MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Feb 27 16:12:44 2010
Length of input sequence	578 amino acids
Number of nanomers from input sequence	570
Number of nanomers with obligatory P1 anchor residue	159
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	57

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	FRLLPPRTM	173	4.0700	67.83
2	MRALLARIC	181	2.1900	36.50
3	MRGATAPRL	342	1.9700	32.83
4	IVLQSVPDA	292	1.1700	19.50
5	VRSMWPTVR	428	1.0900	18.17
6	YLFSGPRGC	37	0.9900	16.50
7	YRPASFAEV	6	0.7000	11.67
8	FRDLIVLQS	288	0.7000	11.67

9	LGLLGVTDV	237	0.6900	11.50
10	YRKYRPASF	3	0.5000	8.33
11	VMLAGATVR	448	0.1900	3.17
12	LEVVCARLL	352	0.1400	2.33
13	MVTTAGFNA	128	0.1000	1.67
14	VVGQEHVTA	14	-0.1000	0
15	YTRALGLLG	233	-0.1000	0
16	VRCETGEPA	499	-0.1000	0
17	VVELDAASH	88	-0.3000	0
18	LIVLQSVPD	291	-0.3000	0
19	YRVFIVDEA	118	-0.3200	0
20	FIVDEAHMV	121	-0.4000	0
21	VTYTRALGL	231	-0.4000	0
22	LIFIFATTE	148	-0.4100	0
23	LNCAQGPTA	58	-0.4300	0
24	LAACDAAAL	255	-0.5000	0
25	LQRVERIET	372	-0.5500	0
26	MREQAARIG	316	-0.6100	0
27	LLEVVCARL	351	-0.7500	0
28	IVEEPPEHL	140	-0.8000	0
29	FGAIESVID	264	-0.8000	0
30	VLTHESAPL	464	-0.8000	0
31	IFIFATTEP	149	-0.8300	0
32	IRAGGGSPR	205	-1.0000	0
33	LQNELGARR	565	-1.0000	0
34	LGVNWRVRC	493	-1.0600	0
35	VFIVDEAHM	120	-1.0700	0
36	LLLPSASDA	359	-1.1000	0
37	LTHESAPLA	465	-1.1300	0
38	VVVDDAVYP	194	-1.2000	0
39	LVIRAGGGS	203	-1.2000	0
40	LGEMRGATA	339	-1.2000	0
41	MLAGATVRA	449	-1.2000	0
42	LAPNAPGSI	78	-1.2600	0

43	YAPVQSRYR	111	-1.2600	0
44	LAGATVRAL	450	-1.3100	0
45	LLGVTDVAL	239	-1.3500	0
46	ICEQEGVVV	188	-1.4000	0
47	LSVLDQLLA	216	-1.4000	0
48	LGVTDVALI	240	-1.4000	0
49	VDALAACDA	252	-1.4000	0
50	MSIPAPQAV	384	-1.4000	0
51	VATAKAVNP	519	-1.4000	0
52	VNPAPTANS	525	-1.4000	0
53	FATTEPEKV	152	-1.5000	0
54	LLLEVVCAR	350	-1.5000	0
55	LELLQNELG	562	-1.5000	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	FRLLPPRTM	173	4.0700	67.83
2	MRALLARIC	181	3.1900	53.17
3	MRGATAPRL	342	2.9700	49.50
4	IVLQSVPDA	292	2.1700	36.17
5	VRSMWPTVR	428	2.0900	34.83
6	LGLLGVTDV	237	1.6900	28.17
7	VMLAGATVR	448	1.1900	19.83
8	LEVVCARLL	352	1.1400	19.00
9	MVTTAGFNA	128	1.1000	18.33
10	VRALEDNTL	455	1.0000	16.67
11	VVGQEHVTA	14	0.9000	15.00
12	VRCETGEPA	499	0.9000	15.00
13	VVELDAASH	88	0.7000	11.67
14	FRDLIVLQS	288	0.7000	11.67
15	LIVLQSVPD	291	0.7000	11.67
16	VTYTRALGL	231	0.6000	10.00

17	LIFIFATTE	148	0.5900	9.83
18	LNCAQGPTA	58	0.5700	9.50
19	LAACDAAAL	255	0.5000	8.33
20	LQRVERIET	372	0.4500	7.50
21	MREQAARIG	316	0.3900	6.50
22	LLEVVCARL	351	0.2500	4.17
23	IVEEPPEHL	140	0.2000	3.33
24	VLTHESAPL	464	0.2000	3.33
25	IFIFATTEP	149	0.1700	2.83
26	YLFSGPRGC	37	-0.0100	0
27	LGVNWRVRC	493	-0.0600	0
28	VFIVDEAHM	120	-0.0700	0
29	LLLPSASDA	359	-0.1000	0
30	LTHESAPLA	465	-0.1300	0
31	VVVDDAVYP	194	-0.2000	0
32	LVIRAGGGS	203	-0.2000	0
33	LGEMRGATA	339	-0.2000	0
34	MLAGATVRA	449	-0.2000	0
35	LAPNAPGSI	78	-0.2600	0
36	YRPASFAEV	6	-0.3000	0
37	LAGATVRAL	450	-0.3100	0
38	LLGVTDVAL	239	-0.3500	0
39	FIVDEAHMV	121	-0.4000	0
40	ICEQEGVVV	188	-0.4000	0
41	LSVLDQLLA	216	-0.4000	0
42	LGVTDVALI	240	-0.4000	0
43	VDALAACDA	252	-0.4000	0
44	MSIPAPQAV	384	-0.4000	0
45	VATAKAVNP	519	-0.4000	0
46	VNPAPTANS	525	-0.4000	0
47	YRKYRPASF	3	-0.5000	0
48	LLLEVVCAR	350	-0.5000	0
49	LELLQNELG	562	-0.5000	0
50	VYPLVIRAG	200	-0.5100	0

51	VGGGANVAT	513	-0.6000	0
52	VIRAGGGSP	204	-0.7000	0
53	VVCARLLLP	354	-0.7000	0
54	FGAIESVID	264	-0.8000	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	IVLQSVPDA	292	5.0000	52.63
2	VVVDDAVYP	194	4.8000	50.53
3	VVDDAVYPL	195	4.2100	44.32
4	VELDAASHG	89	3.8700	40.74
5	VVQAGLGEM	334	3.5000	36.84
6	LYRKYRPAS	2	3.4000	35.79
7	VRSMWPTVR	428	3.3000	34.74
8	LVIRAGGGS	203	3.1000	32.63
9	LRSRTTEVM	441	3.1000	32.63
10	MRGATAPRL	342	3.0600	32.21
11	LFSGPRGCG	38	3.0000	31.58
12	VNPAPTANS	525	3.0000	31.58
13	FRLLPPRTM	173	2.9000	30.53
14	LGLLGVTDV	237	2.9000	30.53
15	LQRVERIET	372	2.8000	29.47
16	VRLRSRTTE	439	2.8000	29.47
17	LLLEVVCAR	350	2.7000	28.42
18	LIDDAVDAL	247	2.6600	28.00
19	IRAGGGSPR	205	2.5700	27.05
20	VMLAGATVR	448	2.5000	26.32
21	MLAGATVRA	449	2.5000	26.32
22	VVGQEHVTA	14	2.4000	25.26
23	FIVDEAHMV	121	2.4000	25.26
24	FRDLIVLQS	288	2.4000	25.26
25	LGVNWRVRC	493	2.4000	25.26

26	VQSRYRVFI	114	2.2000	23.16
27	LLPPRTMRA	175	2.2000	23.16
28	FATDLLERF	280	2.2000	23.16
29	VVCARLLLP	354	2.2000	23.16
30	VRDKVRLRS	435	2.2000	23.16
31	INHAYLFSG	33	2.1000	22.11
32	VFIVDEAHM	120	2.0000	21.05
33	LIFIFATTE	148	2.0000	21.05
34	LLQNELGAR	564	2.0000	21.05
35	LGVTDVALI	240	1.8000	18.95
36	LAPNAPGSI	78	1.7000	17.89
37	IFIFATTEP	149	1.7000	17.89
38	YRKYRPASF	3	1.6000	16.84
39	LKIVEEPPE	138	1.6000	16.84
40	VLQSVPDAA	293	1.6000	16.84
41	IGRATLTRY	323	1.6000	16.84
42	VLAPTPASS	413	1.6000	16.84
43	VYPLVIRAG	200	1.4000	14.74
44	YRVFIVDEA	118	1.3000	13.68
45	MRALLARIC	181	1.3000	13.68
46	VQAGLGEMR	335	1.3000	13.68
47	FNALLKIVE	134	1.2000	12.63
48	FIFATTEPE	150	1.2000	12.63
49	VALDAGRIN	26	1.1000	11.58
50	YLFSGPRGC	37	1.1000	11.58
51	LIVLQSVPD	291	1.1000	11.58
52	LDMSIPAPQ	382	1.1000	11.58
53	LLLPSASDA	359	1.0700	11.26
54	LLPSASDAE	360	1.0000	10.53
55	MALYRKYRP	0	0.9500	10.00
56	MVTTAGFNA	128	0.9000	9.47
57	YPLVIRAGG	201	0.9000	9.47

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	IVLQSVPDA	292	4.0000	43.96
2	FRDLIVLQS	288	3.0000	32.97
3	VVVDDAVYP	194	2.8000	30.77
4	FIVDEAHMV	121	2.4000	26.37
5	FRLLPPRTM	173	2.4000	26.37
6	YRVFIVDEA	118	2.3000	25.27
7	VVDDAVYPL	195	2.2500	24.73
8	YLFSGPRGC	37	2.1000	23.08
9	LYRKYRPAS	2	2.0000	21.98
10	LVIRAGGGS	203	1.7000	18.68
11	VNPAPTANS	525	1.6000	17.58
12	MLAGATVRA	449	1.5000	16.48
13	VELDAASHG	89	1.4700	16.15
14	VVGQEHVTA	14	1.4000	15.38
15	LGVNWRVRC	493	1.4000	15.38
16	FATDLLERF	280	1.3000	14.29
17	LLPPRTMRA	175	1.2000	13.19
18	MRGATAPRL	342	1.1000	12.09
19	LQRVERIET	372	1.1000	12.09
20	VVQAGLGEM	334	1.0000	10.99
21	LGLLGVTDV	237	0.9000	9.89
22	FNALLKIVE	134	0.8000	8.79
23	FIFATTEPE	150	0.8000	8.79
24	LDMSIPAPQ	382	0.8000	8.79
25	VRSMWPTVR	428	0.8000	8.79
26	VRDKVRLRS	435	0.8000	8.79
27	YRKYRPASF	3	0.7000	7.69
28	LIDDAVDAL	247	0.7000	7.69
29	LFSGPRGCG	38	0.6000	6.59
30	VLQSVPDAA	293	0.6000	6.59
31	LRSRTTEVM	441	0.6000	6.59

32	YPLVIRAGG	201	0.5000	5.49
33	YRPASFAEV	6	0.4000	4.40
34	VRLRSRTTE	439	0.4000	4.40
35	LARSLNCAQ	54	0.3000	3.30
36	VQSRYRVFI	114	0.3000	3.30
37	MRALLARIC	181	0.3000	3.30
38	LLLEVVCAR	350	0.2000	2.20
39	VVCARLLLP	354	0.2000	2.20
40	VLAPTPASS	413	0.2000	2.20
41	IRAGGGSPR	205	0.0700	0.77
42	LLLPSASDA	359	0.0700	0.77
43	VVELDAASH	88	-0.0200	0
44	LLAGAADTH	222	-0.0200	0
45	MVTTAGFNA	128	-0.1000	0
46	LGVTDVALI	240	-0.1000	0
47	LNCAQGPTA	58	-0.2000	0
48	LAPNAPGSI	78	-0.2000	0
49	VCESCVSLA	71	-0.2300	0
50	INHAYLFSG	33	-0.3000	0
51	IFIFATTEP	149	-0.3000	0
52	LIFIFATTE	148	-0.4000	0
53	VFIVDEAHM	120	-0.5000	0
54	LLQNELGAR	564	-0.5000	0
55	FGAIESVID	264	-0.6000	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	VVVDDAVYP	194	3.6800	41.82
2	IVLQSVPDA	292	3.6000	40.91
3	VNPAPTANS	525	2.6000	29.55
4	FRDLIVLQS	288	2.5000	28.41
5	MLAGATVRA	449	2.3800	27.05

6	VRDKVRLRS	435	2.3000	26.14
7	VVGQEHVTA	14	2.2800	25.91
8	LGVNWRVRC	493	2.2800	25.91
9	VELDAASHG	89	2.2000	25.00
10	FIVDEAHMV	121	2.2000	25.00
11	VVDDAVYPL	195	2.1000	23.86
12	LIDDAVDAL	247	2.0000	22.73
13	LRSRTTEVM	441	2.0000	22.73
14	LLPPRTMRA	175	1.9000	21.59
15	LGLLGVTDV	237	1.9000	21.59
16	VLQSVPDAA	293	1.9000	21.59
17	LDMSIPAPQ	382	1.8000	20.45
18	VRSMWPTVR	428	1.8000	20.45
19	LQRVERIET	372	1.7800	20.23
20	VVCARLLLP	354	1.7000	19.32
21	LYRKYRPAS	2	1.6000	18.18
22	YRVFIVDEA	118	1.6000	18.18
23	VRLRSRTTE	439	1.4000	15.91
24	LARSLNCAQ	54	1.3000	14.77
25	LVIRAGGGS	203	1.3000	14.77
26	LLAGAADTH	222	1.2800	14.55
27	LLLEVVCAR	350	1.2000	13.64
28	VLAPTPASS	413	1.2000	13.64
29	VQSRYRVFI	114	1.1800	13.41
30	FRLLPPRTM	173	1.1000	12.50
31	MRALLARIC	181	1.0000	11.36
32	VMLAGATVR	448	1.0000	11.36
33	VVELDAASH	88	0.9800	11.14
34	LGVTDVALI	240	0.9000	10.23
35	YLFSGPRGC	37	0.8000	9.09
36	ILARSLNCA	53	0.8000	9.09
37	IRAGGGSPR	205	0.8000	9.09
38	LLLPSASDA	359	0.8000	9.09
39	IFIFATTEP	149	0.7000	7.95

40	FATDLLERF	280	0.7000	7.95
41	MRGATAPRL	342	0.7000	7.95
42	VRCETGEPA	499	0.7000	7.95
43	LIFIFATTE	148	0.6000	6.82
44	LSVLDQLLA	216	0.6000	6.82
45	VVQAGLGEM	334	0.6000	6.82
46	VCARLLLPS	355	0.6000	6.82
47	LDAGRINHA	28	0.5000	5.68
48	VCESCVSLA	71	0.5000	5.68
49	VFIVDEAHM	120	0.5000	5.68
50	IGRATLTRY	323	0.3000	3.41
51	LFSGPRGCG	38	0.2000	2.27
52	FIFATTEPE	150	0.2000	2.27
53	VQAGLGEMR	335	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	VVVDDAVYP	194	3.6800	41.82
2	IVLQSVPDA	292	3.6000	40.91
3	VNPAPTANS	525	2.6000	29.55
4	FRDLIVLQS	288	2.5000	28.41
5	MLAGATVRA	449	2.3800	27.05
6	VRDKVRLRS	435	2.3000	26.14
7	VVGQEHVTA	14	2.2800	25.91
8	LGVNWRVRC	493	2.2800	25.91
9	VELDAASHG	89	2.2000	25.00
10	FIVDEAHMV	121	2.2000	25.00
11	VVDDAVYPL	195	2.1000	23.86
12	LIDDAVDAL	247	2.0000	22.73
13	LRSRTTEVM	441	2.0000	22.73
14	LLPPRTMRA	175	1.9000	21.59
15	LGLLGVTDV	237	1.9000	21.59

16	VLQSVPDAA	293	1.9000	21.59
17	LDMSIPAPQ	382	1.8000	20.45
18	VRSMWPTVR	428	1.8000	20.45
19	LQRVERIET	372	1.7800	20.23
20	VVCARLLLP	354	1.7000	19.32
21	LYRKYRPAS	2	1.6000	18.18
22	YRVFIVDEA	118	1.6000	18.18
23	VRLRSRTTE	439	1.4000	15.91
24	LARSLNCAQ	54	1.3000	14.77
25	LVIRAGGGS	203	1.3000	14.77
26	LLAGAADTH	222	1.2800	14.55
27	LLLEVVCAR	350	1.2000	13.64
28	VLAPTPASS	413	1.2000	13.64
29	VQSRYRVFI	114	1.1800	13.41
30	FRLLPPRTM	173	1.1000	12.50
31	MRALLARIC	181	1.0000	11.36
32	VMLAGATVR	448	1.0000	11.36
33	VVELDAASH	88	0.9800	11.14
34	LGVTDVALI	240	0.9000	10.23
35	YLFSGPRGC	37	0.8000	9.09
36	ILARSLNCA	53	0.8000	9.09
37	IRAGGGSPR	205	0.8000	9.09
38	LLLPSASDA	359	0.8000	9.09
39	IFIFATTEP	149	0.7000	7.95
40	FATDLLERF	280	0.7000	7.95
41	MRGATAPRL	342	0.7000	7.95
42	VRCETGEPA	499	0.7000	7.95
43	LIFIFATTE	148	0.6000	6.82
44	LSVLDQLLA	216	0.6000	6.82
45	VVQAGLGEM	334	0.6000	6.82
46	VCARLLLPS	355	0.6000	6.82
47	LDAGRINHA	28	0.5000	5.68
48	VCESCVSLA	71	0.5000	5.68
49	VFIVDEAHM	120	0.5000	5.68

50	IGRATLTRY	323	0.3000	3.41
51	LFSGPRGCG	38	0.2000	2.27
52	FIFATTEPE	150	0.2000	2.27
53	VQAGLGEMR	335	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	VVVDDAVYP	194	3.6800	41.82
2	IVLQSVPDA	292	3.6000	40.91
3	VNPAPTANS	525	2.6000	29.55
4	FRDLIVLQS	288	2.5000	28.41
5	MLAGATVRA	449	2.3800	27.05
6	VRDKVRLRS	435	2.3000	26.14
7	VVGQEHVTA	14	2.2800	25.91
8	LGVNWRVRC	493	2.2800	25.91
9	VELDAASHG	89	2.2000	25.00
10	FIVDEAHMV	121	2.2000	25.00
11	VVDDAVYPL	195	2.1000	23.86
12	LIDDAVDAL	247	2.0000	22.73
13	LRSRTTEVM	441	2.0000	22.73
14	LLPPRTMRA	175	1.9000	21.59
15	LGLLGVTDV	237	1.9000	21.59
16	VLQSVPDAA	293	1.9000	21.59
17	LDMSIPAPQ	382	1.8000	20.45
18	VRSMWPTVR	428	1.8000	20.45
19	LQRVERIET	372	1.7800	20.23
20	VVCARLLLP	354	1.7000	19.32
21	LYRKYRPAS	2	1.6000	18.18
22	YRVFIVDEA	118	1.6000	18.18
23	VRLRSRTTE	439	1.4000	15.91
24	LARSLNCAQ	54	1.3000	14.77
25	LVIRAGGGS	203	1.3000	14.77

