MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Apr 14 00:08:01 2010
Length of input sequence	358 amino acids
Number of nanomers from input sequence	350
Number of nanomers with obligatory P1 anchor residue	101
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	35

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WVSQTASNT	294	2.0000	33.33
2	VIFLPGPAA	106	1.5700	26.17
3	LLMLSVLVA	15	1.5000	25.00
4	YGLAGSREL	284	1.4900	24.83
5	VRPLSGHPR	60	1.2000	20.00
6	FLPGPAAAL	108	1.1000	18.33
7	FIGLLMLSV	12	1.0000	16.67
8	FARVDALVT	200	0.7500	12.50

9	VYGVDPLIL	265	0.6500	10.83
10	VVSGSGAGV	339	0.6000	10.00
11	LVTQGNTTV	206	0.4900	8.17
12	YTLAKNPAV	176	0.2700	4.50
13	FAPGYPPTI	33	0.1700	2.83
14	VNVADAAHT	145	0.1000	1.67
15	LRQAYPVRQ	273	0.1000	1.67
16	LYVVSGSGA	337	-0.1500	0
17	LILRQAYPV	271	-0.2000	0
18	IGLLMLSVL	13	-0.3000	0
19	VLIADTRGG	253	-0.4100	0
20	LVLGSADGA	166	-0.6000	0
21	YVVSGSGAG	338	-0.6000	0
22	VVLDRGQTS	214	-0.7000	0
23	YDLTTGIPV	306	-0.7000	0
24	LVYGVDPLI	264	-0.7300	0
25	VAGCSSNPL	22	-0.8000	0
26	FLAARGGYF	125	-0.8000	0
27	VLVAGCSSN	20	-0.9000	0
28	MLSVLVAGC	17	-0.9500	0
29	IMVFDDVHV	94	-1.0200	0
30	IEPAQPAVS	41	-1.1000	0
31	VYTLAKNPA	175	-1.1000	0
32	LVALRPGAD	79	-1.2000	0
33	VHVAPRVIF	100	-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	VIFLPGPAA	106	2.5700	42.83
2	LLMLSVLVA	15	2.5000	41.67
3	VRPLSGHPR	60	2.2000	36.67
4	VYGVDPLIL	265	1.6500	27.50

5	VVSGSGAGV	339	1.6000	26.67
6	LVTQGNTTV	206	1.4900	24.83
7	FLPGPAAAL	108	1.1000	18.33
8	VNVADAAHT	145	1.1000	18.33
9	LRQAYPVRQ	273	1.1000	18.33
10	FIGLLMLSV	12	1.0000	16.67
11	LRAGQGATT	236	1.0000	16.67
12	WVSQTASNT	294	1.0000	16.67
13	LYVVSGSGA	337	0.8500	14.17
14	LILRQAYPV	271	0.8000	13.33
15	FARVDALVT	200	0.7500	12.50
16	IGLLMLSVL	13	0.7000	11.67
17	VLIADTRGG	253	0.5900	9.83
18	YGLAGSREL	284	0.4900	8.17
19	LVLGSADGA	166	0.4000	6.67
20	VVLDRGQTS	214	0.3000	5.00
21	LVYGVDPLI	264	0.2700	4.50
22	VAGCSSNPL	22	0.2000	3.33
23	FAPGYPPTI	33	0.1700	2.83
24	VLVAGCSSN	20	0.1000	1.67
25	MLSVLVAGC	17	0.0500	0.83
26	IMVFDDVHV	94	-0.0200	0
27	IEPAQPAVS	41	-0.1000	0
28	VYTLAKNPA	175	-0.1000	0
29	LVALRPGAD	79	-0.2000	0
30	VHVAPRVIF	100	-0.2000	0
31	LSVLVAGCS	18	-0.3000	0
32	IFLPGPAAA	107	-0.3000	0
33	LAKNPAVDP	178	-0.3600	0
34	LVAGCSSNP	21	-0.5000	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	VVLDRGQTS	214	5.7000	60.00
2	MVFDDVHVA	95	5.6000	58.95
3	IGYDLTTGI	304	4.9000	51.58
4	LIADTRGGQ	254	4.3000	45.26
5	LLTGNKPAV	0	3.8000	40.00
6	LLMLSVLVA	15	3.8000	40.00
7	LMLSVLVAG	16	3.6000	37.89
8	LAFDETSDT	328	3.4700	36.53
9	VHVAPRVIF	100	3.4000	35.79
10	YGVDPLILR	266	3.4000	35.79
11	LVLGSADGA	166	3.0000	31.58
12	MAADPLGRV	245	2.9000	30.53
13	FVADLSSGH	133	2.8700	30.21
14	VLIADTRGG	253	2.8000	29.47
15	VRYPTVQQP	317	2.8000	29.47
16	LRQAYPVRQ	273	2.7000	28.42
17	YVVSGSGAG	338	2.7000	28.42
18	LTSDDHGTA	116	2.5000	26.32
19	IGADGHAQQ	226	2.5000	26.32
20	VQVIEHAAG	347	2.5000	26.32
21	MLSVLVAGC	17	2.4000	25.26
22	VVSGSGAGV	339	2.4000	25.26
23	LVYGVDPLI	264	2.3000	24.21
24	LVAGCSSNP	21	2.2700	23.89
25	VYTLAKNPA	175	2.1100	22.21
26	LVALRPGAD	79	2.1000	22.11
27	IEPAQPAVS	41	2.0000	21.05
28	VIFLPGPAA	106	1.9000	20.00
29	VYGVDPLIL	265	1.7600	18.53
30	IGLLMLSVL	13	1.7300	18.21
31	LVTQGNTTV	206	1.7000	17.89
32	VQRRFIGLL	8	1.6600	17.47
33	FAPGYPPTI	33	1.6000	16.84

34	VFDDVHVAP	96	1.6000	16.84
35	VRPLSGHPR	60	1.5000	15.79

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	MVFDDVHVA	95	4.6000	50.55
2	FVADLSSGH	133	4.4500	48.90
3	VVLDRGQTS	214	4.3000	47.25
4	LIADTRGGQ	254	4.0000	43.96
5	IGYDLTTGI	304	3.0000	32.97
6	YGVDPLILR	266	2.9000	31.87
7	LLMLSVLVA	15	2.8000	30.77
8	LRQAYPVRQ	273	2.4000	26.37
9	YVVSGSGAG	338	2.3000	25.27
10	IGADGHAQQ	226	2.2000	24.18
11	LVLGSADGA	166	2.0000	21.98
12	LLTGNKPAV	0	1.8000	19.78
13	LAFDETSDT	328	1.7700	19.45
14	FAPGYPPTI	33	1.7000	18.68
15	LTSDDHGTA	116	1.5000	16.48
16	MLSVLVAGC	17	1.4000	15.38
17	LMLSVLVAG	16	1.2000	13.19
18	WVSQTASNT	294	1.1700	12.86
19	VYTLAKNPA	175	1.1100	12.20
20	VIFLPGPAA	106	0.9000	9.89
21	MAADPLGRV	245	0.9000	9.89
22	FLPGPAAAL	108	0.8000	8.79
23	VRYPTVQQP	317	0.8000	8.79
24	IEPAQPAVS	41	0.6000	6.59
25	YPTVQQPNS	319	0.6000	6.59
26	YFVADLSSG	132	0.5700	6.26
27	VHVAPRVIF	100	0.5000	5.49

28	LTGNKPAVQ	1	0.4000	4.40
29	YTLAKNPAV	176	0.4000	4.40
30	VLIADTRGG	253	0.4000	4.40
31	LVYGVDPLI	264	0.4000	4.40
32	VVSGSGAGV	339	0.4000	4.40
33	IFLPGPAAA	107	0.3000	3.30
34	LVAGCSSNP	21	0.2700	2.97
35	VSGSGAGVQ	340	0.2000	2.20

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	MVFDDVHVA	95	6.4000	72.73
2	VVLDRGQTS	214	5.4000	61.36
3	LLMLSVLVA	15	4.3000	48.86
4	IGYDLTTGI	304	4.0000	45.45
5	LIADTRGGQ	254	3.6000	40.91
6	LVLGSADGA	166	3.3000	37.50
7	LRQAYPVRQ	273	3.2800	37.27
8	IGADGHAQQ	226	3.2000	36.36
9	FVADLSSGH	133	3.1800	36.14
10	VYTLAKNPA	175	2.8000	31.82
11	LAFDETSDT	328	2.5000	28.41
12	MLSVLVAGC	17	2.4000	27.27
13	LMLSVLVAG	16	2.0800	23.64
14	VRYPTVQQP	317	1.9000	21.59
15	IEPAQPAVS	41	1.6000	18.18
16	YGVDPLILR	266	1.5800	17.95
17	LLTGNKPAV	0	1.4000	15.91
18	LTGNKPAVQ	1	1.4000	15.91
19	VVSGSGAGV	339	1.4000	15.91
20	VHVAPRVIF	100	1.3800	15.68
21	IFLPGPAAA	107	1.3000	14.77

22	VYGVDPLIL	265	1.3000	14.77
23	LTSDDHGTA	116	1.1000	12.50
24	VLIADTRGG	253	1.1000	12.50
25	VQVIEHAAG	347	1.1000	12.50
26	LVAGCSSNP	21	1.0000	11.36
27	VRPLSGHPR	60	0.8000	9.09
28	LRAGQGATT	236	0.8000	9.09
29	LTTGIPVEK	308	0.7800	8.86
30	LVTQGNTTV	206	0.7000	7.95
31	LGRVLIADT	250	0.7000	7.95
32	VASRTKIFA	193	0.5800	6.59
33	IGLLMLSVL	13	0.5000	5.68
34	VIFLPGPAA	106	0.5000	5.68
35	LSSGHTARV	137	0.5000	5.68

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	MVFDDVHVA	95	6.4000	72.73
2	VVLDRGQTS	214	5.4000	61.36
3	LLMLSVLVA	15	4.3000	48.86
4	IGYDLTTGI	304	4.0000	45.45
5	LIADTRGGQ	254	3.6000	40.91
6	LVLGSADGA	166	3.3000	37.50
7	LRQAYPVRQ	273	3.2800	37.27
8	IGADGHAQQ	226	3.2000	36.36
9	FVADLSSGH	133	3.1800	36.14
10	VYTLAKNPA	175	2.8000	31.82
11	LAFDETSDT	328	2.5000	28.41
12	MLSVLVAGC	17	2.4000	27.27
13	LMLSVLVAG	16	2.0800	23.64
14	VRYPTVQQP	317	1.9000	21.59
15	IEPAQPAVS	41	1.6000	18.18

16	YGVDPLILR	266	1.5800	17.95
17	LLTGNKPAV	0	1.4000	15.91
18	LTGNKPAVQ	1	1.4000	15.91
19	VVSGSGAGV	339	1.4000	15.91
20	VHVAPRVIF	100	1.3800	15.68
21	IFLPGPAAA	107	1.3000	14.77
22	VYGVDPLIL	265	1.3000	14.77
23	LTSDDHGTA	116	1.1000	12.50
24	VLIADTRGG	253	1.1000	12.50
25	VQVIEHAAG	347	1.1000	12.50
26	LVAGCSSNP	21	1.0000	11.36
27	VRPLSGHPR	60	0.8000	9.09
28	LRAGQGATT	236	0.8000	9.09
29	LTTGIPVEK	308	0.7800	8.86
30	LVTQGNTTV	206	0.7000	7.95
31	LGRVLIADT	250	0.7000	7.95
32	VASRTKIFA	193	0.5800	6.59
33	IGLLMLSVL	13	0.5000	5.68
34	VIFLPGPAA	106	0.5000	5.68
35	LSSGHTARV	137	0.5000	5.68

