MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Apr 14 00:46:41 2010
Length of input sequence	486 amino acids
Number of nanomers from input sequence	478
Number of nanomers with obligatory P1 anchor residue	147
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	48

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	FQLHWAPSL	169	2.0700	34.50
2	VQQITGYAL	60	1.4000	23.33
3	LRPEAGAVL	177	1.3000	21.67
4	FRLGEPAAR	238	1.3000	21.67
5	MLIAGGRRA	133	1.2900	21.50
6	VGVLDALAA	278	1.2000	20.00
7	VVWIAGGLL	347	0.7000	11.67
8	YTAAKARVL	201	0.5900	9.83

9	LLPVASIPV	266	0.5500	9.17
10	LTLLPVASI	264	0.5000	8.33
11	WLVVTGTNG	114	0.4400	7.33
12	FSPATPLLA	75	0.1000	1.67
13	VLVAGGRVT	10	0.0900	1.50
14	YALVVASPG	66	-0.0500	0
15	LGPGAPVLV	4	-0.1000	0
16	LTRFGATPT	26	-0.3300	0
17	VLLAPAGAS	454	-0.4000	0
18	VAAMASRLV	364	-0.4100	0
19	VQVVAGEDT	398	-0.4500	0
20	LARSVGVPA	289	-0.6000	0
21	LHAEVAAMA	360	-0.6000	0
22	VVASPGFSP	69	-0.7000	0
23	LAAAAAAGV	82	-0.7000	0
24	LLAAAAAAG	81	-0.8000	0
25	VGRHRAEVV	309	-0.8000	0
26	LDALAAAAL	281	-0.9000	0
27	LCGNIGSAV	143	-0.9600	0
28	WHATMAEYT	194	-1.0000	0
29	LLKGASLHA	354	-1.0000	0
30	VMTAAVAAA	436	-1.0000	0
31	LRPHAERGL	43	-1.0100	0
32	VAVADGITY	317	-1.1000	0
33	LVGAVLIGR	371	-1.1000	0
34	FATAVRAVI	476	-1.1000	0
35	WRLDAAGCY	100	-1.2000	0
36	VLDALAAAA	280	-1.3000	0
37	VWIAGGLLK	348	-1.3000	0
38	VELAWRLDA	96	-1.4000	0
39	YGPPRSWLV	108	-1.4800	0
40	LVAGGRVTG	11	-1.5000	0
41	VTGQAVAAV	17	-1.5000	0
42	VPVACVLDV	414	-1.5000	0

43	LHWAPSLRP	171	-1.6000	0
44	LTGGVAVAG	209	-1.6000	0
45	LGVRDAHLV	248	-1.7000	0
46	VLDEPAELL	154	-1.8000	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	VQQITGYAL	60	2.4000	40.00
2	LRPEAGAVL	177	2.3000	38.33
3	MLIAGGRRA	133	2.2900	38.17
4	VGVLDALAA	278	2.2000	36.67
5	FQLHWAPSL	169	2.0700	34.50
6	VVWIAGGLL	347	1.7000	28.33
7	LLPVASIPV	266	1.5500	25.83
8	LTLLPVASI	264	1.5000	25.00
9	FRLGEPAAR	238	1.3000	21.67
10	VLVAGGRVT	10	1.0900	18.17
11	LVVASPGFS	68	1.0000	16.67
12	LGPGAPVLV	4	0.9000	15.00
13	LTRFGATPT	26	0.6700	11.17
14	VLLAPAGAS	454	0.6000	10.00
15	VAAMASRLV	364	0.5900	9.83
16	VQVVAGEDT	398	0.5500	9.17
17	LARSVGVPA	289	0.4000	6.67
18	LHAEVAAMA	360	0.4000	6.67
19	VVASPGFSP	69	0.3000	5.00
20	LAAAAAAGV	82	0.3000	5.00
21	LLAAAAAAG	81	0.2000	3.33
22	VGRHRAEVV	309	0.2000	3.33
23	FSPATPLLA	75	0.1000	1.67
24	LDALAAAAL	281	0.1000	1.67
25	LCGNIGSAV	143	0.0400	0.67

26	LRPHAERGL	43	-0.0100	0
27	VAVADGITY	317	-0.1000	0
28	LVGAVLIGR	371	-0.1000	0
29	VLDALAAAA	280	-0.3000	0
30	VWIAGGLLK	348	-0.3000	0
31	VELAWRLDA	96	-0.4000	0
32	YTAAKARVL	201	-0.4100	0
33	LVAGGRVTG	11	-0.5000	0
34	VTGQAVAAV	17	-0.5000	0
35	VPVACVLDV	414	-0.5000	0
36	WLVVTGTNG	114	-0.5600	0
37	LHWAPSLRP	171	-0.6000	0
38	LTGGVAVAG	209	-0.6000	0
39	LGVRDAHLV	248	-0.7000	0
40	VLDEPAELL	154	-0.8000	0
41	VLTGGVAVA	208	-0.8000	0
42	LAYPRVVWI	342	-0.8000	0
43	VEVPVACVL	412	-0.8000	0
44	VLIGRDRAA	375	-0.8100	0
45	LLDGSPAQV	226	-0.9000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WRLDAAGCY	100	4.9000	51.58
2	LVVASPGFS	68	4.3000	45.26
3	LVAGGRVTG	11	4.2000	44.21
4	VRVGFRLGE	234	4.1000	43.16
5	FRLGEPAAR	238	3.7000	38.95
6	IGRDRAAVA	377	3.5000	36.84
7	LVGAVLIGR	371	3.4000	35.79
8	VAKDDKAGE	422	3.3000	34.74
9	VLLAPAGAS	454	3.2000	33.68

10	LTLLPVASI	264	2.8000	29.47
11	YVDDSKATN	325	2.8000	29.47
12	VLTGGVAVA	208	2.7000	28.42
13	LGPGAPVLV	4	2.3000	24.21
14	VVASPGFSP	69	2.3000	24.21
15	VELAWRLDA	96	2.3000	24.21
16	VLCGNIGSA	142	2.3000	24.21
17	VASIPVPGP	269	2.3000	24.21
18	VMTAAVAAA	436	2.3000	24.21
19	MLHAMLIAG	129	2.2000	23.16
20	LLAVELSSF	161	2.1700	22.84
21	LVVTGTNGK	115	2.1100	22.21
22	LIAGGRRAV	134	2.0000	21.05
23	VVWIAGGLL	347	1.9600	20.63
24	LHAMLIAGG	130	1.9000	20.00
25	LLPVASIPV	266	1.9000	20.00
26	VAAARRMAQ	441	1.9000	20.00
27	FQLHWAPSL	169	1.8600	19.58
28	VRDAHLVDR	250	1.8000	18.95
29	LAYPRVVWI	342	1.8000	18.95
30	VPVVQVVAG	395	1.8000	18.95
31	VTGQAVAAV	17	1.7000	17.89
32	WAPSLRPEA	173	1.7000	17.89
33	VPVACVLDV	414	1.7000	17.89
34	VCDDDPVML	35	1.6600	17.47
35	IAGGRRAVL	135	1.6600	17.47
36	VAGGRVTGQ	12	1.6000	16.84
37	VVTGTNGKT	116	1.6000	16.84
38	LLKGASLHA	354	1.6000	16.84
39	LIGRDRAAV	376	1.6000	16.84
40	VVQVVAGED	397	1.6000	16.84
41	VMLRPHAER	41	1.5000	15.79
42	LLAAAAAAG	81	1.4000	14.74
43	WIAGGLLKG	349	1.4000	14.74

44	LTGGVAVAG	209	1.3000	13.68
45	LAAAALARS	284	1.3000	13.68
46	VGRHRAEVV	309	1.3000	13.68
47	VAVAGLDDS	213	1.2000	12.63
48	VGVLDALAA	278	1.2000	12.63

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	WRLDAAGCY	100	4.6000	50.55
2	FRLGEPAAR	238	3.2000	35.16
3	YVDDSKATN	325	3.0000	32.97
4	LVVASPGFS	68	2.9000	31.87
5	WAPSLRPEA	173	2.7000	29.67
6	IGRDRAAVA	377	2.5000	27.47
7	FQLHWAPSL	169	1.9000	20.88
8	LVAGGRVTG	11	1.8000	19.78
9	VLLAPAGAS	454	1.8000	19.78
10	VLTGGVAVA	208	1.7000	18.68
11	VRVGFRLGE	234	1.7000	18.68
12	VAAARRMAQ	441	1.6000	17.58
13	VAGGRVTGQ	12	1.3000	14.29
14	VELAWRLDA	96	1.3000	14.29
15	VLCGNIGSA	142	1.3000	14.29
16	VMTAAVAAA	436	1.3000	14.29
17	LVVTGTNGK	115	1.0100	11.10
18	WIAGGLLKG	349	1.0000	10.99
19	LTLLPVASI	264	0.9000	9.89
20	LVGAVLIGR	371	0.9000	9.89
21	VAKDDKAGE	422	0.9000	9.89
22	FSPATPLLA	75	0.7000	7.69
23	FATAVRAVI	476	0.7000	7.69
24	LLKGASLHA	354	0.6000	6.59

25	FRVGRHRAE	307	0.5000	5.49
26	FSDDLTLLP	260	0.4000	4.40
27	LGPGAPVLV	4	0.3000	3.30
28	VSSSDAVQQ	54	0.3000	3.30
29	VVASPGFSP	69	0.3000	3.30
30	VASIPVPGP	269	0.3000	3.30
31	VGVLDALAA	278	0.2000	2.20
32	YALVVASPG	66	0.0700	0.77
33	VVTGTNGKT	116	-0.1000	0
34	MLIAGGRRA	133	-0.1000	0
35	LLPVASIPV	266	-0.1000	0
36	LAAAALARS	284	-0.1000	0
37	LARSVGVPA	289	-0.1000	0
38	LAYPRVVWI	342	-0.1000	0
39	MLHAMLIAG	129	-0.2000	0
40	VAVAGLDDS	213	-0.2000	0
41	IAEDHLDWH	187	-0.2200	0
42	VTGQAVAAV	17	-0.3000	0
43	VCDDDPVML	35	-0.3000	0
44	WLVVTGTNG	114	-0.3000	0
45	IAGGRRAVL	135	-0.3000	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	IGRDRAAVA	377	3.5000	39.77
2	VRVGFRLGE	234	3.2000	36.36
3	VELAWRLDA	96	2.8000	31.82
4	LVVTGTNGK	115	2.7000	30.68
5	VLTGGVAVA	208	2.7000	30.68
6	LVAGGRVTG	11	2.6800	30.45
7	LVVASPGFS	68	2.5000	28.41
8	VAGGRVTGQ	12	2.3000	26.14

9	VMTAAVAAA	436	2.3000	26.14
10	VAAARRMAQ	441	2.3000	26.14
11	WRLDAAGCY	100	2.2000	25.00
12	FRLGEPAAR	238	2.2000	25.00
13	LLKGASLHA	354	2.1000	23.86
14	YVDDSKATN	325	2.0000	22.73
15	LTLLPVASI	264	1.9000	21.59
16	VAKDDKAGE	422	1.9000	21.59
17	VGVLDALAA	278	1.7000	19.32
18	LVGAVLIGR	371	1.5800	17.95
19	VLLAPAGAS	454	1.4000	15.91
20	VPVACVLDV	414	1.2000	13.64
21	LGPGAPVLV	4	1.1800	13.41
22	VSSSDAVQQ	54	1.1800	13.41
23	VAVAGLDDS	213	1.1000	12.50
24	VWIAGGLLK	348	1.1000	12.50
25	IAEDHLDWH	187	1.0800	12.27
26	VLCGNIGSA	142	0.9000	10.23
27	LAAAALARS	284	0.9000	10.23
28	LARSVGVPA	289	0.7800	8.86
29	LAYPRVVWI	342	0.7800	8.86
30	VTGQAVAAV	17	0.7000	7.95
31	IWGDVELAW	92	0.7000	7.95
32	LIAGGRRAV	134	0.7000	7.95
33	IAGGRRAVL	135	0.7000	7.95
34	VPAGAIADA	295	0.7000	7.95
35	VGRHRAEVV	309	0.7000	7.95
36	MLIAGGRRA	133	0.6000	6.82
37	IAGGLLKGA	350	0.6000	6.82
38	LIGRDRAAV	376	0.6000	6.82
39	VCDDDPVML	35	0.5800	6.59
40	LLPVASIPV	266	0.5800	6.59
41	LHAMLIAGG	130	0.5000	5.68
42	WIAGGLLKG	349	0.5000	5.68

43	MLHAMLIAG	129	0.4800	5.45
44	VELSSFQLH	164	0.4800	5.45
45	VLDVAKDDK	419	0.4000	4.55
46	WAPSLRPEA	173	0.3000	3.41
47	VPVVQVVAG	395	0.2800	3.18
48	FSPATPLLA	75	0.2000	2.27

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	IGRDRAAVA	377	3.5000	39.77
2	VRVGFRLGE	234	3.2000	36.36
3	VELAWRLDA	96	2.8000	31.82
4	LVVTGTNGK	115	2.7000	30.68
5	VLTGGVAVA	208	2.7000	30.68
6	LVAGGRVTG	11	2.6800	30.45
7	LVVASPGFS	68	2.5000	28.41
8	VAGGRVTGQ	12	2.3000	26.14
9	VMTAAVAAA	436	2.3000	26.14
10	VAAARRMAQ	441	2.3000	26.14
11	WRLDAAGCY	100	2.2000	25.00
12	FRLGEPAAR	238	2.2000	25.00
13	LLKGASLHA	354	2.1000	23.86
14	YVDDSKATN	325	2.0000	22.73
15	LTLLPVASI	264	1.9000	21.59
16	VAKDDKAGE	422	1.9000	21.59
17	VGVLDALAA	278	1.7000	19.32
18	LVGAVLIGR	371	1.5800	17.95
19	VLLAPAGAS	454	1.4000	15.91
20	VPVACVLDV	414	1.2000	13.64
21	LGPGAPVLV	4	1.1800	13.41
22	VSSSDAVQQ	54	1.1800	13.41
23	VAVAGLDDS	213	1.1000	12.50

24	VWIAGGLLK	348	1.1000	12.50
25	IAEDHLDWH	187	1.0800	12.27
26	VLCGNIGSA	142	0.9000	10.23
27	LAAAALARS	284	0.9000	10.23
28	LARSVGVPA	289	0.7800	8.86
29	LAYPRVVWI	342	0.7800	8.86
30	VTGQAVAAV	17	0.7000	7.95
31	IWGDVELAW	92	0.7000	7.95
32	LIAGGRRAV	134	0.7000	7.95
33	IAGGRRAVL	135	0.7000	7.95
34	VPAGAIADA	295	0.7000	7.95
35	VGRHRAEVV	309	0.7000	7.95
36	MLIAGGRRA	133	0.6000	6.82
37	IAGGLLKGA	350	0.6000	6.82
38	LIGRDRAAV	376	0.6000	6.82
39	VCDDDPVML	35	0.5800	6.59
40	LLPVASIPV	266	0.5800	6.59
41	LHAMLIAGG	130	0.5000	5.68
42	WIAGGLLKG	349	0.5000	5.68
43	MLHAMLIAG	129	0.4800	5.45
44	VELSSFQLH	164	0.4800	5.45
45	VLDVAKDDK	419	0.4000	4.55
46	WAPSLRPEA	173	0.3000	3.41
47	VPVVQVVAG	395	0.2800	3.18
48	FSPATPLLA	75	0.2000	2.27

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	IGRDRAAVA	377	3.5000	39.77
2	VRVGFRLGE	234	3.2000	36.36
3	VELAWRLDA	96	2.8000	31.82
4	LVVTGTNGK	115	2.7000	30.68