26	LLAGAADTH	222	1.2800	14.55
27	LLLEVVCAR	350	1.2000	13.64
28	VLAPTPASS	413	1.2000	13.64
29	VQSRYRVFI	114	1.1800	13.41
30	FRLLPPRTM	173	1.1000	12.50
31	MRALLARIC	181	1.0000	11.36
32	VMLAGATVR	448	1.0000	11.36
33	VVELDAASH	88	0.9800	11.14
34	LGVTDVALI	240	0.9000	10.23
35	YLFSGPRGC	37	0.8000	9.09
36	ILARSLNCA	53	0.8000	9.09
37	IRAGGGSPR	205	0.8000	9.09
38	LLLPSASDA	359	0.8000	9.09
39	IFIFATTEP	149	0.7000	7.95
40	FATDLLERF	280	0.7000	7.95
41	MRGATAPRL	342	0.7000	7.95
42	VRCETGEPA	499	0.7000	7.95
43	LIFIFATTE	148	0.6000	6.82
44	LSVLDQLLA	216	0.6000	6.82
45	VVQAGLGEM	334	0.6000	6.82
46	VCARLLLPS	355	0.6000	6.82
47	LDAGRINHA	28	0.5000	5.68
48	VCESCVSLA	71	0.5000	5.68
49	VFIVDEAHM	120	0.5000	5.68
50	IGRATLTRY	323	0.3000	3.41
51	LFSGPRGCG	38	0.2000	2.27
52	FIFATTEPE	150	0.2000	2.27
53	VQAGLGEMR	335	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	IVLQSVPDA	292	4.0000	42.11

2	FRLLPPRTM	173	3.9000	41.05
3	VVVDDAVYP	194	3.8000	40.00
4	FIVDEAHMV	121	3.4000	35.79
5	FRDLIVLQS	288	3.4000	35.79
6	VVDDAVYPL	195	3.2100	33.79
7	FATDLLERF	280	3.2000	33.68
8	VELDAASHG	89	2.8700	30.21
9	YRKYRPASF	3	2.6000	27.37
10	VVQAGLGEM	334	2.5000	26.32
11	LYRKYRPAS	2	2.4000	25.26
12	YRVFIVDEA	118	2.3000	24.21
13	VRSMWPTVR	428	2.3000	24.21
14	FNALLKIVE	134	2.2000	23.16
15	FIFATTEPE	150	2.2000	23.16
16	YLFSGPRGC	37	2.1000	22.11
17	LVIRAGGGS	203	2.1000	22.11
18	LRSRTTEVM	441	2.1000	22.11
19	MRGATAPRL	342	2.0600	21.68
20	LFSGPRGCG	38	2.0000	21.05
21	VNPAPTANS	525	2.0000	21.05
22	YPLVIRAGG	201	1.9000	20.00
23	LGLLGVTDV	237	1.9000	20.00
24	LQRVERIET	372	1.8000	18.95
25	VRLRSRTTE	439	1.8000	18.95
26	LLLEVVCAR	350	1.7000	17.89
27	LIDDAVDAL	247	1.6600	17.47
28	IRAGGGSPR	205	1.5700	16.53
29	VMLAGATVR	448	1.5000	15.79
30	MLAGATVRA	449	1.5000	15.79
31	YRPASFAEV	6	1.4000	14.74
32	VVGQEHVTA	14	1.4000	14.74
33	LGVNWRVRC	493	1.4000	14.74
34	VQSRYRVFI	114	1.2000	12.63
35	LLPPRTMRA	175	1.2000	12.63

36	VVCARLLLP	354	1.2000	12.63
37	VRDKVRLRS	435	1.2000	12.63
38	INHAYLFSG	33	1.1000	11.58
39	VFIVDEAHM	120	1.0000	10.53
40	LIFIFATTE	148	1.0000	10.53
41	LLQNELGAR	564	1.0000	10.53
42	LGVTDVALI	240	0.8000	8.42
43	LAPNAPGSI	78	0.7000	7.37
44	IFIFATTEP	149	0.7000	7.37
45	YPFRLLPPR	171	0.7000	7.37
46	LKIVEEPPE	138	0.6000	6.32
47	YTRALGLLG	233	0.6000	6.32
48	VLQSVPDAA	293	0.6000	6.32
49	IGRATLTRY	323	0.6000	6.32
50	VLAPTPASS	413	0.6000	6.32
51	FGAIESVID	264	0.5000	5.26
52	VYPLVIRAG	200	0.4000	4.21
53	MRALLARIC	181	0.3000	3.16
54	VQAGLGEMR	335	0.3000	3.16
55	VALDAGRIN	26	0.1000	1.05
56	LIVLQSVPD	291	0.1000	1.05
57	LDMSIPAPQ	382	0.1000	1.05

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	VVVDDAVYP	194	3.6800	41.82
2	IVLQSVPDA	292	3.6000	40.91
3	VNPAPTANS	525	2.6000	29.55
4	FRDLIVLQS	288	2.5000	28.41
5	MLAGATVRA	449	2.3800	27.05
6	VRDKVRLRS	435	2.3000	26.14
7	VVGQEHVTA	14	2.2800	25.91

8	LGVNWRVRC	493	2.2800	25.91
9	VELDAASHG	89	2.2000	25.00
10	FIVDEAHMV	121	2.2000	25.00
11	VVDDAVYPL	195	2.1000	23.86
12	LIDDAVDAL	247	2.0000	22.73
13	LRSRTTEVM	441	2.0000	22.73
14	LLPPRTMRA	175	1.9000	21.59
15	LGLLGVTDV	237	1.9000	21.59
16	VLQSVPDAA	293	1.9000	21.59
17	LDMSIPAPQ	382	1.8000	20.45
18	VRSMWPTVR	428	1.8000	20.45
19	LQRVERIET	372	1.7800	20.23
20	VVCARLLLP	354	1.7000	19.32
21	LYRKYRPAS	2	1.6000	18.18
22	YRVFIVDEA	118	1.6000	18.18
23	VRLRSRTTE	439	1.4000	15.91
24	LARSLNCAQ	54	1.3000	14.77
25	LVIRAGGGS	203	1.3000	14.77
26	LLAGAADTH	222	1.2800	14.55
27	LLLEVVCAR	350	1.2000	13.64
28	VLAPTPASS	413	1.2000	13.64
29	VQSRYRVFI	114	1.1800	13.41
30	FRLLPPRTM	173	1.1000	12.50
31	MRALLARIC	181	1.0000	11.36
32	VMLAGATVR	448	1.0000	11.36
33	VVELDAASH	88	0.9800	11.14
34	LGVTDVALI	240	0.9000	10.23
35	YLFSGPRGC	37	0.8000	9.09
36	ILARSLNCA	53	0.8000	9.09
37	IRAGGGSPR	205	0.8000	9.09
38	LLLPSASDA	359	0.8000	9.09
39	IFIFATTEP	149	0.7000	7.95
40	FATDLLERF	280	0.7000	7.95
41	MRGATAPRL	342	0.7000	7.95

42	VRCETGEPA	499	0.7000	7.95
43	LIFIFATTE	148	0.6000	6.82
44	LSVLDQLLA	216	0.6000	6.82
45	VVQAGLGEM	334	0.6000	6.82
46	VCARLLLPS	355	0.6000	6.82
47	LDAGRINHA	28	0.5000	5.68
48	VCESCVSLA	71	0.5000	5.68
49	VFIVDEAHM	120	0.5000	5.68
50	IGRATLTRY	323	0.3000	3.41
51	LFSGPRGCG	38	0.2000	2.27
52	FIFATTEPE	150	0.2000	2.27
53	VQAGLGEMR	335	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	FRDLIVLQS	288	4.0000	46.51
2	IVLQSVPDA	292	3.1000	36.05
3	VNPAPTANS	525	2.7000	31.40
4	YRVFIVDEA	118	2.4000	27.91
5	FRLLPPRTM	173	2.4000	27.91
6	LLLEVVCAR	350	2.4000	27.91
7	LARSLNCAQ	54	2.3000	26.74
8	FIVDEAHMV	121	2.3000	26.74
9	FIFATTEPE	150	2.3000	26.74
10	VVVDDAVYP	194	1.7800	20.70
11	YLFSGPRGC	37	1.4000	16.28
12	LLPPRTMRA	175	1.4000	16.28
13	LGLLGVTDV	237	1.4000	16.28
14	VRCETGEPA	499	1.4000	16.28
15	LELLQNELG	562	1.4000	16.28
16	LGVTDVALI	240	1.3000	15.12
17	VRSMWPTVR	428	1.2000	13.95

18	LRSRTTEVM	441	1.2000	13.95
19	VLTHESAPL	464	1.1000	12.79
20	IFIFATTEP	149	0.9000	10.47
21	MRALLARIC	181	0.8000	9.30
22	VVGQEHVTA	14	0.7800	9.07
23	VVELDAASH	88	0.7800	9.07
24	LIVLQSVPD	291	0.7800	9.07
25	YRPASFAEV	6	0.7000	8.14
26	FGAIESVID	264	0.6800	7.91
27	IVEEPPEHL	140	0.6000	6.98
28	VGQEHVTAP	15	0.5000	5.81
29	VLQSVPDAA	293	0.5000	5.81
30	VRALEDNTL	455	0.5000	5.81
31	LDMSIPAPQ	382	0.4000	4.65
32	MLAGATVRA	449	0.3800	4.42
33	VELDAASHG	89	0.3000	3.49
34	FATTEPEKV	152	0.2000	2.33
35	VTYTRALGL	231	0.2000	2.33
36	LLPSASDAE	360	0.1000	1.16
37	VLAEALKDA	484	0.1000	1.16
38	LIFIFATTE	148	-0.1000	0
39	VVDDAVYPL	195	-0.1000	0
40	LIDDAVDAL	247	-0.2000	0
41	MRGATAPRL	342	-0.3000	0
42	LQNELGARR	565	-0.3000	0
43	YRKYRPASF	3	-0.4000	0
44	VERIETRLD	375	-0.4000	0
45	IVDEAHMVT	122	-0.5000	0
46	FATDLLERF	280	-0.5000	0
47	VVCARLLLP	354	-0.6000	0
48	VCESCVSLA	71	-0.7000	0
49	MVTTAGFNA	128	-0.7000	0
50	LSVLDQLLA	216	-0.8000	0
51	LLLPSASDA	359	-0.8000	0

52	LPTIRSRTH	161	-0.8200	0
53	LQSVPDAAS	294	-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	LRSRTTEVM	441	3.7000	38.54
2	VNPAPTANS	525	3.7000	38.54
3	IFIFATTEP	149	3.3000	34.38
4	MRALLARIC	181	3.3000	34.38
5	FRLLPPRTM	173	2.9000	30.21
6	VERIETRLD	375	2.7800	28.96
7	LLPPRTMRA	175	2.7000	28.13
8	IVLQSVPDA	292	2.6000	27.08
9	MLAGATVRA	449	2.4000	25.00
10	LPTIRSRTH	161	2.3600	24.58
11	VLTHESAPL	464	2.2000	22.92
12	VRSMWPTVR	428	2.1000	21.88
13	FRDLIVLQS	288	1.9000	19.79
14	LAGATVRAL	450	1.8000	18.75
15	LVIRAGGGS	203	1.7000	17.71
16	VCARLLLPS	355	1.6000	16.67
17	YLFSGPRGC	37	1.5000	15.62
18	ILARSLNCA	53	1.5000	15.62
19	LARSLNCAQ	54	1.5000	15.62
20	MREQAARIG	316	1.3000	13.54
21	IRSRTHHYP	164	1.2000	12.50
22	VYPLVIRAG	200	1.2000	12.50
23	LGLLGVTDV	237	1.2000	12.50
24	VMLAGATVR	448	1.2000	12.50
25	LGVTDVALI	240	1.1000	11.46
26	VSLAPNAPG	76	1.0000	10.42
27	YRVFIVDEA	118	0.8000	8.33

28	VVGQEHVTA	14	0.7000	7.29
29	VVCARLLLP	354	0.7000	7.29
30	MVTTAGFNA	128	0.6000	6.25
31	LEVVCARLL	352	0.6000	6.25
32	LIVLQSVPD	291	0.5000	5.21
33	IETRLDMSI	378	0.5000	5.21
34	LARRLSEQR	472	0.5000	5.21
35	LRDRAFYAP	105	0.4000	4.17
36	LPPRTMRAL	176	0.4000	4.17
37	MRGATAPRL	342	0.4000	4.17
38	VLAPTPASS	413	0.4000	4.17
39	VVELDAASH	88	0.3800	3.96
40	LIFIFATTE	148	0.3800	3.96
41	YAPVQSRYR	111	0.3000	3.12
42	VTYTRALGL	231	0.3000	3.12
43	LERFRDLIV	285	0.3000	3.12
44	LQSVPDAAS	294	0.3000	3.12
45	LLLPSASDA	359	0.3000	3.12
46	MSIPAPQAV	384	0.3000	3.12
47	VRDKVRLRS	435	0.3000	3.12
48	VGGGANVAT	513	0.3000	3.12
49	VPDAASRGV	297	0.2000	2.08
50	VRLRSRTTE	439	0.2000	2.08
51	VRALEDNTL	455	0.1000	1.04
52	VQSRYRVFI	114	-0.1000	0
53	FIFATTEPE	150	-0.1000	0
54	YRKYRPASF	3	-0.2000	0
55	VAAVRSMWP	425	-0.2000	0
56	YRPASFAEV	6	-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	IFIFATTEP	149	4.3000	48.86
2	VNPAPTANS	525	3.7000	42.05
3	VRSMWPTVR	428	3.6000	40.91
4	LGLLGVTDV	237	3.1000	35.23
5	IVLQSVPDA	292	3.0000	34.09
6	FRDLIVLQS	288	2.8000	31.82
7	LLPPRTMRA	175	2.6000	29.55
8	YRVFIVDEA	118	2.4000	27.27
9	MRALLARIC	181	2.3000	26.14
10	VVELDAASH	88	1.9800	22.50
11	FRLLPPRTM	173	1.9000	21.59
12	LARSLNCAQ	54	1.8000	20.45
13	LIVLQSVPD	291	1.8000	20.45
14	VRALEDNTL	455	1.8000	20.45
15	LIFIFATTE	148	1.7000	19.32
16	LELLQNELG	562	1.7000	19.32
17	LQSVPDAAS	294	1.5000	17.05
18	VMLAGATVR	448	1.5000	17.05
19	LLLPSASDA	359	1.2000	13.64
20	VERIETRLD	375	1.2000	13.64
21	VSLAPNAPG	76	1.0000	11.36
22	VAAVRSMWP	425	0.9000	10.23
23	VVGQEHVTA	14	0.8000	9.09
24	LLLEVVCAR	350	0.8000	9.09
25	LRSRTTEVM	441	0.8000	9.09
26	LPTIRSRTH	161	0.7800	8.86
27	LGVTDVALI	240	0.7000	7.95
28	FIFATTEPE	150	0.4000	4.55
29	MRGATAPRL	342	0.4000	4.55
30	VLAPTPASS	413	0.4000	4.55
31	MLAGATVRA	449	0.4000	4.55
32	LERFRDLIV	285	0.3000	3.41
33	VYPLVIRAG	200	0.2000	2.27
34	VVVDDAVYP	194	0.1000	1.14

35	LDMSIPAPQ	382	-0.1000	0
36	YRKYRPASF	3	-0.2000	0
37	FGAIESVID	264	-0.2000	0
38	YRPASFAEV	6	-0.3000	0
39	VDALAACDA	252	-0.3000	0
40	MVTTAGFNA	128	-0.3500	0
41	LGEMRGATA	339	-0.4000	0
42	VCESCVSLA	71	-0.5000	0
43	VELDAASHG	89	-0.5000	0
44	LLGVTDVAL	239	-0.5000	0
45	IGRATLTRY	323	-0.5000	0
46	VGQEHVTAP	15	-0.6000	0
47	VVDDAVYPL	195	-0.6000	0
48	VVQAGLGEM	334	-0.6000	0
49	VALIDDAVD	245	-0.7000	0
50	LLEVVCARL	351	-0.7000	0
51	LPSASDAES	361	-0.7000	0
52	YLFSGPRGC	37	-0.8000	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	FIFATTEPE	150	4.4000	46.81
2	FRLLPPRTM	173	4.0000	42.55
3	FRDLIVLQS	288	3.8000	40.43
4	LIFIFATTE	148	3.7000	39.36
5	IFIFATTEP	149	3.7000	39.36
6	FGAIESVID	264	3.5000	37.23
7	LIVLQSVPD	291	3.5000	37.23
8	YRVFIVDEA	118	3.4000	36.17
9	VERIETRLD	375	2.9000	30.85
10	VNPAPTANS	525	2.7000	28.72
11	VRSMWPTVR	428	2.6000	27.66

12	LGLLGVTDV	237	2.4000	25.53
13	VVELDAASH	88	2.2000	23.40
14	IVLQSVPDA	292	2.0000	21.28
15	LELLQNELG	562	2.0000	21.28
16	VRALEDNTL	455	1.8000	19.15
17	YRKYRPASF	3	1.7000	18.09
18	LARSLNCAQ	54	1.6000	17.02
19	LLPPRTMRA	175	1.6000	17.02
20	VSLAPNAPG	76	1.3000	13.83
21	MRALLARIC	181	1.3000	13.83
22	YRPASFAEV	6	1.0000	10.64
23	LPTIRSRTH	161	1.0000	10.64
24	VALIDDAVD	245	1.0000	10.64
25	LRSRTTEVM	441	0.9000	9.57
26	FNALLKIVE	134	0.7800	8.30
27	LLPSASDAE	360	0.7000	7.45
28	VYPLVIRAG	200	0.5000	5.32
29	LQSVPDAAS	294	0.5000	5.32
30	VMLAGATVR	448	0.5000	5.32
31	MRGATAPRL	342	0.4000	4.26
32	VAAVRSMWP	425	0.3000	3.19
33	YLFSGPRGC	37	0.2000	2.13
34	LLLPSASDA	359	0.2000	2.13
35	LAPTPASSE	414	0.2000	2.13
36	VFIVDEAHM	120	0.1000	1.06
37	YAPVQSRYR	111	-0.1000	0
38	LGVTDVALI	240	-0.1000	0
39	VVGQEHVTA	14	-0.2000	0
40	VELDAASHG	89	-0.2000	0
41	YTRALGLLG	233	-0.2000	0
42	LLLEVVCAR	350	-0.2000	0
43	FIVDEAHMV	121	-0.3000	0
44	LDMSIPAPQ	382	-0.3000	0
45	LERFRDLIV	285	-0.4000	0