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	MVFDDVHVA	95	6.4000	72.73
2	VVLDRGQTS	214	5.4000	61.36
3	LLMLSVLVA	15	4.3000	48.86
4	IGYDLTTGI	304	4.0000	45.45
5	LIADTRGGQ	254	3.6000	40.91
6	LVLGSADGA	166	3.3000	37.50
7	LRQAYPVRQ	273	3.2800	37.27
8	IGADGHAQQ	226	3.2000	36.36
9	FVADLSSGH	133	3.1800	36.14

10	VYTLAKNPA	175	2.8000	31.82
11	LAFDETSDT	328	2.5000	28.41
12	MLSVLVAGC	17	2.4000	27.27
13	LMLSVLVAG	16	2.0800	23.64
14	VRYPTVQQP	317	1.9000	21.59
15	IEPAQPAVS	41	1.6000	18.18
16	YGVDPLILR	266	1.5800	17.95
17	LLTGNKPAV	0	1.4000	15.91
18	LTGNKPAVQ	1	1.4000	15.91
19	VVSGSGAGV	339	1.4000	15.91
20	VHVAPRVIF	100	1.3800	15.68
21	IFLPGPAAA	107	1.3000	14.77
22	VYGVDPLIL	265	1.3000	14.77
23	LTSDDHGTA	116	1.1000	12.50
24	VLIADTRGG	253	1.1000	12.50
25	VQVIEHAAG	347	1.1000	12.50
26	LVAGCSSNP	21	1.0000	11.36
27	VRPLSGHPR	60	0.8000	9.09
28	LRAGQGATT	236	0.8000	9.09
29	LTTGIPVEK	308	0.7800	8.86
30	LVTQGNTTV	206	0.7000	7.95
31	LGRVLIADT	250	0.7000	7.95
32	VASRTKIFA	193	0.5800	6.59
33	IGLLMLSVL	13	0.5000	5.68
34	VIFLPGPAA	106	0.5000	5.68
35	LSSGHTARV	137	0.5000	5.68

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	VVLDRGQTS	214	4.7000	49.47
2	MVFDDVHVA	95	4.6000	48.42
3	YGVDPLILR	266	4.4000	46.32

4	IGYDLTTGI	304	3.9000	41.05
5	FVADLSSGH	133	3.8700	40.74
6	YVVSGSGAG	338	3.7000	38.95
7	LIADTRGGQ	254	3.3000	34.74
8	LLTGNKPAV	0	2.8000	29.47
9	LLMLSVLVA	15	2.8000	29.47
10	LMLSVLVAG	16	2.6000	27.37
11	FAPGYPPTI	33	2.6000	27.37
12	LAFDETSDT	328	2.4700	26.00
13	VHVAPRVIF	100	2.4000	25.26
14	LVLGSADGA	166	2.0000	21.05
15	YFVADLSSG	132	1.9700	20.74
16	MAADPLGRV	245	1.9000	20.00
17	WVSQTASNT	294	1.8700	19.68
18	VLIADTRGG	253	1.8000	18.95
19	VRYPTVQQP	317	1.8000	18.95
20	FLPGPAAAL	108	1.7600	18.53
21	LRQAYPVRQ	273	1.7000	17.89
22	LTSDDHGTA	116	1.5000	15.79
23	IGADGHAQQ	226	1.5000	15.79
24	VQVIEHAAG	347	1.5000	15.79
25	MLSVLVAGC	17	1.4000	14.74
26	YTLAKNPAV	176	1.4000	14.74
27	VVSGSGAGV	339	1.4000	14.74
28	FLAARGGYF	125	1.3000	13.68
29	LVYGVDPLI	264	1.3000	13.68
30	LVAGCSSNP	21	1.2700	13.37
31	VYTLAKNPA	175	1.1100	11.68
32	LVALRPGAD	79	1.1000	11.58
33	IEPAQPAVS	41	1.0000	10.53
34	YPTVQQPNS	319	1.0000	10.53
35	FIGLLMLSV	12	0.9000	9.47

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	MVFDDVHVA	95	6.4000	72.73
2	VVLDRGQTS	214	5.4000	61.36
3	LLMLSVLVA	15	4.3000	48.86
4	IGYDLTTGI	304	4.0000	45.45
5	LIADTRGGQ	254	3.6000	40.91
6	LVLGSADGA	166	3.3000	37.50
7	LRQAYPVRQ	273	3.2800	37.27
8	IGADGHAQQ	226	3.2000	36.36
9	FVADLSSGH	133	3.1800	36.14
10	VYTLAKNPA	175	2.8000	31.82
11	LAFDETSDT	328	2.5000	28.41
12	MLSVLVAGC	17	2.4000	27.27
13	LMLSVLVAG	16	2.0800	23.64
14	VRYPTVQQP	317	1.9000	21.59
15	IEPAQPAVS	41	1.6000	18.18
16	YGVDPLILR	266	1.5800	17.95
17	LLTGNKPAV	0	1.4000	15.91
18	LTGNKPAVQ	1	1.4000	15.91
19	VVSGSGAGV	339	1.4000	15.91
20	VHVAPRVIF	100	1.3800	15.68
21	IFLPGPAAA	107	1.3000	14.77
22	VYGVDPLIL	265	1.3000	14.77
23	LTSDDHGTA	116	1.1000	12.50
24	VLIADTRGG	253	1.1000	12.50
25	VQVIEHAAG	347	1.1000	12.50
26	LVAGCSSNP	21	1.0000	11.36
27	VRPLSGHPR	60	0.8000	9.09
28	LRAGQGATT	236	0.8000	9.09
29	LTTGIPVEK	308	0.7800	8.86
30	LVTQGNTTV	206	0.7000	7.95
31	LGRVLIADT	250	0.7000	7.95

32	VASRTKIFA	193	0.5800	6.59
33	IGLLMLSVL	13	0.5000	5.68
34	VIFLPGPAA	106	0.5000	5.68
35	LSSGHTARV	137	0.5000	5.68

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	FVADLSSGH	133	4.3800	50.93
2	MVFDDVHVA	95	4.2000	48.84
3	LLMLSVLVA	15	3.8000	44.19
4	IGYDLTTGI	304	3.2000	37.21
5	VVLDRGQTS	214	2.7000	31.40
6	LVTQGNTTV	206	2.4000	27.91
7	YVVSGSGAG	338	2.1000	24.42
8	LRQAYPVRQ	273	1.7800	20.70
9	WVSQTASNT	294	1.7000	19.77
10	LAFDETSDT	328	1.7000	19.77
11	VLIADTRGG	253	1.2000	13.95
12	FIGLLMLSV	12	1.0000	11.63
13	YTLAKNPAV	176	0.9000	10.47
14	LTGNKPAVQ	1	0.6000	6.98
15	YGVDPLILR	266	0.3800	4.42
16	YGLAGSREL	284	0.3000	3.49
17	VSQTASNTV	295	0.3000	3.49
18	MLSVLVAGC	17	0.2000	2.33
19	LVLGSADGA	166	0.2000	2.33
20	IEPAQPAVS	41	0.1000	1.16
21	LMLSVLVAG	16	-0.1200	0
22	VAGCSSNPL	22	-0.2000	0
23	VRPLSGHPR	60	-0.2000	0
24	VTTIGADGH	223	-0.4200	0
25	VIFLPGPAA	106	-0.5000	0

26	LSVLVAGCS	18	-0.6000	0
27	FARVDALVT	200	-0.7000	0
28	VQQPNSLAF	322	-0.7000	0
29	IFLPGPAAA	107	-0.8000	0
30	LFDNGTRQL	71	-0.9000	0
31	VNVADAAHT	145	-0.9000	0
32	VQVIEHAAG	347	-0.9000	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	VLIADTRGG	253	5.1000	53.12
2	LLMLSVLVA	15	3.7000	38.54
3	LILRQAYPV	271	3.3000	34.38
4	LRQAYPVRQ	273	2.9000	30.21
5	LVTQGNTTV	206	2.4000	25.00
6	VRYPTVQQP	317	2.4000	25.00
7	YGLAGSREL	284	2.2000	22.92
8	MVFDDVHVA	95	2.0000	20.83
9	LFDNGTRQL	71	1.7000	17.71
10	MLSVLVAGC	17	1.4000	14.58
11	VALRPGADS	80	1.2000	12.50
12	IEPAQPAVS	41	1.1000	11.46
13	VVLDRGQTS	214	1.1000	11.46
14	VQQPNSLAF	322	0.9000	9.38
15	VAGCSSNPL	22	0.8000	8.33
16	LVAGCSSNP	21	0.7000	7.29
17	IGYDLTTGI	304	0.7000	7.29
18	VTQGNTTVV	207	0.6000	6.25
19	IFLPGPAAA	107	0.5000	5.21
20	VAPRVIFLP	102	0.4000	4.17
21	LSSGHTARV	137	0.4000	4.17
22	VYGVDPLIL	265	0.4000	4.17

23	LTGNKPAVQ	1	0.3000	3.12
24	LRPGADSAA	82	0.3000	3.12
25	IMVFDDVHV	94	0.3000	3.12
26	LVLGSADGA	166	0.3000	3.12
27	VNVADAAHT	145	0.1000	1.04
28	VSQTASNTV	295	0.1000	1.04
29	VRPLSGHPR	60	-0.1000	0
30	LVYGVDPLI	264	-0.2000	0
31	VQRRFIGLL	8	-0.3000	0
32	VLVAGCSSN	20	-0.3000	0
33	LAARGGYFV	126	-0.3000	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	LLMLSVLVA	15	4.6000	52.27
2	LVTQGNTTV	206	3.1000	35.23
3	MLSVLVAGC	17	2.6000	29.55
4	LRQAYPVRQ	273	2.6000	29.55
5	VLIADTRGG	253	2.5000	28.41
6	MVFDDVHVA	95	2.3000	26.14
7	IGYDLTTGI	304	2.2000	25.00
8	FVADLSSGH	133	1.5800	17.95
9	IEPAQPAVS	41	1.1000	12.50
10	VRYPTVQQP	317	1.1000	12.50
11	VVLDRGQTS	214	1.0000	11.36
12	IGLLMLSVL	13	0.9000	10.23
13	VAGCSSNPL	22	0.9000	10.23
14	VYGVDPLIL	265	0.9000	10.23
15	LAFDETSDT	328	0.9000	10.23
16	LYVVSGSGA	337	0.9000	10.23
17	LSVLVAGCS	18	0.7000	7.95
18	IMVFDDVHV	94	0.7000	7.95

19	VLVAGCSSN	20	0.6000	6.82
20	VRPLSGHPR	60	0.6000	6.82
21	WVSQTASNT	294	0.6000	6.82
22	IFLPGPAAA	107	0.5000	5.68
23	VIFLPGPAA	106	0.4000	4.55
24	LGRVLIADT	250	0.4000	4.55
25	VQVIEHAAG	347	0.4000	4.55
26	LVALRPGAD	79	0.2000	2.27
27	VYTLAKNPA	175	0.2000	2.27
28	VQQPNSLAF	322	0.2000	2.27
29	VNVADAAHT	145	0.1000	1.14
30	LAWVSQTAS	292	0.1000	1.14
31	VTTIGADGH	223	-0.0200	0
32	LVAGCSSNP	21	-0.1000	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	FVADLSSGH	133	3.8000	40.43
2	LLMLSVLVA	15	3.6000	38.30
3	VLIADTRGG	253	2.8000	29.79
4	WVSQTASNT	294	2.5000	26.60
5	LVTQGNTTV	206	2.4000	25.53
6	LRQAYPVRQ	273	2.4000	25.53
7	YVVSGSGAG	338	2.0000	21.28
8	LVALRPGAD	79	1.9000	20.21
9	MLSVLVAGC	17	1.6000	17.02
10	VLVAGCSSN	20	1.6000	17.02
11	YGLAGSREL	284	1.6000	17.02
12	IGYDLTTGI	304	1.4000	14.89
13	MVFDDVHVA	95	1.3000	13.83
14	FARVDALVT	200	1.2000	12.77
15	FIGLLMLSV	12	1.1000	11.70

