MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Feb 15 20:16:43 2010
Length of input sequence	582 amino acids
Number of nanomers from input sequence	574
Number of nanomers with obligatory P1 anchor residue	170
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	58

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	VVLLVGARL	277	3.2000	53.33
2	YRIGQVQDI	139	2.8000	46.67
3	YVVNEGANA	395	2.3400	39.00
4	YNALGAIRS	378	2.0000	33.33
5	YAIAAAVET	434	2.0000	33.33
6	FRSAAPVWR	491	1.9000	31.67
7	VVNEGANAL	396	1.8000	30.00
8	VVILNNGGV	474	1.6000	26.67

9	YRLPVTVVI	468	1.5000	25.00
10	WRPVDPAPR	189	1.2500	20.83
11	MRFYNALGA	375	1.2000	20.00
12	MGIGMGYAI	428	1.2000	20.00
13	IYGVVGIPI	30	1.0500	17.50
14	YHVSTPTEL	525	0.9900	16.50
15	IGMGYAIAA	430	0.8000	13.33
16	FLNGLPALA	86	0.6000	10.00
17	MGYAIAAAV	432	0.6000	10.00
18	VVGIPITDL	33	0.4900	8.17
19	WRHDPAPTV	498	0.3700	6.17
20	IGRGVARAI	147	0.2900	4.83
21	FRHEASAGN	55	0.2000	3.33
22	LVLSKGAAY	220	0.2000	3.33
23	FVEHTGIPF	238	0.1000	1.67
24	FYNALGAIR	377	0.1000	1.67
25	ILNNGGVYR	476	-0.0600	0
26	LVGARLNWL	280	-0.1000	0
27	VLLVGARLN	278	-0.1600	0
28	MIQISGSSS	103	-0.2000	0
29	MARADVVLL	272	-0.2000	0
30	FETICRYRL	462	-0.2000	0
31	FLTARPGVC	70	-0.3000	0
32	YRGDEATIF	483	-0.3100	0
33	IGSVMSALL	327	-0.4500	0
34	LASNGPSLI	541	-0.4600	0
35	FLPMSMAKG	246	-0.5000	0
36	LPMSMAKGL	247	-0.5000	0
37	FVKAAYRIG	134	-0.6100	0
38	FDSNRPIVA	313	-0.6600	0
39	YQDLDQLNA	122	-0.7000	0
40	WLLGNGESP	287	-0.7000	0
41	VVAIEGDSA	446	-0.7000	0
42	LQRNPDVYV	388	-0.7600	0

43	IQISGSSSR	104	-0.8000	0
44	VDALKANDV	19	-1.0000	0
45	FPMIQISGS	101	-1.0000	0
46	MSMAKGLLP	249	-1.0000	0
47	YGVVGIPIT	31	-1.0800	0
48	LQRGDYQDL	117	-1.1000	0
49	VETGRPVVA	440	-1.1000	0
50	VLAQAQRPL	211	-1.1100	0
51	VILNNGGVY	475	-1.1600	0
52	LAKLNTTSA	564	-1.2100	0
53	LAMARADVV	270	-1.3000	0
54	FSGMEFETI	457	-1.3000	0
55	VLNAHARHE	506	-1.3100	0
56	YAQADNVIR	228	-1.4000	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	VVLLVGARL	277	4.2000	70.00
2	VVNEGANAL	396	2.8000	46.67
3	VVILNNGGV	474	2.6000	43.33
4	MRFYNALGA	375	2.2000	36.67
5	MGIGMGYAI	428	2.2000	36.67
6	IYGVVGIPI	30	2.0500	34.17
7	FRSAAPVWR	491	1.9000	31.67
8	YRIGQVQDI	139	1.8000	30.00
9	IGMGYAIAA	430	1.8000	30.00
10	MGYAIAAAV	432	1.6000	26.67
11	VVGIPITDL	33	1.4900	24.83
12	YVVNEGANA	395	1.3400	22.33
13	IGRGVARAI	147	1.2900	21.50
14	LVLSKGAAY	220	1.2000	20.00
15	LNGLPALAN	87	1.0000	16.67

16	YNALGAIRS	378	1.0000	16.67
17	YAIAAAVET	434	1.0000	16.67
18	ILNNGGVYR	476	0.9400	15.67
19	LVGARLNWL	280	0.9000	15.00
20	VLLVGARLN	278	0.8400	14.00
21	MIQISGSSS	103	0.8000	13.33
22	MARADVVLL	272	0.8000	13.33
23	FLNGLPALA	86	0.6000	10.00
24	IGSVMSALL	327	0.5500	9.17
25	LASNGPSLI	541	0.5400	9.00
26	LPMSMAKGL	247	0.5000	8.33
27	YRLPVTVVI	468	0.5000	8.33
28	VVAIEGDSA	446	0.3000	5.00
29	WRPVDPAPR	189	0.2500	4.17
30	LQRNPDVYV	388	0.2400	4.00
31	FRHEASAGN	55	0.2000	3.33
32	IQISGSSSR	104	0.2000	3.33
33	FVEHTGIPF	238	0.1000	1.67
34	FYNALGAIR	377	0.1000	1.67
35	YHVSTPTEL	525	-0.0100	0
36	LQRGDYQDL	117	-0.1000	0
37	VETGRPVVA	440	-0.1000	0
38	VLAQAQRPL	211	-0.1100	0
39	VILNNGGVY	475	-0.1600	0
40	FETICRYRL	462	-0.2000	0
41	LAKLNTTSA	564	-0.2100	0
42	FLTARPGVC	70	-0.3000	0
43	LAMARADVV	270	-0.3000	0
44	VLNAHARHE	506	-0.3100	0
45	LNWLLGNGE	285	-0.4000	0
46	IRYIGFRHE	50	-0.4100	0
47	IRSVLQRNP	384	-0.4600	0
48	VIREFVEHT	234	-0.5000	0
49	FLPMSMAKG	246	-0.5000	0