46	IGRATLTRY	323	-0.4000	0
47	WRVRCETGE	497	-0.4000	0
48	VVVDDAVYP	194	-0.5000	0
49	LLGVTDVAL	239	-0.5000	0
50	VVQAGLGEM	334	-0.5000	0
51	VVDDAVYPL	195	-0.6000	0
52	MREQAARIG	316	-0.6000	0
53	VVCARLLLP	354	-0.6000	0
54	VLAPTPASS	413	-0.6000	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	FRDLIVLQS	288	3.8000	43.18
2	YRVFIVDEA	118	3.4000	38.64
3	IFIFATTEP	149	3.3000	37.50
4	FRLLPPRTM	173	2.9000	32.95
5	VNPAPTANS	525	2.7000	30.68
6	VRSMWPTVR	428	2.6000	29.55
7	LGLLGVTDV	237	2.1000	23.86
8	IVLQSVPDA	292	2.0000	22.73
9	LLPPRTMRA	175	1.6000	18.18
10	FIFATTEPE	150	1.4000	15.91
11	MRALLARIC	181	1.3000	14.77
12	VVELDAASH	88	0.9800	11.14
13	YRKYRPASF	3	0.8000	9.09
14	LARSLNCAQ	54	0.8000	9.09
15	FGAIESVID	264	0.8000	9.09
16	LIVLQSVPD	291	0.8000	9.09
17	VRALEDNTL	455	0.8000	9.09
18	YRPASFAEV	6	0.7000	7.95
19	LIFIFATTE	148	0.7000	7.95
20	LELLQNELG	562	0.7000	7.95

21	LQSVPDAAS	294	0.5000	5.68
22	VMLAGATVR	448	0.5000	5.68
23	YLFSGPRGC	37	0.2000	2.27
24	LLLPSASDA	359	0.2000	2.27
25	VERIETRLD	375	0.2000	2.27
26	YAPVQSRYR	111	-0.1000	0
27	VAAVRSMWP	425	-0.1000	0
28	VVGQEHVTA	14	-0.2000	0
29	LLLEVVCAR	350	-0.2000	0
30	LRSRTTEVM	441	-0.2000	0
31	LPTIRSRTH	161	-0.2200	0
32	LGVTDVALI	240	-0.3000	0
33	FIVDEAHMV	121	-0.6000	0
34	MRGATAPRL	342	-0.6000	0
35	VLAPTPASS	413	-0.6000	0
36	MLAGATVRA	449	-0.6000	0
37	LERFRDLIV	285	-0.7000	0
38	VYPLVIRAG	200	-0.8000	0
39	VVVDDAVYP	194	-0.9000	0
40	VFIVDEAHM	120	-1.0000	0
41	LSVLDQLLA	216	-1.0000	0
42	VVCARLLLP	354	-1.0000	0
43	VLTHESAPL	464	-1.0000	0
44	LDMSIPAPQ	382	-1.1000	0
45	VDALAACDA	252	-1.3000	0
46	MVTTAGFNA	128	-1.3500	0
47	LGEMRGATA	339	-1.4000	0
48	VCESCVSLA	71	-1.5000	0
49	VELDAASHG	89	-1.5000	0
50	YTRALGLLG	233	-1.5000	0
51	LLGVTDVAL	239	-1.5000	0
52	IGRATLTRY	323	-1.5000	0
53	VGQEHVTAP	15	-1.6000	0
54	VVDDAVYPL	195	-1.6000	0

55	VVQAGLGEM	334	-1.6000	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	LIFIFATTE	148	4.7000	50.00
2	IFIFATTEP	149	4.7000	50.00
3	LIVLQSVPD	291	4.5000	47.87
4	VERIETRLD	375	3.9000	41.49
5	VNPAPTANS	525	3.7000	39.36
6	VRSMWPTVR	428	3.6000	38.30
7	FIFATTEPE	150	3.4000	36.17
8	LGLLGVTDV	237	3.4000	36.17
9	VVELDAASH	88	3.2000	34.04
10	FRLLPPRTM	173	3.0000	31.91
11	IVLQSVPDA	292	3.0000	31.91
12	LELLQNELG	562	3.0000	31.91
13	FRDLIVLQS	288	2.8000	29.79
14	VRALEDNTL	455	2.8000	29.79
15	LARSLNCAQ	54	2.6000	27.66
16	LLPPRTMRA	175	2.6000	27.66
17	FGAIESVID	264	2.5000	26.60
18	YRVFIVDEA	118	2.4000	25.53
19	VSLAPNAPG	76	2.3000	24.47
20	MRALLARIC	181	2.3000	24.47
21	LPTIRSRTH	161	2.0000	21.28
22	VALIDDAVD	245	2.0000	21.28
23	LRSRTTEVM	441	1.9000	20.21
24	LLPSASDAE	360	1.7000	18.09
25	VYPLVIRAG	200	1.5000	15.96
26	LQSVPDAAS	294	1.5000	15.96
27	VMLAGATVR	448	1.5000	15.96
28	MRGATAPRL	342	1.4000	14.89

29	VAAVRSMWP	425	1.3000	13.83
30	LLLPSASDA	359	1.2000	12.77
31	LAPTPASSE	414	1.2000	12.77
32	VFIVDEAHM	120	1.1000	11.70
33	LKIVEEPPE	138	1.0000	10.64
34	VLTHESAPL	464	1.0000	10.64
35	LGVTDVALI	240	0.9000	9.57
36	VVGQEHVTA	14	0.8000	8.51
37	VELDAASHG	89	0.8000	8.51
38	LLLEVVCAR	350	0.8000	8.51
39	YRKYRPASF	3	0.7000	7.45
40	LDMSIPAPQ	382	0.7000	7.45
41	LERFRDLIV	285	0.6000	6.38
42	IGRATLTRY	323	0.6000	6.38
43	VVVDDAVYP	194	0.5000	5.32
44	LLGVTDVAL	239	0.5000	5.32
45	VVQAGLGEM	334	0.5000	5.32
46	VVDDAVYPL	195	0.4000	4.26
47	MREQAARIG	316	0.4000	4.26
48	VVCARLLLP	354	0.4000	4.26
49	VLAPTPASS	413	0.4000	4.26
50	MLAGATVRA	449	0.4000	4.26
51	LLEVVCARL	351	0.3000	3.19
52	VTYTRALGL	231	0.2000	2.13
53	LEVVCARLL	352	0.2000	2.13
54	LAGATVRAL	450	0.2000	2.13
55	INHAYLFSG	33	0.1500	1.60
56	VRLRSRTTE	439	0.1000	1.06

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	FRDLIVLQS	288	4.4000	48.89

2	FRLLPPRTM	173	3.9000	43.33
3	LLLEVVCAR	350	3.9000	43.33
4	FIFATTEPE	150	3.7000	41.11
5	FIVDEAHMV	121	3.3000	36.67
6	IVLQSVPDA	292	3.1000	34.44
7	VNPAPTANS	525	3.1000	34.44
8	LELLQNELG	562	2.8000	31.11
9	VVVDDAVYP	194	2.7800	30.89
10	VRSMWPTVR	428	2.7000	30.00
11	LRSRTTEVM	441	2.7000	30.00
12	YRVFIVDEA	118	2.4000	26.67
13	LGLLGVTDV	237	2.4000	26.67
14	LGVTDVALI	240	2.2000	24.44
15	VLTHESAPL	464	2.0600	22.89
16	IFIFATTEP	149	1.9000	21.11
17	LIVLQSVPD	291	1.8800	20.89
18	FGAIESVID	264	1.7800	19.78
19	YRPASFAEV	6	1.7000	18.89
20	VELDAASHG	89	1.7000	18.89
21	LARSLNCAQ	54	1.6000	17.78
22	IVEEPPEHL	140	1.5600	17.33
23	YRKYRPASF	3	1.5000	16.67
24	VGQEHVTAP	15	1.5000	16.67
25	LLPSASDAE	360	1.5000	16.67
26	VMLAGATVR	448	1.5000	16.67
27	VRALEDNTL	455	1.4600	16.22
28	YLFSGPRGC	37	1.4000	15.56
29	VSLAPNAPG	76	1.4000	15.56
30	LLPPRTMRA	175	1.4000	15.56
31	FATDLLERF	280	1.4000	15.56
32	VRCETGEPA	499	1.4000	15.56
33	LIFIFATTE	148	1.3000	14.44
34	FATTEPEKV	152	1.2000	13.33
35	LQNELGARR	565	1.2000	13.33

36	VTYTRALGL	231	1.1600	12.89
37	VVDDAVYPL	195	0.8600	9.56
38	MRALLARIC	181	0.8000	8.89
39	VVGQEHVTA	14	0.7800	8.67
40	LIDDAVDAL	247	0.7600	8.44
41	VERIETRLD	375	0.7000	7.78
42	MRGATAPRL	342	0.6600	7.33
43	VLQSVPDAA	293	0.5000	5.56
44	VVCARLLLP	354	0.4000	4.44
45	MLAGATVRA	449	0.3800	4.22
46	YTRALGLLG	233	0.3000	3.33
47	VVELDAASH	88	0.2000	2.22
48	IVDEAHMVT	122	0.2000	2.22
49	VYPLVIRAG	200	0.1000	1.11
50	VLAEALKDA	484	0.1000	1.11
51	VALELLQNE	560	0.1000	1.11
52	LVLTHESAP	463	-0.1000	0
53	LSEQRNADV	476	-0.1000	0
54	VVQAGLGEM	334	-0.2000	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	IFIFATTEP	149	4.3000	48.86
2	VNPAPTANS	525	3.7000	42.05
3	VRSMWPTVR	428	3.6000	40.91
4	LGLLGVTDV	237	3.1000	35.23
5	IVLQSVPDA	292	3.0000	34.09
6	FRDLIVLQS	288	2.8000	31.82
7	LLPPRTMRA	175	2.6000	29.55
8	YRVFIVDEA	118	2.4000	27.27
9	MRALLARIC	181	2.3000	26.14
10	VVELDAASH	88	1.9800	22.50

11	FRLLPPRTM	173	1.9000	21.59
12	LARSLNCAQ	54	1.8000	20.45
13	LIVLQSVPD	291	1.8000	20.45
14	VRALEDNTL	455	1.8000	20.45
15	LIFIFATTE	148	1.7000	19.32
16	LELLQNELG	562	1.7000	19.32
17	LQSVPDAAS	294	1.5000	17.05
18	VMLAGATVR	448	1.5000	17.05
19	LLLPSASDA	359	1.2000	13.64
20	VERIETRLD	375	1.2000	13.64
21	VSLAPNAPG	76	1.0000	11.36
22	VAAVRSMWP	425	0.9000	10.23
23	VVGQEHVTA	14	0.8000	9.09
24	LLLEVVCAR	350	0.8000	9.09
25	LRSRTTEVM	441	0.8000	9.09
26	LPTIRSRTH	161	0.7800	8.86
27	LGVTDVALI	240	0.7000	7.95
28	FIFATTEPE	150	0.4000	4.55
29	MRGATAPRL	342	0.4000	4.55
30	VLAPTPASS	413	0.4000	4.55
31	MLAGATVRA	449	0.4000	4.55
32	LERFRDLIV	285	0.3000	3.41
33	VYPLVIRAG	200	0.2000	2.27
34	VVVDDAVYP	194	0.1000	1.14
35	LDMSIPAPQ	382	-0.1000	0
36	YRKYRPASF	3	-0.2000	0
37	FGAIESVID	264	-0.2000	0
38	YRPASFAEV	6	-0.3000	0
39	VDALAACDA	252	-0.3000	0
40	MVTTAGFNA	128	-0.3500	0
41	LGEMRGATA	339	-0.4000	0
42	VCESCVSLA	71	-0.5000	0
43	VELDAASHG	89	-0.5000	0
44	LLGVTDVAL	239	-0.5000	0

45	IGRATLTRY	323	-0.5000	0
46	VGQEHVTAP	15	-0.6000	0
47	VVDDAVYPL	195	-0.6000	0
48	VVQAGLGEM	334	-0.6000	0
49	VALIDDAVD	245	-0.7000	0
50	LLEVVCARL	351	-0.7000	0
51	LPSASDAES	361	-0.7000	0
52	YLFSGPRGC	37	-0.8000	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	FRDLIVLQS	288	4.0000	46.51
2	IVLQSVPDA	292	3.1000	36.05
3	VNPAPTANS	525	2.7000	31.40
4	YRVFIVDEA	118	2.4000	27.91
5	FRLLPPRTM	173	2.4000	27.91
6	LLLEVVCAR	350	2.4000	27.91
7	LARSLNCAQ	54	2.3000	26.74
8	FIVDEAHMV	121	2.3000	26.74
9	FIFATTEPE	150	2.3000	26.74
10	VVVDDAVYP	194	1.7800	20.70
11	YLFSGPRGC	37	1.4000	16.28
12	LLPPRTMRA	175	1.4000	16.28
13	LGLLGVTDV	237	1.4000	16.28
14	VRCETGEPA	499	1.4000	16.28
15	LELLQNELG	562	1.4000	16.28
16	LGVTDVALI	240	1.3000	15.12
17	VRSMWPTVR	428	1.2000	13.95
18	LRSRTTEVM	441	1.2000	13.95
19	VLTHESAPL	464	1.1000	12.79
20	IFIFATTEP	149	0.9000	10.47
21	MRALLARIC	181	0.8000	9.30

22	VVGQEHVTA	14	0.7800	9.07
23	VVELDAASH	88	0.7800	9.07
24	LIVLQSVPD	291	0.7800	9.07
25	YRPASFAEV	6	0.7000	8.14
26	FGAIESVID	264	0.6800	7.91
27	IVEEPPEHL	140	0.6000	6.98
28	VGQEHVTAP	15	0.5000	5.81
29	VLQSVPDAA	293	0.5000	5.81
30	VRALEDNTL	455	0.5000	5.81
31	LDMSIPAPQ	382	0.4000	4.65
32	MLAGATVRA	449	0.3800	4.42
33	VELDAASHG	89	0.3000	3.49
34	FATTEPEKV	152	0.2000	2.33
35	VTYTRALGL	231	0.2000	2.33
36	LLPSASDAE	360	0.1000	1.16
37	VLAEALKDA	484	0.1000	1.16
38	LIFIFATTE	148	-0.1000	0
39	VVDDAVYPL	195	-0.1000	0
40	LIDDAVDAL	247	-0.2000	0
41	MRGATAPRL	342	-0.3000	0
42	LQNELGARR	565	-0.3000	0
43	YRKYRPASF	3	-0.4000	0
44	VERIETRLD	375	-0.4000	0
45	IVDEAHMVT	122	-0.5000	0
46	FATDLLERF	280	-0.5000	0
47	VVCARLLLP	354	-0.6000	0
48	VCESCVSLA	71	-0.7000	0
49	MVTTAGFNA	128	-0.7000	0
50	LSVLDQLLA	216	-0.8000	0
51	LLLPSASDA	359	-0.8000	0
52	LPTIRSRTH	161	-0.8200	0
53	LQSVPDAAS	294	-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	VTYTRALGL	231	6.8000	58.62
2	LGVTDVALI	240	4.9000	42.24
3	FRLLPPRTM	173	4.6000	39.66
4	MRGATAPRL	342	4.6000	39.66
5	LEVVCARLL	352	4.6000	39.66
6	VLTHESAPL	464	4.1000	35.34
7	MVTTAGFNA	128	4.0000	34.48
8	FATTEPEKV	152	3.8000	32.76
9	YRPASFAEV	6	3.7000	31.90
10	LLGVTDVAL	239	3.6000	31.03
11	YLFSGPRGC	37	3.5000	30.17
12	LQRVERIET	372	3.5000	30.17
13	VTAPLSVAL	20	3.4000	29.31
14	VVDDAVYPL	195	3.4000	29.31
15	LAGATVRAL	450	3.4000	29.31
16	VQSRYRVFI	114	3.2000	27.59
17	LRSRTTEVM	441	3.1200	26.90
18	LLEVVCARL	351	3.1000	26.72
19	VTTAGFNAL	129	3.0000	25.86
20	YRKYRPASF	3	2.9000	25.00
21	FIVDEAHMV	121	2.9000	25.00
22	LGLLGVTDV	237	2.7000	23.28
23	VRALEDNTL	455	2.7000	23.28
24	LIFIFATTE	148	2.6000	22.41
25	FGAIESVID	264	2.6000	22.41
26	FIFATTEPE	150	2.4200	20.86
27	LAACDAAAL	255	2.4000	20.69
28	IVEEPPEHL	140	2.3000	19.83
29	VVQAGLGEM	334	2.2000	18.97
30	FRDLIVLQS	288	2.1000	18.10
31	YAEVVQAGL	331	2.0000	17.24

32	VVCARLLLP	354	1.8000	15.52
33	IFIFATTEP	149	1.7200	14.83
34	YAPVQSRYR	111	1.7000	14.66
35	YRVFIVDEA	118	1.7000	14.66
36	VFIVDEAHM	120	1.7000	14.66
37	YTRALGLLG	233	1.7000	14.66
38	LERFRDLIV	285	1.7000	14.66
39	VAAVRSMWP	425	1.7000	14.66
40	MSIPAPQAV	384	1.6000	13.79
41	VLPTIRSRT	160	1.4000	12.07
42	LFGAIESVI	263	1.3000	11.21
43	IGRATLTRY	323	1.3000	11.21
44	VMLAGATVR	448	1.2000	10.34
45	LAPNAPGSI	78	1.1000	9.48
46	MRALLARIC	181	1.1000	9.48
47	FNALLKIVE	134	1.0000	8.62
48	LPPRTMRAL	176	1.0000	8.62
49	VVVDDAVYP	194	1.0000	8.62
50	LLPPRTMRA	175	0.8200	7.07
51	LIVLQSVPD	291	0.8000	6.90
52	LLPSASDAE	360	0.8000	6.90
53	LAPTPASSE	414	0.8000	6.90
54	LVLTHESAP	463	0.8000	6.90
55	LPTIRSRTH	161	0.7000	6.03
56	IETRLDMSI	378	0.7000	6.03
57	VVGQEHVTA	14	0.6000	5.17

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	VTYTRALGL	231	6.8000	58.62
2	LGVTDVALI	240	4.9000	42.24
3	FRLLPPRTM	173	4.6000	39.66

4	MRGATAPRL	342	4.6000	39.66
5	LEVVCARLL	352	4.6000	39.66
6	VLTHESAPL	464	4.1000	35.34
7	MVTTAGFNA	128	4.0000	34.48
8	FATTEPEKV	152	3.8000	32.76
9	YRPASFAEV	6	3.7000	31.90
10	LLGVTDVAL	239	3.6000	31.03
11	YLFSGPRGC	37	3.5000	30.17
12	LQRVERIET	372	3.5000	30.17
13	VTAPLSVAL	20	3.4000	29.31
14	VVDDAVYPL	195	3.4000	29.31
15	LAGATVRAL	450	3.4000	29.31
16	VQSRYRVFI	114	3.2000	27.59
17	LRSRTTEVM	441	3.1200	26.90
18	LLEVVCARL	351	3.1000	26.72
19	VTTAGFNAL	129	3.0000	25.86
20	YRKYRPASF	3	2.9000	25.00
21	FIVDEAHMV	121	2.9000	25.00
22	LGLLGVTDV	237	2.7000	23.28
23	VRALEDNTL	455	2.7000	23.28
24	LIFIFATTE	148	2.6000	22.41
25	FGAIESVID	264	2.6000	22.41
26	FIFATTEPE	150	2.4200	20.86
27	LAACDAAAL	255	2.4000	20.69
28	IVEEPPEHL	140	2.3000	19.83
29	VVQAGLGEM	334	2.2000	18.97
30	FRDLIVLQS	288	2.1000	18.10
31	YAEVVQAGL	331	2.0000	17.24
32	VVCARLLLP	354	1.8000	15.52
33	IFIFATTEP	149	1.7200	14.83
34	YAPVQSRYR	111	1.7000	14.66
35	YRVFIVDEA	118	1.7000	14.66
36	VFIVDEAHM	120	1.7000	14.66
37	YTRALGLLG	233	1.7000	14.66