5	VLTGGVAVA	208	2.7000	30.68
6	LVAGGRVTG	11	2.6800	30.45
7	LVVASPGFS	68	2.5000	28.41
8	VAGGRVTGQ	12	2.3000	26.14
9	VMTAAVAAA	436	2.3000	26.14
10	VAAARRMAQ	441	2.3000	26.14
11	WRLDAAGCY	100	2.2000	25.00
12	FRLGEPAAR	238	2.2000	25.00
13	LLKGASLHA	354	2.1000	23.86
14	YVDDSKATN	325	2.0000	22.73
15	LTLLPVASI	264	1.9000	21.59
16	VAKDDKAGE	422	1.9000	21.59
17	VGVLDALAA	278	1.7000	19.32
18	LVGAVLIGR	371	1.5800	17.95
19	VLLAPAGAS	454	1.4000	15.91
20	VPVACVLDV	414	1.2000	13.64
21	LGPGAPVLV	4	1.1800	13.41
22	VSSSDAVQQ	54	1.1800	13.41
23	VAVAGLDDS	213	1.1000	12.50
24	VWIAGGLLK	348	1.1000	12.50
25	IAEDHLDWH	187	1.0800	12.27
26	VLCGNIGSA	142	0.9000	10.23
27	LAAAALARS	284	0.9000	10.23
28	LARSVGVPA	289	0.7800	8.86
29	LAYPRVVWI	342	0.7800	8.86
30	VTGQAVAAV	17	0.7000	7.95
31	IWGDVELAW	92	0.7000	7.95
32	LIAGGRRAV	134	0.7000	7.95
33	IAGGRRAVL	135	0.7000	7.95
34	VPAGAIADA	295	0.7000	7.95
35	VGRHRAEVV	309	0.7000	7.95
36	MLIAGGRRA	133	0.6000	6.82
37	IAGGLLKGA	350	0.6000	6.82
38	LIGRDRAAV	376	0.6000	6.82

39	VCDDDPVML	35	0.5800	6.59
40	LLPVASIPV	266	0.5800	6.59
41	LHAMLIAGG	130	0.5000	5.68
42	WIAGGLLKG	349	0.5000	5.68
43	MLHAMLIAG	129	0.4800	5.45
44	VELSSFQLH	164	0.4800	5.45
45	VLDVAKDDK	419	0.4000	4.55
46	WAPSLRPEA	173	0.3000	3.41
47	VPVVQVVAG	395	0.2800	3.18
48	FSPATPLLA	75	0.2000	2.27

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	WRLDAAGCY	100	5.9000	62.11
2	FRLGEPAAR	238	4.7000	49.47
3	YVDDSKATN	325	3.8000	40.00
4	LVVASPGFS	68	3.3000	34.74
5	LVAGGRVTG	11	3.2000	33.68
6	VRVGFRLGE	234	3.1000	32.63
7	FQLHWAPSL	169	2.8600	30.11
8	WAPSLRPEA	173	2.7000	28.42
9	IGRDRAAVA	377	2.5000	26.32
10	WIAGGLLKG	349	2.4000	25.26
11	LVGAVLIGR	371	2.4000	25.26
12	VAKDDKAGE	422	2.3000	24.21
13	VLLAPAGAS	454	2.2000	23.16
14	FRVGRHRAE	307	1.9000	20.00
15	LTLLPVASI	264	1.8000	18.95
16	VLTGGVAVA	208	1.7000	17.89
17	FATAVRAVI	476	1.6000	16.84
18	YALVVASPG	66	1.4700	15.47
19	FSDDLTLLP	260	1.4000	14.74

20	LGPGAPVLV	4	1.3000	13.68
21	VVASPGFSP	69	1.3000	13.68
22	VELAWRLDA	96	1.3000	13.68
23	VLCGNIGSA	142	1.3000	13.68
24	VASIPVPGP	269	1.3000	13.68
25	VMTAAVAAA	436	1.3000	13.68
26	MLHAMLIAG	129	1.2000	12.63
27	LLAVELSSF	161	1.1700	12.32
28	LVVTGTNGK	115	1.1100	11.68
29	WLVVTGTNG	114	1.1000	11.58
30	LIAGGRRAV	134	1.0000	10.53
31	VVWIAGGLL	347	0.9600	10.11
32	LHAMLIAGG	130	0.9000	9.47
33	LLPVASIPV	266	0.9000	9.47
34	VAAARRMAQ	441	0.9000	9.47
35	VRDAHLVDR	250	0.8000	8.42
36	LAYPRVVWI	342	0.8000	8.42
37	VPVVQVVAG	395	0.8000	8.42
38	VTGQAVAAV	17	0.7000	7.37
39	FSPATPLLA	75	0.7000	7.37
40	VPVACVLDV	414	0.7000	7.37
41	VCDDDPVML	35	0.6600	6.95
42	IAGGRRAVL	135	0.6600	6.95
43	VAGGRVTGQ	12	0.6000	6.32
44	VVTGTNGKT	116	0.6000	6.32
45	LLKGASLHA	354	0.6000	6.32
46	LIGRDRAAV	376	0.6000	6.32
47	VVQVVAGED	397	0.6000	6.32
48	VMLRPHAER	41	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	IGRDRAAVA	377	3.5000	39.77
2	VRVGFRLGE	234	3.2000	36.36
3	VELAWRLDA	96	2.8000	31.82
4	LVVTGTNGK	115	2.7000	30.68
5	VLTGGVAVA	208	2.7000	30.68
6	LVAGGRVTG	11	2.6800	30.45
7	LVVASPGFS	68	2.5000	28.41
8	VAGGRVTGQ	12	2.3000	26.14
9	VMTAAVAAA	436	2.3000	26.14
10	VAAARRMAQ	441	2.3000	26.14
11	WRLDAAGCY	100	2.2000	25.00
12	FRLGEPAAR	238	2.2000	25.00
13	LLKGASLHA	354	2.1000	23.86
14	YVDDSKATN	325	2.0000	22.73
15	LTLLPVASI	264	1.9000	21.59
16	VAKDDKAGE	422	1.9000	21.59
17	VGVLDALAA	278	1.7000	19.32
18	LVGAVLIGR	371	1.5800	17.95
19	VLLAPAGAS	454	1.4000	15.91
20	VPVACVLDV	414	1.2000	13.64
21	LGPGAPVLV	4	1.1800	13.41
22	VSSSDAVQQ	54	1.1800	13.41
23	VAVAGLDDS	213	1.1000	12.50
24	VWIAGGLLK	348	1.1000	12.50
25	IAEDHLDWH	187	1.0800	12.27
26	VLCGNIGSA	142	0.9000	10.23
27	LAAAALARS	284	0.9000	10.23
28	LARSVGVPA	289	0.7800	8.86
29	LAYPRVVWI	342	0.7800	8.86
30	VTGQAVAAV	17	0.7000	7.95
31	IWGDVELAW	92	0.7000	7.95
32	LIAGGRRAV	134	0.7000	7.95
33	IAGGRRAVL	135	0.7000	7.95
34	VPAGAIADA	295	0.7000	7.95

35	VGRHRAEVV	309	0.7000	7.95
36	MLIAGGRRA	133	0.6000	6.82
37	IAGGLLKGA	350	0.6000	6.82
38	LIGRDRAAV	376	0.6000	6.82
39	VCDDDPVML	35	0.5800	6.59
40	LLPVASIPV	266	0.5800	6.59
41	LHAMLIAGG	130	0.5000	5.68
42	WIAGGLLKG	349	0.5000	5.68
43	MLHAMLIAG	129	0.4800	5.45
44	VELSSFQLH	164	0.4800	5.45
45	VLDVAKDDK	419	0.4000	4.55
46	WAPSLRPEA	173	0.3000	3.41
47	VPVVQVVAG	395	0.2800	3.18
48	FSPATPLLA	75	0.2000	2.27

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	LVVTGTNGK	115	4.5000	52.33
2	WRLDAAGCY	100	2.3000	26.74
3	LAVELSSFQ	162	2.3000	26.74
4	FQLHWAPSL	169	1.6000	18.60
5	IGRDRAAVA	377	1.6000	18.60
6	VGVLDALAA	278	1.5000	17.44
7	FGATPTVCD	29	1.4800	17.21
8	LTLLPVASI	264	1.4000	16.28
9	LHAEVAAMA	360	1.3000	15.12
10	FSDDLTLLP	260	1.1000	12.79
11	LVVASPGFS	68	1.0000	11.63
12	VMTAAVAAA	436	1.0000	11.63
13	VGRHRAEVV	309	0.8000	9.30
14	FSPATPLLA	75	0.7000	8.14
15	FRLGEPAAR	238	0.6000	6.98

16	LRPEAGAVL	177	0.5000	5.81
17	WHATMAEYT	194	0.5000	5.81
18	VLLAPAGAS	454	0.4000	4.65
19	VSSSDAVQQ	54	0.2800	3.26
20	VTGQAVAAV	17	0.2000	2.33
21	LHWAPSLRP	171	0.2000	2.33
22	LLKGASLHA	354	0.1000	1.16
23	VPVACVLDV	414	-0.1000	0
24	VELSSFQLH	164	-0.1200	0
25	LDWHATMAE	192	-0.2000	0
26	LLPVASIPV	266	-0.2200	0
27	LHAMLIAGG	130	-0.4000	0
28	VLDEPAELL	154	-0.6000	0
29	VLTGGVAVA	208	-0.7000	0
30	VWIAGGLLK	348	-0.7000	0
31	LVGAVLIGR	371	-0.7200	0
32	LARSVGVPA	289	-0.9200	0
33	LLAAAAAAG	81	-1.0000	0
34	VAAMASRLV	364	-1.0000	0
35	VAGGRVTGQ	12	-1.1000	0
36	YALVVASPG	66	-1.1000	0
37	VASIPVPGP	269	-1.1000	0
38	LSRHAPDVP	388	-1.1000	0
39	LAYPRVVWI	342	-1.1200	0
40	MLIAGGRRA	133	-1.2000	0
41	VAVAGLDDS	213	-1.2000	0
42	VAGLDDSRA	215	-1.3000	0
43	VLDALAAAA	280	-1.3000	0
44	LAAAALARS	284	-1.4000	0
45	LNIAEDHLD	185	-1.5000	0
46	LPTVSSSDA	51	-1.6000	0

ALLELE: DRB1_0402	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	1.8	9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVTGTNGK	115	4.3000	44.79
2	MLIAGGRRA	133	2.7000	28.13
3	VAAMASRLV	364	2.6000	27.08
4	VLIGRDRAA	375	2.4000	25.00
5	LLKGASLHA	354	2.3000	23.96
6	LRPHAERGL	43	2.0000	20.83
7	VMTAAVAAA	436	2.0000	20.83
8	VAAVLTRFG	22	1.9000	19.79
9	LGVRDAHLV	248	1.8000	18.75
10	LHWAPSLRP	171	1.5000	15.62
11	VAEALSRHA	384	1.5000	15.62
12	LLPVASIPV	266	1.4000	14.58
13	VGVLDALAA	278	1.4000	14.58
14	LVVASPGFS	68	1.2000	12.50
15	VLTGGVAVA	208	1.2000	12.50
16	VPVACVLDV	414	1.2000	12.50
17	VAGGRVTGQ	12	1.0000	10.42
18	LTLLPVASI	264	1.0000	10.42
19	LDWHATMAE	192	0.9000	9.38
20	VMLRPHAER	41	0.7000	7.29
21	VPIWGDVEL	90	0.7000	7.29
22	LVGAVLIGR	371	0.7000	7.29
23	VWIAGGLLK	348	0.6000	6.25
24	VLLAPAGAS	454	0.6000	6.25
25	VLVAGGRVT	10	0.5000	5.21
26	FRLGEPAAR	238	0.5000	5.21
27	VGRHRAEVV	309	0.5000	5.21
28	FQLHWAPSL	169	0.4000	4.17
29	LHAMLIAGG	130	0.3000	3.12
30	LAYPRVVWI	342	0.3000	3.12
31	YGPPRSWLV	108	0.2000	2.08
32	VELSSFQLH	164	0.1800	1.88

33	LTRFGATPT	26	-0.1000	0
34	VELAWRLDA	96	-0.3000	0
35	YTAAKARVL	201	-0.3000	0
36	VLDALAAAA	280	-0.3000	0
37	VQQITGYAL	60	-0.3200	0
38	LGPGAPVLV	4	-0.4000	0
39	VSSSDAVQQ	54	-0.4000	0
40	MLHAMLIAG	129	-0.4000	0
41	LSSFQLHWA	166	-0.4000	0
42	VGFRLGEPA	236	-0.4000	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	LVVTGTNGK	115	4.0000	45.45
2	LTLLPVASI	264	2.6000	29.55
3	VGVLDALAA	278	2.3000	26.14
4	LLPVASIPV	266	2.1800	24.77
5	LVVASPGFS	68	2.1000	23.86
6	VMTAAVAAA	436	2.0000	22.73
7	LPTVSSSDA	51	1.5000	17.05
8	LHAMLIAGG	130	1.5000	17.05
9	VLLAPAGAS	454	1.5000	17.05
10	LAVELSSFQ	162	1.4000	15.91
11	VAAMASRLV	364	1.2000	13.64
12	VTSFRVGRH	304	0.9800	11.14
13	LTRFGATPT	26	0.9000	10.23
14	LHWAPSLRP	171	0.8000	9.09
15	ITYVDDSKA	323	0.7000	7.95
16	VAGLDDSRA	215	0.6000	6.82
17	VAAVLTRFG	22	0.5000	5.68
18	VPVACVLDV	414	0.5000	5.68
19	VTGQAVAAV	17	0.4000	4.55

20	VPVVQVVAG	395	0.3000	3.41
21	LVGAVLIGR	371	0.2800	3.18
22	MLIAGGRRA	133	0.1000	1.14
23	IADAVTSFR	300	0.1000	1.14
24	IGRDRAAVA	377	0.1000	1.14
25	LLAVELSSF	161	-0.1000	0
26	VASIPVPGP	269	-0.1000	0
27	VWIAGGLLK	348	-0.1000	0
28	LLKGASLHA	354	-0.1000	0
29	VGAAVMTAA	432	-0.2000	0
30	VLDALAAAA	280	-0.3000	0
31	LHAEVAAMA	360	-0.3000	0
32	VVQVVAGED	397	-0.3000	0
33	VAGGRVTGQ	12	-0.4000	0
34	VSSSDAVQQ	54	-0.4000	0
35	VQQITGYAL	60	-0.4000	0
36	LAAAALARS	284	-0.4000	0
37	VLTGGVAVA	208	-0.5000	0
38	VVWIAGGLL	347	-0.5000	0
39	LSSFQLHWA	166	-0.6000	0
40	FSPATPLLA	75	-0.7000	0
41	LAAAAAAGV	82	-0.7000	0
42	MLHAMLIAG	129	-0.8200	0
43	VELSSFQLH	164	-0.8200	0
44	LNIAEDHLD	185	-0.9000	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	FGATPTVCD	29	2.4000	25.53
2	YALVVASPG	66	2.3000	24.47
3	LVVTGTNGK	115	2.3000	24.47
4	LHAMLIAGG	130	1.8000	19.15

5	LTLLPVASI	264	1.8000	19.15
6	LLPVASIPV	266	1.4800	15.74
7	VVQVVAGED	397	1.4000	14.89
8	VGVLDALAA	278	1.3000	13.83
9	WLVVTGTNG	114	1.2000	12.77
10	LAVELSSFQ	162	1.2000	12.77
11	VTSFRVGRH	304	1.2000	12.77
12	LVVASPGFS	68	1.1000	11.70
13	WRLDAAGCY	100	1.0000	10.64
14	VMTAAVAAA	436	1.0000	10.64
15	VAAVLTRFG	22	0.8000	8.51
16	LTRFGATPT	26	0.8000	8.51
17	LNIAEDHLD	185	0.8000	8.51
18	LAPAGASFD	456	0.8000	8.51
19	LDWHATMAE	192	0.6000	6.38
20	VPVVQVVAG	395	0.6000	6.38
21	LPTVSSSDA	51	0.5000	5.32
22	VAAMASRLV	364	0.5000	5.32
23	VLLAPAGAS	454	0.5000	5.32
24	FSPATPLLA	75	0.3000	3.19
25	LLAAAAAAG	81	0.3000	3.19
26	FQLHWAPSL	169	0.2000	2.13
27	LHWAPSLRP	171	0.2000	2.13
28	LKGASLHAE	355	0.1000	1.06
29	YPRVVWIAG	344	0.0800	0.85
30	LLAVELSSF	161	-0.2000	0
31	FRLGEPAAR	238	-0.2000	0
32	VPVACVLDV	414	-0.2000	0
33	VTGQAVAAV	17	-0.3000	0
34	ITYVDDSKA	323	-0.3000	0
35	VGAVLIGRD	372	-0.3000	0
36	VQQITGYAL	60	-0.4000	0
37	VAGLDDSRA	215	-0.4000	0
38	VVWIAGGLL	347	-0.5000	0