50	LGAIRSVLQ	381	-0.5000	0
51	VWRHDPAPT	497	-0.5000	0
52	IFRSAAPVW	490	-0.5300	0
53	IRTATSGRP	155	-0.6000	0
54	FVKAAYRIG	134	-0.6100	0
55	WRHDPAPTV	498	-0.6300	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	LLPDSHPQS	255	5.3000	55.79
2	VYLDIPGDV	166	5.1000	53.68
3	YRIGQVQDI	139	4.9000	51.58
4	WRHDPAPTV	498	4.7000	49.47
5	YRGDEATIF	483	4.5000	47.37
6	IEGDSAFGF	449	4.0000	42.11
7	IQISGSSSR	104	3.8700	40.74
8	LVVDALKAN	17	3.6000	37.89
9	LVLSKGAAY	220	3.4000	35.79
10	VVILNNGGV	474	3.4000	35.79
11	VVGIPITDL	33	3.3600	35.37
12	LNNGGVYRG	477	3.3500	35.26
13	VLGQAVEAS	174	3.3000	34.74
14	LTGDIGSVM	323	2.9700	31.26
15	LLVLSKGAA	219	2.9000	30.53
16	VLTDGCHLV	10	2.8000	29.47
17	IGMGYAIAA	430	2.8000	29.47
18	YRLPVTVVI	468	2.8000	29.47
19	WSADAKFIQ	297	2.6000	27.37
20	IVAPLTGDI	319	2.6000	27.37
21	FRSAAPVWR	491	2.6000	27.37
22	LKANDVDTI	22	2.5000	26.32
23	WRPVDPAPR	189	2.5000	26.32

24	MAKGLLPDS	251	2.5000	26.32
25	LVGARLNWL	280	2.3700	24.95
26	VVLLVGARL	277	2.3600	24.84
27	MGIGMGYAI	428	2.3500	24.74
28	VKAAYRIGQ	135	2.3000	24.21
29	IPGDVLGQA	170	2.3000	24.21
30	IQVDIEASE	304	2.3000	24.21
31	FPMIQISGS	101	2.2700	23.89
32	MVDLQRGDY	114	2.2000	23.16
33	LLVGARLNW	279	2.2000	23.16
34	MRFYNALGA	375	2.2000	23.16
35	LANATTNCF	93	2.1100	22.21
36	LADDHHPMR	368	2.1000	22.11
37	MIQISGSSS	103	2.0700	21.79
38	MARADVVLL	272	2.0600	21.68
39	VILNNGGVY	475	2.0000	21.05
40	IRTATSGRP	155	1.9000	20.00
41	IFRSAAPVW	490	1.9000	20.00
42	FIQVDIEAS	303	1.7000	17.89
43	ILNNGGVYR	476	1.7000	17.89
44	LAQAQRPLL	212	1.6600	17.47
45	LNAARPFVK	128	1.6000	16.84
46	MGYAIAAAV	432	1.6000	16.84
47	LASNGPSLI	541	1.5700	16.53
48	VVDALKAND	18	1.5000	15.79
49	FLNGLPALA	86	1.5000	15.79
50	VQDIGRGVA	144	1.5000	15.79
51	VVNEGANAL	396	1.4700	15.47
52	IYGVVGIPI	30	1.4000	14.74
53	IGRGVARAI	147	1.4000	14.74
54	YHVSTPTEL	525	1.3600	14.32
55	VIREFVEHT	234	1.3000	13.68
56	VMSALLEAA	330	1.3000	13.68
57	YNALGAIRS	378	1.3000	13.68

58	VETGRPVVA	440	1.3000	13.68

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	YRIGQVQDI	139	5.0000	54.95
2	WRHDPAPTV	498	4.7000	51.65
3	WSADAKFIQ	297	4.3000	47.25
4	LLPDSHPQS	255	3.9000	42.86
5	YRGDEATIF	483	3.6000	39.56
6	VYLDIPGDV	166	3.1000	34.07
7	YRLPVTVVI	468	2.9000	31.87
8	FPMIQISGS	101	2.8700	31.54
9	FLNGLPALA	86	2.5000	27.47
10	FIQVDIEAS	303	2.3000	25.27
11	YVVNEGANA	395	2.1000	23.08
12	FRSAAPVWR	491	2.1000	23.08
13	VKAAYRIGQ	135	2.0000	21.98
14	WRPVDPAPR	189	2.0000	21.98
15	VLGQAVEAS	174	1.9000	20.88
16	LLVLSKGAA	219	1.9000	20.88
17	YNALGAIRS	378	1.9000	20.88
18	LVVDALKAN	17	1.8000	19.78
19	IGMGYAIAA	430	1.8000	19.78
20	FLTARPGVC	70	1.6000	17.58
21	VVGIPITDL	33	1.4000	15.38
22	VVILNNGGV	474	1.4000	15.38
23	YHVSTPTEL	525	1.4000	15.38
24	IQISGSSSR	104	1.3700	15.05
25	IPGDVLGQA	170	1.3000	14.29
26	YGVVGIPIT	31	1.2000	13.19
27	LLVGARLNW	279	1.2000	13.19
28	MRFYNALGA	375	1.2000	13.19

29	LVLSKGAAY	220	1.1000	12.09
30	MAKGLLPDS	251	1.1000	12.09
31	IEGDSAFGF	449	1.1000	12.09
32	LNNGGVYRG	477	0.9500	10.44
33	IFRSAAPVW	490	0.9000	9.89
34	VLTDGCHLV	10	0.8000	8.79
35	WGVMGIGMG	425	0.8000	8.79
36	YIGFRHEAS	52	0.7000	7.69
37	IVAPLTGDI	319	0.7000	7.69
38	MIQISGSSS	103	0.6700	7.36
39	LKANDVDTI	22	0.6000	6.59
40	LGAIRSVLQ	381	0.6000	6.59
41	FETICRYRL	462	0.5500	6.04
42	LNAARPFVK	128	0.5000	5.49
43	VQDIGRGVA	144	0.5000	5.49
44	YAIAAAVET	434	0.5000	5.49
45	LTGDIGSVM	323	0.4700	5.16
46	MGIGMGYAI	428	0.4500	4.95
47	LVGARLNWL	280	0.4100	4.51
48	VVLLVGARL	277	0.4000	4.40
49	MRRRLADDH	364	0.3800	4.18
50	WLLGNGESP	287	0.3000	3.30
51	VMSALLEAA	330	0.3000	3.30
52	VETGRPVVA	440	0.3000	3.30
53	VVAIEGDSA	446	0.3000	3.30
54	VGIPITDLA	34	0.2000	2.20
55	MARADVVLL	272	0.1000	1.10
56	LGNGESPQW	289	0.1000	1.10
57	LARNIIDMH	406	0.0800	0.88