16	YFVADLSSG	132	1.0000	10.64
17	VDALVTQGN	203	1.0000	10.64
18	IGLLMLSVL	13	0.9000	9.57
19	VAGCSSNPL	22	0.9000	9.57
20	YTLAKNPAV	176	0.9000	9.57
21	VYGVDPLIL	265	0.9000	9.57
22	LAFDETSDT	328	0.8000	8.51
23	VQVIEHAAG	347	0.7000	7.45
24	VRYPTVQQP	317	0.5000	5.32
25	LGRVLIADT	250	0.3000	3.19
26	VTTIGADGH	223	0.2000	2.13
27	IEPAQPAVS	41	0.1000	1.06
28	VQQPNSLAF	322	0.1000	1.06
29	LYVVSGSGA	337	-0.1000	0
30	LTGNKPAVQ	1	-0.2000	0
31	LLVYGVDPL	263	-0.2000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LLMLSVLVA	15	3.6000	40.91
2	FVADLSSGH	133	2.5800	29.32
3	LVTQGNTTV	206	2.1000	23.86
4	MLSVLVAGC	17	1.6000	18.18
5	LRQAYPVRQ	273	1.6000	18.18
6	WVSQTASNT	294	1.6000	18.18
7	VLIADTRGG	253	1.5000	17.05
8	MVFDDVHVA	95	1.3000	14.77
9	IGYDLTTGI	304	1.2000	13.64
10	FIGLLMLSV	12	0.8000	9.09
11	YVVSGSGAG	338	0.7000	7.95
12	YTLAKNPAV	176	0.6000	6.82
13	YGLAGSREL	284	0.6000	6.82

14	FARVDALVT	200	0.3000	3.41
15	IEPAQPAVS	41	0.1000	1.14
16	VRYPTVQQP	317	0.1000	1.14
17	IGLLMLSVL	13	-0.1000	0
18	VAGCSSNPL	22	-0.1000	0
19	VYGVDPLIL	265	-0.1000	0
20	LAFDETSDT	328	-0.1000	0
21	LYVVSGSGA	337	-0.1000	0
22	LSVLVAGCS	18	-0.3000	0
23	IMVFDDVHV	94	-0.3000	0
24	YFVADLSSG	132	-0.3000	0
25	VLVAGCSSN	20	-0.4000	0
26	VRPLSGHPR	60	-0.4000	0
27	IFLPGPAAA	107	-0.5000	0
28	VIFLPGPAA	106	-0.6000	0
29	LGRVLIADT	250	-0.6000	0
30	VQVIEHAAG	347	-0.6000	0
31	LVALRPGAD	79	-0.8000	0
32	VYTLAKNPA	175	-0.8000	0
33	VQQPNSLAF	322	-0.8000	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	LLMLSVLVA	15	4.6000	48.94
2	VLIADTRGG	253	3.8000	40.43
3	LVTQGNTTV	206	3.4000	36.17
4	LRQAYPVRQ	273	3.4000	36.17
5	LVALRPGAD	79	2.9000	30.85
6	FVADLSSGH	133	2.8000	29.79
7	MLSVLVAGC	17	2.6000	27.66
8	VLVAGCSSN	20	2.6000	27.66
9	IGYDLTTGI	304	2.4000	25.53

10	MVFDDVHVA	95	2.3000	24.47
11	VDALVTQGN	203	2.0000	21.28
12	IGLLMLSVL	13	1.9000	20.21
13	VAGCSSNPL	22	1.9000	20.21
14	VYGVDPLIL	265	1.9000	20.21
15	LAFDETSDT	328	1.8000	19.15
16	VQVIEHAAG	347	1.7000	18.09
17	WVSQTASNT	294	1.5000	15.96
18	VRYPTVQQP	317	1.5000	15.96
19	LGRVLIADT	250	1.3000	13.83
20	VTTIGADGH	223	1.2000	12.77
21	IEPAQPAVS	41	1.1000	11.70
22	VQQPNSLAF	322	1.1000	11.70
23	IMVFDDVHV	94	1.0000	10.64
24	VNVADAAHT	145	1.0000	10.64
25	VVLDRGQTS	214	1.0000	10.64
26	YVVSGSGAG	338	1.0000	10.64
27	LYVVSGSGA	337	0.9000	9.57
28	LTGNKPAVQ	1	0.8000	8.51
29	LLVYGVDPL	263	0.8000	8.51
30	LSVLVAGCS	18	0.7000	7.45
31	VRPLSGHPR	60	0.6000	6.38
32	YGLAGSREL	284	0.6000	6.38
33	LMLSVLVAG	16	0.5000	5.32
34	IFLPGPAAA	107	0.5000	5.32
35	VIGYDLTTG	303	0.5000	5.32

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	MVFDDVHVA	95	4.2000	46.67
2	IGYDLTTGI	304	4.1000	45.56
3	LLMLSVLVA	15	3.8000	42.22

4	FVADLSSGH	133	3.8000	42.22
5	YVVSGSGAG	338	3.5000	38.89
6	LVTQGNTTV	206	3.4000	37.78
7	VVLDRGQTS	214	3.1000	34.44
8	VLIADTRGG	253	2.6000	28.89
9	WVSQTASNT	294	2.4000	26.67
10	LAFDETSDT	328	2.4000	26.67
11	FIGLLMLSV	12	2.0000	22.22
12	YTLAKNPAV	176	1.9000	21.11
13	YGVDPLILR	266	1.8800	20.89
14	VRPLSGHPR	60	1.3000	14.44
15	VSQTASNTV	295	1.3000	14.44
16	LMLSVLVAG	16	1.2800	14.22
17	YGLAGSREL	284	1.2600	14.00
18	VQQPNSLAF	322	1.2000	13.33
19	LRQAYPVRQ	273	1.0800	12.00
20	VRYPTVQQP	317	1.0000	11.11
21	VAGCSSNPL	22	0.7600	8.44
22	IEPAQPAVS	41	0.5000	5.56
23	VQVIEHAAG	347	0.5000	5.56
24	YFVADLSSG	132	0.4000	4.44
25	MLSVLVAGC	17	0.2000	2.22
26	LVLGSADGA	166	0.2000	2.22
27	LFDNGTRQL	71	0.0600	0.67
28	IGLLMLSVL	13	-0.0400	0
29	LTGNKPAVQ	1	-0.1000	0
30	IPVEKVRYP	312	-0.1000	0
31	VYGVDPLIL	265	-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	LLMLSVLVA	15	4.6000	52.27

2	LVTQGNTTV	206	3.1000	35.23
3	MLSVLVAGC	17	2.6000	29.55
4	LRQAYPVRQ	273	2.6000	29.55
5	VLIADTRGG	253	2.5000	28.41
6	MVFDDVHVA	95	2.3000	26.14
7	IGYDLTTGI	304	2.2000	25.00
8	FVADLSSGH	133	1.5800	17.95
9	IEPAQPAVS	41	1.1000	12.50
10	VRYPTVQQP	317	1.1000	12.50
11	VVLDRGQTS	214	1.0000	11.36
12	IGLLMLSVL	13	0.9000	10.23
13	VAGCSSNPL	22	0.9000	10.23
14	VYGVDPLIL	265	0.9000	10.23
15	LAFDETSDT	328	0.9000	10.23
16	LYVVSGSGA	337	0.9000	10.23
17	LSVLVAGCS	18	0.7000	7.95
18	IMVFDDVHV	94	0.7000	7.95
19	VLVAGCSSN	20	0.6000	6.82
20	VRPLSGHPR	60	0.6000	6.82
21	WVSQTASNT	294	0.6000	6.82
22	IFLPGPAAA	107	0.5000	5.68
23	VIFLPGPAA	106	0.4000	4.55
24	LGRVLIADT	250	0.4000	4.55
25	VQVIEHAAG	347	0.4000	4.55
26	LVALRPGAD	79	0.2000	2.27
27	VYTLAKNPA	175	0.2000	2.27
28	VQQPNSLAF	322	0.2000	2.27
29	VNVADAAHT	145	0.1000	1.14
30	LAWVSQTAS	292	0.1000	1.14
31	VTTIGADGH	223	-0.0200	0
32	LVAGCSSNP	21	-0.1000	0

ALLELE: DRB1_0426	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	1.6	8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	FVADLSSGH	133	4.3800	50.93
2	MVFDDVHVA	95	4.2000	48.84
3	LLMLSVLVA	15	3.8000	44.19
4	IGYDLTTGI	304	3.2000	37.21
5	VVLDRGQTS	214	2.7000	31.40
6	LVTQGNTTV	206	2.4000	27.91
7	YVVSGSGAG	338	2.1000	24.42
8	LRQAYPVRQ	273	1.7800	20.70
9	WVSQTASNT	294	1.7000	19.77
10	LAFDETSDT	328	1.7000	19.77
11	VLIADTRGG	253	1.2000	13.95
12	FIGLLMLSV	12	1.0000	11.63
13	YTLAKNPAV	176	0.9000	10.47
14	LTGNKPAVQ	1	0.6000	6.98
15	YGVDPLILR	266	0.3800	4.42
16	YGLAGSREL	284	0.3000	3.49
17	VSQTASNTV	295	0.3000	3.49
18	MLSVLVAGC	17	0.2000	2.33
19	LVLGSADGA	166	0.2000	2.33
20	IEPAQPAVS	41	0.1000	1.16
21	LMLSVLVAG	16	-0.1200	0
22	VAGCSSNPL	22	-0.2000	0
23	VRPLSGHPR	60	-0.2000	0
24	VTTIGADGH	223	-0.4200	0
25	VIFLPGPAA	106	-0.5000	0
26	LSVLVAGCS	18	-0.6000	0
27	FARVDALVT	200	-0.7000	0
28	VQQPNSLAF	322	-0.7000	0
29	IFLPGPAAA	107	-0.8000	0
30	LFDNGTRQL	71	-0.9000	0
31	VNVADAAHT	145	-0.9000	0

32	VQVIEHAAG	347	-0.9000	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	YGLAGSREL	284	6.2000	53.45
2	VYGVDPLIL	265	6.1000	52.59
3	YDLTTGIPV	306	4.9000	42.24
4	VAGCSSNPL	22	4.6000	39.66
5	FARVDALVT	200	4.2000	36.21
6	VSQTASNTV	295	4.1000	35.34
7	YVVSGSGAG	338	4.1000	35.34
8	FIGLLMLSV	12	3.9000	33.62
9	VQQPNSLAF	322	3.9000	33.62
10	LILRQAYPV	271	3.7000	31.90
11	FLPGPAAAL	108	3.6000	31.03
12	IGYDLTTGI	304	2.9200	25.17
13	LLMLSVLVA	15	2.9000	25.00
14	VHVAPRVIF	100	2.9000	25.00
15	VQRRFIGLL	8	2.7000	23.28
16	LMLSVLVAG	16	2.7000	23.28
17	IGLLMLSVL	13	2.6000	22.41
18	FLAARGGYF	125	2.5000	21.55
19	YTLAKNPAV	176	2.2000	18.97
20	FAPGYPPTI	33	1.9000	16.38
21	IMVFDDVHV	94	1.9000	16.38
22	LVTQGNTTV	206	1.9000	16.38
23	IADTRGGQL	255	1.9000	16.38
24	LLVYGVDPL	263	1.8000	15.52
25	WVSQTASNT	294	1.6000	13.79
26	VVSGSGAGV	339	1.6000	13.79
27	VLIADTRGG	253	1.5200	13.10
28	LVYGVDPLI	264	1.5000	12.93

29	LFDNGTRQL	71	1.4200	12.24
30	LRQAYPVRQ	273	1.4000	12.07
31	VRYPTVQQP	317	1.4000	12.07
32	LSGHPRAAL	63	1.3000	11.21
33	MVFDDVHVA	95	1.3000	11.21
34	FVADLSSGH	133	1.3000	11.21
35	MLSVLVAGC	17	1.2000	10.34