38	LERFRDLIV	285	1.7000	14.66
39	VAAVRSMWP	425	1.7000	14.66
40	MSIPAPQAV	384	1.6000	13.79
41	VLPTIRSRT	160	1.4000	12.07
42	LFGAIESVI	263	1.3000	11.21
43	IGRATLTRY	323	1.3000	11.21
44	VMLAGATVR	448	1.2000	10.34
45	LAPNAPGSI	78	1.1000	9.48
46	MRALLARIC	181	1.1000	9.48
47	FNALLKIVE	134	1.0000	8.62
48	LPPRTMRAL	176	1.0000	8.62
49	VVVDDAVYP	194	1.0000	8.62
50	LLPPRTMRA	175	0.8200	7.07
51	LIVLQSVPD	291	0.8000	6.90
52	LLPSASDAE	360	0.8000	6.90
53	LAPTPASSE	414	0.8000	6.90
54	LVLTHESAP	463	0.8000	6.90
55	LPTIRSRTH	161	0.7000	6.03
56	IETRLDMSI	378	0.7000	6.03
57	VVGQEHVTA	14	0.6000	5.17

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	YRKYRPASF	3	4.8000	55.81
2	FRLLPPRTM	173	4.5000	52.33
3	LVIRAGGGS	203	4.4000	51.16
4	VRLRSRTTE	439	4.4000	51.16
5	VRDKVRLRS	435	3.6000	41.86
6	LYRKYRPAS	2	3.4000	39.53
7	FNALLKIVE	134	3.3000	38.37
8	FRDLIVLQS	288	3.2000	37.21
9	LRSRTTEVM	441	2.8000	32.56

10	VNWRVRCET	495	2.8000	32.56
11	VQSRYRVFI	114	2.5000	29.07
12	WRVRCETGE	497	2.5000	29.07
13	YPLVIRAGG	201	2.1000	24.42
14	YRVFIVDEA	118	2.0000	23.26
15	VVELDAASH	88	1.9000	22.09
16	VCARLLLPS	355	1.9000	22.09
17	IRSRTHHYP	164	1.8000	20.93
18	FIFATTEPE	150	1.6000	18.60
19	LLQRVERIE	371	1.6000	18.60
20	VNPAPTANS	525	1.6000	18.60
21	MALYRKYRP	0	1.5000	17.44
22	VVQAGLGEM	334	1.5000	17.44
23	MRALLARIC	181	1.3000	15.12
24	VYPLVIRAG	200	1.3000	15.12
25	VERIETRLD	375	1.3000	15.12
26	ILARSLNCA	53	1.2000	13.95
27	LLARICEQE	184	1.2000	13.95
28	LIVLQSVPD	291	1.1000	12.79
29	IVLQSVPDA	292	1.1000	12.79
30	LQRVERIET	372	1.1000	12.79
31	VFIVDEAHM	120	0.9000	10.47
32	YRPASFAEV	6	0.7000	8.14
33	YLFSGPRGC	37	0.7000	8.14
34	LTRYAEVVQ	328	0.7000	8.14
35	LKIVEEPPE	138	0.6000	6.98
36	YPFRLLPPR	171	0.6000	6.98
37	FGAIESVID	264	0.6000	6.98
38	MRGATAPRL	342	0.2000	2.33
39	LLLEVVCAR	350	0.2000	2.33
40	VLAPTPASS	413	0.2000	2.33
41	LIFIFATTE	148	0.1000	1.16
42	LGVTDVALI	240	0.1000	1.16
43	VVCARLLLP	354	0.1000	1.16

44	LGARRIDNA	569	0.1000	1.16
45	LDMSIPAPQ	382	-0.1000	0
46	VRSMWPTVR	428	-0.1000	0
47	LGVNWRVRC	493	-0.1000	0
48	LFSGPRGCG	38	-0.2000	0
49	LLPPRTMRA	175	-0.2000	0
50	LAGATVRAL	450	-0.2000	0
51	INHAYLFSG	33	-0.4000	0
52	LPPRTMRAL	176	-0.4000	0
53	LGLLGVTDV	237	-0.4000	0
54	LLERFRDLI	284	-0.4000	0
55	LARSLNCAQ	54	-0.6000	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	LVIRAGGGS	203	4.4000	55.00
2	YRKYRPASF	3	3.9000	48.75
3	VRDKVRLRS	435	3.6000	45.00
4	LYRKYRPAS	2	3.4000	42.50
5	FRLLPPRTM	173	3.4000	42.50
6	FRDLIVLQS	288	3.2000	40.00
7	VQSRYRVFI	114	2.3000	28.75
8	YRVFIVDEA	118	2.0000	25.00
9	VCARLLLPS	355	1.9000	23.75
10	VNWRVRCET	495	1.9000	23.75
11	LRSRTTEVM	441	1.7000	21.25
12	VNPAPTANS	525	1.6000	20.00
13	IRSRTHHYP	164	1.4000	17.50
14	VRLRSRTTE	439	1.4000	17.50
15	MRALLARIC	181	1.3000	16.25
16	ILARSLNCA	53	1.2000	15.00
17	MALYRKYRP	0	1.1000	13.75

18	IVLQSVPDA	292	1.1000	13.75
19	YPLVIRAGG	201	0.8000	10.00
20	YLFSGPRGC	37	0.7000	8.75
21	VVELDAASH	88	0.6800	8.50
22	YPFRLLPPR	171	0.6000	7.50
23	YRPASFAEV	6	0.4000	5.00
24	VVQAGLGEM	334	0.4000	5.00
25	FNALLKIVE	134	0.3000	3.75
26	LLLEVVCAR	350	0.2000	2.50
27	LQRVERIET	372	0.2000	2.50
28	VLAPTPASS	413	0.2000	2.50
29	LGARRIDNA	569	0.1000	1.25
30	LGVTDVALI	240	-0.1000	0
31	LTRYAEVVQ	328	-0.1000	0
32	VRSMWPTVR	428	-0.1000	0
33	LGVNWRVRC	493	-0.1000	0
34	VFIVDEAHM	120	-0.2000	0
35	LLPPRTMRA	175	-0.2000	0
36	VVCARLLLP	354	-0.3000	0
37	WRVRCETGE	497	-0.5000	0
38	LLERFRDLI	284	-0.6000	0
39	LSVLDQLLA	216	-0.7000	0
40	LGLLGVTDV	237	-0.7000	0
41	MRGATAPRL	342	-0.8000	0
42	VVGQEHVTA	14	-0.9000	0
43	LDMSIPAPQ	382	-0.9000	0
44	LAPNAPGSI	78	-1.0000	0
45	FIVDEAHMV	121	-1.0000	0
46	LQSVPDAAS	294	-1.0000	0
47	LGEMRGATA	339	-1.0000	0
48	YAPVQSRYR	111	-1.1000	0
49	IFIFATTEP	149	-1.1000	0
50	LAGATVRAL	450	-1.2000	0
51	YTRALGLLG	233	-1.3000	0

52	LLLPSASDA	359	-1.3000	0
53	MLAGATVRA	449	-1.3000	0
54	LLQNELGAR	564	-1.3000	0
55	LARSLNCAQ	54	-1.4000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVIRAGGGS	203	5.4000	67.50
2	VRDKVRLRS	435	4.6000	57.50
3	LYRKYRPAS	2	4.4000	55.00
4	VQSRYRVFI	114	3.3000	41.25
5	YRKYRPASF	3	2.9000	36.25
6	VCARLLLPS	355	2.9000	36.25
7	VNWRVRCET	495	2.9000	36.25
8	LRSRTTEVM	441	2.7000	33.75
9	VNPAPTANS	525	2.6000	32.50
10	IRSRTHHYP	164	2.4000	30.00
11	FRLLPPRTM	173	2.4000	30.00
12	VRLRSRTTE	439	2.4000	30.00
13	MRALLARIC	181	2.3000	28.75
14	ILARSLNCA	53	2.2000	27.50
15	FRDLIVLQS	288	2.2000	27.50
16	MALYRKYRP	0	2.1000	26.25
17	IVLQSVPDA	292	2.1000	26.25
18	VVELDAASH	88	1.6800	21.00
19	VVQAGLGEM	334	1.4000	17.50
20	LLLEVVCAR	350	1.2000	15.00
21	LQRVERIET	372	1.2000	15.00
22	VLAPTPASS	413	1.2000	15.00
23	LGARRIDNA	569	1.1000	13.75
24	YRVFIVDEA	118	1.0000	12.50
25	VYPLVIRAG	200	1.0000	12.50

26	LGVTDVALI	240	0.9000	11.25
27	LTRYAEVVQ	328	0.9000	11.25
28	VRSMWPTVR	428	0.9000	11.25
29	LGVNWRVRC	493	0.9000	11.25
30	VFIVDEAHM	120	0.8000	10.00
31	LLPPRTMRA	175	0.8000	10.00
32	VVCARLLLP	354	0.7000	8.75
33	LLERFRDLI	284	0.4000	5.00
34	LSVLDQLLA	216	0.3000	3.75
35	LGLLGVTDV	237	0.3000	3.75
36	MRGATAPRL	342	0.2000	2.50
37	VVGQEHVTA	14	0.1000	1.25
38	LDMSIPAPQ	382	0.1000	1.25
39	IFIFATTEP	149	-0.1000	0
40	YPLVIRAGG	201	-0.2000	0
41	LAGATVRAL	450	-0.2000	0
42	YLFSGPRGC	37	-0.3000	0
43	LLLPSASDA	359	-0.3000	0
44	MLAGATVRA	449	-0.3000	0
45	LLQNELGAR	564	-0.3000	0
46	LARSLNCAQ	54	-0.4000	0
47	YPFRLLPPR	171	-0.4000	0
48	LPPRTMRAL	176	-0.4000	0
49	LLQRVERIE	371	-0.4000	0
50	VERIETRLD	375	-0.4000	0
51	LFSGPRGCG	38	-0.5000	0
52	MVTTAGFNA	128	-0.5000	0
53	LARRLSEQR	472	-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	LVIRAGGGS	203	5.4000	62.79

2	VRLRSRTTE	439	5.4000	62.79
3	VRDKVRLRS	435	4.6000	53.49
4	LYRKYRPAS	2	4.4000	51.16
5	YRKYRPASF	3	3.8000	44.19
6	LRSRTTEVM	441	3.8000	44.19
7	VNWRVRCET	495	3.8000	44.19
8	VQSRYRVFI	114	3.5000	40.70
9	FRLLPPRTM	173	3.5000	40.70
10	VVELDAASH	88	2.9000	33.72
11	VCARLLLPS	355	2.9000	33.72
12	IRSRTHHYP	164	2.8000	32.56
13	LLQRVERIE	371	2.6000	30.23
14	VNPAPTANS	525	2.6000	30.23
15	MALYRKYRP	0	2.5000	29.07
16	VVQAGLGEM	334	2.5000	29.07
17	FNALLKIVE	134	2.3000	26.74
18	MRALLARIC	181	2.3000	26.74
19	VYPLVIRAG	200	2.3000	26.74
20	VERIETRLD	375	2.3000	26.74
21	ILARSLNCA	53	2.2000	25.58
22	LLARICEQE	184	2.2000	25.58
23	FRDLIVLQS	288	2.2000	25.58
24	LIVLQSVPD	291	2.1000	24.42
25	IVLQSVPDA	292	2.1000	24.42
26	LQRVERIET	372	2.1000	24.42
27	VFIVDEAHM	120	1.9000	22.09
28	LTRYAEVVQ	328	1.7000	19.77
29	LKIVEEPPE	138	1.6000	18.60
30	WRVRCETGE	497	1.5000	17.44
31	MRGATAPRL	342	1.2000	13.95
32	LLLEVVCAR	350	1.2000	13.95
33	VLAPTPASS	413	1.2000	13.95
34	LIFIFATTE	148	1.1000	12.79
35	YPLVIRAGG	201	1.1000	12.79

36	LGVTDVALI	240	1.1000	12.79
37	VVCARLLLP	354	1.1000	12.79
38	LGARRIDNA	569	1.1000	12.79
39	YRVFIVDEA	118	1.0000	11.63
40	LDMSIPAPQ	382	0.9000	10.47
41	VRSMWPTVR	428	0.9000	10.47
42	LGVNWRVRC	493	0.9000	10.47
43	LFSGPRGCG	38	0.8000	9.30
44	LLPPRTMRA	175	0.8000	9.30
45	LAGATVRAL	450	0.8000	9.30
46	INHAYLFSG	33	0.6000	6.98
47	FIFATTEPE	150	0.6000	6.98
48	LPPRTMRAL	176	0.6000	6.98
49	LGLLGVTDV	237	0.6000	6.98
50	LLERFRDLI	284	0.6000	6.98
51	LARSLNCAQ	54	0.4000	4.65
52	VSLAPNAPG	76	0.4000	4.65
53	LPTIRSRTH	161	0.4000	4.65
54	IFIFATTEP	149	0.3000	3.49
55	LSVLDQLLA	216	0.3000	3.49
56	LEVVCARLL	352	0.3000	3.49
57	VALELLQNE	560	0.3000	3.49

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	VRDKVRLRS	435	4.2000	48.28
2	VRLRSRTTE	439	4.2000	48.28
3	YRKYRPASF	3	3.9000	44.83
4	FRDLIVLQS	288	3.8000	43.68
5	LVIRAGGGS	203	3.7000	42.53
6	LYRKYRPAS	2	3.6000	41.38
7	LRSRTTEVM	441	3.4000	39.08

8	VQSRYRVFI	114	3.3000	37.93
9	ILARSLNCA	53	3.2000	36.78
10	YRVFIVDEA	118	3.2000	36.78
11	FRLLPPRTM	173	3.1000	35.63
12	VRSMWPTVR	428	2.7000	31.03
13	VCARLLLPS	355	2.5000	28.74
14	WRVRCETGE	497	2.3000	26.44
15	LGLLGVTDV	237	2.1000	24.14
16	MALYRKYRP	0	2.0000	22.99
17	IRSRTHHYP	164	1.9000	21.84
18	VNWRVRCET	495	1.9000	21.84
19	IFIFATTEP	149	1.7000	19.54
20	VNPAPTANS	525	1.6000	18.39
21	IVLQSVPDA	292	1.3000	14.94
22	LGARRIDNA	569	1.3000	14.94
23	FNALLKIVE	134	1.1800	13.56
24	LQRVERIET	372	1.0800	12.41
25	MRALLARIC	181	1.0000	11.49
26	LTRYAEVVQ	328	0.9000	10.34
27	LGVNWRVRC	493	0.9000	10.34
28	YPFRLLPPR	171	0.8000	9.20
29	LLPPRTMRA	175	0.8000	9.20
30	YPLVIRAGG	201	0.8000	9.20
31	VVELDAASH	88	0.6800	7.82
32	LLERFRDLI	284	0.6000	6.90
33	LLLPSASDA	359	0.5000	5.75
34	VMLAGATVR	448	0.5000	5.75
35	YRPASFAEV	6	0.4000	4.60
36	YLFSGPRGC	37	0.4000	4.60
37	FIFATTEPE	150	0.3000	3.45
38	VVCARLLLP	354	0.3000	3.45
39	LLLEVVCAR	350	0.2000	2.30
40	VLAPTPASS	413	0.2000	2.30
41	LARRLSEQR	472	0.2000	2.30

42	VVGQEHVTA	14	0.1000	1.15
43	LIFIFATTE	148	-0.1000	0
44	LLARICEQE	184	-0.1000	0
45	LSVLDQLLA	216	-0.1000	0
46	LGVTDVALI	240	-0.1000	0
47	VFIVDEAHM	120	-0.2000	0
48	IGRATLTRY	323	-0.2000	0
49	VYPLVIRAG	200	-0.3000	0
50	VVQAGLGEM	334	-0.3000	0
51	MLAGATVRA	449	-0.3000	0
52	VLPTIRSRT	160	-0.4000	0
53	FIVDEAHMV	121	-0.5000	0
54	LIVLQSVPD	291	-0.6000	0
55	MRGATAPRL	342	-0.6000	0
56	IETRLDMSI	378	-0.6000	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	VRLRSRTTE	439	5.5000	54.46
2	VRDKVRLRS	435	5.4000	53.47
3	FRDLIVLQS	288	5.0000	49.50
4	FNALLKIVE	134	4.9000	48.51
5	YRKYRPASF	3	4.8000	47.52
6	FRLLPPRTM	173	4.7000	46.53
7	LYRKYRPAS	2	4.5500	45.05
8	LVIRAGGGS	203	4.5000	44.55
9	LRSRTTEVM	441	3.9000	38.61
10	VCARLLLPS	355	3.7000	36.63
11	WRVRCETGE	497	3.6000	35.64
12	VQSRYRVFI	114	3.0000	29.70
13	VNWRVRCET	495	2.8000	27.72
14	FIFATTEPE	150	2.7000	26.73

15	LQRVERIET	372	2.7000	26.73
16	IRSRTHHYP	164	2.5000	24.75
17	LLARICEQE	184	2.3000	22.77
18	IVLQSVPDA	292	2.2500	22.28
19	MALYRKYRP	0	2.2000	21.78
20	YPLVIRAGG	201	2.1000	20.79
21	VVELDAASH	88	1.9000	18.81
22	VVCARLLLP	354	1.9000	18.81
23	YTRALGLLG	233	1.8000	17.82
24	LLQRVERIE	371	1.8000	17.82
25	LKIVEEPPE	138	1.7500	17.33
26	YPFRLLPPR	171	1.7500	17.33
27	YRVFIVDEA	118	1.7000	16.83
28	LIVLQSVPD	291	1.6000	15.84
29	VVQAGLGEM	334	1.6000	15.84
30	VNPAPTANS	525	1.6000	15.84
31	ILARSLNCA	53	1.5000	14.85
32	MRALLARIC	181	1.5000	14.85
33	VYPLVIRAG	200	1.5000	14.85
34	VERIETRLD	375	1.5000	14.85
35	LLPPRTMRA	175	1.4000	13.86
36	MRGATAPRL	342	1.3500	13.37
37	LIFIFATTE	148	1.2000	11.88
38	LTRYAEVVQ	328	1.2000	11.88
39	LSVLDQLLA	216	1.1000	10.89
40	FGAIESVID	264	1.1000	10.89
41	VRSMWPTVR	428	1.0000	9.90
42	YLFSGPRGC	37	0.9000	8.91
43	VFIVDEAHM	120	0.9000	8.91
44	YRPASFAEV	6	0.7000	6.93
45	LGLLGVTDV	237	0.7000	6.93
46	IFIFATTEP	149	0.4000	3.96
47	LGVNWRVRC	493	0.4000	3.96
48	VTYTRALGL	231	0.3000	2.97