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	YRIGQVQDI	139	4.1000	46.59
2	LLPDSHPQS	255	3.5000	39.77
3	LVVDALKAN	17	3.4000	38.64
4	VLGQAVEAS	174	3.3000	37.50
5	VYLDIPGDV	166	2.7000	30.68
6	LLVGARLNW	279	2.7000	30.68
7	MRFYNALGA	375	2.7000	30.68
8	VKAAYRIGQ	135	2.6800	30.45
9	VLTDGCHLV	10	2.6000	29.55
10	YRGDEATIF	483	2.6000	29.55
11	IGMGYAIAA	430	2.4800	28.18
12	VVGIPITDL	33	2.4000	27.27
13	WRHDPAPTV	498	2.3000	26.14
14	IQISGSSSR	104	2.1000	23.86
15	LVLSKGAAY	220	2.1000	23.86
16	LVGARLNWL	280	2.1000	23.86
17	LKANDVDTI	22	1.9000	21.59
18	WSADAKFIQ	297	1.8000	20.45
19	YRLPVTVVI	468	1.7800	20.23
20	FIQVDIEAS	303	1.7000	19.32
21	VMSALLEAA	330	1.7000	19.32
22	MRRRLADDH	364	1.6800	19.09
23	FPMIQISGS	101	1.6000	18.18
24	VVAIEGDSA	446	1.6000	18.18
25	VGIPITDLA	34	1.5000	17.05
26	FLNGLPALA	86	1.5000	17.05
27	LLVLSKGAA	219	1.5000	17.05
28	LGAIRSVLQ	381	1.4800	16.82
29	MIQISGSSS	103	1.4000	15.91
30	VVLLVGARL	277	1.4000	15.91
31	LARNIIDMH	406	1.3800	15.68
32	LTGDIGSVM	323	1.2000	13.64
33	VVNEGANAL	396	1.2000	13.64
34	VETGRPVVA	440	1.1800	13.41

35	YVVNEGANA	395	1.1000	12.50
36	WRPVDPAPR	189	1.0000	11.36
37	VIREFVEHT	234	1.0000	11.36
38	VVILNNGGV	474	1.0000	11.36
39	MARADVVLL	272	0.9800	11.14
40	FRSAAPVWR	491	0.9800	11.14
41	LANATTNCF	93	0.9000	10.23
42	IPGDVLGQA	170	0.9000	10.23
43	IQVDIEASE	304	0.9000	10.23
44	LNNGGVYRG	477	0.8000	9.09
45	LNAHARHEL	507	0.8000	9.09
46	MAKGLLPDS	251	0.7000	7.95
47	LAKLNTTSA	564	0.7000	7.95
48	VEASAASGA	179	0.6000	6.82
49	MGYAIAAAV	432	0.6000	6.82
50	IEGDSAFGF	449	0.6000	6.82
51	YNALGAIRS	378	0.5800	6.59
52	IFRSAAPVW	490	0.5000	5.68
53	VVDALKAND	18	0.4000	4.55
54	VARAIRTAT	151	0.4000	4.55
55	LAMARADVV	270	0.4000	4.55
56	VYRGDEATI	482	0.4000	4.55
57	YHVSTPTEL	525	0.4000	4.55
58	LASNGPSLI	541	0.4000	4.55

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	YRIGQVQDI	139	4.1000	46.59
2	LLPDSHPQS	255	3.5000	39.77
3	LVVDALKAN	17	3.4000	38.64
4	VLGQAVEAS	174	3.3000	37.50
5	VYLDIPGDV	166	2.7000	30.68

6	LLVGARLNW	279	2.7000	30.68
7	MRFYNALGA	375	2.7000	30.68
8	VKAAYRIGQ	135	2.6800	30.45
9	VLTDGCHLV	10	2.6000	29.55
10	YRGDEATIF	483	2.6000	29.55
11	IGMGYAIAA	430	2.4800	28.18
12	VVGIPITDL	33	2.4000	27.27
13	WRHDPAPTV	498	2.3000	26.14
14	IQISGSSSR	104	2.1000	23.86
15	LVLSKGAAY	220	2.1000	23.86
16	LVGARLNWL	280	2.1000	23.86
17	LKANDVDTI	22	1.9000	21.59
18	WSADAKFIQ	297	1.8000	20.45
19	YRLPVTVVI	468	1.7800	20.23
20	FIQVDIEAS	303	1.7000	19.32
21	VMSALLEAA	330	1.7000	19.32
22	MRRRLADDH	364	1.6800	19.09
23	FPMIQISGS	101	1.6000	18.18
24	VVAIEGDSA	446	1.6000	18.18
25	VGIPITDLA	34	1.5000	17.05
26	FLNGLPALA	86	1.5000	17.05
27	LLVLSKGAA	219	1.5000	17.05
28	LGAIRSVLQ	381	1.4800	16.82
29	MIQISGSSS	103	1.4000	15.91
30	VVLLVGARL	277	1.4000	15.91
31	LARNIIDMH	406	1.3800	15.68
32	LTGDIGSVM	323	1.2000	13.64
33	VVNEGANAL	396	1.2000	13.64
34	VETGRPVVA	440	1.1800	13.41
35	YVVNEGANA	395	1.1000	12.50
36	WRPVDPAPR	189	1.0000	11.36
37	VIREFVEHT	234	1.0000	11.36
38	VVILNNGGV	474	1.0000	11.36
39	MARADVVLL	272	0.9800	11.14

40	FRSAAPVWR	491	0.9800	11.14
41	LANATTNCF	93	0.9000	10.23
42	IPGDVLGQA	170	0.9000	10.23
43	IQVDIEASE	304	0.9000	10.23
44	LNNGGVYRG	477	0.8000	9.09
45	LNAHARHEL	507	0.8000	9.09
46	MAKGLLPDS	251	0.7000	7.95
47	LAKLNTTSA	564	0.7000	7.95
48	VEASAASGA	179	0.6000	6.82
49	MGYAIAAAV	432	0.6000	6.82
50	IEGDSAFGF	449	0.6000	6.82
51	YNALGAIRS	378	0.5800	6.59
52	IFRSAAPVW	490	0.5000	5.68
53	VVDALKAND	18	0.4000	4.55
54	VARAIRTAT	151	0.4000	4.55
55	LAMARADVV	270	0.4000	4.55
56	VYRGDEATI	482	0.4000	4.55
57	YHVSTPTEL	525	0.4000	4.55
58	LASNGPSLI	541	0.4000	4.55

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	YRIGQVQDI	139	4.1000	46.59
2	LLPDSHPQS	255	3.5000	39.77
3	LVVDALKAN	17	3.4000	38.64
4	VLGQAVEAS	174	3.3000	37.50
5	VYLDIPGDV	166	2.7000	30.68
6	LLVGARLNW	279	2.7000	30.68
7	MRFYNALGA	375	2.7000	30.68
8	VKAAYRIGQ	135	2.6800	30.45
9	VLTDGCHLV	10	2.6000	29.55
10	YRGDEATIF	483	2.6000	29.55