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	YGLAGSREL	284	6.2000	53.45
2	VYGVDPLIL	265	6.1000	52.59
3	YDLTTGIPV	306	4.9000	42.24
4	VAGCSSNPL	22	4.6000	39.66
5	FARVDALVT	200	4.2000	36.21
6	VSQTASNTV	295	4.1000	35.34
7	YVVSGSGAG	338	4.1000	35.34
8	FIGLLMLSV	12	3.9000	33.62
9	VQQPNSLAF	322	3.9000	33.62
10	LILRQAYPV	271	3.7000	31.90
11	FLPGPAAAL	108	3.6000	31.03
12	IGYDLTTGI	304	2.9200	25.17
13	LLMLSVLVA	15	2.9000	25.00
14	VHVAPRVIF	100	2.9000	25.00
15	VQRRFIGLL	8	2.7000	23.28
16	LMLSVLVAG	16	2.7000	23.28
17	IGLLMLSVL	13	2.6000	22.41
18	FLAARGGYF	125	2.5000	21.55
19	YTLAKNPAV	176	2.2000	18.97
20	FAPGYPPTI	33	1.9000	16.38
21	IMVFDDVHV	94	1.9000	16.38
22	LVTQGNTTV	206	1.9000	16.38

23	IADTRGGQL	255	1.9000	16.38
24	LLVYGVDPL	263	1.8000	15.52
25	WVSQTASNT	294	1.6000	13.79
26	VVSGSGAGV	339	1.6000	13.79
27	VLIADTRGG	253	1.5200	13.10
28	LVYGVDPLI	264	1.5000	12.93
29	LFDNGTRQL	71	1.4200	12.24
30	LRQAYPVRQ	273	1.4000	12.07
31	VRYPTVQQP	317	1.4000	12.07
32	LSGHPRAAL	63	1.3000	11.21
33	MVFDDVHVA	95	1.3000	11.21
34	FVADLSSGH	133	1.3000	11.21
35	MLSVLVAGC	17	1.2000	10.34

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	VQRRFIGLL	8	3.4000	39.53
2	LLMLSVLVA	15	3.0000	34.88
3	LVALRPGAD	79	2.8000	32.56
4	VALRPGADS	80	2.3000	26.74
5	VASRTKIFA	193	2.0000	23.26
6	VLIADTRGG	253	2.0000	23.26
7	LILRQAYPV	271	1.9000	22.09
8	LRQAYPVRQ	273	1.9000	22.09
9	MLSVLVAGC	17	1.7000	19.77
10	FTAIARRSD	155	1.7000	19.77
11	LLVYGVDPL	263	1.5000	17.44
12	YPVRQAPYG	277	1.4000	16.28
13	YVVSGSGAG	338	1.3000	15.12
14	MVFDDVHVA	95	1.2000	13.95
15	VQVIEHAAG	347	1.2000	13.95
16	LTGNKPAVQ	1	1.0000	11.63

17	FVADLSSGH	133	1.0000	11.63
18	LGRVLIADT	250	0.9000	10.47
19	LIADTRGGQ	254	0.9000	10.47
20	YGLAGSREL	284	0.8000	9.30
21	IEPAQPAVS	41	0.6000	6.98
22	VYTLAKNPA	175	0.6000	6.98
23	VYGVDPLIL	265	0.6000	6.98
24	VIGYDLTTG	303	0.6000	6.98
25	VAPRVIFLP	102	0.5000	5.81
26	YFVADLSSG	132	0.5000	5.81
27	FIGLLMLSV	12	0.4000	4.65
28	FARVDALVT	200	0.4000	4.65
29	IFLPGPAAA	107	0.3000	3.49
30	FLPGPAAAL	108	0.3000	3.49
31	IGLLMLSVL	13	0.1000	1.16
32	LSVLVAGCS	18	0.1000	1.16
33	VHVAPRVIF	100	0.1000	1.16
34	VRYPTVQQP	317	0.1000	1.16

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LLMLSVLVA	15	3.0000	37.50
2	VQRRFIGLL	8	2.4000	30.00
3	VALRPGADS	80	2.3000	28.75
4	VASRTKIFA	193	2.0000	25.00
5	MLSVLVAGC	17	1.7000	21.25
6	LILRQAYPV	271	1.6000	20.00
7	MVFDDVHVA	95	1.2000	15.00
8	LRQAYPVRQ	273	1.1000	13.75
9	VLIADTRGG	253	0.7000	8.75
10	IEPAQPAVS	41	0.6000	7.50
11	VYTLAKNPA	175	0.6000	7.50

12	LLVYGVDPL	263	0.5000	6.25
13	IFLPGPAAA	107	0.3000	3.75
14	LTGNKPAVQ	1	0.2000	2.50
15	FIGLLMLSV	12	0.1000	1.25
16	LSVLVAGCS	18	0.1000	1.25
17	LVALRPGAD	79	0.1000	1.25
18	VAPRVIFLP	102	0.1000	1.25
19	LIADTRGGQ	254	0.1000	1.25
20	YPVRQAPYG	277	0.1000	1.25
21	VVLDRGQTS	214	-0.1000	0
22	VQVIEHAAG	347	-0.1000	0
23	YGLAGSREL	284	-0.2000	0
24	FVADLSSGH	133	-0.2200	0
25	VIFLPGPAA	106	-0.3000	0
26	VRYPTVQQP	317	-0.3000	0
27	VRPLSGHPR	60	-0.4000	0
28	VYGVDPLIL	265	-0.4000	0
29	FARVDALVT	200	-0.5000	0
30	FLPGPAAAL	108	-0.7000	0
31	VRQAPYGLA	279	-0.7000	0
32	VIGYDLTTG	303	-0.7000	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	LLMLSVLVA	15	4.0000	50.00
2	VQRRFIGLL	8	3.4000	42.50
3	VALRPGADS	80	3.3000	41.25
4	VASRTKIFA	193	3.0000	37.50
5	MLSVLVAGC	17	2.7000	33.75
6	LILRQAYPV	271	2.6000	32.50
7	MVFDDVHVA	95	2.2000	27.50
8	LRQAYPVRQ	273	2.1000	26.25

9	VLIADTRGG	253	1.7000	21.25
10	IEPAQPAVS	41	1.6000	20.00
11	VYTLAKNPA	175	1.6000	20.00
12	LLVYGVDPL	263	1.5000	18.75
13	IFLPGPAAA	107	1.3000	16.25
14	LTGNKPAVQ	1	1.2000	15.00
15	LSVLVAGCS	18	1.1000	13.75
16	LVALRPGAD	79	1.1000	13.75
17	VAPRVIFLP	102	1.1000	13.75
18	LIADTRGGQ	254	1.1000	13.75
19	LGRVLIADT	250	1.0000	12.50
20	VVLDRGQTS	214	0.9000	11.25
21	VQVIEHAAG	347	0.9000	11.25
22	VIFLPGPAA	106	0.7000	8.75
23	VRYPTVQQP	317	0.7000	8.75
24	VRPLSGHPR	60	0.6000	7.50
25	VYGVDPLIL	265	0.6000	7.50
26	VRQAPYGLA	279	0.3000	3.75
27	VIGYDLTTG	303	0.3000	3.75
28	VHVAPRVIF	100	0.2000	2.50
29	IGLLMLSVL	13	0.1000	1.25
30	VNVADAAHT	145	0.1000	1.25
31	IGADGHAQQ	226	-0.1000	0
32	VVSGSGAGV	339	-0.1000	0
33	LAARGGYFV	126	-0.2000	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	VQRRFIGLL	8	4.4000	51.16
2	LLMLSVLVA	15	4.0000	46.51
3	LVALRPGAD	79	3.8000	44.19
4	VALRPGADS	80	3.3000	38.37

5	VASRTKIFA	193	3.0000	34.88
6	VLIADTRGG	253	3.0000	34.88
7	LILRQAYPV	271	2.9000	33.72
8	LRQAYPVRQ	273	2.9000	33.72
9	MLSVLVAGC	17	2.7000	31.40
10	LLVYGVDPL	263	2.5000	29.07
11	MVFDDVHVA	95	2.2000	25.58
12	VQVIEHAAG	347	2.2000	25.58
13	LTGNKPAVQ	1	2.0000	23.26
14	LGRVLIADT	250	1.9000	22.09
15	LIADTRGGQ	254	1.9000	22.09
16	IEPAQPAVS	41	1.6000	18.60
17	VYTLAKNPA	175	1.6000	18.60
18	VYGVDPLIL	265	1.6000	18.60
19	VIGYDLTTG	303	1.6000	18.60
20	VAPRVIFLP	102	1.5000	17.44
21	IFLPGPAAA	107	1.3000	15.12
22	IGLLMLSVL	13	1.1000	12.79
23	LSVLVAGCS	18	1.1000	12.79
24	VHVAPRVIF	100	1.1000	12.79
25	VRYPTVQQP	317	1.1000	12.79
26	VNVADAAHT	145	1.0000	11.63
27	VVLDRGQTS	214	0.9000	10.47
28	VLVAGCSSN	20	0.8000	9.30
29	VIFLPGPAA	106	0.7000	8.14
30	FTAIARRSD	155	0.7000	8.14
31	IGADGHAQQ	226	0.7000	8.14
32	VRPLSGHPR	60	0.6000	6.98
33	LMLSVLVAG	16	0.5000	5.81
34	YPVRQAPYG	277	0.4000	4.65
35	IFARVDALV	199	0.3000	3.49

ALLELE: DRB1_0813	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	1.9	8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	LLMLSVLVA	15	3.6000	41.38
2	VASRTKIFA	193	2.8800	33.10
3	VYTLAKNPA	175	2.6000	29.89
4	LILRQAYPV	271	2.5000	28.74
5	VALRPGADS	80	2.3000	26.44
6	LRQAYPVRQ	273	2.1000	24.14
7	VIGYDLTTG	303	2.1000	24.14
8	VQRRFIGLL	8	1.7000	19.54
9	MLSVLVAGC	17	1.7000	19.54
10	MVFDDVHVA	95	1.7000	19.54
11	LLVYGVDPL	263	1.7000	19.54
12	FVADLSSGH	133	1.5800	18.16
13	YFVADLSSG	132	1.0000	11.49
14	VAPRVIFLP	102	0.9500	10.92
15	IGLLMLSVL	13	0.9000	10.34
16	VVLDRGQTS	214	0.9000	10.34
17	FIGLLMLSV	12	0.7000	8.05
18	VRYPTVQQP	317	0.7000	8.05
19	IEPAQPAVS	41	0.6000	6.90
20	WVSQTASNT	294	0.6000	6.90
21	LYVVSGSGA	337	0.5000	5.75
22	VLDRGQTSV	215	0.4000	4.60
23	VLIADTRGG	253	0.4000	4.60
24	IFLPGPAAA	107	0.3000	3.45
25	YPVRQAPYG	277	0.3000	3.45
26	LTGNKPAVQ	1	0.2000	2.30
27	VHVAPRVIF	100	0.2000	2.30
28	VYGVDPLIL	265	0.2000	2.30
29	IGYDLTTGI	304	0.2000	2.30
30	VRPLSGHPR	60	0.1000	1.15
31	FARVDALVT	200	0.1000	1.15
32	LAWVSQTAS	292	0.1000	1.15

33	VIFLPGPAA	106	-0.1000	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	LLMLSVLVA	15	4.8000	47.52
2	VASRTKIFA	193	3.6000	35.64
3	VQRRFIGLL	8	3.5000	34.65
4	LVALRPGAD	79	2.9000	28.71
5	LILRQAYPV	271	2.6000	25.74
6	YPVRQAPYG	277	2.5500	25.25
7	VYGVDPLIL	265	2.4000	23.76
8	LRQAYPVRQ	273	2.4000	23.76
9	VALRPGADS	80	2.3000	22.77
10	FIGLLMLSV	12	2.2000	21.78
11	FARVDALVT	200	2.2000	21.78
12	VLIADTRGG	253	2.2000	21.78
13	MVFDDVHVA	95	1.9000	18.81
14	FTAIARRSD	155	1.9000	18.81
15	MLSVLVAGC	17	1.7000	16.83
16	VIGYDLTTG	303	1.7000	16.83
17	YVVSGSGAG	338	1.4000	13.86
18	LLVYGVDPL	263	1.2000	11.88
19	VQVIEHAAG	347	1.2000	11.88
20	LTGNKPAVQ	1	1.0000	9.90
21	VAPRVIFLP	102	1.0000	9.90
22	FVADLSSGH	133	1.0000	9.90
23	LIADTRGGQ	254	1.0000	9.90
24	YGLAGSREL	284	1.0000	9.90
25	VYTLAKNPA	175	0.9000	8.91
26	LGRVLIADT	250	0.9000	8.91
27	VIFLPGPAA	106	0.8500	8.42
28	IEPAQPAVS	41	0.6000	5.94

