	LARLPSRVW	104	0.4000	4.08
33	IHEANARAG	162	0.3000	3.06
34	VPYLDRMEL	286	0.3000	3.06
35	IYVPLPIGN	322	0.3000	3.06
36	LGTLRGLET	70	0.2000	2.04
37	MAVADALVA	52	0.1000	1.02
38	VVVGFGGYV	129	0.1000	1.02
39	LRRAEVVGV	192	0.1000	1.02
40	VLELRRRAQ	270	0.1000	1.02

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVALDPRVR	58	5.7000	58.16
2	YVAVPYLDR	283	5.3000	54.08
3	VVIHEANAR	160	4.2000	42.86
4	VRITALGTL	65	3.9000	39.80
5	YVALPAYLA	136	3.9000	39.80

6	LVICRAGAM	301	3.7000	37.76
7	LITAVPMPR	90	3.2000	32.65
8	VVGVPVRAS	197	3.1000	31.63
9	VLLVFGGSQ	230	3.1000	31.63
10	VLRAEARAH	213	3.0000	30.61
11	LVPQRGYHL	80	2.9000	29.59
12	YLAARGLPL	142	2.6000	26.53
13	YVPLPIGNG	323	2.6000	26.53
14	VVLAGGGTA	37	2.4000	24.49
15	LRGLETRLV	73	2.3000	23.47
16	VVNAGGGMV	340	1.7000	17.35
17	LELITAVPM	88	1.6000	16.33
18	VVGFGGYVA	130	1.6000	16.33
19	MVVADAALT	347	1.4000	14.29
20	VSVVLAGGG	35	1.3000	13.27
21	LPVVNAGGG	338	1.1000	11.22
22	VARQVAGLL	359	0.9000	9.18
23	ITAVPMPRK	91	0.7000	7.14
24	FGGYVALPA	133	0.7000	7.14
25	LAAMTAAAA	373	0.7000	7.14
26	MTAAAARVG	376	0.7000	7.14
27	FGGSQGAVS	234	0.6000	6.12
28	LNRAVSGAA	243	0.6000	6.12
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