39	MLHAMLIAG	129	-0.5200	0
40	VAGGRVTGQ	12	-0.6000	0
41	VSSSDAVQQ	54	-0.6000	0
42	YGPPRSWLV	108	-0.6000	0
43	VELSSFQLH	164	-0.6000	0
44	VASIPVPGP	269	-0.7000	0
45	FRVGRHRAE	307	-0.7000	0
46	LVGAVLIGR	371	-0.7200	0
47	LAYPRVVWI	342	-0.8000	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	LVVTGTNGK	115	3.0000	34.09
2	LTLLPVASI	264	1.6000	18.18
3	VGVLDALAA	278	1.3000	14.77
4	LLPVASIPV	266	1.1800	13.41
5	LVVASPGFS	68	1.1000	12.50
6	YALVVASPG	66	1.0000	11.36
7	VMTAAVAAA	436	1.0000	11.36
8	LPTVSSSDA	51	0.5000	5.68
9	LHAMLIAGG	130	0.5000	5.68
10	VLLAPAGAS	454	0.5000	5.68
11	LAVELSSFQ	162	0.4000	4.55
12	FSPATPLLA	75	0.3000	3.41
13	VAAMASRLV	364	0.2000	2.27
14	VTSFRVGRH	304	-0.0200	0
15	LTRFGATPT	26	-0.1000	0
16	WRLDAAGCY	100	-0.1000	0
17	WLVVTGTNG	114	-0.1000	0
18	LHWAPSLRP	171	-0.2000	0
19	FRLGEPAAR	238	-0.2000	0
20	FGATPTVCD	29	-0.3000	0

21	ITYVDDSKA	323	-0.3000	0
22	VAGLDDSRA	215	-0.4000	0
23	VAAVLTRFG	22	-0.5000	0
24	VPVACVLDV	414	-0.5000	0
25	VTGQAVAAV	17	-0.6000	0
26	VPVVQVVAG	395	-0.7000	0
27	LVGAVLIGR	371	-0.7200	0
28	FQLHWAPSL	169	-0.8000	0
29	YGPPRSWLV	108	-0.9000	0
30	MLIAGGRRA	133	-0.9000	0
31	IADAVTSFR	300	-0.9000	0
32	IGRDRAAVA	377	-0.9000	0
33	LLAAAAAAG	81	-1.0000	0
34	LAYPRVVWI	342	-1.0000	0
35	LLAVELSSF	161	-1.1000	0
36	VASIPVPGP	269	-1.1000	0
37	VWIAGGLLK	348	-1.1000	0
38	LLKGASLHA	354	-1.1000	0
39	VGAAVMTAA	432	-1.2000	0
40	YPRVVWIAG	344	-1.2200	0
41	VLDALAAAA	280	-1.3000	0
42	LHAEVAAMA	360	-1.3000	0
43	VVQVVAGED	397	-1.3000	0
44	VAGGRVTGQ	12	-1.4000	0
45	VSSSDAVQQ	54	-1.4000	0
46	VQQITGYAL	60	-1.4000	0
47	LAAAALARS	284	-1.4000	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	LVVTGTNGK	115	3.3000	35.11
2	LHAMLIAGG	130	2.8000	29.79

3	LTLLPVASI	264	2.8000	29.79
4	LLPVASIPV	266	2.4800	26.38
5	VVQVVAGED	397	2.4000	25.53
6	VGVLDALAA	278	2.3000	24.47
7	LAVELSSFQ	162	2.2000	23.40
8	VTSFRVGRH	304	2.2000	23.40
9	LVVASPGFS	68	2.1000	22.34
10	VMTAAVAAA	436	2.0000	21.28
11	VAAVLTRFG	22	1.8000	19.15
12	LTRFGATPT	26	1.8000	19.15
13	LNIAEDHLD	185	1.8000	19.15
14	LAPAGASFD	456	1.8000	19.15
15	LDWHATMAE	192	1.6000	17.02
16	VPVVQVVAG	395	1.6000	17.02
17	LPTVSSSDA	51	1.5000	15.96
18	VAAMASRLV	364	1.5000	15.96
19	VLLAPAGAS	454	1.5000	15.96
20	FGATPTVCD	29	1.4000	14.89
21	YALVVASPG	66	1.3000	13.83
22	LLAAAAAAG	81	1.3000	13.83
23	LHWAPSLRP	171	1.2000	12.77
24	LKGASLHAE	355	1.1000	11.70
25	LLAVELSSF	161	0.8000	8.51
26	VPVACVLDV	414	0.8000	8.51
27	VTGQAVAAV	17	0.7000	7.45
28	ITYVDDSKA	323	0.7000	7.45
29	VGAVLIGRD	372	0.7000	7.45
30	VQQITGYAL	60	0.6000	6.38
31	VAGLDDSRA	215	0.6000	6.38
32	VVWIAGGLL	347	0.5000	5.32
33	MLHAMLIAG	129	0.4800	5.11
34	VAGGRVTGQ	12	0.4000	4.26
35	VSSSDAVQQ	54	0.4000	4.26
36	VELSSFQLH	164	0.4000	4.26

37	VASIPVPGP	269	0.3000	3.19
38	LVGAVLIGR	371	0.2800	2.98
39	WLVVTGTNG	114	0.2000	2.13
40	LAYPRVVWI	342	0.2000	2.13
41	MLIAGGRRA	133	0.1000	1.06
42	IADAVTSFR	300	0.1000	1.06
43	IGRDRAAVA	377	0.1000	1.06
44	LRPEAGAVL	177	-0.1000	0

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	LVVTGTNGK	115	4.6000	51.11
2	WRLDAAGCY	100	3.6000	40.00
3	FGATPTVCD	29	2.5800	28.67
4	FQLHWAPSL	169	2.5600	28.44
5	LTLLPVASI	264	2.3000	25.56
6	FRLGEPAAR	238	2.1000	23.33
7	FSDDLTLLP	260	2.1000	23.33
8	VGRHRAEVV	309	1.8000	20.00
9	LAVELSSFQ	162	1.6000	17.78
10	IGRDRAAVA	377	1.6000	17.78
11	VGVLDALAA	278	1.5000	16.67
12	LRPEAGAVL	177	1.4600	16.22
13	LVVASPGFS	68	1.4000	15.56
14	LHAEVAAMA	360	1.3000	14.44
15	VTGQAVAAV	17	1.2000	13.33
16	LHWAPSLRP	171	1.2000	13.33
17	LDWHATMAE	192	1.2000	13.33
18	WHATMAEYT	194	1.2000	13.33
19	LHAMLIAGG	130	1.0000	11.11
20	VAGEDTGMP	401	1.0000	11.11
21	VMTAAVAAA	436	1.0000	11.11

22	VPVACVLDV	414	0.9000	10.00
23	VLLAPAGAS	454	0.8000	8.89
24	LLPVASIPV	266	0.7800	8.67
25	LVGAVLIGR	371	0.7800	8.67
26	FSPATPLLA	75	0.7000	7.78
27	LLAAAAAAG	81	0.4000	4.44
28	VLDEPAELL	154	0.3600	4.00
29	YALVVASPG	66	0.3000	3.33
30	LLKGASLHA	354	0.1000	1.11
31	VASIPVPGP	269	-0.1000	0
32	IADAVTSFR	300	-0.1000	0
33	LSRHAPDVP	388	-0.1000	0
34	LAYPRVVWI	342	-0.2200	0
35	MLRPHAERG	42	-0.3000	0
36	LNIAEDHLD	185	-0.4000	0
37	VSSSDAVQQ	54	-0.4200	0
38	MLHAMLIAG	129	-0.4200	0
39	WIAGGLLKG	349	-0.5000	0
40	MTAAVAAAR	437	-0.5000	0
41	VPVVQVVAG	395	-0.5200	0
42	WLVVTGTNG	114	-0.6000	0
43	VWIAGGLLK	348	-0.6000	0
44	VVAGEDTGM	400	-0.6000	0
45	VRDAHLVDR	250	-0.6200	0
46	LAAAAAAGV	82	-0.7000	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	LVVTGTNGK	115	4.0000	45.45
2	LTLLPVASI	264	2.6000	29.55
3	VGVLDALAA	278	2.3000	26.14
4	LLPVASIPV	266	2.1800	24.77

5	LVVASPGFS	68	2.1000	23.86
6	VMTAAVAAA	436	2.0000	22.73
7	LPTVSSSDA	51	1.5000	17.05
8	LHAMLIAGG	130	1.5000	17.05
9	VLLAPAGAS	454	1.5000	17.05
10	LAVELSSFQ	162	1.4000	15.91
11	VAAMASRLV	364	1.2000	13.64
12	VTSFRVGRH	304	0.9800	11.14
13	LTRFGATPT	26	0.9000	10.23
14	LHWAPSLRP	171	0.8000	9.09
15	ITYVDDSKA	323	0.7000	7.95
16	VAGLDDSRA	215	0.6000	6.82
17	VAAVLTRFG	22	0.5000	5.68
18	VPVACVLDV	414	0.5000	5.68
19	VTGQAVAAV	17	0.4000	4.55
20	VPVVQVVAG	395	0.3000	3.41
21	LVGAVLIGR	371	0.2800	3.18
22	MLIAGGRRA	133	0.1000	1.14
23	IADAVTSFR	300	0.1000	1.14
24	IGRDRAAVA	377	0.1000	1.14
25	LLAVELSSF	161	-0.1000	0
26	VASIPVPGP	269	-0.1000	0
27	VWIAGGLLK	348	-0.1000	0
28	LLKGASLHA	354	-0.1000	0
29	VGAAVMTAA	432	-0.2000	0
30	VLDALAAAA	280	-0.3000	0
31	LHAEVAAMA	360	-0.3000	0
32	VVQVVAGED	397	-0.3000	0
33	VAGGRVTGQ	12	-0.4000	0
34	VSSSDAVQQ	54	-0.4000	0
35	VQQITGYAL	60	-0.4000	0
36	LAAAALARS	284	-0.4000	0
37	VLTGGVAVA	208	-0.5000	0
38	VVWIAGGLL	347	-0.5000	0

39	LSSFQLHWA	166	-0.6000	0
40	FSPATPLLA	75	-0.7000	0
41	LAAAAAAGV	82	-0.7000	0
42	MLHAMLIAG	129	-0.8200	0
43	VELSSFQLH	164	-0.8200	0
44	LNIAEDHLD	185	-0.9000	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	LVVTGTNGK	115	4.5000	52.33
2	WRLDAAGCY	100	2.3000	26.74
3	LAVELSSFQ	162	2.3000	26.74
4	FQLHWAPSL	169	1.6000	18.60
5	IGRDRAAVA	377	1.6000	18.60
6	VGVLDALAA	278	1.5000	17.44
7	FGATPTVCD	29	1.4800	17.21
8	LTLLPVASI	264	1.4000	16.28
9	LHAEVAAMA	360	1.3000	15.12
10	FSDDLTLLP	260	1.1000	12.79
11	LVVASPGFS	68	1.0000	11.63
12	VMTAAVAAA	436	1.0000	11.63
13	VGRHRAEVV	309	0.8000	9.30
14	FSPATPLLA	75	0.7000	8.14
15	FRLGEPAAR	238	0.6000	6.98
16	LRPEAGAVL	177	0.5000	5.81
17	WHATMAEYT	194	0.5000	5.81
18	VLLAPAGAS	454	0.4000	4.65
19	VSSSDAVQQ	54	0.2800	3.26
20	VTGQAVAAV	17	0.2000	2.33
21	LHWAPSLRP	171	0.2000	2.33
22	LLKGASLHA	354	0.1000	1.16
23	VPVACVLDV	414	-0.1000	0

24	VELSSFQLH	164	-0.1200	0
25	LDWHATMAE	192	-0.2000	0
26	LLPVASIPV	266	-0.2200	0
27	LHAMLIAGG	130	-0.4000	0
28	VLDEPAELL	154	-0.6000	0
29	VLTGGVAVA	208	-0.7000	0
30	VWIAGGLLK	348	-0.7000	0
31	LVGAVLIGR	371	-0.7200	0
32	LARSVGVPA	289	-0.9200	0
33	LLAAAAAAG	81	-1.0000	0
34	VAAMASRLV	364	-1.0000	0
35	VAGGRVTGQ	12	-1.1000	0
36	YALVVASPG	66	-1.1000	0
37	VASIPVPGP	269	-1.1000	0
38	LSRHAPDVP	388	-1.1000	0
39	LAYPRVVWI	342	-1.1200	0
40	MLIAGGRRA	133	-1.2000	0
41	VAVAGLDDS	213	-1.2000	0
42	VAGLDDSRA	215	-1.3000	0
43	VLDALAAAA	280	-1.3000	0
44	LAAAALARS	284	-1.4000	0
45	LNIAEDHLD	185	-1.5000	0
46	LPTVSSSDA	51	-1.6000	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	LLPVASIPV	266	6.2000	53.45
2	VQQITGYAL	60	5.8000	50.00
3	FQLHWAPSL	169	5.5000	47.41
4	VVWIAGGLL	347	5.0000	43.10
5	YTAAKARVL	201	4.1000	35.34
6	LAYPRVVWI	342	3.7000	31.90

7	YGPPRSWLV	108	3.6000	31.03
8	VVASPGFSP	69	3.5000	30.17
9	WHATMAEYT	194	3.5000	30.17
10	VPVACVLDV	414	3.3000	28.45
11	LVVTGTNGK	115	3.2200	27.76
12	LRPHAERGL	43	3.2000	27.59
13	VGRHRAEVV	309	3.2000	27.59
14	LRPEAGAVL	177	2.9000	25.00
15	WRLDAAGCY	100	2.7000	23.28
16	LTLLPVASI	264	2.7000	23.28
17	LLAVELSSF	161	2.5000	21.55
18	VAVADGITY	317	2.4000	20.69
19	VQVVAGEDT	398	2.3000	19.83
20	FATAVRAVI	476	2.3000	19.83
21	FGATPTVCD	29	2.2200	19.14
22	LARSVGVPA	289	2.2000	18.97
23	WLVVTGTNG	114	2.1000	18.10
24	LHWAPSLRP	171	2.0000	17.24
25	YPRVVWIAG	344	2.0000	17.24
26	LVGAVLIGR	371	2.0000	17.24
27	VAAMASRLV	364	1.9000	16.38
28	LGPGAPVLV	4	1.8000	15.52
29	LGVRDAHLV	248	1.8000	15.52
30	VEVPVACVL	412	1.8000	15.52
31	YALVVASPG	66	1.7000	14.66
32	FSPATPLLA	75	1.7000	14.66
33	VELSSFQLH	164	1.7000	14.66
34	LLKGASLHA	354	1.7000	14.66
35	MLIAGGRRA	133	1.6000	13.79
36	VLDEPAELL	154	1.6000	13.79
37	VPIWGDVEL	90	1.4000	12.07
38	VRVGFRLGE	234	1.4000	12.07
39	VGVLDALAA	278	1.4000	12.07
40	LDDSRAAAL	218	1.3000	11.21

41	LTRFGATPT	26	1.2000	10.34
42	VELAWRLDA	96	1.2000	10.34
43	VLNIAEDHL	184	1.2000	10.34
44	LGEPAAREL	240	1.2000	10.34
45	FRVGRHRAE	307	1.2000	10.34
46	VSSSDAVQQ	54	1.1000	9.48
47	MLHAMLIAG	129	1.1000	9.48
48	VDRAFSDDL	256	1.1000	9.48