29	VHVAPRVIF	100	0.6000	5.94
30	YFVADLSSG	132	0.5000	4.95
31	VQQPNSLAF	322	0.5000	4.95
32	VRPLSGHPR	60	0.3000	2.97
33	IFLPGPAAA	107	0.3000	2.97
34	FLPGPAAAL	108	0.3000	2.97
35	LSVLVAGCS	18	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	LLMLSVLVA	15	5.2000	62.65
2	FIGLLMLSV	12	2.3000	27.71
3	MLSVLVAGC	17	1.8000	21.69
4	LRQAYPVRQ	273	1.6000	19.28
5	VYGVDPLIL	265	1.5000	18.07
6	FARVDALVT	200	1.4000	16.87
7	VYTLAKNPA	175	1.3000	15.66
8	VIFLPGPAA	106	1.2500	15.06
9	MVFDDVHVA	95	1.2000	14.46
10	VLIADTRGG	253	0.9000	10.84
11	VRPLSGHPR	60	0.7000	8.43
12	LSVLVAGCS	18	0.6000	7.23
13	IEPAQPAVS	41	0.6000	7.23
14	LVALRPGAD	79	0.6000	7.23
15	VASRTKIFA	193	0.6000	7.23
16	VQVIEHAAG	347	0.5000	6.02
17	YVVSGSGAG	338	0.4000	4.82
18	YPTVQQPNS	319	0.2500	3.01
19	LTGNKPAVQ	1	0.2000	2.41
20	LGRVLIADT	250	0.1000	1.20
21	FTAIARRSD	155	-0.2000	0
22	VHVAPRVIF	100	-0.3000	0

23	YTLAKNPAV	176	-0.3500	0
24	IFLPGPAAA	107	-0.4000	0
25	VQRRFIGLL	8	-0.5000	0
26	IGLLMLSVL	13	-0.5000	0
27	LIADTRGGQ	254	-0.5000	0
28	VRQAPYGLA	279	-0.6000	0
29	WVSQTASNT	294	-0.6000	0
30	VALRPGADS	80	-0.7000	0
31	VVLDRGQTS	214	-0.7000	0
32	YGVDPLILR	266	-0.7000	0
33	LILRQAYPV	271	-0.7000	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	LLMLSVLVA	15	4.4000	52.38
2	VLIADTRGG	253	3.5000	41.67
3	LRQAYPVRQ	273	3.1000	36.90
4	MVFDDVHVA	95	3.0000	35.71
5	VYTLAKNPA	175	2.7000	32.14
6	IEPAQPAVS	41	1.6000	19.05
7	MLSVLVAGC	17	1.5000	17.86
8	VRPLSGHPR	60	1.5000	17.86
9	LSGHPRAAL	63	1.4000	16.67
10	LILRQAYPV	271	1.4000	16.67
11	LTGNKPAVQ	1	1.3000	15.48
12	VVLDRGQTS	214	1.3000	15.48
13	VALRPGADS	80	1.2000	14.29
14	VHVAPRVIF	100	1.2000	14.29
15	VASRTKIFA	193	1.2000	14.29
16	VIFLPGPAA	106	1.1000	13.10
17	VRYPTVQQP	317	1.0000	11.90
18	IFLPGPAAA	107	0.8000	9.52

19	VDPLILRQA	268	0.8000	9.52
20	LMLSVLVAG	16	0.6000	7.14
21	LFDNGTRQL	71	0.6000	7.14
22	LLVYGVDPL	263	0.6000	7.14
23	YGLAGSREL	284	0.6000	7.14
24	VAPRVIFLP	102	0.5000	5.95
25	LVTQGNTTV	206	0.5000	5.95
26	VQRRFIGLL	8	0.3000	3.57
27	IGLLMLSVL	13	0.2000	2.38
28	VNVADAAHT	145	0.1000	1.19
29	LVLGSADGA	166	0.1000	1.19
30	VYGVDPLIL	265	0.1000	1.19
31	LSVLVAGCS	18	-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	LLMLSVLVA	15	6.2000	74.70
2	MLSVLVAGC	17	2.8000	33.73
3	LRQAYPVRQ	273	2.6000	31.33
4	VYGVDPLIL	265	2.5000	30.12
5	VYTLAKNPA	175	2.3000	27.71
6	VIFLPGPAA	106	2.2500	27.11
7	MVFDDVHVA	95	2.2000	26.51
8	VLIADTRGG	253	1.9000	22.89
9	VRPLSGHPR	60	1.7000	20.48
10	LSVLVAGCS	18	1.6000	19.28
11	IEPAQPAVS	41	1.6000	19.28
12	LVALRPGAD	79	1.6000	19.28
13	VASRTKIFA	193	1.6000	19.28
14	VQVIEHAAG	347	1.5000	18.07
15	FIGLLMLSV	12	1.3000	15.66
16	LTGNKPAVQ	1	1.2000	14.46

17	LGRVLIADT	250	1.1000	13.25
18	VHVAPRVIF	100	0.7000	8.43
19	IFLPGPAAA	107	0.6000	7.23
20	VQRRFIGLL	8	0.5000	6.02
21	IGLLMLSVL	13	0.5000	6.02
22	LIADTRGGQ	254	0.5000	6.02
23	FARVDALVT	200	0.4000	4.82
24	VRQAPYGLA	279	0.4000	4.82
25	VALRPGADS	80	0.3000	3.61
26	VVLDRGQTS	214	0.3000	3.61
27	LILRQAYPV	271	0.3000	3.61
28	VNVADAAHT	145	0.1000	1.20
29	VRYPTVQQP	317	0.1000	1.20
30	VDPLILRQA	268	-0.1000	0
31	VQQPNSLAF	322	-0.1000	0
32	LLTGNKPAV	0	-0.1500	0
33	LYVVSGSGA	337	-0.2000	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	LLMLSVLVA	15	6.2000	74.70
2	MLSVLVAGC	17	2.8000	33.73
3	LRQAYPVRQ	273	2.6000	31.33
4	VYGVDPLIL	265	2.5000	30.12
5	VYTLAKNPA	175	2.3000	27.71
6	VIFLPGPAA	106	2.2500	27.11
7	MVFDDVHVA	95	2.2000	26.51
8	VLIADTRGG	253	1.9000	22.89
9	VRPLSGHPR	60	1.7000	20.48
10	LSVLVAGCS	18	1.6000	19.28
11	IEPAQPAVS	41	1.6000	19.28
12	LVALRPGAD	79	1.6000	19.28

13	VASRTKIFA	193	1.6000	19.28
14	VQVIEHAAG	347	1.5000	18.07
15	FIGLLMLSV	12	1.3000	15.66
16	LTGNKPAVQ	1	1.2000	14.46
17	LGRVLIADT	250	1.1000	13.25
18	VHVAPRVIF	100	0.7000	8.43
19	IFLPGPAAA	107	0.6000	7.23
20	VQRRFIGLL	8	0.5000	6.02
21	IGLLMLSVL	13	0.5000	6.02
22	LIADTRGGQ	254	0.5000	6.02
23	FARVDALVT	200	0.4000	4.82
24	VRQAPYGLA	279	0.4000	4.82
25	VALRPGADS	80	0.3000	3.61
26	VVLDRGQTS	214	0.3000	3.61
27	LILRQAYPV	271	0.3000	3.61
28	VNVADAAHT	145	0.1000	1.20
29	VRYPTVQQP	317	0.1000	1.20
30	VDPLILRQA	268	-0.1000	0
31	VQQPNSLAF	322	-0.1000	0
32	LLTGNKPAV	0	-0.1500	0
33	LYVVSGSGA	337	-0.2000	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	MVFDDVHVA	95	5.6000	61.54
2	VVLDRGQTS	214	5.3000	58.24
3	LIADTRGGQ	254	5.0000	54.95
4	IGYDLTTGI	304	4.0000	43.96
5	LLMLSVLVA	15	3.8000	41.76
6	FVADLSSGH	133	3.4500	37.91
7	LRQAYPVRQ	273	3.4000	37.36
8	IGADGHAQQ	226	3.2000	35.16

9	LVLGSADGA	166	3.0000	32.97
10	LLTGNKPAV	0	2.8000	30.77
11	LAFDETSDT	328	2.7700	30.44
12	LTSDDHGTA	116	2.5000	27.47
13	MLSVLVAGC	17	2.4000	26.37
14	LMLSVLVAG	16	2.2000	24.18
15	VYTLAKNPA	175	2.1100	23.19
16	VIFLPGPAA	106	1.9000	20.88
17	MAADPLGRV	245	1.9000	20.88
18	YGVDPLILR	266	1.9000	20.88
19	VRYPTVQQP	317	1.8000	19.78
20	IEPAQPAVS	41	1.6000	17.58
21	VHVAPRVIF	100	1.5000	16.48
22	LTGNKPAVQ	1	1.4000	15.38
23	VLIADTRGG	253	1.4000	15.38
24	LVYGVDPLI	264	1.4000	15.38
25	VVSGSGAGV	339	1.4000	15.38
26	IFLPGPAAA	107	1.3000	14.29
27	YVVSGSGAG	338	1.3000	14.29
28	LVAGCSSNP	21	1.2700	13.96
29	VSGSGAGVQ	340	1.2000	13.19
30	VQVIEHAAG	347	1.1000	12.09
31	LSVLVAGCS	18	1.0000	10.99
32	LVALRPGAD	79	1.0000	10.99
33	VASRTKIFA	193	0.9000	9.89
34	VRQAPYGLA	279	0.9000	9.89
35	LTTGIPVEK	308	0.9000	9.89

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	LLMLSVLVA	15	3.4000	40.48
2	VLIADTRGG	253	2.5000	29.76

3	LRQAYPVRQ	273	2.1000	25.00
4	MVFDDVHVA	95	2.0000	23.81
5	VYTLAKNPA	175	1.7000	20.24
6	YGLAGSREL	284	1.6000	19.05
7	WVSQTASNT	294	0.8000	9.52
8	IEPAQPAVS	41	0.6000	7.14
9	FIGLLMLSV	12	0.5000	5.95
10	MLSVLVAGC	17	0.5000	5.95
11	VRPLSGHPR	60	0.5000	5.95
12	LSGHPRAAL	63	0.4000	4.76
13	LILRQAYPV	271	0.4000	4.76
14	LTGNKPAVQ	1	0.3000	3.57
15	VVLDRGQTS	214	0.3000	3.57
16	VALRPGADS	80	0.2000	2.38
17	VHVAPRVIF	100	0.2000	2.38
18	VASRTKIFA	193	0.2000	2.38
19	VIFLPGPAA	106	0.1000	1.19
20	FTAIARRSD	155	-0.1000	0
21	IFLPGPAAA	107	-0.2000	0
22	VDPLILRQA	268	-0.2000	0
23	FVADLSSGH	133	-0.2200	0
24	LMLSVLVAG	16	-0.4000	0
25	LFDNGTRQL	71	-0.4000	0
26	YFVADLSSG	132	-0.4000	0
27	LLVYGVDPL	263	-0.4000	0
28	VAPRVIFLP	102	-0.5000	0
29	LVTQGNTTV	206	-0.5000	0
30	YVVSGSGAG	338	-0.6000	0
31	VQRRFIGLL	8	-0.7000	0
32	IGLLMLSVL	13	-0.8000	0
33	YTLAKNPAV	176	-0.8000	0