49	LLLEVVCAR	350	0.2000	1.98
50	IETRLDMSI	378	0.2000	1.98
51	VLAPTPASS	413	0.2000	1.98
52	INHAYLFSG	33	0.1000	0.99
53	LGVTDVALI	240	0.1000	0.99

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	FRDLIVLQS	288	5.4000	65.06
2	FRLLPPRTM	173	4.0000	48.19
3	IVLQSVPDA	292	2.8500	34.34
4	VRDKVRLRS	435	2.6000	31.33
5	FNALLKIVE	134	2.3000	27.71
6	MRALLARIC	181	1.9000	22.89
7	LQRVERIET	372	1.9000	22.89
8	LYRKYRPAS	2	1.7500	21.08
9	YRVFIVDEA	118	1.6000	19.28
10	VNPAPTANS	525	1.6000	19.28
11	LVIRAGGGS	203	1.5000	18.07
12	LSVLDQLLA	216	1.5000	18.07
13	VVCARLLLP	354	1.5000	18.07
14	YLFSGPRGC	37	1.2000	14.46
15	VVELDAASH	88	1.0800	13.01
16	YRKYRPASF	3	1.0000	12.05
17	YPLVIRAGG	201	0.9000	10.84
18	LGLLGVTDV	237	0.8000	9.64
19	LLPPRTMRA	175	0.7000	8.43
20	VCARLLLPS	355	0.7000	8.43
21	VYPLVIRAG	200	0.6000	7.23
22	VRSMWPTVR	428	0.6000	7.23
23	YTRALGLLG	233	0.5000	6.02
24	VVQAGLGEM	334	0.5000	6.02

25	YRPASFAEV	6	0.4000	4.82
26	LGVNWRVRC	493	0.4000	4.82
27	MRGATAPRL	342	0.3500	4.22
28	LGVTDVALI	240	0.3000	3.61
29	VVGQEHVTA	14	0.2000	2.41
30	VFIVDEAHM	120	-0.1000	0
31	IFIFATTEP	149	-0.1000	0
32	VQSRYRVFI	114	-0.2000	0
33	LRSRTTEVM	441	-0.2000	0
34	FIFATTEPE	150	-0.3000	0
35	VTYTRALGL	231	-0.3000	0
36	LLLEVVCAR	350	-0.5000	0
37	VLAPTPASS	413	-0.5000	0
38	VRLRSRTTE	439	-0.5000	0
39	MVTTAGFNA	128	-0.6000	0
40	VERIETRLD	375	-0.6000	0
41	LDMSIPAPQ	382	-0.6000	0
42	LIVLQSVPD	291	-0.7000	0
43	VAAVRSMWP	425	-0.7000	0
44	YAPVQSRYR	111	-0.8000	0
45	LAPNAPGSI	78	-0.9000	0
46	IRSRTHHYP	164	-0.9000	0
47	LQSVPDAAS	294	-0.9000	0
48	LNCAQGPTA	58	-0.9500	0
49	FIVDEAHMV	121	-1.0000	0
50	FGAIESVID	264	-1.0000	0
51	LAGATVRAL	450	-1.0000	0
52	LPTIRSRTH	161	-1.0200	0
53	MALYRKYRP	0	-1.1000	0
54	LARSLNCAQ	54	-1.1000	0
55	VNWRVRCET	495	-1.1000	0
56	LKIVEEPPE	138	-1.1500	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	IVLQSVPDA	292	4.4000	52.38
2	FRLLPPRTM	173	3.9000	46.43
3	MRALLARIC	181	3.8000	45.24
4	VRDKVRLRS	435	3.8000	45.24
5	LYRKYRPAS	2	3.6000	42.86
6	VVGQEHVTA	14	2.7000	32.14
7	FRDLIVLQS	288	2.6000	30.95
8	VNPAPTANS	525	2.6000	30.95
9	VYPLVIRAG	200	2.5000	29.76
10	LVIRAGGGS	203	2.3000	27.38
11	VQSRYRVFI	114	2.2000	26.19
12	YRVFIVDEA	118	2.2000	26.19
13	LRSRTTEVM	441	2.0000	23.81
14	LGVNWRVRC	493	2.0000	23.81
15	YLFSGPRGC	37	1.9000	22.62
16	MREQAARIG	316	1.8000	21.43
17	VRSMWPTVR	428	1.8000	21.43
18	VRLRSRTTE	439	1.8000	21.43
19	IFIFATTEP	149	1.7000	20.24
20	LAGATVRAL	450	1.6000	19.05
21	ILARSLNCA	53	1.5000	17.86
22	IRSRTHHYP	164	1.5000	17.86
23	LGLLGVTDV	237	1.5000	17.86
24	VCARLLLPS	355	1.5000	17.86
25	VVCARLLLP	354	1.4000	16.67
26	VLTHESAPL	464	1.4000	16.67
27	VVELDAASH	88	1.3800	16.43
28	MALYRKYRP	0	1.2000	14.29
29	YRKYRPASF	3	1.1000	13.10
30	LLLEVVCAR	350	1.1000	13.10
31	MVTTAGFNA	128	0.9000	10.71

32	MRGATAPRL	342	0.9000	10.71
33	INHAYLFSG	33	0.8000	9.52
34	LGVTDVALI	240	0.8000	9.52
35	VNWRVRCET	495	0.8000	9.52
36	LSVLDQLLA	216	0.7000	8.33
37	VLAPTPASS	413	0.7000	8.33
38	LLPPRTMRA	175	0.6000	7.14
39	VLDQLLAGA	218	0.5000	5.95
40	VERIETRLD	375	0.5000	5.95
41	LDMSIPAPQ	382	0.5000	5.95
42	VVQAGLGEM	334	0.4000	4.76
43	LQRVERIET	372	0.3000	3.57
44	VMLAGATVR	448	0.2000	2.38
45	MLAGATVRA	449	0.2000	2.38
46	LIVLQSVPD	291	0.1000	1.19
47	LTRYAEVVQ	328	0.1000	1.19
48	VLAEALKDA	484	0.1000	1.19
49	LPTIRSRTH	161	0.0800	0.95
50	LEVVCARLL	352	-0.1000	0
51	LGARRIDNA	569	-0.1000	0
52	VVVDDAVYP	194	-0.2000	0
53	LNCAQGPTA	58	-0.4000	0
54	VFIVDEAHM	120	-0.4000	0
55	LLLPSASDA	359	-0.4000	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	FRDLIVLQS	288	4.4000	53.01
2	IVLQSVPDA	292	3.8500	46.39
3	VRDKVRLRS	435	3.6000	43.37
4	FRLLPPRTM	173	3.0000	36.14
5	MRALLARIC	181	2.9000	34.94

6	LQRVERIET	372	2.9000	34.94
7	LYRKYRPAS	2	2.7500	33.13
8	VNPAPTANS	525	2.6000	31.33
9	LVIRAGGGS	203	2.5000	30.12
10	LSVLDQLLA	216	2.5000	30.12
11	VVCARLLLP	354	2.5000	30.12
12	VVELDAASH	88	2.0800	25.06
13	LGLLGVTDV	237	1.8000	21.69
14	LLPPRTMRA	175	1.7000	20.48
15	VCARLLLPS	355	1.7000	20.48
16	VYPLVIRAG	200	1.6000	19.28
17	VRSMWPTVR	428	1.6000	19.28
18	VVQAGLGEM	334	1.5000	18.07
19	LGVNWRVRC	493	1.4000	16.87
20	MRGATAPRL	342	1.3500	16.27
21	FNALLKIVE	134	1.3000	15.66
22	LGVTDVALI	240	1.3000	15.66
23	VVGQEHVTA	14	1.2000	14.46
24	VFIVDEAHM	120	0.9000	10.84
25	IFIFATTEP	149	0.9000	10.84
26	VQSRYRVFI	114	0.8000	9.64
27	LRSRTTEVM	441	0.8000	9.64
28	VTYTRALGL	231	0.7000	8.43
29	YRVFIVDEA	118	0.6000	7.23
30	LLLEVVCAR	350	0.5000	6.02
31	VLAPTPASS	413	0.5000	6.02
32	VRLRSRTTE	439	0.5000	6.02
33	MVTTAGFNA	128	0.4000	4.82
34	VERIETRLD	375	0.4000	4.82
35	LDMSIPAPQ	382	0.4000	4.82
36	LIVLQSVPD	291	0.3000	3.61
37	VAAVRSMWP	425	0.3000	3.61
38	YLFSGPRGC	37	0.2000	2.41
39	LAPNAPGSI	78	0.1000	1.20

40	IRSRTHHYP	164	0.1000	1.20
41	LQSVPDAAS	294	0.1000	1.20
42	LNCAQGPTA	58	0.0500	0.60
43	LPTIRSRTH	161	-0.0200	0
44	MALYRKYRP	0	-0.1000	0
45	LARSLNCAQ	54	-0.1000	0
46	YPLVIRAGG	201	-0.1000	0
47	VNWRVRCET	495	-0.1000	0
48	LKIVEEPPE	138	-0.1500	0
49	INHAYLFSG	33	-0.2000	0
50	LIFIFATTE	148	-0.2000	0
51	VDALAACDA	252	-0.2000	0
52	VMLAGATVR	448	-0.2000	0
53	LLQNELGAR	564	-0.2000	0
54	LERFRDLIV	285	-0.4000	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	FRDLIVLQS	288	4.4000	53.01
2	IVLQSVPDA	292	3.8500	46.39
3	VRDKVRLRS	435	3.6000	43.37
4	FRLLPPRTM	173	3.0000	36.14
5	MRALLARIC	181	2.9000	34.94
6	LQRVERIET	372	2.9000	34.94
7	LYRKYRPAS	2	2.7500	33.13
8	VNPAPTANS	525	2.6000	31.33
9	LVIRAGGGS	203	2.5000	30.12
10	LSVLDQLLA	216	2.5000	30.12
11	VVCARLLLP	354	2.5000	30.12
12	VVELDAASH	88	2.0800	25.06
13	LGLLGVTDV	237	1.8000	21.69
14	LLPPRTMRA	175	1.7000	20.48

15	VCARLLLPS	355	1.7000	20.48
16	VYPLVIRAG	200	1.6000	19.28
17	VRSMWPTVR	428	1.6000	19.28
18	VVQAGLGEM	334	1.5000	18.07
19	LGVNWRVRC	493	1.4000	16.87
20	MRGATAPRL	342	1.3500	16.27
21	FNALLKIVE	134	1.3000	15.66
22	LGVTDVALI	240	1.3000	15.66
23	VVGQEHVTA	14	1.2000	14.46
24	VFIVDEAHM	120	0.9000	10.84
25	IFIFATTEP	149	0.9000	10.84
26	VQSRYRVFI	114	0.8000	9.64
27	LRSRTTEVM	441	0.8000	9.64
28	VTYTRALGL	231	0.7000	8.43
29	YRVFIVDEA	118	0.6000	7.23
30	LLLEVVCAR	350	0.5000	6.02
31	VLAPTPASS	413	0.5000	6.02
32	VRLRSRTTE	439	0.5000	6.02
33	MVTTAGFNA	128	0.4000	4.82
34	VERIETRLD	375	0.4000	4.82
35	LDMSIPAPQ	382	0.4000	4.82
36	LIVLQSVPD	291	0.3000	3.61
37	VAAVRSMWP	425	0.3000	3.61
38	YLFSGPRGC	37	0.2000	2.41
39	LAPNAPGSI	78	0.1000	1.20
40	IRSRTHHYP	164	0.1000	1.20
41	LQSVPDAAS	294	0.1000	1.20
42	LNCAQGPTA	58	0.0500	0.60
43	LPTIRSRTH	161	-0.0200	0
44	MALYRKYRP	0	-0.1000	0
45	LARSLNCAQ	54	-0.1000	0
46	YPLVIRAGG	201	-0.1000	0
47	VNWRVRCET	495	-0.1000	0
48	LKIVEEPPE	138	-0.1500	0

49	INHAYLFSG	33	-0.2000	0
50	LIFIFATTE	148	-0.2000	0
51	VDALAACDA	252	-0.2000	0
52	VMLAGATVR	448	-0.2000	0
53	LLQNELGAR	564	-0.2000	0
54	LERFRDLIV	285	-0.4000	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	IVLQSVPDA	292	5.0000	54.95
2	VVVDDAVYP	194	3.8000	41.76
3	VVDDAVYPL	195	3.2500	35.71
4	LYRKYRPAS	2	3.0000	32.97
5	LVIRAGGGS	203	2.7000	29.67
6	VNPAPTANS	525	2.6000	28.57
7	MLAGATVRA	449	2.5000	27.47
8	VELDAASHG	89	2.4700	27.14
9	VVGQEHVTA	14	2.4000	26.37
10	LGVNWRVRC	493	2.4000	26.37
11	LLPPRTMRA	175	2.2000	24.18
12	MRGATAPRL	342	2.1000	23.08
13	LQRVERIET	372	2.1000	23.08
14	FRDLIVLQS	288	2.0000	21.98
15	VVQAGLGEM	334	2.0000	21.98
16	LGLLGVTDV	237	1.9000	20.88
17	LDMSIPAPQ	382	1.8000	19.78
18	VRSMWPTVR	428	1.8000	19.78
19	VRDKVRLRS	435	1.8000	19.78
20	LIDDAVDAL	247	1.7000	18.68
21	LFSGPRGCG	38	1.6000	17.58
22	VLQSVPDAA	293	1.6000	17.58
23	LRSRTTEVM	441	1.6000	17.58

24	FIVDEAHMV	121	1.4000	15.38
25	FRLLPPRTM	173	1.4000	15.38
26	VRLRSRTTE	439	1.4000	15.38
27	LARSLNCAQ	54	1.3000	14.29
28	VQSRYRVFI	114	1.3000	14.29
29	YRVFIVDEA	118	1.3000	14.29
30	MRALLARIC	181	1.3000	14.29
31	LLLEVVCAR	350	1.2000	13.19
32	VVCARLLLP	354	1.2000	13.19
33	VLAPTPASS	413	1.2000	13.19
34	YLFSGPRGC	37	1.1000	12.09
35	IRAGGGSPR	205	1.0700	11.76
36	LLLPSASDA	359	1.0700	11.76
37	VMLAGATVR	448	1.0000	10.99
38	VVELDAASH	88	0.9800	10.77
39	LLAGAADTH	222	0.9800	10.77
40	MVTTAGFNA	128	0.9000	9.89
41	LGVTDVALI	240	0.9000	9.89
42	LNCAQGPTA	58	0.8000	8.79
43	LAPNAPGSI	78	0.8000	8.79
44	VCESCVSLA	71	0.7700	8.46
45	INHAYLFSG	33	0.7000	7.69
46	IFIFATTEP	149	0.7000	7.69
47	LIFIFATTE	148	0.6000	6.59
48	VFIVDEAHM	120	0.5000	5.49
49	LLQNELGAR	564	0.5000	5.49
50	VALDAGRIN	26	0.3000	3.30
51	FATDLLERF	280	0.3000	3.30
52	IGRATLTRY	323	0.3000	3.30
53	VRCETGEPA	499	0.3000	3.30
54	LKIVEEPPE	138	0.2000	2.20
55	VLPTIRSRT	160	0.1700	1.87
56	ILARSLNCA	53	0.1100	1.21
57	LSVLDQLLA	216	0.1000	1.10

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	FRLLPPRTM	173	4.9000	58.33
2	FRDLIVLQS	288	3.6000	42.86
3	IVLQSVPDA	292	3.4000	40.48
4	YRVFIVDEA	118	3.2000	38.10
5	YLFSGPRGC	37	2.9000	34.52
6	MRALLARIC	181	2.8000	33.33
7	VRDKVRLRS	435	2.8000	33.33
8	LYRKYRPAS	2	2.6000	30.95
9	YRKYRPASF	3	2.1000	25.00
10	VVGQEHVTA	14	1.7000	20.24
11	VNPAPTANS	525	1.6000	19.05
12	VYPLVIRAG	200	1.5000	17.86
13	LVIRAGGGS	203	1.3000	15.48
14	VQSRYRVFI	114	1.2000	14.29
15	LRSRTTEVM	441	1.0000	11.90
16	LGVNWRVRC	493	1.0000	11.90
17	MREQAARIG	316	0.8000	9.52
18	VRSMWPTVR	428	0.8000	9.52
19	VRLRSRTTE	439	0.8000	9.52
20	IFIFATTEP	149	0.7000	8.33
21	LAGATVRAL	450	0.6000	7.14
22	ILARSLNCA	53	0.5000	5.95
23	IRSRTHHYP	164	0.5000	5.95
24	LGLLGVTDV	237	0.5000	5.95
25	VCARLLLPS	355	0.5000	5.95
26	YRPASFAEV	6	0.4000	4.76
27	VVCARLLLP	354	0.4000	4.76
28	VLTHESAPL	464	0.4000	4.76
29	VVELDAASH	88	0.3800	4.52
30	FNALLKIVE	134	0.3000	3.57

31	MALYRKYRP	0	0.2000	2.38
32	LLLEVVCAR	350	0.1000	1.19
33	MVTTAGFNA	128	-0.1000	0
34	MRGATAPRL	342	-0.1000	0
35	INHAYLFSG	33	-0.2000	0
36	FIVDEAHMV	121	-0.2000	0
37	LGVTDVALI	240	-0.2000	0
38	VNWRVRCET	495	-0.2000	0
39	LSVLDQLLA	216	-0.3000	0
40	VLAPTPASS	413	-0.3000	0
41	LLPPRTMRA	175	-0.4000	0
42	YPLVIRAGG	201	-0.4000	0
43	YAPVQSRYR	111	-0.5000	0
44	VLDQLLAGA	218	-0.5000	0
45	VERIETRLD	375	-0.5000	0
46	LDMSIPAPQ	382	-0.5000	0
47	YTRALGLLG	233	-0.6000	0
48	VVQAGLGEM	334	-0.6000	0
49	LQRVERIET	372	-0.7000	0
50	YPFRLLPPR	171	-0.8000	0
51	VMLAGATVR	448	-0.8000	0
52	MLAGATVRA	449	-0.8000	0
53	LIVLQSVPD	291	-0.9000	0
54	LTRYAEVVQ	328	-0.9000	0
55	VLAEALKDA	484	-0.9000	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	FRLLPPRTM	173	6.4000	72.73
2	YRKYRPASF	3	4.0000	45.45
3	FRDLIVLQS	288	4.0000	45.45
4	IVLQSVPDA	292	3.4000	38.64