11	IGMGYAIAA	430	2.4800	28.18
12	VVGIPITDL	33	2.4000	27.27
13	WRHDPAPTV	498	2.3000	26.14
14	IQISGSSSR	104	2.1000	23.86
15	LVLSKGAAY	220	2.1000	23.86
16	LVGARLNWL	280	2.1000	23.86
17	LKANDVDTI	22	1.9000	21.59
18	WSADAKFIQ	297	1.8000	20.45
19	YRLPVTVVI	468	1.7800	20.23
20	FIQVDIEAS	303	1.7000	19.32
21	VMSALLEAA	330	1.7000	19.32
22	MRRRLADDH	364	1.6800	19.09
23	FPMIQISGS	101	1.6000	18.18
24	VVAIEGDSA	446	1.6000	18.18
25	VGIPITDLA	34	1.5000	17.05
26	FLNGLPALA	86	1.5000	17.05
27	LLVLSKGAA	219	1.5000	17.05
28	LGAIRSVLQ	381	1.4800	16.82
29	MIQISGSSS	103	1.4000	15.91
30	VVLLVGARL	277	1.4000	15.91
31	LARNIIDMH	406	1.3800	15.68
32	LTGDIGSVM	323	1.2000	13.64
33	VVNEGANAL	396	1.2000	13.64
34	VETGRPVVA	440	1.1800	13.41
35	YVVNEGANA	395	1.1000	12.50
36	WRPVDPAPR	189	1.0000	11.36
37	VIREFVEHT	234	1.0000	11.36
38	VVILNNGGV	474	1.0000	11.36
39	MARADVVLL	272	0.9800	11.14
40	FRSAAPVWR	491	0.9800	11.14
41	LANATTNCF	93	0.9000	10.23
42	IPGDVLGQA	170	0.9000	10.23
43	IQVDIEASE	304	0.9000	10.23
44	LNNGGVYRG	477	0.8000	9.09

45	LNAHARHEL	507	0.8000	9.09
46	MAKGLLPDS	251	0.7000	7.95
47	LAKLNTTSA	564	0.7000	7.95
48	VEASAASGA	179	0.6000	6.82
49	MGYAIAAAV	432	0.6000	6.82
50	IEGDSAFGF	449	0.6000	6.82
51	YNALGAIRS	378	0.5800	6.59
52	IFRSAAPVW	490	0.5000	5.68
53	VVDALKAND	18	0.4000	4.55
54	VARAIRTAT	151	0.4000	4.55
55	LAMARADVV	270	0.4000	4.55
56	VYRGDEATI	482	0.4000	4.55
57	YHVSTPTEL	525	0.4000	4.55
58	LASNGPSLI	541	0.4000	4.55

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	YRIGQVQDI	139	5.9000	62.11
2	WRHDPAPTV	498	5.7000	60.00
3	YRGDEATIF	483	5.5000	57.89
4	LLPDSHPQS	255	4.3000	45.26
5	VYLDIPGDV	166	4.1000	43.16
6	YRLPVTVVI	468	3.8000	40.00
7	WSADAKFIQ	297	3.6000	37.89
8	FRSAAPVWR	491	3.6000	37.89
9	WRPVDPAPR	189	3.5000	36.84
10	FPMIQISGS	101	3.2700	34.42
11	IEGDSAFGF	449	3.0000	31.58
12	IQISGSSSR	104	2.8700	30.21
13	FIQVDIEAS	303	2.7000	28.42
14	LVVDALKAN	17	2.6000	27.37
15	FLNGLPALA	86	2.5000	26.32

16	LVLSKGAAY	220	2.4000	25.26
17	VVILNNGGV	474	2.4000	25.26
18	VVGIPITDL	33	2.3600	24.84
19	YHVSTPTEL	525	2.3600	24.84
20	LNNGGVYRG	477	2.3500	24.74
21	VLGQAVEAS	174	2.3000	24.21
22	YNALGAIRS	378	2.3000	24.21
23	WGVMGIGMG	425	2.2000	23.16
24	YVVNEGANA	395	2.1000	22.11
25	LTGDIGSVM	323	1.9700	20.74
26	YGVVGIPIT	31	1.9000	20.00
27	LLVLSKGAA	219	1.9000	20.00
28	VLTDGCHLV	10	1.8000	18.95
29	IGMGYAIAA	430	1.8000	18.95
30	FLTARPGVC	70	1.6000	16.84
31	IVAPLTGDI	319	1.6000	16.84
32	FETICRYRL	462	1.5100	15.89
33	LKANDVDTI	22	1.5000	15.79
34	FVEHTGIPF	238	1.5000	15.79
35	MAKGLLPDS	251	1.5000	15.79
36	LVGARLNWL	280	1.3700	14.42
37	VVLLVGARL	277	1.3600	14.32
38	MGIGMGYAI	428	1.3500	14.21
39	VKAAYRIGQ	135	1.3000	13.68
40	IPGDVLGQA	170	1.3000	13.68
41	WLLGNGESP	287	1.3000	13.68
42	IQVDIEASE	304	1.3000	13.68
43	MVDLQRGDY	114	1.2000	12.63
44	LLVGARLNW	279	1.2000	12.63
45	MRFYNALGA	375	1.2000	12.63
46	FYNALGAIR	377	1.2000	12.63
47	YAIAAAVET	434	1.2000	12.63
48	LANATTNCF	93	1.1100	11.68
49	YIGFRHEAS	52	1.1000	11.58

50	LADDHHPMR	368	1.1000	11.58
51	MIQISGSSS	103	1.0700	11.26
52	MARADVVLL	272	1.0600	11.16
53	VILNNGGVY	475	1.0000	10.53
54	IRTATSGRP	155	0.9000	9.47
55	IFRSAAPVW	490	0.9000	9.47
56	FLPMSMAKG	246	0.8000	8.42
57	FRHEASAGN	55	0.7000	7.37
58	ILNNGGVYR	476	0.7000	7.37