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LLPVASIPV	266	6.2000	53.45
2	VQQITGYAL	60	5.8000	50.00
3	FQLHWAPSL	169	5.5000	47.41
4	VVWIAGGLL	347	5.0000	43.10
5	YTAAKARVL	201	4.1000	35.34
6	LAYPRVVWI	342	3.7000	31.90
7	YGPPRSWLV	108	3.6000	31.03
8	VVASPGFSP	69	3.5000	30.17
9	WHATMAEYT	194	3.5000	30.17
10	VPVACVLDV	414	3.3000	28.45
11	LVVTGTNGK	115	3.2200	27.76
12	LRPHAERGL	43	3.2000	27.59
13	VGRHRAEVV	309	3.2000	27.59
14	LRPEAGAVL	177	2.9000	25.00
15	WRLDAAGCY	100	2.7000	23.28
16	LTLLPVASI	264	2.7000	23.28
17	LLAVELSSF	161	2.5000	21.55
18	VAVADGITY	317	2.4000	20.69
19	VQVVAGEDT	398	2.3000	19.83
20	FATAVRAVI	476	2.3000	19.83
21	FGATPTVCD	29	2.2200	19.14

22	LARSVGVPA	289	2.2000	18.97
23	WLVVTGTNG	114	2.1000	18.10
24	LHWAPSLRP	171	2.0000	17.24
25	YPRVVWIAG	344	2.0000	17.24
26	LVGAVLIGR	371	2.0000	17.24
27	VAAMASRLV	364	1.9000	16.38
28	LGPGAPVLV	4	1.8000	15.52
29	LGVRDAHLV	248	1.8000	15.52
30	VEVPVACVL	412	1.8000	15.52
31	YALVVASPG	66	1.7000	14.66
32	FSPATPLLA	75	1.7000	14.66
33	VELSSFQLH	164	1.7000	14.66
34	LLKGASLHA	354	1.7000	14.66
35	MLIAGGRRA	133	1.6000	13.79
36	VLDEPAELL	154	1.6000	13.79
37	VPIWGDVEL	90	1.4000	12.07
38	VRVGFRLGE	234	1.4000	12.07
39	VGVLDALAA	278	1.4000	12.07
40	LDDSRAAAL	218	1.3000	11.21
41	LTRFGATPT	26	1.2000	10.34
42	VELAWRLDA	96	1.2000	10.34
43	VLNIAEDHL	184	1.2000	10.34
44	LGEPAAREL	240	1.2000	10.34
45	FRVGRHRAE	307	1.2000	10.34
46	VSSSDAVQQ	54	1.1000	9.48
47	MLHAMLIAG	129	1.1000	9.48
48	VDRAFSDDL	256	1.1000	9.48

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LIGRDRAAV	376	3.2000	37.21
2	VRVGFRLGE	234	2.7000	31.40

3	VMLRPHAER	41	2.3000	26.74
4	LVVASPGFS	68	2.3000	26.74
5	FRVGRHRAE	307	2.3000	26.74
6	LHAMLIAGG	130	2.2000	25.58
7	VLAYPRVVW	341	2.0000	23.26
8	VVQVVAGED	397	1.9000	22.09
9	WRLDAAGCY	100	1.8000	20.93
10	LTLLPVASI	264	1.8000	20.93
11	MASRLVGAV	367	1.8000	20.93
12	FRLGEPAAR	238	1.7000	19.77
13	VTSFRVGRH	304	1.7000	19.77
14	YVDDSKATN	325	1.7000	19.77
15	VMTAAVAAA	436	1.3000	15.12
16	VLLAPAGAS	454	1.2000	13.95
17	LGVRDAHLV	248	1.0000	11.63
18	VGAVLIGRD	372	1.0000	11.63
19	VAAARRMAQ	441	1.0000	11.63
20	LKGASLHAE	355	0.9000	10.47
21	FATAVRAVI	476	0.9000	10.47
22	VELAWRLDA	96	0.8000	9.30
23	VLTRFGATP	25	0.7000	8.14
24	FTGYADRGE	466	0.7000	8.14
25	VAKDDKAGE	422	0.6000	6.98
26	ITGYALVVA	63	0.5000	5.81
27	LVDRAFSDD	255	0.4000	4.65
28	VGVLDALAA	278	0.4000	4.65
29	LVAGGRVTG	11	0.3000	3.49
30	YALVVASPG	66	0.3000	3.49
31	LLAAAAAAG	81	0.3000	3.49
32	WIAGGLLKG	349	0.3000	3.49
33	FGATPTVCD	29	0.2000	2.33
34	FSPATPLLA	75	0.2000	2.33
35	MLIAGGRRA	133	0.2000	2.33
36	VLTGGVAVA	208	0.2000	2.33

37	VVWIAGGLL	347	0.2000	2.33
38	MLHAMLIAG	129	-0.1000	0
39	LAAAALARS	284	-0.1000	0
40	VAAVLTRFG	22	-0.2000	0
41	LRPEAGAVL	177	-0.2000	0
42	LVGAVLIGR	371	-0.3000	0
43	VPVVQVVAG	395	-0.3000	0
44	YADRGEAFA	469	-0.4000	0
45	VGFRLGEPA	236	-0.5000	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	LIGRDRAAV	376	2.9000	36.25
2	VMLRPHAER	41	2.3000	28.75
3	LVVASPGFS	68	2.3000	28.75
4	FRLGEPAAR	238	1.7000	21.25
5	LTLLPVASI	264	1.6000	20.00
6	MASRLVGAV	367	1.5000	18.75
7	VMTAAVAAA	436	1.3000	16.25
8	VLLAPAGAS	454	1.2000	15.00
9	VLAYPRVVW	341	1.1000	13.75
10	LHAMLIAGG	130	0.9000	11.25
11	VELAWRLDA	96	0.8000	10.00
12	WRLDAAGCY	100	0.7000	8.75
13	LGVRDAHLV	248	0.7000	8.75
14	FATAVRAVI	476	0.7000	8.75
15	ITGYALVVA	63	0.5000	6.25
16	VTSFRVGRH	304	0.4800	6.00
17	VGVLDALAA	278	0.4000	5.00
18	VLTRFGATP	25	0.3000	3.75
19	FSPATPLLA	75	0.2000	2.50
20	MLIAGGRRA	133	0.2000	2.50

21	VLTGGVAVA	208	0.2000	2.50
22	VAAARRMAQ	441	0.2000	2.50
23	LAAAALARS	284	-0.1000	0
24	LVVTGTNGK	115	-0.2000	0
25	VRVGFRLGE	234	-0.3000	0
26	YVDDSKATN	325	-0.3000	0
27	LVGAVLIGR	371	-0.3000	0
28	YADRGEAFA	469	-0.4000	0
29	VGFRLGEPA	236	-0.5000	0
30	FRVGRHRAE	307	-0.7000	0
31	VLCGNIGSA	142	-0.8000	0
32	VVWIAGGLL	347	-0.8000	0
33	IGRDRAAVA	377	-0.8000	0
34	VVQVVAGED	397	-0.8000	0
35	VPVACVLDV	414	-0.8000	0
36	WAPSLRPEA	173	-0.9000	0
37	VWIAGGLLK	348	-0.9000	0
38	LVAGGRVTG	11	-1.0000	0
39	YALVVASPG	66	-1.0000	0
40	LLAAAAAAG	81	-1.0000	0
41	FQLHWAPSL	169	-1.0000	0
42	LLPVASIPV	266	-1.0000	0
43	WIAGGLLKG	349	-1.0000	0
44	VAAMASRLV	364	-1.0000	0
45	LIAGGRRAV	134	-1.2000	0
46	LRPEAGAVL	177	-1.2000	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	LIGRDRAAV	376	3.9000	48.75
2	VMLRPHAER	41	3.3000	41.25
3	LVVASPGFS	68	3.3000	41.25

4	LTLLPVASI	264	2.6000	32.50
5	MASRLVGAV	367	2.5000	31.25
6	VMTAAVAAA	436	2.3000	28.75
7	VLLAPAGAS	454	2.2000	27.50
8	VLAYPRVVW	341	2.1000	26.25
9	LHAMLIAGG	130	1.9000	23.75
10	VELAWRLDA	96	1.8000	22.50
11	LGVRDAHLV	248	1.7000	21.25
12	ITGYALVVA	63	1.5000	18.75
13	VTSFRVGRH	304	1.4800	18.50
14	VGVLDALAA	278	1.4000	17.50
15	VLTRFGATP	25	1.3000	16.25
16	MLIAGGRRA	133	1.2000	15.00
17	VLTGGVAVA	208	1.2000	15.00
18	VAAARRMAQ	441	1.2000	15.00
19	MAEYTAAKA	198	1.0000	12.50
20	LAAAALARS	284	0.9000	11.25
21	LVVTGTNGK	115	0.8000	10.00
22	VRVGFRLGE	234	0.7000	8.75
23	FRLGEPAAR	238	0.7000	8.75
24	LVGAVLIGR	371	0.7000	8.75
25	VGFRLGEPA	236	0.5000	6.25
26	VLCGNIGSA	142	0.2000	2.50
27	VVWIAGGLL	347	0.2000	2.50
28	IGRDRAAVA	377	0.2000	2.50
29	VVQVVAGED	397	0.2000	2.50
30	VPVACVLDV	414	0.2000	2.50
31	VWIAGGLLK	348	0.1000	1.25
32	LIAGGRRAV	134	-0.2000	0
33	LRPEAGAVL	177	-0.2000	0
34	LHAEVAAMA	360	-0.2000	0
35	VTGQAVAAV	17	-0.3000	0
36	WRLDAAGCY	100	-0.3000	0
37	LSSFQLHWA	166	-0.3000	0

38	VLDALAAAA	280	-0.3000	0
39	FATAVRAVI	476	-0.3000	0
40	MLHAMLIAG	129	-0.4000	0
41	LAYPRVVWI	342	-0.4000	0
42	LLKGASLHA	354	-0.4000	0
43	VAAVLTRFG	22	-0.5000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LIGRDRAAV	376	4.2000	48.84
2	VRVGFRLGE	234	3.7000	43.02
3	VMLRPHAER	41	3.3000	38.37
4	LVVASPGFS	68	3.3000	38.37
5	LHAMLIAGG	130	3.2000	37.21
6	VLAYPRVVW	341	3.0000	34.88
7	VVQVVAGED	397	2.9000	33.72
8	LTLLPVASI	264	2.8000	32.56
9	MASRLVGAV	367	2.8000	32.56
10	VTSFRVGRH	304	2.7000	31.40
11	VMTAAVAAA	436	2.3000	26.74
12	VLLAPAGAS	454	2.2000	25.58
13	LGVRDAHLV	248	2.0000	23.26
14	VGAVLIGRD	372	2.0000	23.26
15	VAAARRMAQ	441	2.0000	23.26
16	LKGASLHAE	355	1.9000	22.09
17	VELAWRLDA	96	1.8000	20.93
18	VLTRFGATP	25	1.7000	19.77
19	VAKDDKAGE	422	1.6000	18.60
20	ITGYALVVA	63	1.5000	17.44
21	LVDRAFSDD	255	1.4000	16.28
22	VGVLDALAA	278	1.4000	16.28
23	LVAGGRVTG	11	1.3000	15.12

24	LLAAAAAAG	81	1.3000	15.12
25	FRVGRHRAE	307	1.3000	15.12
26	MLIAGGRRA	133	1.2000	13.95
27	VLTGGVAVA	208	1.2000	13.95
28	VVWIAGGLL	347	1.2000	13.95
29	MAEYTAAKA	198	1.0000	11.63
30	MLHAMLIAG	129	0.9000	10.47
31	LAAAALARS	284	0.9000	10.47
32	VAAVLTRFG	22	0.8000	9.30
33	WRLDAAGCY	100	0.8000	9.30
34	LRPEAGAVL	177	0.8000	9.30
35	FRLGEPAAR	238	0.7000	8.14
36	YVDDSKATN	325	0.7000	8.14
37	LVGAVLIGR	371	0.7000	8.14
38	VPVVQVVAG	395	0.7000	8.14
39	VGFRLGEPA	236	0.5000	5.81
40	VPVACVLDV	414	0.5000	5.81
41	LLPVASIPV	266	0.3000	3.49
42	VAAMASRLV	364	0.3000	3.49
43	LAWRLDAAG	98	0.2000	2.33
44	IAGGRRAVL	135	0.2000	2.33
45	VLCGNIGSA	142	0.2000	2.33
46	IGRDRAAVA	377	0.2000	2.33
47	LVVTGTNGK	115	0.1000	1.16
48	LIAGGRRAV	134	0.1000	1.16

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	LIGRDRAAV	376	2.9000	33.33
2	VMLRPHAER	41	2.3000	26.44
3	VLAYPRVVW	341	2.1000	24.14
4	LVVTGTNGK	115	1.8000	20.69

5	FRLGEPAAR	238	1.7000	19.54
6	LVVASPGFS	68	1.6000	18.39
7	LTLLPVASI	264	1.6000	18.39
8	ITGYALVVA	63	1.5000	17.24
9	VELAWRLDA	96	1.4000	16.09
10	VMTAAVAAA	436	1.3000	14.94
11	VGFRLGEPA	236	1.2000	13.79
12	LGVRDAHLV	248	1.2000	13.79
13	VAAARRMAQ	441	1.2000	13.79
14	VGVLDALAA	278	1.0000	11.49
15	LHAMLIAGG	130	0.9000	10.34
16	YALVVASPG	66	0.8000	9.20
17	FSPATPLLA	75	0.8000	9.20
18	MASRLVGAV	367	0.8000	9.20
19	FATAVRAVI	476	0.7000	8.05
20	LVGAVLIGR	371	0.5800	6.67
21	WLVVTGTNG	114	0.5000	5.75
22	VLLAPAGAS	454	0.5000	5.75
23	VAGGRVTGQ	12	0.3000	3.45
24	VLTRFGATP	25	0.3000	3.45
25	VRVGFRLGE	234	0.3000	3.45
26	VLTGGVAVA	208	0.2000	2.30
27	MLIAGGRRA	133	-0.1000	0
28	LAAAALARS	284	-0.1000	0
29	LLPVASIPV	266	-0.1200	0
30	VPVACVLDV	414	-0.2000	0
31	VTSFRVGRH	304	-0.2200	0
32	YVDDSKATN	325	-0.3000	0
33	VWIAGGLLK	348	-0.3000	0
34	LAYPRVVWI	342	-0.4000	0
35	WIAGGLLKG	349	-0.4000	0
36	YADRGEAFA	469	-0.4000	0
37	LVDRAFSDD	255	-0.5000	0
38	MLHAMLIAG	129	-0.5200	0

39	LTRFGATPT	26	-0.6000	0
40	LAVELSSFQ	162	-0.6000	0
41	VPVVQVVAG	395	-0.6000	0
42	WAPSLRPEA	173	-0.7000	0
43	LPTVSSSDA	51	-0.8000	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	VRVGFRLGE	234	4.5000	44.55
2	LIGRDRAAV	376	3.2000	31.68
3	VELAWRLDA	96	2.6000	25.74
4	VAAARRMAQ	441	2.6000	25.74
5	FRVGRHRAE	307	2.5000	24.75
6	VLAYPRVVW	341	2.5000	24.75
7	LVVASPGFS	68	2.4000	23.76
8	VMLRPHAER	41	2.3000	22.77
9	LHAMLIAGG	130	2.2000	21.78
10	VGVLDALAA	278	2.2000	21.78
11	WIAGGLLKG	349	2.1000	20.79
12	FSPATPLLA	75	2.0000	19.80
13	VVQVVAGED	397	2.0000	19.80
14	WRLDAAGCY	100	1.9000	18.81
15	MASRLVGAV	367	1.9000	18.81
16	LTLLPVASI	264	1.8000	17.82
17	VTSFRVGRH	304	1.8000	17.82
18	FRLGEPAAR	238	1.7000	16.83
19	LGVRDAHLV	248	1.7000	16.83
20	YVDDSKATN	325	1.7000	16.83
21	LKGASLHAE	355	1.6000	15.84
22	MLHAMLIAG	129	1.5000	14.85
23	LVGAVLIGR	371	1.3000	12.87
24	VPVACVLDV	414	1.3000	12.87