5	YRVFIVDEA	118	3.2000	36.36
6	VRDKVRLRS	435	3.2000	36.36
7	LYRKYRPAS	2	3.0000	34.09
8	YLFSGPRGC	37	2.9000	32.95
9	VYPLVIRAG	200	2.9000	32.95
10	MRALLARIC	181	2.8000	31.82
11	LRSRTTEVM	441	2.5000	28.41
12	VRSMWPTVR	428	2.3000	26.14
13	MREQAARIG	316	2.2000	25.00
14	VRLRSRTTE	439	2.2000	25.00
15	VQSRYRVFI	114	2.1000	23.86
16	VNPAPTANS	525	2.0000	22.73
17	VVGQEHVTA	14	1.7000	19.32
18	FNALLKIVE	134	1.7000	19.32
19	IFIFATTEP	149	1.7000	19.32
20	LVIRAGGGS	203	1.7000	19.32
21	LLLEVVCAR	350	1.6000	18.18
22	LAGATVRAL	450	1.5600	17.73
23	IRSRTHHYP	164	1.5000	17.05
24	LGLLGVTDV	237	1.5000	17.05
25	YRPASFAEV	6	1.4000	15.91
26	FIFATTEPE	150	1.4000	15.91
27	VVCARLLLP	354	1.4000	15.91
28	VLTHESAPL	464	1.3600	15.45
29	MALYRKYRP	0	1.2000	13.64
30	INHAYLFSG	33	1.2000	13.64
31	YAPVQSRYR	111	1.0000	11.36
32	YPLVIRAGG	201	1.0000	11.36
33	LGVNWRVRC	493	1.0000	11.36
34	VVQAGLGEM	334	0.9000	10.23
35	VCARLLLPS	355	0.9000	10.23
36	MRGATAPRL	342	0.8600	9.77
37	FIVDEAHMV	121	0.8000	9.09
38	YTRALGLLG	233	0.8000	9.09

39	YPFRLLPPR	171	0.7000	7.95
40	LGVTDVALI	240	0.7000	7.95
41	VMLAGATVR	448	0.7000	7.95
42	VERIETRLD	375	0.6000	6.82
43	ILARSLNCA	53	0.5000	5.68
44	VNWRVRCET	495	0.5000	5.68
45	WRVRCETGE	497	0.3000	3.41
46	LIVLQSVPD	291	0.2000	2.27
47	VFIVDEAHM	120	0.1000	1.14
48	VLAPTPASS	413	0.1000	1.14
49	MVTTAGFNA	128	-0.1000	0
50	LEVVCARLL	352	-0.1400	0
51	VVELDAASH	88	-0.2000	0
52	VVVDDAVYP	194	-0.2000	0
53	IGRATLTRY	323	-0.2000	0
54	LSVLDQLLA	216	-0.3000	0
55	LLQRVERIE	371	-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	IVLQSVPDA	292	4.4000	52.38
2	FRLLPPRTM	173	3.9000	46.43
3	MRALLARIC	181	3.8000	45.24
4	VRDKVRLRS	435	3.8000	45.24
5	LYRKYRPAS	2	3.6000	42.86
6	VVGQEHVTA	14	2.7000	32.14
7	FRDLIVLQS	288	2.6000	30.95
8	VNPAPTANS	525	2.6000	30.95
9	VYPLVIRAG	200	2.5000	29.76
10	LVIRAGGGS	203	2.3000	27.38
11	VQSRYRVFI	114	2.2000	26.19
12	YRVFIVDEA	118	2.2000	26.19

13	LRSRTTEVM	441	2.0000	23.81
14	LGVNWRVRC	493	2.0000	23.81
15	YLFSGPRGC	37	1.9000	22.62
16	MREQAARIG	316	1.8000	21.43
17	VRSMWPTVR	428	1.8000	21.43
18	VRLRSRTTE	439	1.8000	21.43
19	IFIFATTEP	149	1.7000	20.24
20	LAGATVRAL	450	1.6000	19.05
21	ILARSLNCA	53	1.5000	17.86
22	IRSRTHHYP	164	1.5000	17.86
23	LGLLGVTDV	237	1.5000	17.86
24	VCARLLLPS	355	1.5000	17.86
25	VVCARLLLP	354	1.4000	16.67
26	VLTHESAPL	464	1.4000	16.67
27	VVELDAASH	88	1.3800	16.43
28	MALYRKYRP	0	1.2000	14.29
29	YRKYRPASF	3	1.1000	13.10
30	LLLEVVCAR	350	1.1000	13.10
31	MVTTAGFNA	128	0.9000	10.71
32	MRGATAPRL	342	0.9000	10.71
33	INHAYLFSG	33	0.8000	9.52
34	LGVTDVALI	240	0.8000	9.52
35	VNWRVRCET	495	0.8000	9.52
36	LSVLDQLLA	216	0.7000	8.33
37	VLAPTPASS	413	0.7000	8.33
38	LLPPRTMRA	175	0.6000	7.14
39	VLDQLLAGA	218	0.5000	5.95
40	VERIETRLD	375	0.5000	5.95
41	LDMSIPAPQ	382	0.5000	5.95
42	VVQAGLGEM	334	0.4000	4.76
43	LQRVERIET	372	0.3000	3.57
44	VMLAGATVR	448	0.2000	2.38
45	MLAGATVRA	449	0.2000	2.38
46	LIVLQSVPD	291	0.1000	1.19

47	LTRYAEVVQ	328	0.1000	1.19
48	VLAEALKDA	484	0.1000	1.19
49	LPTIRSRTH	161	0.0800	0.95
50	LEVVCARLL	352	-0.1000	0
51	LGARRIDNA	569	-0.1000	0
52	VVVDDAVYP	194	-0.2000	0
53	LNCAQGPTA	58	-0.4000	0
54	VFIVDEAHM	120	-0.4000	0
55	LLLPSASDA	359	-0.4000	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	FRDLIVLQS	288	5.8000	66.67
2	FRLLPPRTM	173	5.5000	63.22
3	FNALLKIVE	134	3.7000	42.53
4	VRDKVRLRS	435	3.0000	34.48
5	YRKYRPASF	3	2.9000	33.33
6	IVLQSVPDA	292	2.8500	32.76
7	LQRVERIET	372	2.6000	29.89
8	VVCARLLLP	354	2.5000	28.74
9	YPLVIRAGG	201	2.3000	26.44
10	LYRKYRPAS	2	2.1500	24.71
11	VRSMWPTVR	428	2.1000	24.14
12	VYPLVIRAG	200	2.0000	22.99
13	VVQAGLGEM	334	2.0000	22.99
14	VNPAPTANS	525	2.0000	22.99
15	MRALLARIC	181	1.9000	21.84
16	LVIRAGGGS	203	1.9000	21.84
17	YTRALGLLG	233	1.9000	21.84
18	LGLLGVTDV	237	1.8000	20.69
19	YRVFIVDEA	118	1.6000	18.39
20	LSVLDQLLA	216	1.5000	17.24

21	YRPASFAEV	6	1.4000	16.09
22	VFIVDEAHM	120	1.4000	16.09
23	MRGATAPRL	342	1.3100	15.06
24	LRSRTTEVM	441	1.3000	14.94
25	YLFSGPRGC	37	1.2000	13.79
26	LGVTDVALI	240	1.2000	13.79
27	FIFATTEPE	150	1.1000	12.64
28	VCARLLLPS	355	1.1000	12.64
29	LLLEVVCAR	350	1.0000	11.49
30	IFIFATTEP	149	0.9000	10.34
31	VRLRSRTTE	439	0.9000	10.34
32	YAPVQSRYR	111	0.7000	8.05
33	VQSRYRVFI	114	0.7000	8.05
34	LLPPRTMRA	175	0.7000	8.05
35	VTYTRALGL	231	0.6600	7.59
36	VVELDAASH	88	0.5000	5.75
37	VERIETRLD	375	0.5000	5.75
38	LIVLQSVPD	291	0.4000	4.60
39	LGVNWRVRC	493	0.4000	4.60
40	VAAVRSMWP	425	0.3000	3.45
41	VMLAGATVR	448	0.3000	3.45
42	LLQNELGAR	564	0.3000	3.45
43	LKIVEEPPE	138	0.2500	2.87
44	YPFRLLPPR	171	0.2500	2.87
45	VVGQEHVTA	14	0.2000	2.30
46	INHAYLFSG	33	0.2000	2.30
47	LIFIFATTE	148	0.2000	2.30
48	IRSRTHHYP	164	0.1000	1.15
49	FGAIESVID	264	0.1000	1.15
50	LAGATVRAL	450	-0.0400	0
51	MALYRKYRP	0	-0.1000	0
52	VLAPTPASS	413	-0.1000	0
53	LELLQNELG	562	-0.3000	0
54	LERFRDLIV	285	-0.4000	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	FRLLPPRTM	173	5.4000	61.36
2	IVLQSVPDA	292	4.4000	50.00
3	VRDKVRLRS	435	4.2000	47.73
4	LYRKYRPAS	2	4.0000	45.45
5	VYPLVIRAG	200	3.9000	44.32
6	MRALLARIC	181	3.8000	43.18
7	LRSRTTEVM	441	3.5000	39.77
8	VRSMWPTVR	428	3.3000	37.50
9	MREQAARIG	316	3.2000	36.36
10	VRLRSRTTE	439	3.2000	36.36
11	VQSRYRVFI	114	3.1000	35.23
12	YRKYRPASF	3	3.0000	34.09
13	FRDLIVLQS	288	3.0000	34.09
14	VNPAPTANS	525	3.0000	34.09
15	VVGQEHVTA	14	2.7000	30.68
16	IFIFATTEP	149	2.7000	30.68
17	LVIRAGGGS	203	2.7000	30.68
18	LLLEVVCAR	350	2.6000	29.55
19	LAGATVRAL	450	2.5600	29.09
20	IRSRTHHYP	164	2.5000	28.41
21	LGLLGVTDV	237	2.5000	28.41
22	VVCARLLLP	354	2.4000	27.27
23	VLTHESAPL	464	2.3600	26.82
24	MALYRKYRP	0	2.2000	25.00
25	INHAYLFSG	33	2.2000	25.00
26	YRVFIVDEA	118	2.2000	25.00
27	LGVNWRVRC	493	2.0000	22.73
28	YLFSGPRGC	37	1.9000	21.59
29	VVQAGLGEM	334	1.9000	21.59
30	VCARLLLPS	355	1.9000	21.59

31	MRGATAPRL	342	1.8600	21.14
32	LGVTDVALI	240	1.7000	19.32
33	VMLAGATVR	448	1.7000	19.32
34	VERIETRLD	375	1.6000	18.18
35	ILARSLNCA	53	1.5000	17.05
36	VNWRVRCET	495	1.5000	17.05
37	LIVLQSVPD	291	1.2000	13.64
38	VFIVDEAHM	120	1.1000	12.50
39	VLAPTPASS	413	1.1000	12.50
40	LQRVERIET	372	1.0000	11.36
41	MVTTAGFNA	128	0.9000	10.23
42	LEVVCARLL	352	0.8600	9.77
43	VVELDAASH	88	0.8000	9.09
44	VVVDDAVYP	194	0.8000	9.09
45	IGRATLTRY	323	0.8000	9.09
46	FNALLKIVE	134	0.7000	7.95
47	LSVLDQLLA	216	0.7000	7.95
48	LLQRVERIE	371	0.7000	7.95
49	LLPPRTMRA	175	0.6000	6.82
50	VSLAPNAPG	76	0.5000	5.68
51	VLDQLLAGA	218	0.5000	5.68
52	YRPASFAEV	6	0.4000	4.55
53	FIFATTEPE	150	0.4000	4.55
54	LQNELGARR	565	0.4000	4.55
55	VVDDAVYPL	195	0.3600	4.09
56	LARRLSEQR	472	0.3000	3.41
57	LELLQNELG	562	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	FRLLPPRTM	173	6.4000	72.73
2	YRKYRPASF	3	4.0000	45.45

3	FRDLIVLQS	288	4.0000	45.45
4	IVLQSVPDA	292	3.4000	38.64
5	YRVFIVDEA	118	3.2000	36.36
6	VRDKVRLRS	435	3.2000	36.36
7	LYRKYRPAS	2	3.0000	34.09
8	YLFSGPRGC	37	2.9000	32.95
9	VYPLVIRAG	200	2.9000	32.95
10	MRALLARIC	181	2.8000	31.82
11	LRSRTTEVM	441	2.5000	28.41
12	VRSMWPTVR	428	2.3000	26.14
13	MREQAARIG	316	2.2000	25.00
14	VRLRSRTTE	439	2.2000	25.00
15	VQSRYRVFI	114	2.1000	23.86
16	VNPAPTANS	525	2.0000	22.73
17	VVGQEHVTA	14	1.7000	19.32
18	FNALLKIVE	134	1.7000	19.32
19	IFIFATTEP	149	1.7000	19.32
20	LVIRAGGGS	203	1.7000	19.32
21	LLLEVVCAR	350	1.6000	18.18
22	LAGATVRAL	450	1.5600	17.73
23	IRSRTHHYP	164	1.5000	17.05
24	LGLLGVTDV	237	1.5000	17.05
25	YRPASFAEV	6	1.4000	15.91
26	FIFATTEPE	150	1.4000	15.91
27	VVCARLLLP	354	1.4000	15.91
28	VLTHESAPL	464	1.3600	15.45
29	MALYRKYRP	0	1.2000	13.64
30	INHAYLFSG	33	1.2000	13.64
31	YAPVQSRYR	111	1.0000	11.36
32	YPLVIRAGG	201	1.0000	11.36
33	LGVNWRVRC	493	1.0000	11.36
34	VVQAGLGEM	334	0.9000	10.23
35	VCARLLLPS	355	0.9000	10.23
36	MRGATAPRL	342	0.8600	9.77

37	FIVDEAHMV	121	0.8000	9.09
38	YTRALGLLG	233	0.8000	9.09
39	YPFRLLPPR	171	0.7000	7.95
40	LGVTDVALI	240	0.7000	7.95
41	VMLAGATVR	448	0.7000	7.95
42	VERIETRLD	375	0.6000	6.82
43	ILARSLNCA	53	0.5000	5.68
44	VNWRVRCET	495	0.5000	5.68
45	WRVRCETGE	497	0.3000	3.41
46	LIVLQSVPD	291	0.2000	2.27
47	VFIVDEAHM	120	0.1000	1.14
48	VLAPTPASS	413	0.1000	1.14
49	MVTTAGFNA	128	-0.1000	0
50	LEVVCARLL	352	-0.1400	0
51	VVELDAASH	88	-0.2000	0
52	VVVDDAVYP	194	-0.2000	0
53	IGRATLTRY	323	-0.2000	0
54	LSVLDQLLA	216	-0.3000	0
55	LLQRVERIE	371	-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	FRLLPPRTM	173	5.0000	55.56
2	VRLRSRTTE	439	4.8000	53.33
3	IVLQSVPDA	292	4.4000	48.89
4	MRALLARIC	181	3.8000	42.22
5	VYPLVIRAG	200	3.8000	42.22
6	VRDKVRLRS	435	3.8000	42.22
7	LYRKYRPAS	2	3.6000	40.00
8	VERIETRLD	375	3.2000	35.56
9	MREQAARIG	316	3.1000	34.44
10	LRSRTTEVM	441	3.1000	34.44

11	LIVLQSVPD	291	2.8000	31.11
12	VVGQEHVTA	14	2.7000	30.00
13	VVELDAASH	88	2.6000	28.89
14	FRDLIVLQS	288	2.6000	28.89
15	LAGATVRAL	450	2.6000	28.89
16	VNPAPTANS	525	2.6000	28.89
17	VQSRYRVFI	114	2.4000	26.67
18	VLTHESAPL	464	2.4000	26.67
19	FNALLKIVE	134	2.3000	25.56
20	LVIRAGGGS	203	2.3000	25.56
21	LLQRVERIE	371	2.3000	25.56
22	YRVFIVDEA	118	2.2000	24.44
23	INHAYLFSG	33	2.1000	23.33
24	IFIFATTEP	149	2.1000	23.33
25	YRKYRPASF	3	2.0000	22.22
26	FIFATTEPE	150	2.0000	22.22
27	LGVNWRVRC	493	2.0000	22.22
28	YLFSGPRGC	37	1.9000	21.11
29	IRSRTHHYP	164	1.9000	21.11
30	MRGATAPRL	342	1.9000	21.11
31	LGLLGVTDV	237	1.8000	20.00
32	VVCARLLLP	354	1.8000	20.00
33	VRSMWPTVR	428	1.8000	20.00
34	LIFIFATTE	148	1.7000	18.89
35	VNWRVRCET	495	1.7000	18.89
36	MALYRKYRP	0	1.6000	17.78
37	ILARSLNCA	53	1.5000	16.67
38	LLARICEQE	184	1.5000	16.67
39	VVQAGLGEM	334	1.5000	16.67
40	VCARLLLPS	355	1.5000	16.67
41	MLAEAGRGD	542	1.4000	15.56
42	LPTIRSRTH	161	1.3000	14.44
43	LDMSIPAPQ	382	1.3000	14.44
44	LQRVERIET	372	1.2000	13.33

45	LKIVEEPPE	138	1.1000	12.22
46	LLLEVVCAR	350	1.1000	12.22
47	LGVTDVALI	240	1.0000	11.11
48	VALELLQNE	560	1.0000	11.11
49	MVTTAGFNA	128	0.9000	10.00
50	LTRYAEVVQ	328	0.9000	10.00
51	LEVVCARLL	352	0.9000	10.00
52	WRVRCETGE	497	0.9000	10.00
53	LARSLNCAQ	54	0.8000	8.89
54	VALDAGRIN	26	0.7000	7.78
55	VFIVDEAHM	120	0.7000	7.78
56	LSVLDQLLA	216	0.7000	7.78
57	VLAPTPASS	413	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	FRDLIVLQS	288	5.8000	66.67
2	FRLLPPRTM	173	5.5000	63.22
3	FNALLKIVE	134	3.7000	42.53
4	VRDKVRLRS	435	3.0000	34.48
5	YRKYRPASF	3	2.9000	33.33
6	IVLQSVPDA	292	2.8500	32.76
7	LQRVERIET	372	2.6000	29.89
8	VVCARLLLP	354	2.5000	28.74
9	YPLVIRAGG	201	2.3000	26.44
10	LYRKYRPAS	2	2.1500	24.71
11	VRSMWPTVR	428	2.1000	24.14
12	VYPLVIRAG	200	2.0000	22.99
13	VVQAGLGEM	334	2.0000	22.99
14	VNPAPTANS	525	2.0000	22.99
15	MRALLARIC	181	1.9000	21.84
16	LVIRAGGGS	203	1.9000	21.84