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	YRIGQVQDI	139	4.1000	46.59
2	LLPDSHPQS	255	3.5000	39.77
3	LVVDALKAN	17	3.4000	38.64
4	VLGQAVEAS	174	3.3000	37.50
5	VYLDIPGDV	166	2.7000	30.68
6	LLVGARLNW	279	2.7000	30.68
7	MRFYNALGA	375	2.7000	30.68
8	VKAAYRIGQ	135	2.6800	30.45
9	VLTDGCHLV	10	2.6000	29.55
10	YRGDEATIF	483	2.6000	29.55
11	IGMGYAIAA	430	2.4800	28.18
12	VVGIPITDL	33	2.4000	27.27
13	WRHDPAPTV	498	2.3000	26.14
14	IQISGSSSR	104	2.1000	23.86
15	LVLSKGAAY	220	2.1000	23.86
16	LVGARLNWL	280	2.1000	23.86
17	LKANDVDTI	22	1.9000	21.59
18	WSADAKFIQ	297	1.8000	20.45
19	YRLPVTVVI	468	1.7800	20.23
20	FIQVDIEAS	303	1.7000	19.32

21	VMSALLEAA	330	1.7000	19.32
22	MRRRLADDH	364	1.6800	19.09
23	FPMIQISGS	101	1.6000	18.18
24	VVAIEGDSA	446	1.6000	18.18
25	VGIPITDLA	34	1.5000	17.05
26	FLNGLPALA	86	1.5000	17.05
27	LLVLSKGAA	219	1.5000	17.05
28	LGAIRSVLQ	381	1.4800	16.82
29	MIQISGSSS	103	1.4000	15.91
30	VVLLVGARL	277	1.4000	15.91
31	LARNIIDMH	406	1.3800	15.68
32	LTGDIGSVM	323	1.2000	13.64
33	VVNEGANAL	396	1.2000	13.64
34	VETGRPVVA	440	1.1800	13.41
35	YVVNEGANA	395	1.1000	12.50
36	WRPVDPAPR	189	1.0000	11.36
37	VIREFVEHT	234	1.0000	11.36
38	VVILNNGGV	474	1.0000	11.36
39	MARADVVLL	272	0.9800	11.14
40	FRSAAPVWR	491	0.9800	11.14
41	LANATTNCF	93	0.9000	10.23
42	IPGDVLGQA	170	0.9000	10.23
43	IQVDIEASE	304	0.9000	10.23
44	LNNGGVYRG	477	0.8000	9.09
45	LNAHARHEL	507	0.8000	9.09
46	MAKGLLPDS	251	0.7000	7.95
47	LAKLNTTSA	564	0.7000	7.95
48	VEASAASGA	179	0.6000	6.82
49	MGYAIAAAV	432	0.6000	6.82
50	IEGDSAFGF	449	0.6000	6.82
51	YNALGAIRS	378	0.5800	6.59
52	IFRSAAPVW	490	0.5000	5.68
53	VVDALKAND	18	0.4000	4.55
54	VARAIRTAT	151	0.4000	4.55

55	LAMARADVV	270	0.4000	4.55
56	VYRGDEATI	482	0.4000	4.55
57	YHVSTPTEL	525	0.4000	4.55
58	LASNGPSLI	541	0.4000	4.55

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	FRHEASAGN	55	3.5000	40.70
2	YRLPVTVVI	468	3.2800	38.14
3	VLGQAVEAS	174	2.8000	32.56
4	YRIGQVQDI	139	2.7000	31.40
5	VVNEGANAL	396	2.7000	31.40
6	VVILNNGGV	474	2.7000	31.40
7	YRGDEATIF	483	2.7000	31.40
8	WRHDPAPTV	498	2.4000	27.91
9	YNALGAIRS	378	2.3800	27.67
10	IQISGSSSR	104	2.3000	26.74
11	VIREFVEHT	234	2.2000	25.58
12	FPMIQISGS	101	2.1000	24.42
13	YVVNEGANA	395	2.0000	23.26
14	LGAIRSVLQ	381	1.8800	21.86
15	LAKLNTTSA	564	1.6000	18.60
16	FRSAAPVWR	491	1.4800	17.21
17	LKANDVDTI	22	1.3000	15.12
18	WTGELADRK	349	1.1000	12.79
19	MRFYNALGA	375	1.1000	12.79
20	VGIPITDLA	34	1.0000	11.63
21	LANATTNCF	93	1.0000	11.63
22	FIQVDIEAS	303	1.0000	11.63
23	YHVSTPTEL	525	1.0000	11.63
24	VVGIPITDL	33	0.9000	10.47
25	VLTDGCHLV	10	0.7000	8.14

26	WRPVDPAPR	189	0.6000	6.98
27	LVLSKGAAY	220	0.4000	4.65
28	VVLLVGARL	277	0.4000	4.65
29	YAQADNVIR	228	0.3800	4.42
30	YAIAAAVET	434	0.3800	4.42
31	VYLDIPGDV	166	0.3000	3.49
32	LLPDSHPQS	255	0.3000	3.49
33	MEFETICRY	460	0.3000	3.49
34	LARNIIDMH	406	0.2800	3.26
35	LVVDALKAN	17	0.2000	2.33
36	VDIEASEFD	306	0.2000	2.33
37	LNGLPALAN	87	0.1000	1.16
38	FLPMSMAKG	246	0.1000	1.16
39	VVAIEGDSA	446	0.1000	1.16
40	LQRNPDVYV	388	0.0800	0.93
41	YIGFRHEAS	52	-0.1000	0
42	FLNGLPALA	86	-0.1000	0
43	MIQISGSSS	103	-0.1000	0
44	YQDLDQLNA	122	-0.1000	0
45	LESALTDAL	533	-0.1000	0
46	FDSNRPIVA	313	-0.1200	0
47	LVGARLNWL	280	-0.2000	0
48	IVAPLTGDI	319	-0.2000	0
49	MRRRLADDH	364	-0.2200	0
50	FLTARPGVC	70	-0.3000	0
51	VEASAASGA	179	-0.3000	0
52	VAIEGDSAF	447	-0.3000	0
53	MARADVVLL	272	-0.3200	0
54	IPITDLARA	36	-0.4000	0
55	IRTATSGRP	155	-0.4000	0
56	MGYAIAAAV	432	-0.4000	0
57	FSGMEFETI	457	-0.4000	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	YRIGQVQDI	139	3.7000	38.54
2	MRFYNALGA	375	3.6000	37.50
3	VGARLNWLL	281	3.2000	33.33
4	YRLPVTVVI	468	2.7000	28.13
5	LGAIRSVLQ	381	2.2800	23.75
6	LADRKARNS	353	2.1000	21.88
7	LANATTNCF	93	2.0000	20.83
8	IDMHLPRHR	411	2.0000	20.83
9	IRYIGFRHE	50	1.9800	20.62
10	IGRGVARAI	147	1.9000	19.79
11	MRRRLADDH	364	1.8800	19.58
12	IGMGYAIAA	430	1.7000	17.71
13	VLLVGARLN	278	1.6000	16.67
14	VVILNNGGV	474	1.5000	15.62
15	VLNAHARHE	506	1.5000	15.62
16	LEAAADRSS	335	1.4000	14.58
17	LNNGGVYRG	477	1.4000	14.58
18	LAKLNTTSA	564	1.4000	14.58
19	VVGIPITDL	33	1.3800	14.37
20	IQISGSSSR	104	1.3000	13.54
21	VLSKGAAYA	221	1.3000	13.54
22	ISGSSSRPM	106	1.2000	12.50
23	VLGQAVEAS	174	1.2000	12.50
24	LNAARPFVK	128	1.0000	10.42
25	MARADVVLL	272	0.8000	8.33
26	LVGARLNWL	280	0.8000	8.33
27	MTTRSASPC	0	0.6000	6.25
28	IRSVLQRNP	384	0.6000	6.25
29	MGYAIAAAV	432	0.6000	6.25
30	FRSAAPVWR	491	0.6000	6.25
31	VWRHDPAPT	497	0.6000	6.25