25	VMTAAVAAA	436	1.3000	12.87
26	VLLAPAGAS	454	1.3000	12.87
27	FQLHWAPSL	169	1.1500	11.39
28	VGAVLIGRD	372	1.1000	10.89
29	ITGYALVVA	63	1.0000	9.90
30	LLPVASIPV	266	0.9000	8.91
31	FTGYADRGE	466	0.9000	8.91
32	FATAVRAVI	476	0.9000	8.91
33	LVAGGRVTG	11	0.8000	7.92
34	VLTRFGATP	25	0.7000	6.93
35	FGATPTVCD	29	0.7000	6.93
36	VGFRLGEPA	236	0.6000	5.94
37	VAKDDKAGE	422	0.6000	5.94
38	MLIAGGRRA	133	0.4000	3.96
39	LVDRAFSDD	255	0.4000	3.96
40	LLKGASLHA	354	0.4000	3.96
41	YALVVASPG	66	0.3000	2.97
42	LLAAAAAAG	81	0.3000	2.97
43	LHWAPSLRP	171	0.3000	2.97
44	VVWIAGGLL	347	0.3000	2.97
45	WAPSLRPEA	173	0.2500	2.48
46	VLTGGVAVA	208	0.2000	1.98
47	YPRVVWIAG	344	0.2000	1.98
48	VWIAGGLLK	348	0.2000	1.98

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	VELAWRLDA	96	2.6000	31.33
2	VGVLDALAA	278	2.6000	31.33
3	LVVASPGFS	68	2.4000	28.92
4	FSPATPLLA	75	2.0000	24.10
5	LTLLPVASI	264	2.0000	24.10

6	VAAARRMAQ	441	1.8000	21.69
7	LVGAVLIGR	371	1.3000	15.66
8	VMTAAVAAA	436	1.3000	15.66
9	VLLAPAGAS	454	1.3000	15.66
10	FRLGEPAAR	238	1.0000	12.05
11	VPVACVLDV	414	1.0000	12.05
12	VWIAGGLLK	348	0.9000	10.84
13	VRVGFRLGE	234	0.8000	9.64
14	LLPVASIPV	266	0.7000	8.43
15	FATAVRAVI	476	0.7000	8.43
16	FQLHWAPSL	169	0.5500	6.63
17	WAPSLRPEA	173	0.5500	6.63
18	LVVTGTNGK	115	0.5000	6.02
19	LHAMLIAGG	130	0.5000	6.02
20	VTSFRVGRH	304	0.4800	5.78
21	MLIAGGRRA	133	0.4000	4.82
22	MLHAMLIAG	129	0.2000	2.41
23	WRLDAAGCY	100	0.1000	1.20
24	WIAGGLLKG	349	0.1000	1.20
25	VASIPVPGP	269	-0.0500	0
26	LHWAPSLRP	171	-0.1000	0
27	LAAAALARS	284	-0.1000	0
28	VVWIAGGLL	347	-0.1000	0
29	LIGRDRAAV	376	-0.1000	0
30	LLKGASLHA	354	-0.3000	0
31	VLTGGVAVA	208	-0.5000	0
32	VVQVVAGED	397	-0.6000	0
33	VTGQAVAAV	17	-0.7000	0
34	VMLRPHAER	41	-0.7000	0
35	LSSFQLHWA	166	-0.7000	0
36	YALVVASPG	66	-0.9000	0
37	VQQITGYAL	60	-1.0000	0
38	LLAAAAAAG	81	-1.0000	0
39	YVDDSKATN	325	-1.0000	0

40	YPRVVWIAG	344	-1.0000	0
41	VPVVQVVAG	395	-1.0000	0
42	WLVVTGTNG	114	-1.1000	0
43	LVAGGRVTG	11	-1.2000	0
44	VAAVLTRFG	22	-1.2000	0
45	WGDVELAWR	93	-1.2000	0
46	FRVGRHRAE	307	-1.2000	0
47	VAAMASRLV	364	-1.2000	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	MLIAGGRRA	133	3.0000	35.71
2	LRPHAERGL	43	2.8000	33.33
3	VELAWRLDA	96	2.5000	29.76
4	LVVASPGFS	68	2.3000	27.38
5	LTLLPVASI	264	2.3000	27.38
6	VMTAAVAAA	436	2.3000	27.38
7	LVVTGTNGK	115	2.1000	25.00
8	VGVLDALAA	278	1.8000	21.43
9	LIGRDRAAV	376	1.8000	21.43
10	VAAARRMAQ	441	1.5000	17.86
11	VTGQAVAAV	17	1.3000	15.48
12	LHAMLIAGG	130	1.3000	15.48
13	VLAYPRVVW	341	1.3000	15.48
14	VMLRPHAER	41	1.2000	14.29
15	LSSFQLHWA	166	1.2000	14.29
16	FQLHWAPSL	169	1.2000	14.29
17	VAAMASRLV	364	1.2000	14.29
18	VLLAPAGAS	454	1.2000	14.29
19	LIAGGRRAV	134	1.1000	13.10
20	VGRHRAEVV	309	1.0000	11.90
21	LVGAVLIGR	371	1.0000	11.90

22	VRVGFRLGE	234	0.9000	10.71
23	LAAAALARS	284	0.9000	10.71
24	VPVACVLDV	414	0.9000	10.71
25	VLVAGGRVT	10	0.8000	9.52
26	LGVRDAHLV	248	0.8000	9.52
27	VWIAGGLLK	348	0.8000	9.52
28	VTSFRVGRH	304	0.7800	9.29
29	ITGYALVVA	63	0.7000	8.33
30	VLTGGVAVA	208	0.7000	8.33
31	LVAGGRVTG	11	0.5000	5.95
32	FRLGEPAAR	238	0.2000	2.38
33	VAAVLTRFG	22	0.1000	1.19
34	VVASPGFSP	69	0.1000	1.19
35	LAYPRVVWI	342	0.1000	1.19
36	LKGASLHAE	355	0.1000	1.19
37	FSPATPLLA	75	-0.1000	0
38	MLHAMLIAG	129	-0.1000	0
39	VAVAGLDDS	213	-0.1000	0
40	VAEALSRHA	384	-0.1000	0
41	LHWAPSLRP	171	-0.2000	0
42	VGFRLGEPA	236	-0.2000	0
43	LLKGASLHA	354	-0.2000	0
44	VLIGRDRAA	375	-0.2000	0
45	IGRDRAAVA	377	-0.2000	0

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	VELAWRLDA	96	3.6000	43.37
2	VGVLDALAA	278	3.6000	43.37
3	LVVASPGFS	68	3.4000	40.96
4	LTLLPVASI	264	3.0000	36.14
5	VAAARRMAQ	441	2.8000	33.73

6	LVGAVLIGR	371	2.3000	27.71
7	VMTAAVAAA	436	2.3000	27.71
8	VLLAPAGAS	454	2.3000	27.71
9	VPVACVLDV	414	2.0000	24.10
10	VWIAGGLLK	348	1.9000	22.89
11	VRVGFRLGE	234	1.8000	21.69
12	LLPVASIPV	266	1.7000	20.48
13	LVVTGTNGK	115	1.5000	18.07
14	LHAMLIAGG	130	1.5000	18.07
15	VTSFRVGRH	304	1.4800	17.83
16	MLIAGGRRA	133	1.4000	16.87
17	MLHAMLIAG	129	1.2000	14.46
18	FSPATPLLA	75	1.0000	12.05
19	VASIPVPGP	269	0.9500	11.45
20	LHWAPSLRP	171	0.9000	10.84
21	LAAAALARS	284	0.9000	10.84
22	VVWIAGGLL	347	0.9000	10.84
23	LIGRDRAAV	376	0.9000	10.84
24	LLKGASLHA	354	0.7000	8.43
25	VLTGGVAVA	208	0.5000	6.02
26	VVQVVAGED	397	0.4000	4.82
27	VTGQAVAAV	17	0.3000	3.61
28	VMLRPHAER	41	0.3000	3.61
29	LSSFQLHWA	166	0.3000	3.61
30	LVAGGRVTG	11	-0.2000	0
31	VAAVLTRFG	22	-0.2000	0
32	VAAMASRLV	364	-0.2000	0
33	VLDALAAAA	280	-0.3000	0
34	VLAYPRVVW	341	-0.3000	0
35	FATAVRAVI	476	-0.3000	0
36	VLCGNIGSA	142	-0.4000	0
37	VAVADGITY	317	-0.4000	0
38	LKGASLHAE	355	-0.4000	0
39	MASRLVGAV	367	-0.4000	0

40	FQLHWAPSL	169	-0.4500	0
41	WAPSLRPEA	173	-0.4500	0
42	VRDAHLVDR	250	-0.5000	0
43	VGAVLIGRD	372	-0.5000	0

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	VELAWRLDA	96	3.6000	43.37
2	VGVLDALAA	278	3.6000	43.37
3	LVVASPGFS	68	3.4000	40.96
4	LTLLPVASI	264	3.0000	36.14
5	VAAARRMAQ	441	2.8000	33.73
6	LVGAVLIGR	371	2.3000	27.71
7	VMTAAVAAA	436	2.3000	27.71
8	VLLAPAGAS	454	2.3000	27.71
9	VPVACVLDV	414	2.0000	24.10
10	VWIAGGLLK	348	1.9000	22.89
11	VRVGFRLGE	234	1.8000	21.69
12	LLPVASIPV	266	1.7000	20.48
13	LVVTGTNGK	115	1.5000	18.07
14	LHAMLIAGG	130	1.5000	18.07
15	VTSFRVGRH	304	1.4800	17.83
16	MLIAGGRRA	133	1.4000	16.87
17	MLHAMLIAG	129	1.2000	14.46
18	FSPATPLLA	75	1.0000	12.05
19	VASIPVPGP	269	0.9500	11.45
20	LHWAPSLRP	171	0.9000	10.84
21	LAAAALARS	284	0.9000	10.84
22	VVWIAGGLL	347	0.9000	10.84
23	LIGRDRAAV	376	0.9000	10.84
24	LLKGASLHA	354	0.7000	8.43
25	VLTGGVAVA	208	0.5000	6.02

26	VVQVVAGED	397	0.4000	4.82
27	VTGQAVAAV	17	0.3000	3.61
28	VMLRPHAER	41	0.3000	3.61
29	LSSFQLHWA	166	0.3000	3.61
30	LVAGGRVTG	11	-0.2000	0
31	VAAVLTRFG	22	-0.2000	0
32	VAAMASRLV	364	-0.2000	0
33	VLDALAAAA	280	-0.3000	0
34	VLAYPRVVW	341	-0.3000	0
35	FATAVRAVI	476	-0.3000	0
36	VLCGNIGSA	142	-0.4000	0
37	VAVADGITY	317	-0.4000	0
38	LKGASLHAE	355	-0.4000	0
39	MASRLVGAV	367	-0.4000	0
40	FQLHWAPSL	169	-0.4500	0
41	WAPSLRPEA	173	-0.4500	0
42	VRDAHLVDR	250	-0.5000	0
43	VGAVLIGRD	372	-0.5000	0

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	LVVASPGFS	68	3.9000	42.86
2	WRLDAAGCY	100	3.6000	39.56
3	IGRDRAAVA	377	3.5000	38.46
4	LVAGGRVTG	11	2.8000	30.77
5	VLLAPAGAS	454	2.8000	30.77
6	VLTGGVAVA	208	2.7000	29.67
7	VRVGFRLGE	234	2.7000	29.67
8	VAAARRMAQ	441	2.6000	28.57
9	VAGGRVTGQ	12	2.3000	25.27
10	VELAWRLDA	96	2.3000	25.27
11	VLCGNIGSA	142	2.3000	25.27

12	VMTAAVAAA	436	2.3000	25.27
13	FRLGEPAAR	238	2.2000	24.18
14	LVVTGTNGK	115	2.0100	22.09
15	YVDDSKATN	325	2.0000	21.98
16	LTLLPVASI	264	1.9000	20.88
17	LVGAVLIGR	371	1.9000	20.88
18	VAKDDKAGE	422	1.9000	20.88
19	WAPSLRPEA	173	1.7000	18.68
20	LLKGASLHA	354	1.6000	17.58
21	LGPGAPVLV	4	1.3000	14.29
22	VSSSDAVQQ	54	1.3000	14.29
23	VVASPGFSP	69	1.3000	14.29
24	VASIPVPGP	269	1.3000	14.29
25	VGVLDALAA	278	1.2000	13.19
26	LIAGGRRAV	134	1.0000	10.99
27	VVWIAGGLL	347	1.0000	10.99
28	VVTGTNGKT	116	0.9000	9.89
29	MLIAGGRRA	133	0.9000	9.89
30	FQLHWAPSL	169	0.9000	9.89
31	LLPVASIPV	266	0.9000	9.89
32	LAAAALARS	284	0.9000	9.89
33	LARSVGVPA	289	0.9000	9.89
34	LAYPRVVWI	342	0.9000	9.89
35	MLHAMLIAG	129	0.8000	8.79
36	VAVAGLDDS	213	0.8000	8.79
37	IAEDHLDWH	187	0.7800	8.57
38	VTGQAVAAV	17	0.7000	7.69
39	VCDDDPVML	35	0.7000	7.69
40	IAGGRRAVL	135	0.7000	7.69
41	VPAGAIADA	295	0.7000	7.69
42	VPVACVLDV	414	0.7000	7.69
43	VWIAGGLLK	348	0.6000	6.59
44	LIGRDRAAV	376	0.6000	6.59
45	VTSFRVGRH	304	0.5800	6.37

46	LHAMLIAGG	130	0.5000	5.49
47	VVQVVAGED	397	0.5000	5.49
48	VPVVQVVAG	395	0.4000	4.40

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	FQLHWAPSL	169	2.2000	26.19
2	MLIAGGRRA	133	2.0000	23.81
3	LRPHAERGL	43	1.8000	21.43
4	VELAWRLDA	96	1.5000	17.86
5	LVVASPGFS	68	1.3000	15.48
6	LTLLPVASI	264	1.3000	15.48
7	VMTAAVAAA	436	1.3000	15.48
8	FRLGEPAAR	238	1.2000	14.29
9	LVVTGTNGK	115	1.1000	13.10
10	FSPATPLLA	75	0.9000	10.71
11	VGVLDALAA	278	0.8000	9.52
12	LIGRDRAAV	376	0.8000	9.52
13	FATAVRAVI	476	0.7000	8.33
14	FRVGRHRAE	307	0.6000	7.14
15	VAAARRMAQ	441	0.5000	5.95
16	VTGQAVAAV	17	0.3000	3.57
17	LHAMLIAGG	130	0.3000	3.57
18	VLAYPRVVW	341	0.3000	3.57
19	VMLRPHAER	41	0.2000	2.38
20	LSSFQLHWA	166	0.2000	2.38
21	WAPSLRPEA	173	0.2000	2.38
22	YTAAKARVL	201	0.2000	2.38
23	VAAMASRLV	364	0.2000	2.38
24	VLLAPAGAS	454	0.2000	2.38
25	LIAGGRRAV	134	0.1000	1.19
26	VRVGFRLGE	234	-0.1000	0

27	LAAAALARS	284	-0.1000	0
28	VPVACVLDV	414	-0.1000	0
29	VLVAGGRVT	10	-0.2000	0
30	LGVRDAHLV	248	-0.2000	0
31	VWIAGGLLK	348	-0.2000	0
32	VTSFRVGRH	304	-0.2200	0
33	ITGYALVVA	63	-0.3000	0
34	VLTGGVAVA	208	-0.3000	0
35	LVAGGRVTG	11	-0.5000	0
36	WRLDAAGCY	100	-0.7000	0
37	YVDDSKATN	325	-0.7000	0
38	WIAGGLLKG	349	-0.8000	0
39	VAAVLTRFG	22	-0.9000	0
40	VVASPGFSP	69	-0.9000	0
41	LAYPRVVWI	342	-0.9000	0
42	LKGASLHAE	355	-0.9000	0
43	LLAAAAAAG	81	-1.0000	0
44	VRDAHLVDR	250	-1.0000	0
45	YGPPRSWLV	108	-1.1000	0