17	YTRALGLLG	233	1.9000	21.84
18	LGLLGVTDV	237	1.8000	20.69
19	YRVFIVDEA	118	1.6000	18.39
20	LSVLDQLLA	216	1.5000	17.24
21	YRPASFAEV	6	1.4000	16.09
22	VFIVDEAHM	120	1.4000	16.09
23	MRGATAPRL	342	1.3100	15.06
24	LRSRTTEVM	441	1.3000	14.94
25	YLFSGPRGC	37	1.2000	13.79
26	LGVTDVALI	240	1.2000	13.79
27	FIFATTEPE	150	1.1000	12.64
28	VCARLLLPS	355	1.1000	12.64
29	LLLEVVCAR	350	1.0000	11.49
30	IFIFATTEP	149	0.9000	10.34
31	VRLRSRTTE	439	0.9000	10.34
32	YAPVQSRYR	111	0.7000	8.05
33	VQSRYRVFI	114	0.7000	8.05
34	LLPPRTMRA	175	0.7000	8.05
35	VTYTRALGL	231	0.6600	7.59
36	VVELDAASH	88	0.5000	5.75
37	VERIETRLD	375	0.5000	5.75
38	LIVLQSVPD	291	0.4000	4.60
39	LGVNWRVRC	493	0.4000	4.60
40	VAAVRSMWP	425	0.3000	3.45
41	VMLAGATVR	448	0.3000	3.45
42	LLQNELGAR	564	0.3000	3.45
43	LKIVEEPPE	138	0.2500	2.87
44	YPFRLLPPR	171	0.2500	2.87
45	VVGQEHVTA	14	0.2000	2.30
46	INHAYLFSG	33	0.2000	2.30
47	LIFIFATTE	148	0.2000	2.30
48	IRSRTHHYP	164	0.1000	1.15
49	FGAIESVID	264	0.1000	1.15
50	LAGATVRAL	450	-0.0400	0

51	MALYRKYRP	0	-0.1000	0
52	VLAPTPASS	413	-0.1000	0
53	LELLQNELG	562	-0.3000	0
54	LERFRDLIV	285	-0.4000	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	FRLLPPRTM	173	3.8000	55.88
2	FRDLIVLQS	288	3.6000	52.94
3	YRVFIVDEA	118	1.9000	27.94
4	MRALLARIC	181	1.7000	25.00
5	IVLQSVPDA	292	1.7000	25.00
6	VNPAPTANS	525	1.6000	23.53
7	LVIRAGGGS	203	1.4000	20.59
8	VVELDAASH	88	1.0800	15.88
9	YRKYRPASF	3	1.0000	14.71
10	YLFSGPRGC	37	1.0000	14.71
11	YPLVIRAGG	201	0.9000	13.24
12	VRDKVRLRS	435	0.8000	11.76
13	FNALLKIVE	134	0.7000	10.29
14	LYRKYRPAS	2	0.6000	8.82
15	YRPASFAEV	6	0.4000	5.88
16	VYPLVIRAG	200	0.4000	5.88
17	VVQAGLGEM	334	0.4000	5.88
18	LGVTDVALI	240	0.3000	4.41
19	LQRVERIET	372	0.3000	4.41
20	VFIVDEAHM	120	-0.1000	0
21	LGVNWRVRC	493	-0.1000	0
22	VVGQEHVTA	14	-0.3000	0
23	LSVLDQLLA	216	-0.3000	0
24	LGLLGVTDV	237	-0.3000	0
25	VVCARLLLP	354	-0.3000	0

26	LLLEVVCAR	350	-0.5000	0
27	VLAPTPASS	413	-0.5000	0
28	VRSMWPTVR	428	-0.5000	0
29	LDMSIPAPQ	382	-0.6000	0
30	VQSRYRVFI	114	-0.7000	0
31	MRGATAPRL	342	-0.8000	0
32	VERIETRLD	375	-0.8000	0
33	LLPPRTMRA	175	-0.9000	0
34	LQSVPDAAS	294	-0.9000	0
35	LAPNAPGSI	78	-1.0000	0
36	YAPVQSRYR	111	-1.0000	0
37	LARSLNCAQ	54	-1.1000	0
38	MVTTAGFNA	128	-1.1000	0
39	VCARLLLPS	355	-1.1000	0
40	VNWRVRCET	495	-1.1000	0
41	IFIFATTEP	149	-1.2000	0
42	VDALAACDA	252	-1.2000	0
43	LIVLQSVPD	291	-1.2000	0
44	LAGATVRAL	450	-1.2000	0
45	LPTIRSRTH	161	-1.2200	0
46	YTRALGLLG	233	-1.3000	0
47	LRSRTTEVM	441	-1.3000	0
48	LLQNELGAR	564	-1.3000	0
49	FIFATTEPE	150	-1.4000	0
50	LGEMRGATA	339	-1.4000	0
51	VLDQLLAGA	218	-1.5000	0
52	FGAIESVID	264	-1.5000	0
53	IRSRTHHYP	164	-1.6000	0
54	LEVVCARLL	352	-1.6000	0
55	VRLRSRTTE	439	-1.6000	0
56	INHAYLFSG	33	-1.7000	0

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

	2.0	

Rank	Sequence	At Position	Score	% of Highest Score
1	FRDLIVLQS	288	4.4000	53.01
2	IVLQSVPDA	292	3.8500	46.39
3	VRDKVRLRS	435	3.6000	43.37
4	FRLLPPRTM	173	3.0000	36.14
5	MRALLARIC	181	2.9000	34.94
6	LQRVERIET	372	2.9000	34.94
7	LYRKYRPAS	2	2.7500	33.13
8	VNPAPTANS	525	2.6000	31.33
9	LVIRAGGGS	203	2.5000	30.12
10	LSVLDQLLA	216	2.5000	30.12
11	VVCARLLLP	354	2.5000	30.12
12	VVELDAASH	88	2.0800	25.06
13	LGLLGVTDV	237	1.8000	21.69
14	LLPPRTMRA	175	1.7000	20.48
15	VCARLLLPS	355	1.7000	20.48
16	VYPLVIRAG	200	1.6000	19.28
17	VRSMWPTVR	428	1.6000	19.28
18	VVQAGLGEM	334	1.5000	18.07
19	LGVNWRVRC	493	1.4000	16.87
20	MRGATAPRL	342	1.3500	16.27
21	FNALLKIVE	134	1.3000	15.66
22	LGVTDVALI	240	1.3000	15.66
23	VVGQEHVTA	14	1.2000	14.46
24	VFIVDEAHM	120	0.9000	10.84
25	IFIFATTEP	149	0.9000	10.84
26	VQSRYRVFI	114	0.8000	9.64
27	LRSRTTEVM	441	0.8000	9.64
28	VTYTRALGL	231	0.7000	8.43
29	YRVFIVDEA	118	0.6000	7.23
30	LLLEVVCAR	350	0.5000	6.02
31	VLAPTPASS	413	0.5000	6.02
32	VRLRSRTTE	439	0.5000	6.02

33	MVTTAGFNA	128	0.4000	4.82
34	VERIETRLD	375	0.4000	4.82
35	LDMSIPAPQ	382	0.4000	4.82
36	LIVLQSVPD	291	0.3000	3.61
37	VAAVRSMWP	425	0.3000	3.61
38	YLFSGPRGC	37	0.2000	2.41
39	LAPNAPGSI	78	0.1000	1.20
40	IRSRTHHYP	164	0.1000	1.20
41	LQSVPDAAS	294	0.1000	1.20
42	LNCAQGPTA	58	0.0500	0.60
43	LPTIRSRTH	161	-0.0200	0
44	MALYRKYRP	0	-0.1000	0
45	LARSLNCAQ	54	-0.1000	0
46	YPLVIRAGG	201	-0.1000	0
47	VNWRVRCET	495	-0.1000	0
48	LKIVEEPPE	138	-0.1500	0
49	INHAYLFSG	33	-0.2000	0
50	LIFIFATTE	148	-0.2000	0
51	VDALAACDA	252	-0.2000	0
52	VMLAGATVR	448	-0.2000	0
53	LLQNELGAR	564	-0.2000	0
54	LERFRDLIV	285	-0.4000	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	FRDLIVLQS	288	5.4000	60.67
2	FNALLKIVE	134	5.3000	59.55
3	FRLLPPRTM	173	5.1000	57.30
4	IVLQSVPDA	292	2.8500	32.02
5	LQRVERIET	372	2.8000	31.46
6	FIFATTEPE	150	2.7000	30.34
7	VRDKVRLRS	435	2.6000	29.21

8	VRLRSRTTE	439	2.5000	28.09
9	VVELDAASH	88	2.3000	25.84
10	YPLVIRAGG	201	2.2000	24.72
11	VERIETRLD	375	2.1000	23.60
12	LIVLQSVPD	291	2.0000	22.47
13	YRKYRPASF	3	1.9000	21.35
14	MRALLARIC	181	1.9000	21.35
15	VYPLVIRAG	200	1.9000	21.35
16	VVCARLLLP	354	1.9000	21.35
17	LKIVEEPPE	138	1.8500	20.79
18	LIFIFATTE	148	1.8000	20.22
19	YTRALGLLG	233	1.8000	20.22
20	LYRKYRPAS	2	1.7500	19.66
21	FGAIESVID	264	1.7000	19.10
22	YRVFIVDEA	118	1.6000	17.98
23	VVQAGLGEM	334	1.6000	17.98
24	VNPAPTANS	525	1.6000	17.98
25	LVIRAGGGS	203	1.5000	16.85
26	LSVLDQLLA	216	1.5000	16.85
27	MRGATAPRL	342	1.3500	15.17
28	YLFSGPRGC	37	1.2000	13.48
29	LGLLGVTDV	237	1.1000	12.36
30	VFIVDEAHM	120	1.0000	11.24
31	LRSRTTEVM	441	0.9000	10.11
32	YRPASFAEV	6	0.7000	7.87
33	LLPPRTMRA	175	0.7000	7.87
34	VTYTRALGL	231	0.7000	7.87
35	VCARLLLPS	355	0.7000	7.87
36	VRSMWPTVR	428	0.6000	6.74
37	WRVRCETGE	497	0.6000	6.74
38	LGVTDVALI	240	0.5000	5.62
39	LGVNWRVRC	493	0.4000	4.49
40	IFIFATTEP	149	0.3000	3.37
41	VVGQEHVTA	14	0.2000	2.25

42	LPTIRSRTH	161	0.2000	2.25
43	LDMSIPAPQ	382	0.2000	2.25
44	INHAYLFSG	33	0.1000	1.12
45	VTDVALIDD	242	0.1000	1.12
46	VNWRVRCET	495	-0.2000	0
47	LARSLNCAQ	54	-0.3000	0
48	VAAVRSMWP	425	-0.3000	0
49	LEVVCARLL	352	-0.4000	0
50	LELLQNELG	562	-0.4000	0
51	IRSRTHHYP	164	-0.5000	0
52	VALIDDAVD	245	-0.5000	0
53	MREQAARIG	316	-0.5000	0
54	LLLEVVCAR	350	-0.5000	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	IVLQSVPDA	292	4.4000	52.38
2	FRLLPPRTM	173	3.9000	46.43
3	MRALLARIC	181	3.8000	45.24
4	VRDKVRLRS	435	3.8000	45.24
5	LYRKYRPAS	2	3.6000	42.86
6	VVGQEHVTA	14	2.7000	32.14
7	FRDLIVLQS	288	2.6000	30.95
8	VNPAPTANS	525	2.6000	30.95
9	VYPLVIRAG	200	2.5000	29.76
10	LVIRAGGGS	203	2.3000	27.38
11	VQSRYRVFI	114	2.2000	26.19
12	YRVFIVDEA	118	2.2000	26.19
13	LRSRTTEVM	441	2.0000	23.81
14	LGVNWRVRC	493	2.0000	23.81
15	YLFSGPRGC	37	1.9000	22.62
16	MREQAARIG	316	1.8000	21.43

17	VRSMWPTVR	428	1.8000	21.43
18	VRLRSRTTE	439	1.8000	21.43
19	IFIFATTEP	149	1.7000	20.24
20	LAGATVRAL	450	1.6000	19.05
21	ILARSLNCA	53	1.5000	17.86
22	IRSRTHHYP	164	1.5000	17.86
23	LGLLGVTDV	237	1.5000	17.86
24	VCARLLLPS	355	1.5000	17.86
25	VVCARLLLP	354	1.4000	16.67
26	VLTHESAPL	464	1.4000	16.67
27	VVELDAASH	88	1.3800	16.43
28	MALYRKYRP	0	1.2000	14.29
29	YRKYRPASF	3	1.1000	13.10
30	LLLEVVCAR	350	1.1000	13.10
31	MVTTAGFNA	128	0.9000	10.71
32	MRGATAPRL	342	0.9000	10.71
33	INHAYLFSG	33	0.8000	9.52
34	LGVTDVALI	240	0.8000	9.52
35	VNWRVRCET	495	0.8000	9.52
36	LSVLDQLLA	216	0.7000	8.33
37	VLAPTPASS	413	0.7000	8.33
38	LLPPRTMRA	175	0.6000	7.14
39	VLDQLLAGA	218	0.5000	5.95
40	VERIETRLD	375	0.5000	5.95
41	LDMSIPAPQ	382	0.5000	5.95
42	VVQAGLGEM	334	0.4000	4.76
43	LQRVERIET	372	0.3000	3.57
44	VMLAGATVR	448	0.2000	2.38
45	MLAGATVRA	449	0.2000	2.38
46	LIVLQSVPD	291	0.1000	1.19
47	LTRYAEVVQ	328	0.1000	1.19
48	VLAEALKDA	484	0.1000	1.19
49	LPTIRSRTH	161	0.0800	0.95
50	LEVVCARLL	352	-0.1000	0

51	LGARRIDNA	569	-0.1000	0
52	VVVDDAVYP	194	-0.2000	0
53	LNCAQGPTA	58	-0.4000	0
54	VFIVDEAHM	120	-0.4000	0
55	LLLPSASDA	359	-0.4000	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	FRLLPPRTM	173	4.9000	58.33
2	FRDLIVLQS	288	3.6000	42.86
3	IVLQSVPDA	292	3.4000	40.48
4	YRVFIVDEA	118	3.2000	38.10
5	YLFSGPRGC	37	2.9000	34.52
6	MRALLARIC	181	2.8000	33.33
7	VRDKVRLRS	435	2.8000	33.33
8	LYRKYRPAS	2	2.6000	30.95
9	YRKYRPASF	3	2.1000	25.00
10	VVGQEHVTA	14	1.7000	20.24
11	VNPAPTANS	525	1.6000	19.05
12	VYPLVIRAG	200	1.5000	17.86
13	LVIRAGGGS	203	1.3000	15.48
14	VQSRYRVFI	114	1.2000	14.29
15	LRSRTTEVM	441	1.0000	11.90
16	LGVNWRVRC	493	1.0000	11.90
17	MREQAARIG	316	0.8000	9.52
18	VRSMWPTVR	428	0.8000	9.52
19	VRLRSRTTE	439	0.8000	9.52
20	IFIFATTEP	149	0.7000	8.33
21	LAGATVRAL	450	0.6000	7.14
22	ILARSLNCA	53	0.5000	5.95
23	IRSRTHHYP	164	0.5000	5.95
24	LGLLGVTDV	237	0.5000	5.95

25	VCARLLLPS	355	0.5000	5.95
26	YRPASFAEV	6	0.4000	4.76
27	VVCARLLLP	354	0.4000	4.76
28	VLTHESAPL	464	0.4000	4.76
29	VVELDAASH	88	0.3800	4.52
30	FNALLKIVE	134	0.3000	3.57
31	MALYRKYRP	0	0.2000	2.38
32	LLLEVVCAR	350	0.1000	1.19
33	MVTTAGFNA	128	-0.1000	0
34	MRGATAPRL	342	-0.1000	0
35	INHAYLFSG	33	-0.2000	0
36	FIVDEAHMV	121	-0.2000	0
37	LGVTDVALI	240	-0.2000	0
38	VNWRVRCET	495	-0.2000	0
39	LSVLDQLLA	216	-0.3000	0
40	VLAPTPASS	413	-0.3000	0
41	LLPPRTMRA	175	-0.4000	0
42	YPLVIRAGG	201	-0.4000	0
43	YAPVQSRYR	111	-0.5000	0
44	VLDQLLAGA	218	-0.5000	0
45	VERIETRLD	375	-0.5000	0
46	LDMSIPAPQ	382	-0.5000	0
47	YTRALGLLG	233	-0.6000	0
48	VVQAGLGEM	334	-0.6000	0
49	LQRVERIET	372	-0.7000	0
50	YPFRLLPPR	171	-0.8000	0
51	VMLAGATVR	448	-0.8000	0
52	MLAGATVRA	449	-0.8000	0
53	LIVLQSVPD	291	-0.9000	0
54	LTRYAEVVQ	328	-0.9000	0
55	VLAEALKDA	484	-0.9000	0

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

	2.6	8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FRLLPPRTM	173	5.4000	61.36
2	IVLQSVPDA	292	4.4000	50.00
3	VRDKVRLRS	435	4.2000	47.73
4	LYRKYRPAS	2	4.0000	45.45
5	VYPLVIRAG	200	3.9000	44.32
6	MRALLARIC	181	3.8000	43.18
7	LRSRTTEVM	441	3.5000	39.77
8	VRSMWPTVR	428	3.3000	37.50
9	MREQAARIG	316	3.2000	36.36
10	VRLRSRTTE	439	3.2000	36.36
11	VQSRYRVFI	114	3.1000	35.23
12	YRKYRPASF	3	3.0000	34.09
13	FRDLIVLQS	288	3.0000	34.09
14	VNPAPTANS	525	3.0000	34.09
15	VVGQEHVTA	14	2.7000	30.68
16	IFIFATTEP	149	2.7000	30.68
17	LVIRAGGGS	203	2.7000	30.68
18	LLLEVVCAR	350	2.6000	29.55
19	LAGATVRAL	450	2.5600	29.09
20	IRSRTHHYP	164	2.5000	28.41
21	LGLLGVTDV	237	2.5000	28.41
22	VVCARLLLP	354	2.4000	27.27
23	VLTHESAPL	464	2.3600	26.82
24	MALYRKYRP	0	2.2000	25.00
25	INHAYLFSG	33	2.2000	25.00
26	YRVFIVDEA	118	2.2000	25.00
27	LGVNWRVRC	493	2.0000	22.73
28	YLFSGPRGC	37	1.9000	21.59
29	VVQAGLGEM	334	1.9000	21.59
30	VCARLLLPS	355	1.9000	21.59
31	MRGATAPRL	342	1.8600	21.14
32	LGVTDVALI	240	1.7000	19.32