32	VGIPITDLA	34	0.5000	5.21
33	LSKGAAYAQ	222	0.4000	4.17
34	YNALGAIRS	378	0.4000	4.17
35	MGIGMGYAI	428	0.4000	4.17
36	FVKAAYRIG	134	0.3000	3.12
37	IVAPLTGDI	319	0.3000	3.12
38	FPMIQISGS	101	0.1800	1.88
39	MIQISGSSS	103	-0.0200	0
40	IGFRHEASA	53	-0.1000	0
41	LQRNPDVYV	388	-0.1000	0
42	VVNEGANAL	396	-0.1000	0
43	FLNGLPALA	86	-0.2000	0
44	LQRGDYQDL	117	-0.2000	0
45	IRTATSGRP	155	-0.2000	0
46	WRPVDPAPR	189	-0.2000	0
47	VLAQAQRPL	211	-0.2000	0
48	LDLARNIID	404	-0.2000	0
49	VKAAYRIGQ	135	-0.3000	0
50	YVVNEGANA	395	-0.3000	0
51	LVLSKGAAY	220	-0.4000	0
52	VETGRPVVA	440	-0.4000	0
53	YAQADNVIR	228	-0.5000	0
54	YAIAAAVET	434	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVILNNGGV	474	4.0000	45.45
2	LAKLNTTSA	564	3.3000	37.50
3	LGAIRSVLQ	381	3.0000	34.09
4	MRFYNALGA	375	2.9000	32.95
5	VVGIPITDL	33	2.7000	30.68
6	IQISGSSSR	104	2.5000	28.41

7	YRLPVTVVI	468	2.4000	27.27
8	LANATTNCF	93	2.1000	23.86
9	FPMIQISGS	101	2.1000	23.86
10	VLGQAVEAS	174	2.1000	23.86
11	MIQISGSSS	103	1.9000	21.59
12	VVLLVGARL	277	1.6000	18.18
13	YNALGAIRS	378	1.5800	17.95
14	VGIPITDLA	34	1.4000	15.91
15	IVAPLTGDI	319	1.2000	13.64
16	IGSVMSALL	327	1.2000	13.64
17	VVNEGANAL	396	1.2000	13.64
18	WRPVDPAPR	189	1.0000	11.36
19	LNGLPALAN	87	0.9000	10.23
20	LVGARLNWL	280	0.9000	10.23
21	YRIGQVQDI	139	0.7000	7.95
22	IRTATSGRP	155	0.7000	7.95
23	IPFLPMSMA	244	0.7000	7.95
24	LPALANATT	90	0.6000	6.82
25	MGYAIAAAV	432	0.6000	6.82
26	MARADVVLL	272	0.5000	5.68
27	FIQVDIEAS	303	0.5000	5.68
28	VVAIEGDSA	446	0.5000	5.68
29	LNAARPFVK	128	0.4500	5.11
30	IRYIGFRHE	50	0.4000	4.55
31	FRSAAPVWR	491	0.3000	3.41
32	VLLVGARLN	278	0.2000	2.27
33	VMGIGMGYA	427	0.1000	1.14
34	YIGFRHEAS	52	-0.1000	0
35	FRHEASAGN	55	-0.1000	0
36	VEASAASGA	179	-0.1000	0
37	LVLSKGAAY	220	-0.1000	0
38	IYGVVGIPI	30	-0.1200	0
39	LKANDVDTI	22	-0.2000	0
40	VDALKANDV	19	-0.3000	0

41	VLSKGAAYA	221	-0.3000	0
42	VIREFVEHT	234	-0.3000	0
43	YRGDEATIF	483	-0.3000	0
44	LASNGPSLI	541	-0.3000	0
45	VTVVILNNG	472	-0.4000	0
46	IIDMHLPRH	410	-0.4200	0
47	IGMGYAIAA	430	-0.4200	0
48	LAMARADVV	270	-0.5000	0
49	VMSALLEAA	330	-0.5000	0
50	WGVMGIGMG	425	-0.5000	0
51	YVVNEGANA	395	-0.6000	0
52	MRRRLADDH	364	-0.6200	0
53	LDLARNIID	404	-0.6200	0
54	LNWLLGNGE	285	-0.7000	0
55	LLEAAADRS	334	-0.7000	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	YRLPVTVVI	468	3.6000	38.30
2	VVILNNGGV	474	3.3000	35.11
3	FPMIQISGS	101	3.1000	32.98
4	FRHEASAGN	55	2.9000	30.85
5	LGAIRSVLQ	381	2.8000	29.79
6	VVGIPITDL	33	2.7000	28.72
7	YNALGAIRS	378	2.5800	27.45
8	IRYIGFRHE	50	2.4000	25.53
9	FLPMSMAKG	246	2.3000	24.47
10	LAKLNTTSA	564	2.3000	24.47
11	LANATTNCF	93	2.0000	21.28
12	WRPVDPAPR	189	2.0000	21.28
13	LNGLPALAN	87	1.9000	20.21
14	YRIGQVQDI	139	1.9000	20.21