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FQLHWAPSL	169	3.1600	35.91
2	LRPHAERGL	43	2.7600	31.36
3	FRLGEPAAR	238	2.7000	30.68
4	LTLLPVASI	264	2.2000	25.00
5	MLIAGGRRA	133	2.0000	22.73
6	FRVGRHRAE	307	2.0000	22.73
7	LIGRDRAAV	376	1.8000	20.45
8	VMLRPHAER	41	1.7000	19.32
9	LVVASPGFS	68	1.7000	19.32
10	LHAMLIAGG	130	1.7000	19.32

11	FATAVRAVI	476	1.6000	18.18
12	VELAWRLDA	96	1.5000	17.05
13	LVGAVLIGR	371	1.5000	17.05
14	VTGQAVAAV	17	1.3000	14.77
15	VRVGFRLGE	234	1.3000	14.77
16	VMTAAVAAA	436	1.3000	14.77
17	LVVTGTNGK	115	1.2000	13.64
18	VAAMASRLV	364	1.2000	13.64
19	YTAAKARVL	201	1.1600	13.18
20	LIAGGRRAV	134	1.1000	12.50
21	VGRHRAEVV	309	1.0000	11.36
22	LVAGGRVTG	11	0.9000	10.23
23	FSPATPLLA	75	0.9000	10.23
24	VPVACVLDV	414	0.9000	10.23
25	LGVRDAHLV	248	0.8000	9.09
26	VGVLDALAA	278	0.8000	9.09
27	WRLDAAGCY	100	0.6000	6.82
28	WIAGGLLKG	349	0.6000	6.82
29	VLLAPAGAS	454	0.6000	6.82
30	VLVAGGRVT	10	0.5000	5.68
31	VAAVLTRFG	22	0.5000	5.68
32	VRDAHLVDR	250	0.5000	5.68
33	LKGASLHAE	355	0.5000	5.68
34	LLAAAAAAG	81	0.4000	4.55
35	MLHAMLIAG	129	0.3000	3.41
36	LAAAALARS	284	0.3000	3.41
37	VLAYPRVVW	341	0.3000	3.41
38	LSSFQLHWA	166	0.2000	2.27
39	WAPSLRPEA	173	0.2000	2.27
40	VVASPGFSP	69	0.1000	1.14
41	YVDDSKATN	325	0.1000	1.14
42	YGPPRSWLV	108	-0.1000	0
43	VWIAGGLLK	348	-0.1000	0
44	LHWAPSLRP	171	-0.2000	0

45	VAAARRMAQ	441	-0.2000	0
46	ITGYALVVA	63	-0.3000	0

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	MLIAGGRRA	133	3.0000	35.71
2	LRPHAERGL	43	2.8000	33.33
3	VELAWRLDA	96	2.5000	29.76
4	LVVASPGFS	68	2.3000	27.38
5	LTLLPVASI	264	2.3000	27.38
6	VMTAAVAAA	436	2.3000	27.38
7	LVVTGTNGK	115	2.1000	25.00
8	VGVLDALAA	278	1.8000	21.43
9	LIGRDRAAV	376	1.8000	21.43
10	VAAARRMAQ	441	1.5000	17.86
11	VTGQAVAAV	17	1.3000	15.48
12	LHAMLIAGG	130	1.3000	15.48
13	VLAYPRVVW	341	1.3000	15.48
14	VMLRPHAER	41	1.2000	14.29
15	LSSFQLHWA	166	1.2000	14.29
16	FQLHWAPSL	169	1.2000	14.29
17	VAAMASRLV	364	1.2000	14.29
18	VLLAPAGAS	454	1.2000	14.29
19	LIAGGRRAV	134	1.1000	13.10
20	VGRHRAEVV	309	1.0000	11.90
21	LVGAVLIGR	371	1.0000	11.90
22	VRVGFRLGE	234	0.9000	10.71
23	LAAAALARS	284	0.9000	10.71
24	VPVACVLDV	414	0.9000	10.71
25	VLVAGGRVT	10	0.8000	9.52
26	LGVRDAHLV	248	0.8000	9.52
27	VWIAGGLLK	348	0.8000	9.52

28	VTSFRVGRH	304	0.7800	9.29
29	ITGYALVVA	63	0.7000	8.33
30	VLTGGVAVA	208	0.7000	8.33
31	LVAGGRVTG	11	0.5000	5.95
32	FRLGEPAAR	238	0.2000	2.38
33	VAAVLTRFG	22	0.1000	1.19
34	VVASPGFSP	69	0.1000	1.19
35	LAYPRVVWI	342	0.1000	1.19
36	LKGASLHAE	355	0.1000	1.19
37	FSPATPLLA	75	-0.1000	0
38	MLHAMLIAG	129	-0.1000	0
39	VAVAGLDDS	213	-0.1000	0
40	VAEALSRHA	384	-0.1000	0
41	LHWAPSLRP	171	-0.2000	0
42	VGFRLGEPA	236	-0.2000	0
43	LLKGASLHA	354	-0.2000	0
44	VLIGRDRAA	375	-0.2000	0
45	IGRDRAAVA	377	-0.2000	0

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	LTLLPVASI	264	2.9000	33.33
2	LVVASPGFS	68	2.8000	32.18
3	LVGAVLIGR	371	2.8000	32.18
4	VELAWRLDA	96	2.6000	29.89
5	VGVLDALAA	278	2.6000	29.89
6	FRLGEPAAR	238	2.5000	28.74
7	VRVGFRLGE	234	2.2000	25.29
8	FSPATPLLA	75	2.0000	22.99
9	VPVACVLDV	414	2.0000	22.99
10	LHAMLIAGG	130	1.9000	21.84
11	LLPVASIPV	266	1.7000	19.54

12	VLLAPAGAS	454	1.7000	19.54
13	MLHAMLIAG	129	1.6000	18.39
14	FATAVRAVI	476	1.6000	18.39
15	FQLHWAPSL	169	1.5100	17.36
16	WIAGGLLKG	349	1.5000	17.24
17	WRLDAAGCY	100	1.4000	16.09
18	VMTAAVAAA	436	1.3000	14.94
19	VAAARRMAQ	441	1.1000	12.64
20	VWIAGGLLK	348	1.0000	11.49
21	VASIPVPGP	269	0.9500	10.92
22	LHWAPSLRP	171	0.9000	10.34
23	LIGRDRAAV	376	0.9000	10.34
24	VVWIAGGLL	347	0.8600	9.89
25	VMLRPHAER	41	0.8000	9.20
26	LVVTGTNGK	115	0.6000	6.90
27	WAPSLRPEA	173	0.5500	6.32
28	YALVVASPG	66	0.5000	5.75
29	VVQVVAGED	397	0.5000	5.75
30	LLAAAAAAG	81	0.4000	4.60
31	MLIAGGRRA	133	0.4000	4.60
32	YPRVVWIAG	344	0.4000	4.60
33	VPVVQVVAG	395	0.4000	4.60
34	VTGQAVAAV	17	0.3000	3.45
35	WGDVELAWR	93	0.3000	3.45
36	WLVVTGTNG	114	0.3000	3.45
37	LAAAALARS	284	0.3000	3.45
38	LVAGGRVTG	11	0.2000	2.30
39	VAAVLTRFG	22	0.2000	2.30
40	LLAVELSSF	161	0.2000	2.30
41	FRVGRHRAE	307	0.2000	2.30
42	VQQITGYAL	60	-0.0400	0
43	VTSFRVGRH	304	-0.1000	0
44	VAVADGITY	317	-0.1000	0
45	YVDDSKATN	325	-0.2000	0

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	LRPHAERGL	43	3.7600	42.73
2	LTLLPVASI	264	3.2000	36.36
3	MLIAGGRRA	133	3.0000	34.09
4	LIGRDRAAV	376	2.8000	31.82
5	VMLRPHAER	41	2.7000	30.68
6	LVVASPGFS	68	2.7000	30.68
7	LHAMLIAGG	130	2.7000	30.68
8	VELAWRLDA	96	2.5000	28.41
9	LVGAVLIGR	371	2.5000	28.41
10	VTGQAVAAV	17	2.3000	26.14
11	VRVGFRLGE	234	2.3000	26.14
12	VMTAAVAAA	436	2.3000	26.14
13	LVVTGTNGK	115	2.2000	25.00
14	VAAMASRLV	364	2.2000	25.00
15	FQLHWAPSL	169	2.1600	24.55
16	LIAGGRRAV	134	2.1000	23.86
17	VGRHRAEVV	309	2.0000	22.73
18	LVAGGRVTG	11	1.9000	21.59
19	VPVACVLDV	414	1.9000	21.59
20	LGVRDAHLV	248	1.8000	20.45
21	VGVLDALAA	278	1.8000	20.45
22	FRLGEPAAR	238	1.7000	19.32
23	VLLAPAGAS	454	1.6000	18.18
24	VLVAGGRVT	10	1.5000	17.05
25	VAAVLTRFG	22	1.5000	17.05
26	VRDAHLVDR	250	1.5000	17.05
27	LKGASLHAE	355	1.5000	17.05
28	LLAAAAAAG	81	1.4000	15.91
29	MLHAMLIAG	129	1.3000	14.77
30	LAAAALARS	284	1.3000	14.77

31	VLAYPRVVW	341	1.3000	14.77
32	LSSFQLHWA	166	1.2000	13.64
33	VVASPGFSP	69	1.1000	12.50
34	FRVGRHRAE	307	1.0000	11.36
35	LAYPRVVWI	342	1.0000	11.36
36	VWIAGGLLK	348	0.9000	10.23
37	LHWAPSLRP	171	0.8000	9.09
38	VAAARRMAQ	441	0.8000	9.09
39	ITGYALVVA	63	0.7000	7.95
40	LDWHATMAE	192	0.7000	7.95
41	VLTGGVAVA	208	0.7000	7.95
42	LRPEAGAVL	177	0.6600	7.50
43	LSRHAPDVP	388	0.6000	6.82
44	VPVVQVVAG	395	0.6000	6.82
45	FATAVRAVI	476	0.6000	6.82
46	MTAAVAAAR	437	0.5000	5.68
47	MASRLVGAV	367	0.4000	4.55
48	LAAAAAAGV	82	0.3000	3.41

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	FQLHWAPSL	169	3.1600	35.91
2	LRPHAERGL	43	2.7600	31.36
3	FRLGEPAAR	238	2.7000	30.68
4	LTLLPVASI	264	2.2000	25.00
5	MLIAGGRRA	133	2.0000	22.73
6	FRVGRHRAE	307	2.0000	22.73
7	LIGRDRAAV	376	1.8000	20.45
8	VMLRPHAER	41	1.7000	19.32
9	LVVASPGFS	68	1.7000	19.32
10	LHAMLIAGG	130	1.7000	19.32
11	FATAVRAVI	476	1.6000	18.18

12	VELAWRLDA	96	1.5000	17.05
13	LVGAVLIGR	371	1.5000	17.05
14	VTGQAVAAV	17	1.3000	14.77
15	VRVGFRLGE	234	1.3000	14.77
16	VMTAAVAAA	436	1.3000	14.77
17	LVVTGTNGK	115	1.2000	13.64
18	VAAMASRLV	364	1.2000	13.64
19	YTAAKARVL	201	1.1600	13.18
20	LIAGGRRAV	134	1.1000	12.50
21	VGRHRAEVV	309	1.0000	11.36
22	LVAGGRVTG	11	0.9000	10.23
23	FSPATPLLA	75	0.9000	10.23
24	VPVACVLDV	414	0.9000	10.23
25	LGVRDAHLV	248	0.8000	9.09
26	VGVLDALAA	278	0.8000	9.09
27	WRLDAAGCY	100	0.6000	6.82
28	WIAGGLLKG	349	0.6000	6.82
29	VLLAPAGAS	454	0.6000	6.82
30	VLVAGGRVT	10	0.5000	5.68
31	VAAVLTRFG	22	0.5000	5.68
32	VRDAHLVDR	250	0.5000	5.68
33	LKGASLHAE	355	0.5000	5.68
34	LLAAAAAAG	81	0.4000	4.55
35	MLHAMLIAG	129	0.3000	3.41
36	LAAAALARS	284	0.3000	3.41
37	VLAYPRVVW	341	0.3000	3.41
38	LSSFQLHWA	166	0.2000	2.27
39	WAPSLRPEA	173	0.2000	2.27
40	VVASPGFSP	69	0.1000	1.14
41	YVDDSKATN	325	0.1000	1.14
42	YGPPRSWLV	108	-0.1000	0
43	VWIAGGLLK	348	-0.1000	0
44	LHWAPSLRP	171	-0.2000	0
45	VAAARRMAQ	441	-0.2000	0

46	ITGYALVVA	63	-0.3000	0

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	VRVGFRLGE	234	3.9000	43.33
2	LRPHAERGL	43	3.8000	42.22
3	LKGASLHAE	355	3.1000	34.44
4	MLIAGGRRA	133	3.0000	33.33
5	LHAMLIAGG	130	2.6000	28.89
6	FRVGRHRAE	307	2.6000	28.89
7	VELAWRLDA	96	2.5000	27.78
8	LTLLPVASI	264	2.5000	27.78
9	LVVASPGFS	68	2.3000	25.56
10	LDWHATMAE	192	2.3000	25.56
11	VMTAAVAAA	436	2.3000	25.56
12	VAAARRMAQ	441	2.3000	25.56
13	FQLHWAPSL	169	2.2000	24.44
14	VLAYPRVVW	341	2.2000	24.44
15	LIGRDRAAV	376	2.1000	23.33
16	VTSFRVGRH	304	2.0000	22.22
17	LVAGGRVTG	11	1.8000	20.00
18	VGVLDALAA	278	1.8000	20.00
19	VLVAGGRVT	10	1.7000	18.89
20	VTGQAVAAV	17	1.6000	17.78
21	VAAMASRLV	364	1.5000	16.67
22	VAAVLTRFG	22	1.4000	15.56
23	LVVTGTNGK	115	1.4000	15.56
24	LIAGGRRAV	134	1.4000	15.56
25	LLAAAAAAG	81	1.3000	14.44
26	VGRHRAEVV	309	1.3000	14.44
27	VMLRPHAER	41	1.2000	13.33
28	MLHAMLIAG	129	1.2000	13.33

29	LSSFQLHWA	166	1.2000	13.33
30	LNIAEDHLD	185	1.2000	13.33
31	VPVACVLDV	414	1.2000	13.33
32	VAKDDKAGE	422	1.2000	13.33
33	VLLAPAGAS	454	1.2000	13.33
34	LGVRDAHLV	248	1.1000	12.22
35	LVGAVLIGR	371	1.0000	11.11
36	LAAAALARS	284	0.9000	10.00
37	ITGYALVVA	63	0.7000	7.78
38	LRPEAGAVL	177	0.7000	7.78
39	VLTGGVAVA	208	0.7000	7.78
40	VVQVVAGED	397	0.7000	7.78
41	VSSSDAVQQ	54	0.5000	5.56
42	VVASPGFSP	69	0.5000	5.56
43	VPVVQVVAG	395	0.5000	5.56
44	LAPAGASFD	456	0.4000	4.44
45	VAGGRVTGQ	12	0.3000	3.33
46	LTRFGATPT	26	0.3000	3.33
47	YVDDSKATN	325	0.3000	3.33
48	LAYPRVVWI	342	0.3000	3.33

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	LTLLPVASI	264	2.9000	33.33
2	LVVASPGFS	68	2.8000	32.18
3	LVGAVLIGR	371	2.8000	32.18
4	VELAWRLDA	96	2.6000	29.89
5	VGVLDALAA	278	2.6000	29.89
6	FRLGEPAAR	238	2.5000	28.74
7	VRVGFRLGE	234	2.2000	25.29
8	FSPATPLLA	75	2.0000	22.99
9	VPVACVLDV	414	2.0000	22.99