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

	2.1	

Rank	Sequence	At Position	Score	% of Highest Score
1	VLIADTRGG	253	3.9000	44.32
2	LLMLSVLVA	15	3.4000	38.64
3	YGLAGSREL	284	2.5600	29.09
4	VHVAPRVIF	100	2.1000	23.86
5	VRPLSGHPR	60	2.0000	22.73
6	MVFDDVHVA	95	2.0000	22.73
7	VYTLAKNPA	175	1.7000	19.32
8	FIGLLMLSV	12	1.5000	17.05
9	WVSQTASNT	294	1.5000	17.05
10	LILRQAYPV	271	1.4000	15.91
11	LRQAYPVRQ	273	1.4000	15.91
12	LSGHPRAAL	63	1.3600	15.45
13	LMLSVLVAG	16	1.0000	11.36
14	IEPAQPAVS	41	1.0000	11.36
15	YFVADLSSG	132	1.0000	11.36
16	FTAIARRSD	155	1.0000	11.36
17	VRYPTVQQP	317	1.0000	11.36
18	YVVSGSGAG	338	0.8000	9.09
19	VVLDRGQTS	214	0.7000	7.95
20	VALRPGADS	80	0.6000	6.82
21	LFDNGTRQL	71	0.5600	6.36
22	LLVYGVDPL	263	0.5600	6.36
23	MLSVLVAGC	17	0.5000	5.68
24	VAPRVIFLP	102	0.5000	5.68
25	LVTQGNTTV	206	0.5000	5.68
26	VIGYDLTTG	303	0.4000	4.55
27	VQVIEHAAG	347	0.4000	4.55
28	VQRRFIGLL	8	0.2600	2.95
29	YTLAKNPAV	176	0.2000	2.27
30	VASRTKIFA	193	0.2000	2.27
31	IGLLMLSVL	13	0.1600	1.82
32	VIFLPGPAA	106	0.1000	1.14

33	YPVRQAPYG	277	0.1000	1.14
34	VYGVDPLIL	265	0.0600	0.68

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	LLMLSVLVA	15	4.4000	52.38
2	VLIADTRGG	253	3.5000	41.67
3	LRQAYPVRQ	273	3.1000	36.90
4	MVFDDVHVA	95	3.0000	35.71
5	VYTLAKNPA	175	2.7000	32.14
6	IEPAQPAVS	41	1.6000	19.05
7	MLSVLVAGC	17	1.5000	17.86
8	VRPLSGHPR	60	1.5000	17.86
9	LSGHPRAAL	63	1.4000	16.67
10	LILRQAYPV	271	1.4000	16.67
11	LTGNKPAVQ	1	1.3000	15.48
12	VVLDRGQTS	214	1.3000	15.48
13	VALRPGADS	80	1.2000	14.29
14	VHVAPRVIF	100	1.2000	14.29
15	VASRTKIFA	193	1.2000	14.29
16	VIFLPGPAA	106	1.1000	13.10
17	VRYPTVQQP	317	1.0000	11.90
18	IFLPGPAAA	107	0.8000	9.52
19	VDPLILRQA	268	0.8000	9.52
20	LMLSVLVAG	16	0.6000	7.14
21	LFDNGTRQL	71	0.6000	7.14
22	LLVYGVDPL	263	0.6000	7.14
23	YGLAGSREL	284	0.6000	7.14
24	VAPRVIFLP	102	0.5000	5.95
25	LVTQGNTTV	206	0.5000	5.95
26	VQRRFIGLL	8	0.3000	3.57
27	IGLLMLSVL	13	0.2000	2.38

28	VNVADAAHT	145	0.1000	1.19
29	LVLGSADGA	166	0.1000	1.19
30	VYGVDPLIL	265	0.1000	1.19
31	LSVLVAGCS	18	-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	LLMLSVLVA	15	5.2000	59.77
2	FIGLLMLSV	12	3.3000	37.93
3	VYGVDPLIL	265	2.4600	28.28
4	VLIADTRGG	253	2.3000	26.44
5	VRPLSGHPR	60	2.2000	25.29
6	FARVDALVT	200	2.1000	24.14
7	VQVIEHAAG	347	1.9000	21.84
8	MLSVLVAGC	17	1.8000	20.69
9	YVVSGSGAG	338	1.8000	20.69
10	LVALRPGAD	79	1.7000	19.54
11	VHVAPRVIF	100	1.6000	18.39
12	VYTLAKNPA	175	1.3000	14.94
13	VIFLPGPAA	106	1.2500	14.37
14	MVFDDVHVA	95	1.2000	13.79
15	LSVLVAGCS	18	1.0000	11.49
16	IEPAQPAVS	41	1.0000	11.49
17	YGLAGSREL	284	0.9600	11.03
18	FTAIARRSD	155	0.9000	10.34
19	LRQAYPVRQ	273	0.9000	10.34
20	FLAARGGYF	125	0.8000	9.20
21	LGRVLIADT	250	0.8000	9.20
22	YGVDPLILR	266	0.8000	9.20
23	VQQPNSLAF	322	0.8000	9.20
24	YTLAKNPAV	176	0.6500	7.47
25	YPTVQQPNS	319	0.6500	7.47

26	YFVADLSSG	132	0.6000	6.90
27	VASRTKIFA	193	0.6000	6.90
28	VQRRFIGLL	8	0.4600	5.29
29	IGLLMLSVL	13	0.4600	5.29
30	LMLSVLVAG	16	0.4000	4.60
31	LILRQAYPV	271	0.3000	3.45
32	WVSQTASNT	294	0.1000	1.15
33	VRYPTVQQP	317	0.1000	1.15
34	LLTGNKPAV	0	-0.1500	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	VLIADTRGG	253	4.9000	55.68
2	LLMLSVLVA	15	4.4000	50.00
3	VHVAPRVIF	100	3.1000	35.23
4	VRPLSGHPR	60	3.0000	34.09
5	MVFDDVHVA	95	3.0000	34.09
6	VYTLAKNPA	175	2.7000	30.68
7	LILRQAYPV	271	2.4000	27.27
8	LRQAYPVRQ	273	2.4000	27.27
9	LSGHPRAAL	63	2.3600	26.82
10	LMLSVLVAG	16	2.0000	22.73
11	IEPAQPAVS	41	2.0000	22.73
12	VRYPTVQQP	317	2.0000	22.73
13	VVLDRGQTS	214	1.7000	19.32
14	VALRPGADS	80	1.6000	18.18
15	LFDNGTRQL	71	1.5600	17.73
16	LLVYGVDPL	263	1.5600	17.73
17	YGLAGSREL	284	1.5600	17.73
18	MLSVLVAGC	17	1.5000	17.05
19	VAPRVIFLP	102	1.5000	17.05
20	LVTQGNTTV	206	1.5000	17.05

21	VIGYDLTTG	303	1.4000	15.91
22	VQVIEHAAG	347	1.4000	15.91
23	VQRRFIGLL	8	1.2600	14.32
24	VASRTKIFA	193	1.2000	13.64
25	IGLLMLSVL	13	1.1600	13.18
26	VIFLPGPAA	106	1.1000	12.50
27	VYGVDPLIL	265	1.0600	12.05
28	IPVEKVRYP	312	1.0000	11.36
29	LVALRPGAD	79	0.9000	10.23
30	ILRQAYPVR	272	0.9000	10.23
31	VQQPNSLAF	322	0.9000	10.23
32	IFLPGPAAA	107	0.8000	9.09
33	VNVADAAHT	145	0.8000	9.09
34	VDPLILRQA	268	0.8000	9.09
35	LLTGNKPAV	0	0.6000	6.82

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	VLIADTRGG	253	3.9000	44.32
2	LLMLSVLVA	15	3.4000	38.64
3	YGLAGSREL	284	2.5600	29.09
4	VHVAPRVIF	100	2.1000	23.86
5	VRPLSGHPR	60	2.0000	22.73
6	MVFDDVHVA	95	2.0000	22.73
7	VYTLAKNPA	175	1.7000	19.32
8	FIGLLMLSV	12	1.5000	17.05
9	WVSQTASNT	294	1.5000	17.05
10	LILRQAYPV	271	1.4000	15.91
11	LRQAYPVRQ	273	1.4000	15.91
12	LSGHPRAAL	63	1.3600	15.45
13	LMLSVLVAG	16	1.0000	11.36
14	IEPAQPAVS	41	1.0000	11.36

15	YFVADLSSG	132	1.0000	11.36
16	FTAIARRSD	155	1.0000	11.36
17	VRYPTVQQP	317	1.0000	11.36
18	YVVSGSGAG	338	0.8000	9.09
19	VVLDRGQTS	214	0.7000	7.95
20	VALRPGADS	80	0.6000	6.82
21	LFDNGTRQL	71	0.5600	6.36
22	LLVYGVDPL	263	0.5600	6.36
23	MLSVLVAGC	17	0.5000	5.68
24	VAPRVIFLP	102	0.5000	5.68
25	LVTQGNTTV	206	0.5000	5.68
26	VIGYDLTTG	303	0.4000	4.55
27	VQVIEHAAG	347	0.4000	4.55
28	VQRRFIGLL	8	0.2600	2.95
29	YTLAKNPAV	176	0.2000	2.27
30	VASRTKIFA	193	0.2000	2.27
31	IGLLMLSVL	13	0.1600	1.82
32	VIFLPGPAA	106	0.1000	1.14
33	YPVRQAPYG	277	0.1000	1.14
34	VYGVDPLIL	265	0.0600	0.68

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	VLIADTRGG	253	4.8000	53.33
2	LLMLSVLVA	15	4.4000	48.89
3	LRQAYPVRQ	273	3.9000	43.33
4	MVFDDVHVA	95	3.0000	33.33
5	VYTLAKNPA	175	2.7000	30.00
6	LVALRPGAD	79	2.5000	27.78
7	LSGHPRAAL	63	2.4000	26.67
8	LTGNKPAVQ	1	2.1000	23.33
9	VHVAPRVIF	100	2.1000	23.33

10	LMLSVLVAG	16	1.9000	21.11
11	LILRQAYPV	271	1.7000	18.89
12	IEPAQPAVS	41	1.6000	17.78
13	LFDNGTRQL	71	1.6000	17.78
14	FTAIARRSD	155	1.6000	17.78
15	LLVYGVDPL	263	1.6000	17.78
16	YGLAGSREL	284	1.6000	17.78
17	MLSVLVAGC	17	1.5000	16.67
18	VRPLSGHPR	60	1.5000	16.67
19	VRYPTVQQP	317	1.4000	15.56
20	VQRRFIGLL	8	1.3000	14.44
21	VVLDRGQTS	214	1.3000	14.44
22	VIGYDLTTG	303	1.3000	14.44
23	VQVIEHAAG	347	1.3000	14.44
24	IGLLMLSVL	13	1.2000	13.33
25	VLVAGCSSN	20	1.2000	13.33
26	VALRPGADS	80	1.2000	13.33
27	VASRTKIFA	193	1.2000	13.33
28	VIFLPGPAA	106	1.1000	12.22
29	VYGVDPLIL	265	1.1000	12.22
30	VNVADAAHT	145	1.0000	11.11
31	VAPRVIFLP	102	0.9000	10.00
32	IFLPGPAAA	107	0.8000	8.89
33	LVTQGNTTV	206	0.8000	8.89
34	VDPLILRQA	268	0.8000	8.89
35	LGRVLIADT	250	0.7000	7.78

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	LLMLSVLVA	15	5.2000	59.77
2	FIGLLMLSV	12	3.3000	37.93
3	VYGVDPLIL	265	2.4600	28.28