15	MRFYNALGA	375	1.9000	20.21
16	WGVMGIGMG	425	1.8000	19.15
17	VVLLVGARL	277	1.6000	17.02
18	YRGDEATIF	483	1.6000	17.02
19	IQISGSSSR	104	1.5000	15.96
20	FIQVDIEAS	303	1.5000	15.96
21	LNWLLGNGE	285	1.3000	13.83
22	FRSAAPVWR	491	1.3000	13.83
23	VLLVGARLN	278	1.2000	12.77
24	IGSVMSALL	327	1.2000	12.77
25	VVNEGANAL	396	1.2000	12.77
26	VLGQAVEAS	174	1.1000	11.70
27	YAIAAAVET	434	1.1000	11.70
28	LDLARNIID	404	1.0800	11.49
29	YHVSTPTEL	525	1.0000	10.64
30	YIGFRHEAS	52	0.9000	9.57
31	MIQISGSSS	103	0.9000	9.57
32	LVGARLNWL	280	0.9000	9.57
33	VLNAHARHE	506	0.9000	9.57
34	LPALANATT	90	0.5000	5.32
35	MARADVVLL	272	0.5000	5.32
36	VGIPITDLA	34	0.4000	4.26
37	IVAPLTGDI	319	0.4000	4.26
38	YVVNEGANA	395	0.4000	4.26
39	YAQADNVIR	228	0.2000	2.13
40	YGVVGIPIT	31	0.1000	1.06
41	IRTATSGRP	155	0.1000	1.06
42	FGFSGMEFE	455	0.1000	1.06
43	VASAAWTGE	344	-0.1000	0
44	MGYAIAAAV	432	-0.1000	0
45	VTVVILNNG	472	-0.1000	0
46	WRHDPAPTV	498	-0.1000	0
47	FLTARPGVC	70	-0.2000	0
48	IIDMHLPRH	410	-0.2000	0

49	FSGMEFETI	457	-0.2000	0
50	YQDLDQLNA	122	-0.3000	0
51	IPFLPMSMA	244	-0.3000	0
52	LPVTVVILN	470	-0.3200	0
53	VIREFVEHT	234	-0.4000	0
54	MRRRLADDH	364	-0.4000	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	YRLPVTVVI	468	3.4000	38.64
2	FPMIQISGS	101	3.1000	35.23
3	VVILNNGGV	474	3.0000	34.09
4	YNALGAIRS	378	2.5800	29.32
5	LAKLNTTSA	564	2.3000	26.14
6	WRPVDPAPR	189	2.0000	22.73
7	LGAIRSVLQ	381	2.0000	22.73
8	MRFYNALGA	375	1.9000	21.59
9	VVGIPITDL	33	1.7000	19.32
10	YRIGQVQDI	139	1.7000	19.32
11	IQISGSSSR	104	1.5000	17.05
12	FIQVDIEAS	303	1.5000	17.05
13	FRSAAPVWR	491	1.3000	14.77
14	LANATTNCF	93	1.1000	12.50
15	VLGQAVEAS	174	1.1000	12.50
16	FLPMSMAKG	246	1.0000	11.36
17	YIGFRHEAS	52	0.9000	10.23
18	FRHEASAGN	55	0.9000	10.23
19	MIQISGSSS	103	0.9000	10.23
20	YRGDEATIF	483	0.7000	7.95
21	VVLLVGARL	277	0.6000	6.82
22	WGVMGIGMG	425	0.5000	5.68
23	VGIPITDLA	34	0.4000	4.55

24	YVVNEGANA	395	0.4000	4.55
25	YAQADNVIR	228	0.2000	2.27
26	IVAPLTGDI	319	0.2000	2.27
27	IGSVMSALL	327	0.2000	2.27
28	VVNEGANAL	396	0.2000	2.27
29	YAIAAAVET	434	0.2000	2.27
30	LNGLPALAN	87	-0.1000	0
31	LVGARLNWL	280	-0.1000	0
32	FLTARPGVC	70	-0.2000	0
33	YQDLDQLNA	122	-0.3000	0
34	IRTATSGRP	155	-0.3000	0
35	IPFLPMSMA	244	-0.3000	0
36	LPALANATT	90	-0.4000	0
37	MGYAIAAAV	432	-0.4000	0
38	FSGMEFETI	457	-0.4000	0
39	WRHDPAPTV	498	-0.4000	0
40	MARADVVLL	272	-0.5000	0
41	VVAIEGDSA	446	-0.5000	0
42	LNAARPFVK	128	-0.5500	0
43	IRYIGFRHE	50	-0.6000	0
44	YGVVGIPIT	31	-0.8000	0
45	VLLVGARLN	278	-0.8000	0
46	FLNGLPALA	86	-0.9000	0
47	VMGIGMGYA	427	-0.9000	0
48	LESALTDAL	533	-1.0000	0
49	VEASAASGA	179	-1.1000	0
50	LVLSKGAAY	220	-1.1000	0
51	FYNALGAIR	377	-1.1000	0
52	IYGVVGIPI	30	-1.1200	0
53	LKANDVDTI	22	-1.2000	0
54	VDALKANDV	19	-1.3000	0
55	FVKAAYRIG	134	-1.3000	0
56	VLSKGAAYA	221	-1.3000	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	VVILNNGGV	474	4.3000	45.74
2	LGAIRSVLQ	381	3.8000	40.43
3	VVGIPITDL	33	3.7000	39.36
4	IRYIGFRHE	50	3.4000	36.17
5	LAKLNTTSA	564	3.3000	35.11
6	LANATTNCF	93	3.0000	31.91
7	LNGLPALAN	87	2.9000	30.85
8	MRFYNALGA	375	2.9000	30.85
9	VVLLVGARL	277	2.6000	27.66
10	YRLPVTVVI	468	2.6000	27.66
11	IQISGSSSR	104	2.5000	26.60
12	LNWLLGNGE	285	2.3000	24.47
13	VLLVGARLN	278	2.2000	23.40
14	IGSVMSALL	327	2.2000	23.40
15	VVNEGANAL	396	2.2000	23.40
16	FPMIQISGS	101	2.1000	22.34
17	VLGQAVEAS	174	2.1000	22.34
18	LDLARNIID	404	2.0800	22.13
19	FRHEASAGN	55	1.9000	20.21
20	MIQISGSSS	103	1.9000	20.21
21	LVGARLNWL	280	1.9000	20.21
22	VLNAHARHE	506	1.9000	20.21
23	YNALGAIRS	378	1.5800	16.81
24	LPALANATT	90	1.5000	15.96
25	MARADVVLL	272	1.5000	15.96
26	VGIPITDLA	34	1.4000	14.89
27	IVAPLTGDI	319	1.4000	14.89
28	FLPMSMAKG	246	1.3000	13.83
29	IRTATSGRP	155	1.1000	11.70
30	WRPVDPAPR	189	1.0000	10.64