10	LHAMLIAGG	130	1.9000	21.84
11	LLPVASIPV	266	1.7000	19.54
12	VLLAPAGAS	454	1.7000	19.54
13	MLHAMLIAG	129	1.6000	18.39
14	FATAVRAVI	476	1.6000	18.39
15	FQLHWAPSL	169	1.5100	17.36
16	WIAGGLLKG	349	1.5000	17.24
17	WRLDAAGCY	100	1.4000	16.09
18	VMTAAVAAA	436	1.3000	14.94
19	VAAARRMAQ	441	1.1000	12.64
20	VWIAGGLLK	348	1.0000	11.49
21	VASIPVPGP	269	0.9500	10.92
22	LHWAPSLRP	171	0.9000	10.34
23	LIGRDRAAV	376	0.9000	10.34
24	VVWIAGGLL	347	0.8600	9.89
25	VMLRPHAER	41	0.8000	9.20
26	LVVTGTNGK	115	0.6000	6.90
27	WAPSLRPEA	173	0.5500	6.32
28	YALVVASPG	66	0.5000	5.75
29	VVQVVAGED	397	0.5000	5.75
30	LLAAAAAAG	81	0.4000	4.60
31	MLIAGGRRA	133	0.4000	4.60
32	YPRVVWIAG	344	0.4000	4.60
33	VPVVQVVAG	395	0.4000	4.60
34	VTGQAVAAV	17	0.3000	3.45
35	WGDVELAWR	93	0.3000	3.45
36	WLVVTGTNG	114	0.3000	3.45
37	LAAAALARS	284	0.3000	3.45
38	LVAGGRVTG	11	0.2000	2.30
39	VAAVLTRFG	22	0.2000	2.30
40	LLAVELSSF	161	0.2000	2.30
41	FRVGRHRAE	307	0.2000	2.30
42	VQQITGYAL	60	-0.0400	0
43	VTSFRVGRH	304	-0.1000	0

44	VAVADGITY	317	-0.1000	0
45	YVDDSKATN	325	-0.2000	0

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	LVVASPGFS	68	2.3000	33.82
2	LTLLPVASI	264	2.0000	29.41
3	VMTAAVAAA	436	1.3000	19.12
4	VLLAPAGAS	454	1.2000	17.65
5	FRLGEPAAR	238	1.0000	14.71
6	VELAWRLDA	96	0.8000	11.76
7	VGVLDALAA	278	0.8000	11.76
8	FATAVRAVI	476	0.7000	10.29
9	LHAMLIAGG	130	0.5000	7.35
10	VTSFRVGRH	304	0.3800	5.59
11	FSPATPLLA	75	0.2000	2.94
12	LVVTGTNGK	115	0.2000	2.94
13	MLIAGGRRA	133	0.2000	2.94
14	VAAARRMAQ	441	0.2000	2.94
15	LAAAALARS	284	-0.1000	0
16	LIGRDRAAV	376	-0.1000	0
17	VVWIAGGLL	347	-0.2000	0
18	LVGAVLIGR	371	-0.3000	0
19	VLTGGVAVA	208	-0.5000	0
20	FQLHWAPSL	169	-0.6000	0
21	WAPSLRPEA	173	-0.6000	0
22	VTGQAVAAV	17	-0.7000	0
23	VMLRPHAER	41	-0.7000	0
24	VVQVVAGED	397	-0.7000	0
25	VPVACVLDV	414	-0.8000	0
26	YALVVASPG	66	-0.9000	0
27	LLPVASIPV	266	-0.9000	0

28	VWIAGGLLK	348	-0.9000	0
29	LLAAAAAAG	81	-1.0000	0
30	VRVGFRLGE	234	-1.0000	0
31	YVDDSKATN	325	-1.0000	0
32	WGDVELAWR	93	-1.2000	0
33	VASIPVPGP	269	-1.2000	0
34	VLDALAAAA	280	-1.3000	0
35	VAAVLTRFG	22	-1.4000	0
36	MLHAMLIAG	129	-1.4000	0
37	LSSFQLHWA	166	-1.4000	0
38	FRVGRHRAE	307	-1.4000	0
39	VAAMASRLV	364	-1.4000	0
40	VLCGNIGSA	142	-1.5000	0
41	MASRLVGAV	367	-1.5000	0
42	IGRDRAAVA	377	-1.5000	0
43	VPVVQVVAG	395	-1.5000	0
44	YTAAKARVL	201	-1.6000	0
45	VGAVLIGRD	372	-1.6000	0
46	LVAGGRVTG	11	-1.7000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VELAWRLDA	96	3.6000	43.37
2	VGVLDALAA	278	3.6000	43.37
3	LVVASPGFS	68	3.4000	40.96
4	LTLLPVASI	264	3.0000	36.14
5	VAAARRMAQ	441	2.8000	33.73
6	LVGAVLIGR	371	2.3000	27.71
7	VMTAAVAAA	436	2.3000	27.71
8	VLLAPAGAS	454	2.3000	27.71
9	VPVACVLDV	414	2.0000	24.10
10	VWIAGGLLK	348	1.9000	22.89

11	VRVGFRLGE	234	1.8000	21.69
12	LLPVASIPV	266	1.7000	20.48
13	LVVTGTNGK	115	1.5000	18.07
14	LHAMLIAGG	130	1.5000	18.07
15	VTSFRVGRH	304	1.4800	17.83
16	MLIAGGRRA	133	1.4000	16.87
17	MLHAMLIAG	129	1.2000	14.46
18	FSPATPLLA	75	1.0000	12.05
19	VASIPVPGP	269	0.9500	11.45
20	LHWAPSLRP	171	0.9000	10.84
21	LAAAALARS	284	0.9000	10.84
22	VVWIAGGLL	347	0.9000	10.84
23	LIGRDRAAV	376	0.9000	10.84
24	LLKGASLHA	354	0.7000	8.43
25	VLTGGVAVA	208	0.5000	6.02
26	VVQVVAGED	397	0.4000	4.82
27	VTGQAVAAV	17	0.3000	3.61
28	VMLRPHAER	41	0.3000	3.61
29	LSSFQLHWA	166	0.3000	3.61
30	LVAGGRVTG	11	-0.2000	0
31	VAAVLTRFG	22	-0.2000	0
32	VAAMASRLV	364	-0.2000	0
33	VLDALAAAA	280	-0.3000	0
34	VLAYPRVVW	341	-0.3000	0
35	FATAVRAVI	476	-0.3000	0
36	VLCGNIGSA	142	-0.4000	0
37	VAVADGITY	317	-0.4000	0
38	LKGASLHAE	355	-0.4000	0
39	MASRLVGAV	367	-0.4000	0
40	FQLHWAPSL	169	-0.4500	0
41	WAPSLRPEA	173	-0.4500	0
42	VRDAHLVDR	250	-0.5000	0
43	VGAVLIGRD	372	-0.5000	0

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	VRVGFRLGE	234	3.8000	42.70
2	VELAWRLDA	96	2.6000	29.21
3	VGVLDALAA	278	2.6000	29.21
4	VAAARRMAQ	441	2.6000	29.21
5	LVVASPGFS	68	2.4000	26.97
6	LTLLPVASI	264	2.2000	24.72
7	VVQVVAGED	397	2.1000	23.60
8	FSPATPLLA	75	2.0000	22.47
9	LHAMLIAGG	130	1.8000	20.22
10	FRVGRHRAE	307	1.8000	20.22
11	VTSFRVGRH	304	1.7000	19.10
12	LKGASLHAE	355	1.6000	17.98
13	FQLHWAPSL	169	1.5500	17.42
14	MLHAMLIAG	129	1.5000	16.85
15	WIAGGLLKG	349	1.4000	15.73
16	LVGAVLIGR	371	1.3000	14.61
17	VPVACVLDV	414	1.3000	14.61
18	VMTAAVAAA	436	1.3000	14.61
19	VLLAPAGAS	454	1.3000	14.61
20	WRLDAAGCY	100	1.2000	13.48
21	VGAVLIGRD	372	1.2000	13.48
22	FGATPTVCD	29	1.1000	12.36
23	FRLGEPAAR	238	1.0000	11.24
24	LLPVASIPV	266	1.0000	11.24
25	YVDDSKATN	325	1.0000	11.24
26	VVWIAGGLL	347	0.9000	10.11
27	FATAVRAVI	476	0.9000	10.11
28	WAPSLRPEA	173	0.5500	6.18
29	LDWHATMAE	192	0.5000	5.62
30	YALVVASPG	66	0.4000	4.49

31	MLIAGGRRA	133	0.4000	4.49
32	VASIPVPGP	269	0.3500	3.93
33	LLAAAAAAG	81	0.3000	3.37
34	LHWAPSLRP	171	0.3000	3.37
35	YPRVVWIAG	344	0.3000	3.37
36	VPVVQVVAG	395	0.3000	3.37
37	WLVVTGTNG	114	0.2000	2.25
38	VWIAGGLLK	348	0.2000	2.25
39	LIGRDRAAV	376	0.2000	2.25
40	LVAGGRVTG	11	0.1000	1.12
41	VAAVLTRFG	22	0.1000	1.12
42	LAAAALARS	284	-0.1000	0
43	VAKDDKAGE	422	-0.1000	0
44	LVVTGTNGK	115	-0.2000	0
45	LNIAEDHLD	185	-0.3000	0
46	VAVADGITY	317	-0.3000	0

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	MLIAGGRRA	133	3.0000	35.71
2	LRPHAERGL	43	2.8000	33.33
3	VELAWRLDA	96	2.5000	29.76
4	LVVASPGFS	68	2.3000	27.38
5	LTLLPVASI	264	2.3000	27.38
6	VMTAAVAAA	436	2.3000	27.38
7	LVVTGTNGK	115	2.1000	25.00
8	VGVLDALAA	278	1.8000	21.43
9	LIGRDRAAV	376	1.8000	21.43
10	VAAARRMAQ	441	1.5000	17.86
11	VTGQAVAAV	17	1.3000	15.48
12	LHAMLIAGG	130	1.3000	15.48
13	VLAYPRVVW	341	1.3000	15.48

14	VMLRPHAER	41	1.2000	14.29
15	LSSFQLHWA	166	1.2000	14.29
16	FQLHWAPSL	169	1.2000	14.29
17	VAAMASRLV	364	1.2000	14.29
18	VLLAPAGAS	454	1.2000	14.29
19	LIAGGRRAV	134	1.1000	13.10
20	VGRHRAEVV	309	1.0000	11.90
21	LVGAVLIGR	371	1.0000	11.90
22	VRVGFRLGE	234	0.9000	10.71
23	LAAAALARS	284	0.9000	10.71
24	VPVACVLDV	414	0.9000	10.71
25	VLVAGGRVT	10	0.8000	9.52
26	LGVRDAHLV	248	0.8000	9.52
27	VWIAGGLLK	348	0.8000	9.52
28	VTSFRVGRH	304	0.7800	9.29
29	ITGYALVVA	63	0.7000	8.33
30	VLTGGVAVA	208	0.7000	8.33
31	LVAGGRVTG	11	0.5000	5.95
32	FRLGEPAAR	238	0.2000	2.38
33	VAAVLTRFG	22	0.1000	1.19
34	VVASPGFSP	69	0.1000	1.19
35	LAYPRVVWI	342	0.1000	1.19
36	LKGASLHAE	355	0.1000	1.19
37	FSPATPLLA	75	-0.1000	0
38	MLHAMLIAG	129	-0.1000	0
39	VAVAGLDDS	213	-0.1000	0
40	VAEALSRHA	384	-0.1000	0
41	LHWAPSLRP	171	-0.2000	0
42	VGFRLGEPA	236	-0.2000	0
43	LLKGASLHA	354	-0.2000	0
44	VLIGRDRAA	375	-0.2000	0
45	IGRDRAAVA	377	-0.2000	0

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	FQLHWAPSL	169	2.2000	26.19
2	MLIAGGRRA	133	2.0000	23.81
3	LRPHAERGL	43	1.8000	21.43
4	VELAWRLDA	96	1.5000	17.86
5	LVVASPGFS	68	1.3000	15.48
6	LTLLPVASI	264	1.3000	15.48
7	VMTAAVAAA	436	1.3000	15.48
8	FRLGEPAAR	238	1.2000	14.29
9	LVVTGTNGK	115	1.1000	13.10
10	FSPATPLLA	75	0.9000	10.71
11	VGVLDALAA	278	0.8000	9.52
12	LIGRDRAAV	376	0.8000	9.52
13	FATAVRAVI	476	0.7000	8.33
14	FRVGRHRAE	307	0.6000	7.14
15	VAAARRMAQ	441	0.5000	5.95
16	VTGQAVAAV	17	0.3000	3.57
17	LHAMLIAGG	130	0.3000	3.57
18	VLAYPRVVW	341	0.3000	3.57
19	VMLRPHAER	41	0.2000	2.38
20	LSSFQLHWA	166	0.2000	2.38
21	WAPSLRPEA	173	0.2000	2.38
22	YTAAKARVL	201	0.2000	2.38
23	VAAMASRLV	364	0.2000	2.38
24	VLLAPAGAS	454	0.2000	2.38
25	LIAGGRRAV	134	0.1000	1.19
26	VRVGFRLGE	234	-0.1000	0
27	LAAAALARS	284	-0.1000	0
28	VPVACVLDV	414	-0.1000	0
29	VLVAGGRVT	10	-0.2000	0
30	LGVRDAHLV	248	-0.2000	0
31	VWIAGGLLK	348	-0.2000	0

32	VTSFRVGRH	304	-0.2200	0
33	ITGYALVVA	63	-0.3000	0
34	VLTGGVAVA	208	-0.3000	0
35	LVAGGRVTG	11	-0.5000	0
36	WRLDAAGCY	100	-0.7000	0
37	YVDDSKATN	325	-0.7000	0
38	WIAGGLLKG	349	-0.8000	0
39	VAAVLTRFG	22	-0.9000	0
40	VVASPGFSP	69	-0.9000	0
41	LAYPRVVWI	342	-0.9000	0
42	LKGASLHAE	355	-0.9000	0
43	LLAAAAAAG	81	-1.0000	0
44	VRDAHLVDR	250	-1.0000	0
45	YGPPRSWLV	108	-1.1000	0

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRPHAERGL	43	3.7600	42.73
2	LTLLPVASI	264	3.2000	36.36
3	MLIAGGRRA	133	3.0000	34.09
4	LIGRDRAAV	376	2.8000	31.82
5	VMLRPHAER	41	2.7000	30.68
6	LVVASPGFS	68	2.7000	30.68
7	LHAMLIAGG	130	2.7000	30.68
8	VELAWRLDA	96	2.5000	28.41
9	LVGAVLIGR	371	2.5000	28.41
10	VTGQAVAAV	17	2.3000	26.14
11	VRVGFRLGE	234	2.3000	26.14
12	VMTAAVAAA	436	2.3000	26.14
13	LVVTGTNGK	115	2.2000	25.00
14	VAAMASRLV	364	2.2000	25.00
15	FQLHWAPSL	169	2.1600	24.55

16	LIAGGRRAV	134	2.1000	23.86
17	VGRHRAEVV	309	2.0000	22.73
18	LVAGGRVTG	11	1.9000	21.59
19	VPVACVLDV	414	1.9000	21.59
20	LGVRDAHLV	248	1.8000	20.45
21	VGVLDALAA	278	1.8000	20.45
22	FRLGEPAAR	238	1.7000	19.32
23	VLLAPAGAS	454	1.6000	18.18
24	VLVAGGRVT	10	1.5000	17.05
25	VAAVLTRFG	22	1.5000	17.05
26	VRDAHLVDR	250	1.5000	17.05
27	LKGASLHAE	355	1.5000	17.05
28	LLAAAAAAG	81	1.4000	15.91
29	MLHAMLIAG	129	1.3000	14.77
30	LAAAALARS	284	1.3000	14.77
31	VLAYPRVVW	341	1.3000	14.77
32	LSSFQLHWA	166	1.2000	13.64
33	VVASPGFSP	69	1.1000	12.50
34	FRVGRHRAE	307	1.0000	11.36
35	LAYPRVVWI	342	1.0000	11.36
36	VWIAGGLLK	348	0.9000	10.23
37	LHWAPSLRP	171	0.8000	9.09
38	VAAARRMAQ	441	0.8000	9.09
39	ITGYALVVA	63	0.7000	7.95
40	LDWHATMAE	192	0.7000	7.95
41	VLTGGVAVA	208	0.7000	7.95
42	LRPEAGAVL	177	0.6600	7.50
43	LSRHAPDVP	388	0.6000	6.82
44	VPVVQVVAG	395	0.6000	6.82
45	FATAVRAVI	476	0.6000	6.82
46	MTAAVAAAR	437	0.5000	5.68
47	MASRLVGAV	367	0.4000	4.55
48	LAAAAAAGV	82	0.3000	3.41