4	VLIADTRGG	253	2.3000	26.44
5	VRPLSGHPR	60	2.2000	25.29
6	FARVDALVT	200	2.1000	24.14
7	VQVIEHAAG	347	1.9000	21.84
8	MLSVLVAGC	17	1.8000	20.69
9	YVVSGSGAG	338	1.8000	20.69
10	LVALRPGAD	79	1.7000	19.54
11	VHVAPRVIF	100	1.6000	18.39
12	VYTLAKNPA	175	1.3000	14.94
13	VIFLPGPAA	106	1.2500	14.37
14	MVFDDVHVA	95	1.2000	13.79
15	LSVLVAGCS	18	1.0000	11.49
16	IEPAQPAVS	41	1.0000	11.49
17	YGLAGSREL	284	0.9600	11.03
18	FTAIARRSD	155	0.9000	10.34
19	LRQAYPVRQ	273	0.9000	10.34
20	FLAARGGYF	125	0.8000	9.20
21	LGRVLIADT	250	0.8000	9.20
22	YGVDPLILR	266	0.8000	9.20
23	VQQPNSLAF	322	0.8000	9.20
24	YTLAKNPAV	176	0.6500	7.47
25	YPTVQQPNS	319	0.6500	7.47
26	YFVADLSSG	132	0.6000	6.90
27	VASRTKIFA	193	0.6000	6.90
28	VQRRFIGLL	8	0.4600	5.29
29	IGLLMLSVL	13	0.4600	5.29
30	LMLSVLVAG	16	0.4000	4.60
31	LILRQAYPV	271	0.3000	3.45
32	WVSQTASNT	294	0.1000	1.15
33	VRYPTVQQP	317	0.1000	1.15
34	LLTGNKPAV	0	-0.1500	0

ALLELE: DRB1_1307	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	0.6	6.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LLMLSVLVA	15	3.4000	50.00
2	MLSVLVAGC	17	1.8000	26.47
3	LRQAYPVRQ	273	1.1000	16.18
4	VYTLAKNPA	175	1.0000	14.71
5	VLIADTRGG	253	0.7000	10.29
6	IEPAQPAVS	41	0.6000	8.82
7	FIGLLMLSV	12	0.5000	7.35
8	LSVLVAGCS	18	0.5000	7.35
9	LVALRPGAD	79	0.5000	7.35
10	MVFDDVHVA	95	0.5000	7.35
11	VQVIEHAAG	347	0.5000	7.35
12	YVVSGSGAG	338	0.3000	4.41
13	LTGNKPAVQ	1	0.2000	2.94
14	VIFLPGPAA	106	0.1000	1.47
15	LGRVLIADT	250	0.1000	1.47
16	YGLAGSREL	284	-0.2000	0
17	VYGVDPLIL	265	-0.3000	0
18	IFLPGPAAA	107	-0.4000	0
19	FTAIARRSD	155	-0.4000	0
20	FARVDALVT	200	-0.4000	0
21	IGLLMLSVL	13	-0.5000	0
22	VQRRFIGLL	8	-0.6000	0
23	LIADTRGGQ	254	-0.6000	0
24	WVSQTASNT	294	-0.6000	0
25	VALRPGADS	80	-0.7000	0
26	VRQAPYGLA	279	-0.7000	0
27	VHVAPRVIF	100	-0.8000	0
28	YFVADLSSG	132	-0.8000	0
29	VVLDRGQTS	214	-0.8000	0
30	VNVADAAHT	145	-0.9000	0
31	YPTVQQPNS	319	-0.9000	0
32	FVADLSSGH	133	-0.9200	0

33	VASRTKIFA	193	-1.0000	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	LLMLSVLVA	15	6.2000	74.70
2	MLSVLVAGC	17	2.8000	33.73
3	LRQAYPVRQ	273	2.6000	31.33
4	VYGVDPLIL	265	2.5000	30.12
5	VYTLAKNPA	175	2.3000	27.71
6	VIFLPGPAA	106	2.2500	27.11
7	MVFDDVHVA	95	2.2000	26.51
8	VLIADTRGG	253	1.9000	22.89
9	VRPLSGHPR	60	1.7000	20.48
10	LSVLVAGCS	18	1.6000	19.28
11	IEPAQPAVS	41	1.6000	19.28
12	LVALRPGAD	79	1.6000	19.28
13	VASRTKIFA	193	1.6000	19.28
14	VQVIEHAAG	347	1.5000	18.07
15	FIGLLMLSV	12	1.3000	15.66
16	LTGNKPAVQ	1	1.2000	14.46
17	LGRVLIADT	250	1.1000	13.25
18	VHVAPRVIF	100	0.7000	8.43
19	IFLPGPAAA	107	0.6000	7.23
20	VQRRFIGLL	8	0.5000	6.02
21	IGLLMLSVL	13	0.5000	6.02
22	LIADTRGGQ	254	0.5000	6.02
23	FARVDALVT	200	0.4000	4.82
24	VRQAPYGLA	279	0.4000	4.82
25	VALRPGADS	80	0.3000	3.61
26	VVLDRGQTS	214	0.3000	3.61
27	LILRQAYPV	271	0.3000	3.61
28	VNVADAAHT	145	0.1000	1.20

29	VRYPTVQQP	317	0.1000	1.20
30	VDPLILRQA	268	-0.1000	0
31	VQQPNSLAF	322	-0.1000	0
32	LLTGNKPAV	0	-0.1500	0
33	LYVVSGSGA	337	-0.2000	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	LLMLSVLVA	15	5.2000	58.43
2	LVALRPGAD	79	3.3000	37.08
3	FIGLLMLSV	12	2.6000	29.21
4	FTAIARRSD	155	2.5000	28.09
5	VYGVDPLIL	265	2.5000	28.09
6	LRQAYPVRQ	273	2.4000	26.97
7	FARVDALVT	200	2.3000	25.84
8	VLIADTRGG	253	2.2000	24.72
9	MLSVLVAGC	17	1.8000	20.22
10	VQVIEHAAG	347	1.8000	20.22
11	YVVSGSGAG	338	1.7000	19.10
12	VYTLAKNPA	175	1.3000	14.61
13	VIFLPGPAA	106	1.2500	14.04
14	MVFDDVHVA	95	1.2000	13.48
15	LTGNKPAVQ	1	1.0000	11.24
16	LGRVLIADT	250	1.0000	11.24
17	YGLAGSREL	284	1.0000	11.24
18	VRPLSGHPR	60	0.7000	7.87
19	LSVLVAGCS	18	0.6000	6.74
20	IEPAQPAVS	41	0.6000	6.74
21	VHVAPRVIF	100	0.6000	6.74
22	VASRTKIFA	193	0.6000	6.74
23	VQRRFIGLL	8	0.5000	5.62
24	IGLLMLSVL	13	0.5000	5.62

25	YFVADLSSG	132	0.5000	5.62
26	LMLSVLVAG	16	0.3000	3.37
27	FVADLSSGH	133	0.3000	3.37
28	LIADTRGGQ	254	0.3000	3.37
29	WVSQTASNT	294	0.3000	3.37
30	YPTVQQPNS	319	0.2500	2.81
31	YTLAKNPAV	176	-0.0500	0
32	VLVAGCSSN	20	-0.2000	0
33	FLAARGGYF	125	-0.2000	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	LLMLSVLVA	15	4.4000	52.38
2	VLIADTRGG	253	3.5000	41.67
3	LRQAYPVRQ	273	3.1000	36.90
4	MVFDDVHVA	95	3.0000	35.71
5	VYTLAKNPA	175	2.7000	32.14
6	IEPAQPAVS	41	1.6000	19.05
7	MLSVLVAGC	17	1.5000	17.86
8	VRPLSGHPR	60	1.5000	17.86
9	LSGHPRAAL	63	1.4000	16.67
10	LILRQAYPV	271	1.4000	16.67
11	LTGNKPAVQ	1	1.3000	15.48
12	VVLDRGQTS	214	1.3000	15.48
13	VALRPGADS	80	1.2000	14.29
14	VHVAPRVIF	100	1.2000	14.29
15	VASRTKIFA	193	1.2000	14.29
16	VIFLPGPAA	106	1.1000	13.10
17	VRYPTVQQP	317	1.0000	11.90
18	IFLPGPAAA	107	0.8000	9.52
19	VDPLILRQA	268	0.8000	9.52
20	LMLSVLVAG	16	0.6000	7.14

21	LFDNGTRQL	71	0.6000	7.14
22	LLVYGVDPL	263	0.6000	7.14
23	YGLAGSREL	284	0.6000	7.14
24	VAPRVIFLP	102	0.5000	5.95
25	LVTQGNTTV	206	0.5000	5.95
26	VQRRFIGLL	8	0.3000	3.57
27	IGLLMLSVL	13	0.2000	2.38
28	VNVADAAHT	145	0.1000	1.19
29	LVLGSADGA	166	0.1000	1.19
30	VYGVDPLIL	265	0.1000	1.19
31	LSVLVAGCS	18	-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	LLMLSVLVA	15	3.4000	40.48
2	VLIADTRGG	253	2.5000	29.76
3	LRQAYPVRQ	273	2.1000	25.00
4	MVFDDVHVA	95	2.0000	23.81
5	VYTLAKNPA	175	1.7000	20.24
6	YGLAGSREL	284	1.6000	19.05
7	WVSQTASNT	294	0.8000	9.52
8	IEPAQPAVS	41	0.6000	7.14
9	FIGLLMLSV	12	0.5000	5.95
10	MLSVLVAGC	17	0.5000	5.95
11	VRPLSGHPR	60	0.5000	5.95
12	LSGHPRAAL	63	0.4000	4.76
13	LILRQAYPV	271	0.4000	4.76
14	LTGNKPAVQ	1	0.3000	3.57
15	VVLDRGQTS	214	0.3000	3.57
16	VALRPGADS	80	0.2000	2.38
17	VHVAPRVIF	100	0.2000	2.38
18	VASRTKIFA	193	0.2000	2.38

19	VIFLPGPAA	106	0.1000	1.19
20	FTAIARRSD	155	-0.1000	0
21	IFLPGPAAA	107	-0.2000	0
22	VDPLILRQA	268	-0.2000	0
23	FVADLSSGH	133	-0.2200	0
24	LMLSVLVAG	16	-0.4000	0
25	LFDNGTRQL	71	-0.4000	0
26	YFVADLSSG	132	-0.4000	0
27	LLVYGVDPL	263	-0.4000	0
28	VAPRVIFLP	102	-0.5000	0
29	LVTQGNTTV	206	-0.5000	0
30	YVVSGSGAG	338	-0.6000	0
31	VQRRFIGLL	8	-0.7000	0
32	IGLLMLSVL	13	-0.8000	0
33	YTLAKNPAV	176	-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	VLIADTRGG	253	4.9000	55.68
2	LLMLSVLVA	15	4.4000	50.00
3	VHVAPRVIF	100	3.1000	35.23
4	VRPLSGHPR	60	3.0000	34.09
5	MVFDDVHVA	95	3.0000	34.09
6	VYTLAKNPA	175	2.7000	30.68
7	LILRQAYPV	271	2.4000	27.27
8	LRQAYPVRQ	273	2.4000	27.27
9	LSGHPRAAL	63	2.3600	26.82
10	LMLSVLVAG	16	2.0000	22.73
11	IEPAQPAVS	41	2.0000	22.73
12	VRYPTVQQP	317	2.0000	22.73
13	VVLDRGQTS	214	1.7000	19.32
14	VALRPGADS	80	1.6000	18.18

15	LFDNGTRQL	71	1.5600	17.73
16	LLVYGVDPL	263	1.5600	17.73
17	YGLAGSREL	284	1.5600	17.73
18	MLSVLVAGC	17	1.5000	17.05
19	VAPRVIFLP	102	1.5000	17.05
20	LVTQGNTTV	206	1.5000	17.05
21	VIGYDLTTG	303	1.4000	15.91
22	VQVIEHAAG	347	1.4000	15.91
23	VQRRFIGLL	8	1.2600	14.32
24	VASRTKIFA	193	1.2000	13.64
25	IGLLMLSVL	13	1.1600	13.18
26	VIFLPGPAA	106	1.1000	12.50
27	VYGVDPLIL	265	1.0600	12.05
28	IPVEKVRYP	312	1.0000	11.36
29	LVALRPGAD	79	0.9000	10.23
30	ILRQAYPVR	272	0.9000	10.23
31	VQQPNSLAF	322	0.9000	10.23
32	IFLPGPAAA	107	0.8000	9.09
33	VNVADAAHT	145	0.8000	9.09
34	VDPLILRQA	268	0.8000	9.09
35	LLTGNKPAV	0	0.6000	6.82