33	VMLAGATVR	448	1.7000	19.32
34	VERIETRLD	375	1.6000	18.18
35	ILARSLNCA	53	1.5000	17.05
36	VNWRVRCET	495	1.5000	17.05
37	LIVLQSVPD	291	1.2000	13.64
38	VFIVDEAHM	120	1.1000	12.50
39	VLAPTPASS	413	1.1000	12.50
40	LQRVERIET	372	1.0000	11.36
41	MVTTAGFNA	128	0.9000	10.23
42	LEVVCARLL	352	0.8600	9.77
43	VVELDAASH	88	0.8000	9.09
44	VVVDDAVYP	194	0.8000	9.09
45	IGRATLTRY	323	0.8000	9.09
46	FNALLKIVE	134	0.7000	7.95
47	LSVLDQLLA	216	0.7000	7.95
48	LLQRVERIE	371	0.7000	7.95
49	LLPPRTMRA	175	0.6000	6.82
50	VSLAPNAPG	76	0.5000	5.68
51	VLDQLLAGA	218	0.5000	5.68
52	YRPASFAEV	6	0.4000	4.55
53	FIFATTEPE	150	0.4000	4.55
54	LQNELGARR	565	0.4000	4.55
55	VVDDAVYPL	195	0.3600	4.09
56	LARRLSEQR	472	0.3000	3.41
57	LELLQNELG	562	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	FRLLPPRTM	173	5.4000	61.36
2	IVLQSVPDA	292	4.4000	50.00
3	VRDKVRLRS	435	4.2000	47.73
4	LYRKYRPAS	2	4.0000	45.45

5	VYPLVIRAG	200	3.9000	44.32
6	MRALLARIC	181	3.8000	43.18
7	LRSRTTEVM	441	3.5000	39.77
8	VRSMWPTVR	428	3.3000	37.50
9	MREQAARIG	316	3.2000	36.36
10	VRLRSRTTE	439	3.2000	36.36
11	VQSRYRVFI	114	3.1000	35.23
12	YRKYRPASF	3	3.0000	34.09
13	FRDLIVLQS	288	3.0000	34.09
14	VNPAPTANS	525	3.0000	34.09
15	VVGQEHVTA	14	2.7000	30.68
16	IFIFATTEP	149	2.7000	30.68
17	LVIRAGGGS	203	2.7000	30.68
18	LLLEVVCAR	350	2.6000	29.55
19	LAGATVRAL	450	2.5600	29.09
20	IRSRTHHYP	164	2.5000	28.41
21	LGLLGVTDV	237	2.5000	28.41
22	VVCARLLLP	354	2.4000	27.27
23	VLTHESAPL	464	2.3600	26.82
24	MALYRKYRP	0	2.2000	25.00
25	INHAYLFSG	33	2.2000	25.00
26	YRVFIVDEA	118	2.2000	25.00
27	LGVNWRVRC	493	2.0000	22.73
28	YLFSGPRGC	37	1.9000	21.59
29	VVQAGLGEM	334	1.9000	21.59
30	VCARLLLPS	355	1.9000	21.59
31	MRGATAPRL	342	1.8600	21.14
32	LGVTDVALI	240	1.7000	19.32
33	VMLAGATVR	448	1.7000	19.32
34	VERIETRLD	375	1.6000	18.18
35	ILARSLNCA	53	1.5000	17.05
36	VNWRVRCET	495	1.5000	17.05
37	LIVLQSVPD	291	1.2000	13.64
38	VFIVDEAHM	120	1.1000	12.50

39	VLAPTPASS	413	1.1000	12.50
40	LQRVERIET	372	1.0000	11.36
41	MVTTAGFNA	128	0.9000	10.23
42	LEVVCARLL	352	0.8600	9.77
43	VVELDAASH	88	0.8000	9.09
44	VVVDDAVYP	194	0.8000	9.09
45	IGRATLTRY	323	0.8000	9.09
46	FNALLKIVE	134	0.7000	7.95
47	LSVLDQLLA	216	0.7000	7.95
48	LLQRVERIE	371	0.7000	7.95
49	LLPPRTMRA	175	0.6000	6.82
50	VSLAPNAPG	76	0.5000	5.68
51	VLDQLLAGA	218	0.5000	5.68
52	YRPASFAEV	6	0.4000	4.55
53	FIFATTEPE	150	0.4000	4.55
54	LQNELGARR	565	0.4000	4.55
55	VVDDAVYPL	195	0.3600	4.09
56	LARRLSEQR	472	0.3000	3.41
57	LELLQNELG	562	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	LERFRDLIV	285	5.0000	51.02
2	LQRVERIET	372	4.4000	44.90
3	LVIRAGGGS	203	4.0000	40.82
4	IFIFATTEP	149	3.7600	38.37
5	MVTTAGFNA	128	3.7000	37.76
6	VQSRYRVFI	114	3.6000	36.73
7	VRALEDNTL	455	3.5000	35.71
8	MRGATAPRL	342	3.2000	32.65
9	VLTHESAPL	464	3.2000	32.65
10	YRKYRPASF	3	3.1000	31.63

11	YRVFIVDEA	118	3.1000	31.63
12	VVCARLLLP	354	3.1000	31.63
13	VTYTRALGL	231	2.9000	29.59
14	MALYRKYRP	0	2.8000	28.57
15	VRDKVRLRS	435	2.8000	28.57
16	VRLRSRTTE	439	2.7000	27.55
17	LLPPRTMRA	175	2.6600	27.14
18	VRSMWPTVR	428	2.4000	24.49
19	VVQAGLGEM	334	2.3800	24.29
20	IVLQSVPDA	292	2.3000	23.47
21	IETRLDMSI	378	2.3000	23.47
22	MRALLARIC	181	2.2000	22.45
23	LGLLGVTDV	237	2.2000	22.45
24	ILARSLNCA	53	2.1000	21.43
25	VLPTIRSRT	160	2.1000	21.43
26	LGVNWRVRC	493	2.1000	21.43
27	FRLLPPRTM	173	2.0800	21.22
28	IRAGGGSPR	205	2.0000	20.41
29	VCARLLLPS	355	2.0000	20.41
30	LLLPSASDA	359	2.0000	20.41
31	LRSRTTEVM	441	1.9400	19.80
32	LYRKYRPAS	2	1.9000	19.39
33	INHAYLFSG	33	1.8000	18.37
34	LSVLDQLLA	216	1.8000	18.37
35	LLGVTDVAL	239	1.8000	18.37
36	VNWRVRCET	495	1.8000	18.37
37	FRDLIVLQS	288	1.7000	17.35
38	LNCAQGPTA	58	1.6000	16.33
39	IRSRTHHYP	164	1.6000	16.33
40	VFIVDEAHM	120	1.5800	16.12
41	YRPASFAEV	6	1.5000	15.31
42	VGGGANVAT	513	1.5000	15.31
43	VVVDDAVYP	194	1.4000	14.29
44	VAAVRSMWP	425	1.4000	14.29

45	VRCETGEPA	499	1.4000	14.29
46	VVGQEHVTA	14	1.3000	13.27
47	VVDDAVYPL	195	1.3000	13.27
48	YTRALGLLG	233	1.3000	13.27
49	VMLAGATVR	448	1.3000	13.27
50	MLAGATVRA	449	1.2600	12.86
51	LFSGPRGCG	38	1.2000	12.24
52	IVDEAHMVT	122	1.2000	12.24
53	VIRAGGGSP	204	1.2000	12.24
54	VTAPLSVAL	20	1.1000	11.22
55	FIVDEAHMV	121	1.1000	11.22
56	LGVTDVALI	240	1.1000	11.22
57	LIVLQSVPD	291	1.1000	11.22

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YRKYRPASF	3	4.1000	41.84
2	YRVFIVDEA	118	4.1000	41.84
3	LERFRDLIV	285	4.0000	40.82
4	LQRVERIET	372	3.4000	34.69
5	FRLLPPRTM	173	3.0800	31.43
6	LVIRAGGGS	203	3.0000	30.61
7	IFIFATTEP	149	2.7600	28.16
8	MVTTAGFNA	128	2.7000	27.55
9	FRDLIVLQS	288	2.7000	27.55
10	VQSRYRVFI	114	2.6000	26.53
11	YRPASFAEV	6	2.5000	25.51
12	VRALEDNTL	455	2.5000	25.51
13	YTRALGLLG	233	2.3000	23.47
14	MRGATAPRL	342	2.2000	22.45
15	VLTHESAPL	464	2.2000	22.45
16	FIVDEAHMV	121	2.1000	21.43

17	VVCARLLLP	354	2.1000	21.43
18	VTYTRALGL	231	1.9000	19.39
19	MALYRKYRP	0	1.8000	18.37
20	VRDKVRLRS	435	1.8000	18.37
21	VRLRSRTTE	439	1.7000	17.35
22	LLPPRTMRA	175	1.6600	16.94
23	VRSMWPTVR	428	1.4000	14.29
24	VVQAGLGEM	334	1.3800	14.08
25	IVLQSVPDA	292	1.3000	13.27
26	IETRLDMSI	378	1.3000	13.27
27	MRALLARIC	181	1.2000	12.24
28	LGLLGVTDV	237	1.2000	12.24
29	ILARSLNCA	53	1.1000	11.22
30	VLPTIRSRT	160	1.1000	11.22
31	LGVNWRVRC	493	1.1000	11.22
32	IRAGGGSPR	205	1.0000	10.20
33	VCARLLLPS	355	1.0000	10.20
34	LLLPSASDA	359	1.0000	10.20
35	LRSRTTEVM	441	0.9400	9.59
36	LYRKYRPAS	2	0.9000	9.18
37	YPLVIRAGG	201	0.9000	9.18
38	INHAYLFSG	33	0.8000	8.16
39	YLFSGPRGC	37	0.8000	8.16
40	LSVLDQLLA	216	0.8000	8.16
41	LLGVTDVAL	239	0.8000	8.16
42	VNWRVRCET	495	0.8000	8.16
43	LNCAQGPTA	58	0.6000	6.12
44	FNALLKIVE	134	0.6000	6.12
45	IRSRTHHYP	164	0.6000	6.12
46	VFIVDEAHM	120	0.5800	5.92
47	VGGGANVAT	513	0.5000	5.10
48	VVVDDAVYP	194	0.4000	4.08
49	VAAVRSMWP	425	0.4000	4.08
50	VRCETGEPA	499	0.4000	4.08

51	VVGQEHVTA	14	0.3000	3.06
52	VVDDAVYPL	195	0.3000	3.06
53	VMLAGATVR	448	0.3000	3.06
54	MLAGATVRA	449	0.2600	2.65
55	LFSGPRGCG	38	0.2000	2.04
56	IVDEAHMVT	122	0.2000	2.04
57	VIRAGGGSP	204	0.2000	2.04

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	LERFRDLIV	285	5.0000	51.02
2	LQRVERIET	372	4.4000	44.90
3	LVIRAGGGS	203	4.0000	40.82
4	IFIFATTEP	149	3.7600	38.37
5	MVTTAGFNA	128	3.7000	37.76
6	VQSRYRVFI	114	3.6000	36.73
7	VRALEDNTL	455	3.5000	35.71
8	MRGATAPRL	342	3.2000	32.65
9	VLTHESAPL	464	3.2000	32.65
10	YRKYRPASF	3	3.1000	31.63
11	YRVFIVDEA	118	3.1000	31.63
12	VVCARLLLP	354	3.1000	31.63
13	VTYTRALGL	231	2.9000	29.59
14	MALYRKYRP	0	2.8000	28.57
15	VRDKVRLRS	435	2.8000	28.57
16	VRLRSRTTE	439	2.7000	27.55
17	LLPPRTMRA	175	2.6600	27.14
18	VRSMWPTVR	428	2.4000	24.49
19	VVQAGLGEM	334	2.3800	24.29
20	IVLQSVPDA	292	2.3000	23.47
21	IETRLDMSI	378	2.3000	23.47
22	MRALLARIC	181	2.2000	22.45

23	LGLLGVTDV	237	2.2000	22.45
24	ILARSLNCA	53	2.1000	21.43
25	VLPTIRSRT	160	2.1000	21.43
26	LGVNWRVRC	493	2.1000	21.43
27	FRLLPPRTM	173	2.0800	21.22
28	IRAGGGSPR	205	2.0000	20.41
29	VCARLLLPS	355	2.0000	20.41
30	LLLPSASDA	359	2.0000	20.41
31	LRSRTTEVM	441	1.9400	19.80
32	LYRKYRPAS	2	1.9000	19.39
33	INHAYLFSG	33	1.8000	18.37
34	LSVLDQLLA	216	1.8000	18.37
35	LLGVTDVAL	239	1.8000	18.37
36	VNWRVRCET	495	1.8000	18.37
37	FRDLIVLQS	288	1.7000	17.35
38	LNCAQGPTA	58	1.6000	16.33
39	IRSRTHHYP	164	1.6000	16.33
40	VFIVDEAHM	120	1.5800	16.12
41	YRPASFAEV	6	1.5000	15.31
42	VGGGANVAT	513	1.5000	15.31
43	VVVDDAVYP	194	1.4000	14.29
44	VAAVRSMWP	425	1.4000	14.29
45	VRCETGEPA	499	1.4000	14.29
46	VVGQEHVTA	14	1.3000	13.27
47	VVDDAVYPL	195	1.3000	13.27
48	YTRALGLLG	233	1.3000	13.27
49	VMLAGATVR	448	1.3000	13.27
50	MLAGATVRA	449	1.2600	12.86
51	LFSGPRGCG	38	1.2000	12.24
52	IVDEAHMVT	122	1.2000	12.24
53	VIRAGGGSP	204	1.2000	12.24
54	VTAPLSVAL	20	1.1000	11.22
55	FIVDEAHMV	121	1.1000	11.22
56	LGVTDVALI	240	1.1000	11.22

57	LIVLQSVPD	291	1.1000	11.22

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRSMWPTVR	428	6.1000	62.24
2	FRLLPPRTM	173	5.8000	59.18
3	YAPVQSRYR	111	4.7000	47.96
4	VMLAGATVR	448	3.9000	39.80
5	LEVVCARLL	352	3.3000	33.67
6	MRALLARIC	181	3.1000	31.63
7	YRKYRPASF	3	3.0000	30.61
8	YLFSGPRGC	37	2.8000	28.57
9	MVTTAGFNA	128	2.6000	26.53
10	MRGATAPRL	342	2.1000	21.43
11	VTYTRALGL	231	2.0000	20.41
12	WPTVRDKVR	432	2.0000	20.41
13	LIFIFATTE	148	1.9000	19.39
14	LVIRAGGGS	203	1.9000	19.39
15	LQRVERIET	372	1.7000	17.35
16	LPTIRSRTH	161	1.6000	16.33
17	IRAGGGSPR	205	1.6000	16.33
18	VRALEDNTL	455	1.6000	16.33
19	LQNELGARR	565	1.6000	16.33
20	VVELDAASH	88	1.5000	15.31
21	FRDLIVLQS	288	1.5000	15.31
22	YTRALGLLG	233	1.4000	14.29
23	FAEVVGQEH	11	1.3000	13.27
24	VVQAGLGEM	334	1.2000	12.24
25	LLEVVCARL	351	1.2000	12.24
26	VYPLVIRAG	200	1.1000	11.22
27	MREQAARIG	316	1.0000	10.20
28	INHAYLFSG	33	0.9000	9.18

29	VFIVDEAHM	120	0.9000	9.18
30	LLLEVVCAR	350	0.9000	9.18
31	FSGPRGCGK	39	0.8000	8.16
32	IGRATLTRY	323	0.8000	8.16
33	FIVDEAHMV	121	0.7000	7.14
34	YPLVIRAGG	201	0.7000	7.14
35	YRPASFAEV	6	0.6000	6.12
36	FNALLKIVE	134	0.5000	5.10
37	LAGATVRAL	450	0.5000	5.10
38	LLQNELGAR	564	0.4000	4.08
39	VIRAGGGSP	204	0.3000	3.06
40	LLGVTDVAL	239	0.3000	3.06
41	LAACDAAAL	255	0.3000	3.06
42	IFATTEPEK	151	0.2000	2.04
43	LGVTDVALI	240	0.2000	2.04
44	LQSVPDAAS	294	0.2000	2.04
45	LARICEQEG	185	0.1000	1.02
46	VERIETRLD	375	0.1000	1.02
47	LGLLGVTDV	237	-0.1000	0
48	VQAGLGEMR	335	-0.1000	0
49	VVCARLLLP	354	-0.1000	0
50	YAEVVQAGL	331	-0.2000	0
51	LSVALDAGR	24	-0.3000	0
52	LGEMRGATA	339	-0.3000	0
53	LAPNAPGSI	78	-0.4000	0
54	FIFATTEPE	150	-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	VRSMWPTVR	428	6.1000	62.24
2	FRLLPPRTM	173	5.8000	59.18
3	YAPVQSRYR	111	4.7000	47.96

4	VMLAGATVR	448	3.9000	39.80
5	LEVVCARLL	352	3.3000	33.67
6	MRALLARIC	181	3.1000	31.63
7	YRKYRPASF	3	3.0000	30.61
8	YLFSGPRGC	37	2.8000	28.57
9	MVTTAGFNA	128	2.6000	26.53
10	MRGATAPRL	342	2.1000	21.43
11	VTYTRALGL	231	2.0000	20.41
12	WPTVRDKVR	432	2.0000	20.41
13	LIFIFATTE	148	1.9000	19.39
14	LVIRAGGGS	203	1.9000	19.39
15	LQRVERIET	372	1.7000	17.35
16	LPTIRSRTH	161	1.6000	16.33
17	IRAGGGSPR	205	1.6000	16.33
18	VRALEDNTL	455	1.6000	16.33
19	LQNELGARR	565	1.6000	16.33
20	VVELDAASH	88	1.5000	15.31
21	FRDLIVLQS	288	1.5000	15.31
22	YTRALGLLG	233	1.4000	14.29
23	FAEVVGQEH	11	1.3000	13.27
24	VVQAGLGEM	334	1.2000	12.24
25	LLEVVCARL	351	1.2000	12.24
26	VYPLVIRAG	200	1.1000	11.22
27	MREQAARIG	316	1.0000	10.20
28	INHAYLFSG	33	0.9000	9.18
29	VFIVDEAHM	120	0.9000	9.18
30	LLLEVVCAR	350	0.9000	9.18
31	FSGPRGCGK	39	0.8000	8.16
32	IGRATLTRY	323	0.8000	8.16
33	FIVDEAHMV	121	0.7000	7.14
34	YPLVIRAGG	201	0.7000	7.14
35	YRPASFAEV	6	0.6000	6.12
36	FNALLKIVE	134	0.5000	5.10
37	LAGATVRAL	450	0.5000	5.10

38	LLQNELGAR	564	0.4000	4.08
39	VIRAGGGSP	204	0.3000	3.06
40	LLGVTDVAL	239	0.3000	3.06
41	LAACDAAAL	255	0.3000	3.06
42	IFATTEPEK	151	0.2000	2.04
43	LGVTDVALI	240	0.2000	2.04
44	LQSVPDAAS	294	0.2000	2.04
45	LARICEQEG	185	0.1000	1.02
46	VERIETRLD	375	0.1000	1.02
47	LGLLGVTDV	237	-0.1000	0
48	VQAGLGEMR	335	-0.1000	0
49	VVCARLLLP	354	-0.1000	0
50	YAEVVQAGL	331	-0.2000	0
51	LSVALDAGR	24	-0.3000	0
52	LGEMRGATA	339	-0.3000	0
53	LAPNAPGSI	78	-0.4000	0
54	FIFATTEPE	150	-0.4000	0