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	LRPHAERGL	43	3.7600	42.73
2	LTLLPVASI	264	3.2000	36.36
3	MLIAGGRRA	133	3.0000	34.09
4	LIGRDRAAV	376	2.8000	31.82
5	VMLRPHAER	41	2.7000	30.68
6	LVVASPGFS	68	2.7000	30.68
7	LHAMLIAGG	130	2.7000	30.68
8	VELAWRLDA	96	2.5000	28.41
9	LVGAVLIGR	371	2.5000	28.41
10	VTGQAVAAV	17	2.3000	26.14
11	VRVGFRLGE	234	2.3000	26.14
12	VMTAAVAAA	436	2.3000	26.14
13	LVVTGTNGK	115	2.2000	25.00
14	VAAMASRLV	364	2.2000	25.00
15	FQLHWAPSL	169	2.1600	24.55
16	LIAGGRRAV	134	2.1000	23.86
17	VGRHRAEVV	309	2.0000	22.73
18	LVAGGRVTG	11	1.9000	21.59
19	VPVACVLDV	414	1.9000	21.59
20	LGVRDAHLV	248	1.8000	20.45
21	VGVLDALAA	278	1.8000	20.45
22	FRLGEPAAR	238	1.7000	19.32
23	VLLAPAGAS	454	1.6000	18.18
24	VLVAGGRVT	10	1.5000	17.05
25	VAAVLTRFG	22	1.5000	17.05
26	VRDAHLVDR	250	1.5000	17.05
27	LKGASLHAE	355	1.5000	17.05
28	LLAAAAAAG	81	1.4000	15.91
29	MLHAMLIAG	129	1.3000	14.77
30	LAAAALARS	284	1.3000	14.77

31	VLAYPRVVW	341	1.3000	14.77
32	LSSFQLHWA	166	1.2000	13.64
33	VVASPGFSP	69	1.1000	12.50
34	FRVGRHRAE	307	1.0000	11.36
35	LAYPRVVWI	342	1.0000	11.36
36	VWIAGGLLK	348	0.9000	10.23
37	LHWAPSLRP	171	0.8000	9.09
38	VAAARRMAQ	441	0.8000	9.09
39	ITGYALVVA	63	0.7000	7.95
40	LDWHATMAE	192	0.7000	7.95
41	VLTGGVAVA	208	0.7000	7.95
42	LRPEAGAVL	177	0.6600	7.50
43	LSRHAPDVP	388	0.6000	6.82
44	VPVVQVVAG	395	0.6000	6.82
45	FATAVRAVI	476	0.6000	6.82
46	MTAAVAAAR	437	0.5000	5.68
47	MASRLVGAV	367	0.4000	4.55
48	LAAAAAAGV	82	0.3000	3.41

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	VELAWRLDA	96	4.0000	40.82
2	LLPVASIPV	266	3.9000	39.80
3	VRVGFRLGE	234	3.7000	37.76
4	VVWIAGGLL	347	3.7000	37.76
5	VQQITGYAL	60	3.5000	35.71
6	LLKGASLHA	354	3.5000	35.71
7	VGVLDALAA	278	3.4000	34.69
8	VLAYPRVVW	341	3.4000	34.69
9	ITGYALVVA	63	3.2000	32.65
10	LTRFGATPT	26	3.1000	31.63
11	LSSFQLHWA	166	3.1000	31.63

12	FQLHWAPSL	169	3.1000	31.63
13	LVGAVLIGR	371	3.0000	30.61
14	LRPEAGAVL	177	2.9000	29.59
15	LIGRDRAAV	376	2.8000	28.57
16	LVAGGRVTG	11	2.6000	26.53
17	LRPHAERGL	43	2.6000	26.53
18	VVASPGFSP	69	2.6000	26.53
19	VVTGTNGKT	116	2.6000	26.53
20	MLIAGGRRA	133	2.5000	25.51
21	LHWAPSLRP	171	2.2000	22.45
22	LVVASPGFS	68	2.1000	21.43
23	MLHAMLIAG	129	2.1000	21.43
24	LGVRDAHLV	248	2.1000	21.43
25	VWIAGGLLK	348	2.1000	21.43
26	VVAGEDTGM	400	1.9800	20.20
27	LIAGGRRAV	134	1.9000	19.39
28	LTLLPVASI	264	1.9000	19.39
29	VGRHRAEVV	309	1.9000	19.39
30	VPVACVLDV	414	1.9000	19.39
31	VPIWGDVEL	90	1.8000	18.37
32	IAGGRRAVL	135	1.7000	17.35
33	VVAVADGIT	316	1.7000	17.35
34	VLLAPAGAS	454	1.7000	17.35
35	VAVADGITY	317	1.6000	16.33
36	VLIGRDRAA	375	1.6000	16.33
37	VQVVAGEDT	398	1.5000	15.31
38	WIAGGLLKG	349	1.4000	14.29
39	VAAMASRLV	364	1.4000	14.29
40	VLVAGGRVT	10	1.3000	13.27
41	LLAVELSSF	161	1.3000	13.27
42	MAEYTAAKA	198	1.3000	13.27
43	VGFRLGEPA	236	1.3000	13.27
44	LVVTGTNGK	115	1.2600	12.86
45	LGPGAPVLV	4	1.2000	12.24

46	LARSVGVPA	289	1.2000	12.24
47	VGVPAGAIA	293	1.2000	12.24
48	VTSFRVGRH	304	1.2000	12.24

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FQLHWAPSL	169	4.1000	41.84
2	VELAWRLDA	96	3.0000	30.61
3	LLPVASIPV	266	2.9000	29.59
4	VRVGFRLGE	234	2.7000	27.55
5	VVWIAGGLL	347	2.7000	27.55
6	VQQITGYAL	60	2.5000	25.51
7	LLKGASLHA	354	2.5000	25.51
8	VGVLDALAA	278	2.4000	24.49
9	VLAYPRVVW	341	2.4000	24.49
10	WIAGGLLKG	349	2.4000	24.49
11	ITGYALVVA	63	2.2000	22.45
12	LTRFGATPT	26	2.1000	21.43
13	LSSFQLHWA	166	2.1000	21.43
14	YGPPRSWLV	108	2.0000	20.41
15	FRLGEPAAR	238	2.0000	20.41
16	LVGAVLIGR	371	2.0000	20.41
17	WRLDAAGCY	100	1.9000	19.39
18	LRPEAGAVL	177	1.9000	19.39
19	LIGRDRAAV	376	1.8000	18.37
20	FSPATPLLA	75	1.7000	17.35
21	FATAVRAVI	476	1.7000	17.35
22	LVAGGRVTG	11	1.6000	16.33
23	LRPHAERGL	43	1.6000	16.33
24	VVASPGFSP	69	1.6000	16.33
25	WLVVTGTNG	114	1.6000	16.33
26	VVTGTNGKT	116	1.6000	16.33

27	MLIAGGRRA	133	1.5000	15.31
28	WAPSLRPEA	173	1.3000	13.27
29	LHWAPSLRP	171	1.2000	12.24
30	LVVASPGFS	68	1.1000	11.22
31	MLHAMLIAG	129	1.1000	11.22
32	LGVRDAHLV	248	1.1000	11.22
33	VWIAGGLLK	348	1.1000	11.22
34	VVAGEDTGM	400	0.9800	10.00
35	LIAGGRRAV	134	0.9000	9.18
36	LTLLPVASI	264	0.9000	9.18
37	VGRHRAEVV	309	0.9000	9.18
38	VPVACVLDV	414	0.9000	9.18
39	VPIWGDVEL	90	0.8000	8.16
40	YALVVASPG	66	0.7000	7.14
41	IAGGRRAVL	135	0.7000	7.14
42	VVAVADGIT	316	0.7000	7.14
43	YPRVVWIAG	344	0.7000	7.14
44	VLLAPAGAS	454	0.7000	7.14
45	VAVADGITY	317	0.6000	6.12
46	VLIGRDRAA	375	0.6000	6.12
47	VQVVAGEDT	398	0.5000	5.10
48	VAAMASRLV	364	0.4000	4.08

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	VELAWRLDA	96	4.0000	40.82
2	LLPVASIPV	266	3.9000	39.80
3	VRVGFRLGE	234	3.7000	37.76
4	VVWIAGGLL	347	3.7000	37.76
5	VQQITGYAL	60	3.5000	35.71
6	LLKGASLHA	354	3.5000	35.71
7	VGVLDALAA	278	3.4000	34.69

8	VLAYPRVVW	341	3.4000	34.69
9	ITGYALVVA	63	3.2000	32.65
10	LTRFGATPT	26	3.1000	31.63
11	LSSFQLHWA	166	3.1000	31.63
12	FQLHWAPSL	169	3.1000	31.63
13	LVGAVLIGR	371	3.0000	30.61
14	LRPEAGAVL	177	2.9000	29.59
15	LIGRDRAAV	376	2.8000	28.57
16	LVAGGRVTG	11	2.6000	26.53
17	LRPHAERGL	43	2.6000	26.53
18	VVASPGFSP	69	2.6000	26.53
19	VVTGTNGKT	116	2.6000	26.53
20	MLIAGGRRA	133	2.5000	25.51
21	LHWAPSLRP	171	2.2000	22.45
22	LVVASPGFS	68	2.1000	21.43
23	MLHAMLIAG	129	2.1000	21.43
24	LGVRDAHLV	248	2.1000	21.43
25	VWIAGGLLK	348	2.1000	21.43
26	VVAGEDTGM	400	1.9800	20.20
27	LIAGGRRAV	134	1.9000	19.39
28	LTLLPVASI	264	1.9000	19.39
29	VGRHRAEVV	309	1.9000	19.39
30	VPVACVLDV	414	1.9000	19.39
31	VPIWGDVEL	90	1.8000	18.37
32	IAGGRRAVL	135	1.7000	17.35
33	VVAVADGIT	316	1.7000	17.35
34	VLLAPAGAS	454	1.7000	17.35
35	VAVADGITY	317	1.6000	16.33
36	VLIGRDRAA	375	1.6000	16.33
37	VQVVAGEDT	398	1.5000	15.31
38	WIAGGLLKG	349	1.4000	14.29
39	VAAMASRLV	364	1.4000	14.29
40	VLVAGGRVT	10	1.3000	13.27
41	LLAVELSSF	161	1.3000	13.27

42	MAEYTAAKA	198	1.3000	13.27
43	VGFRLGEPA	236	1.3000	13.27
44	LVVTGTNGK	115	1.2600	12.86
45	LGPGAPVLV	4	1.2000	12.24
46	LARSVGVPA	289	1.2000	12.24
47	VGVPAGAIA	293	1.2000	12.24
48	VTSFRVGRH	304	1.2000	12.24

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVTGTNGK	115	4.3000	43.88
2	FRLGEPAAR	238	4.3000	43.88
3	VVWIAGGLL	347	4.0000	40.82
4	LVGAVLIGR	371	4.0000	40.82
5	VQQITGYAL	60	3.7000	37.76
6	VWIAGGLLK	348	3.4000	34.69
7	WRLDAAGCY	100	3.2000	32.65
8	LVVASPGFS	68	3.1000	31.63
9	WLVVTGTNG	114	3.0000	30.61
10	YTAAKARVL	201	2.6000	26.53
11	MLIAGGRRA	133	2.5000	25.51
12	YALVVASPG	66	2.3000	23.47
13	VLLAPAGAS	454	2.3000	23.47
14	LLPVASIPV	266	1.9000	19.39
15	WGDVELAWR	93	1.8000	18.37
16	VAVADGITY	317	1.7000	17.35
17	FQLHWAPSL	169	1.5000	15.31
18	MTAAVAAAR	437	1.5000	15.31
19	VLVAGGRVT	10	1.3000	13.27
20	VAAMASRLV	364	1.3000	13.27
21	VVQVVAGED	397	1.3000	13.27
22	LRPEAGAVL	177	1.2000	12.24

23	VGVLDALAA	278	1.2000	12.24
24	YPRVVWIAG	344	1.2000	12.24
25	LLAVELSSF	161	1.1000	11.22
26	VRDAHLVDR	250	1.1000	11.22
27	VAAVLTRFG	22	1.0000	10.20
28	VVASPGFSP	69	1.0000	10.20
29	FSPATPLLA	75	0.8000	8.16
30	MLHAMLIAG	129	0.8000	8.16
31	VMLRPHAER	41	0.7000	7.14
32	LRPHAERGL	43	0.7000	7.14
33	LDGSPAQVR	227	0.6000	6.12
34	FRVGRHRAE	307	0.6000	6.12
35	VVAVADGIT	316	0.6000	6.12
36	LHAMLIAGG	130	0.5000	5.10
37	LTLLPVASI	264	0.5000	5.10
38	VACVLDVAK	416	0.5000	5.10
39	LLAAAAAAG	81	0.4000	4.08
40	VQVVAGEDT	398	0.4000	4.08
41	VTGTNGKTT	117	-0.1000	0
42	LKGASLHAE	355	-0.1000	0
43	FATAVRAVI	476	-0.1000	0
44	VELSSFQLH	164	-0.4000	0
45	VLNIAEDHL	184	-0.4000	0
46	LDALAAAAL	281	-0.4000	0

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	LVVTGTNGK	115	4.3000	43.88
2	FRLGEPAAR	238	4.3000	43.88
3	VVWIAGGLL	347	4.0000	40.82
4	LVGAVLIGR	371	4.0000	40.82
5	VQQITGYAL	60	3.7000	37.76

6	VWIAGGLLK	348	3.4000	34.69
7	WRLDAAGCY	100	3.2000	32.65
8	LVVASPGFS	68	3.1000	31.63
9	WLVVTGTNG	114	3.0000	30.61
10	YTAAKARVL	201	2.6000	26.53
11	MLIAGGRRA	133	2.5000	25.51
12	YALVVASPG	66	2.3000	23.47
13	VLLAPAGAS	454	2.3000	23.47
14	LLPVASIPV	266	1.9000	19.39
15	WGDVELAWR	93	1.8000	18.37
16	VAVADGITY	317	1.7000	17.35
17	FQLHWAPSL	169	1.5000	15.31
18	MTAAVAAAR	437	1.5000	15.31
19	VLVAGGRVT	10	1.3000	13.27
20	VAAMASRLV	364	1.3000	13.27
21	VVQVVAGED	397	1.3000	13.27
22	LRPEAGAVL	177	1.2000	12.24
23	VGVLDALAA	278	1.2000	12.24
24	YPRVVWIAG	344	1.2000	12.24
25	LLAVELSSF	161	1.1000	11.22
26	VRDAHLVDR	250	1.1000	11.22
27	VAAVLTRFG	22	1.0000	10.20
28	VVASPGFSP	69	1.0000	10.20
29	FSPATPLLA	75	0.8000	8.16
30	MLHAMLIAG	129	0.8000	8.16
31	VMLRPHAER	41	0.7000	7.14
32	LRPHAERGL	43	0.7000	7.14
33	LDGSPAQVR	227	0.6000	6.12
34	FRVGRHRAE	307	0.6000	6.12
35	VVAVADGIT	316	0.6000	6.12
36	LHAMLIAGG	130	0.5000	5.10
37	LTLLPVASI	264	0.5000	5.10
38	VACVLDVAK	416	0.5000	5.10
39	LLAAAAAAG	81	0.4000	4.08

40	VQVVAGEDT	398	0.4000	4.08
41	VTGTNGKTT	117	-0.1000	0
42	LKGASLHAE	355	-0.1000	0
43	FATAVRAVI	476	-0.1000	0
44	VELSSFQLH	164	-0.4000	0
45	VLNIAEDHL	184	-0.4000	0
46	LDALAAAAL	281	-0.4000	0