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	VLIADTRGG	253	4.9000	55.68
2	LLMLSVLVA	15	4.4000	50.00
3	VHVAPRVIF	100	3.1000	35.23
4	VRPLSGHPR	60	3.0000	34.09
5	MVFDDVHVA	95	3.0000	34.09
6	VYTLAKNPA	175	2.7000	30.68
7	LILRQAYPV	271	2.4000	27.27
8	LRQAYPVRQ	273	2.4000	27.27

9	LSGHPRAAL	63	2.3600	26.82
10	LMLSVLVAG	16	2.0000	22.73
11	IEPAQPAVS	41	2.0000	22.73
12	VRYPTVQQP	317	2.0000	22.73
13	VVLDRGQTS	214	1.7000	19.32
14	VALRPGADS	80	1.6000	18.18
15	LFDNGTRQL	71	1.5600	17.73
16	LLVYGVDPL	263	1.5600	17.73
17	YGLAGSREL	284	1.5600	17.73
18	MLSVLVAGC	17	1.5000	17.05
19	VAPRVIFLP	102	1.5000	17.05
20	LVTQGNTTV	206	1.5000	17.05
21	VIGYDLTTG	303	1.4000	15.91
22	VQVIEHAAG	347	1.4000	15.91
23	VQRRFIGLL	8	1.2600	14.32
24	VASRTKIFA	193	1.2000	13.64
25	IGLLMLSVL	13	1.1600	13.18
26	VIFLPGPAA	106	1.1000	12.50
27	VYGVDPLIL	265	1.0600	12.05
28	IPVEKVRYP	312	1.0000	11.36
29	LVALRPGAD	79	0.9000	10.23
30	ILRQAYPVR	272	0.9000	10.23
31	VQQPNSLAF	322	0.9000	10.23
32	IFLPGPAAA	107	0.8000	9.09
33	VNVADAAHT	145	0.8000	9.09
34	VDPLILRQA	268	0.8000	9.09
35	LLTGNKPAV	0	0.6000	6.82

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	LLMLSVLVA	15	4.5000	45.92
2	IMVFDDVHV	94	4.2000	42.86

3	LLVYGVDPL	263	3.5000	35.71
4	LVYGVDPLI	264	3.5000	35.71
5	VYGVDPLIL	265	3.5000	35.71
6	VIGYDLTTG	303	3.4000	34.69
7	LILRQAYPV	271	3.3000	33.67
8	VIFLPGPAA	106	3.2000	32.65
9	FIGLLMLSV	12	3.1000	31.63
10	VRPLSGHPR	60	3.1000	31.63
11	VVSGSGAGV	339	3.1000	31.63
12	IGLLMLSVL	13	3.0000	30.61
13	VQQPNSLAF	322	3.0000	30.61
14	MVFDDVHVA	95	2.8000	28.57
15	VQRRFIGLL	8	2.6500	27.04
16	VVLDRGQTS	214	2.6000	26.53
17	VRQAPYGLA	279	2.6000	26.53
18	LSGHPRAAL	63	2.5000	25.51
19	LVTQGNTTV	206	2.5000	25.51
20	LRAGQGATT	236	2.5000	25.51
21	LRPGADSAA	82	2.4000	24.49
22	LVLGSADGA	166	2.4000	24.49
23	LYVVSGSGA	337	2.4000	24.49
24	VHVAPRVIF	100	2.2000	22.45
25	VAGCSSNPL	22	2.0000	20.41
26	LVAGCSSNP	21	1.9000	19.39
27	VYTLAKNPA	175	1.8000	18.37
28	IGYDLTTGI	304	1.7600	17.96
29	LAARGGYFV	126	1.7000	17.35
30	LANFAPGYP	30	1.6000	16.33
31	VASRTKIFA	193	1.6000	16.33
32	FARVDALVT	200	1.6000	16.33
33	LMLSVLVAG	16	1.5000	15.31
34	VALRPGADS	80	1.4000	14.29
35	LLTGNKPAV	0	1.3000	13.27

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	FIGLLMLSV	12	4.1000	41.84
2	LLMLSVLVA	15	3.5000	35.71
3	IMVFDDVHV	94	3.2000	32.65
4	FARVDALVT	200	2.6000	26.53
5	LLVYGVDPL	263	2.5000	25.51
6	LVYGVDPLI	264	2.5000	25.51
7	VYGVDPLIL	265	2.5000	25.51
8	VIGYDLTTG	303	2.4000	24.49
9	YTLAKNPAV	176	2.3000	23.47
10	LILRQAYPV	271	2.3000	23.47
11	VIFLPGPAA	106	2.2000	22.45
12	VRPLSGHPR	60	2.1000	21.43
13	YGLAGSREL	284	2.1000	21.43
14	YVVSGSGAG	338	2.1000	21.43
15	VVSGSGAGV	339	2.1000	21.43
16	IGLLMLSVL	13	2.0000	20.41
17	VQQPNSLAF	322	2.0000	20.41
18	MVFDDVHVA	95	1.8000	18.37
19	FLPGPAAAL	108	1.8000	18.37
20	YDLTTGIPV	306	1.7000	17.35
21	VQRRFIGLL	8	1.6500	16.84
22	VVLDRGQTS	214	1.6000	16.33
23	VRQAPYGLA	279	1.6000	16.33
24	WVSQTASNT	294	1.6000	16.33
25	LSGHPRAAL	63	1.5000	15.31
26	FVADLSSGH	133	1.5000	15.31
27	LVTQGNTTV	206	1.5000	15.31
28	LRAGQGATT	236	1.5000	15.31
29	LRPGADSAA	82	1.4000	14.29
30	LVLGSADGA	166	1.4000	14.29

31	LYVVSGSGA	337	1.4000	14.29
32	YGVDPLILR	266	1.3000	13.27
33	VHVAPRVIF	100	1.2000	12.24
34	FAPGYPPTI	33	1.1000	11.22
35	FLAARGGYF	125	1.1000	11.22

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	LLMLSVLVA	15	4.5000	45.92
2	IMVFDDVHV	94	4.2000	42.86
3	LLVYGVDPL	263	3.5000	35.71
4	LVYGVDPLI	264	3.5000	35.71
5	VYGVDPLIL	265	3.5000	35.71
6	VIGYDLTTG	303	3.4000	34.69
7	LILRQAYPV	271	3.3000	33.67
8	VIFLPGPAA	106	3.2000	32.65
9	FIGLLMLSV	12	3.1000	31.63
10	VRPLSGHPR	60	3.1000	31.63
11	VVSGSGAGV	339	3.1000	31.63
12	IGLLMLSVL	13	3.0000	30.61
13	VQQPNSLAF	322	3.0000	30.61
14	MVFDDVHVA	95	2.8000	28.57
15	VQRRFIGLL	8	2.6500	27.04
16	VVLDRGQTS	214	2.6000	26.53
17	VRQAPYGLA	279	2.6000	26.53
18	LSGHPRAAL	63	2.5000	25.51
19	LVTQGNTTV	206	2.5000	25.51
20	LRAGQGATT	236	2.5000	25.51
21	LRPGADSAA	82	2.4000	24.49
22	LVLGSADGA	166	2.4000	24.49
23	LYVVSGSGA	337	2.4000	24.49
24	VHVAPRVIF	100	2.2000	22.45

25	VAGCSSNPL	22	2.0000	20.41
26	LVAGCSSNP	21	1.9000	19.39
27	VYTLAKNPA	175	1.8000	18.37
28	IGYDLTTGI	304	1.7600	17.96
29	LAARGGYFV	126	1.7000	17.35
30	LANFAPGYP	30	1.6000	16.33
31	VASRTKIFA	193	1.6000	16.33
32	FARVDALVT	200	1.6000	16.33
33	LMLSVLVAG	16	1.5000	15.31
34	VALRPGADS	80	1.4000	14.29
35	LLTGNKPAV	0	1.3000	13.27

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	VRPLSGHPR	60	5.5000	56.12
2	YGLAGSREL	284	3.6000	36.73
3	VYGVDPLIL	265	3.3000	33.67
4	YVVSGSGAG	338	2.6000	26.53
5	FLAARGGYF	125	2.5000	25.51
6	VLIADTRGG	253	2.4000	24.49
7	FARVDALVT	200	2.2000	22.45
8	YGVDPLILR	266	1.8000	18.37
9	LRQAYPVRQ	273	1.8000	18.37
10	LLMLSVLVA	15	1.3000	13.27
11	VVLDRGQTS	214	1.3000	13.27
12	IGLLMLSVL	13	1.2000	12.24
13	WVSQTASNT	294	1.2000	12.24
14	VQVIEHAAG	347	1.2000	12.24
15	LSVLVAGCS	18	1.1000	11.22
16	LVALRPGAD	79	1.0000	10.20
17	FLPGPAAAL	108	1.0000	10.20
18	LYVVSGSGA	337	1.0000	10.20

19	ILRQAYPVR	272	0.9000	9.18
20	FIGLLMLSV	12	0.8000	8.16
21	VRQAPYGLA	279	0.8000	8.16
22	LGSADGAVY	168	0.7000	7.14
23	YDLTTGIPV	306	0.7000	7.14
24	VIFLPGPAA	106	0.6000	6.12
25	VIEHAAGTR	349	0.6000	6.12
26	VAGCSSNPL	22	0.5000	5.10
27	YFVADLSSG	132	0.5000	5.10
28	FVADLSSGH	133	0.5000	5.10
29	LILRQAYPV	271	0.4000	4.08
30	VLVAGCSSN	20	0.3000	3.06
31	IEPAQPAVS	41	0.3000	3.06
32	VNVADAAHT	145	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	VRPLSGHPR	60	5.5000	56.12
2	YGLAGSREL	284	3.6000	36.73
3	VYGVDPLIL	265	3.3000	33.67
4	YVVSGSGAG	338	2.6000	26.53
5	FLAARGGYF	125	2.5000	25.51
6	VLIADTRGG	253	2.4000	24.49
7	FARVDALVT	200	2.2000	22.45
8	YGVDPLILR	266	1.8000	18.37
9	LRQAYPVRQ	273	1.8000	18.37
10	LLMLSVLVA	15	1.3000	13.27
11	VVLDRGQTS	214	1.3000	13.27
12	IGLLMLSVL	13	1.2000	12.24
13	WVSQTASNT	294	1.2000	12.24
14	VQVIEHAAG	347	1.2000	12.24
15	LSVLVAGCS	18	1.1000	11.22

16	LVALRPGAD	79	1.0000	10.20
17	FLPGPAAAL	108	1.0000	10.20
18	LYVVSGSGA	337	1.0000	10.20
19	ILRQAYPVR	272	0.9000	9.18
20	FIGLLMLSV	12	0.8000	8.16
21	VRQAPYGLA	279	0.8000	8.16
22	LGSADGAVY	168	0.7000	7.14
23	YDLTTGIPV	306	0.7000	7.14
24	VIFLPGPAA	106	0.6000	6.12
25	VIEHAAGTR	349	0.6000	6.12
26	VAGCSSNPL	22	0.5000	5.10
27	YFVADLSSG	132	0.5000	5.10
28	FVADLSSGH	133	0.5000	5.10
29	LILRQAYPV	271	0.4000	4.08
30	VLVAGCSSN	20	0.3000	3.06
31	IEPAQPAVS	41	0.3000	3.06
32	VNVADAAHT	145	0.1000	1.02