31	LVLSKGAAY	220	1.0000	10.64
32	LESALTDAL	533	1.0000	10.64
33	YRIGQVQDI	139	0.9000	9.57
34	VASAAWTGE	344	0.9000	9.57
35	MGYAIAAAV	432	0.9000	9.57
36	VTVVILNNG	472	0.9000	9.57
37	IIDMHLPRH	410	0.8000	8.51
38	WGVMGIGMG	425	0.8000	8.51
39	IPFLPMSMA	244	0.7000	7.45
40	LPVTVVILN	470	0.6800	7.23
41	VIREFVEHT	234	0.6000	6.38
42	MRRRLADDH	364	0.6000	6.38
43	YRGDEATIF	483	0.6000	6.38
44	FIQVDIEAS	303	0.5000	5.32
45	VVAIEGDSA	446	0.5000	5.32
46	VDIEASEFD	306	0.4000	4.26
47	FRSAAPVWR	491	0.3000	3.19
48	VCLTTSGPG	77	0.2000	2.13
49	VMGIGMGYA	427	0.1000	1.06
50	YAIAAAVET	434	0.1000	1.06
51	IYGVVGIPI	30	0.0800	0.85
52	VKAAYRIGQ	135	0.0800	0.85

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	YRGDEATIF	483	4.6000	51.11
2	FRHEASAGN	55	4.3000	47.78
3	YRLPVTVVI	468	4.1800	46.44
4	IQISGSSSR	104	3.8000	42.22
5	VVILNNGGV	474	3.7000	41.11
6	VVNEGANAL	396	3.6600	40.67
7	YRIGQVQDI	139	3.6000	40.00

8	WRHDPAPTV	498	3.4000	37.78
9	VLGQAVEAS	174	3.2000	35.56
10	FRSAAPVWR	491	2.9800	33.11
11	LANATTNCF	93	2.9000	32.22
12	VIREFVEHT	234	2.9000	32.22
13	YNALGAIRS	378	2.7800	30.89
14	FPMIQISGS	101	2.5000	27.78
15	LKANDVDTI	22	2.2000	24.44
16	WRPVDPAPR	189	2.1000	23.33
17	YVVNEGANA	395	2.0000	22.22
18	YHVSTPTEL	525	1.9600	21.78
19	YAQADNVIR	228	1.8800	20.89
20	VVGIPITDL	33	1.8600	20.67
21	VLTDGCHLV	10	1.7000	18.89
22	LVLSKGAAY	220	1.7000	18.89
23	VAIEGDSAF	447	1.6000	17.78
24	MEFETICRY	460	1.6000	17.78
25	LAKLNTTSA	564	1.6000	17.78
26	FLPMSMAKG	246	1.5000	16.67
27	FVEHTGIPF	238	1.4800	16.44
28	FIQVDIEAS	303	1.4000	15.56
29	VVLLVGARL	277	1.3600	15.11
30	VYLDIPGDV	166	1.3000	14.44
31	VDIEASEFD	306	1.3000	14.44
32	WTGELADRK	349	1.2000	13.33
33	LGAIRSVLQ	381	1.1800	13.11
34	MRFYNALGA	375	1.1000	12.22
35	LQRNPDVYV	388	1.0800	12.00
36	YAIAAAVET	434	1.0800	12.00
37	LVVDALKAN	17	1.0000	11.11
38	VGIPITDLA	34	1.0000	11.11
39	LNGLPALAN	87	0.9000	10.00
40	WGVMGIGMG	425	0.9000	10.00
41	FGFSGMEFE	455	0.9000	10.00

42	LESALTDAL	533	0.8600	9.56
43	VCLTTSGPG	77	0.8000	8.89
44	LVGARLNWL	280	0.7600	8.44
45	LLPDSHPQS	255	0.7000	7.78
46	IVAPLTGDI	319	0.7000	7.78
47	MARADVVLL	272	0.6400	7.11
48	ISGSSSRPM	106	0.6000	6.67
49	IRTATSGRP	155	0.6000	6.67
50	MGYAIAAAV	432	0.6000	6.67
51	IEGDSAFGF	449	0.6000	6.67
52	FSGMEFETI	457	0.5000	5.56
53	LASNGPSLI	541	0.5000	5.56
54	ILNNGGVYR	476	0.4800	5.33
55	LAMARADVV	270	0.4000	4.44
56	FYNALGAIR	377	0.4000	4.44
57	LPMSMAKGL	247	0.3600	4.00
58	YIGFRHEAS	52	0.3000	3.33

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVILNNGGV	474	4.0000	45.45
2	LAKLNTTSA	564	3.3000	37.50
3	LGAIRSVLQ	381	3.0000	34.09
4	MRFYNALGA	375	2.9000	32.95
5	VVGIPITDL	33	2.7000	30.68
6	IQISGSSSR	104	2.5000	28.41
7	YRLPVTVVI	468	2.4000	27.27
8	LANATTNCF	93	2.1000	23.86
9	FPMIQISGS	101	2.1000	23.86
10	VLGQAVEAS	174	2.1000	23.86
11	MIQISGSSS	103	1.9000	21.59
12	VVLLVGARL	277	1.6000	18.18

13	YNALGAIRS	378	1.5800	17.95
14	VGIPITDLA	34	1.4000	15.91
15	IVAPLTGDI	319	1.2000	13.64
16	IGSVMSALL	327	1.2000	13.64
17	VVNEGANAL	396	1.2000	13.64
18	WRPVDPAPR	189	1.0000	11.36
19	LNGLPALAN	87	0.9000	10.23
20	LVGARLNWL	280	0.9000	10.23
21	YRIGQVQDI	139	0.7000	7.95
22	IRTATSGRP	155	0.7000	7.95
23	IPFLPMSMA	244	0.7000	7.95
24	LPALANATT	90	0.6000	6.82
25	MGYAIAAAV	432	0.6000	6.82
26	MARADVVLL	272	0.5000	5.68
27	FIQVDIEAS	303	0.5000	5.68
28	VVAIEGDSA	446	0.5000	5.68
29	LNAARPFVK	128	0.4500	5.11
30	IRYIGFRHE	50	0.4000	4.55
31	FRSAAPVWR	491	0.3000	3.41
32	VLLVGARLN	278	0.2000	2.27
33	VMGIGMGYA	427	0.1000	1.14
34	YIGFRHEAS	52	-0.1000	0
35	FRHEASAGN	55	-0.1000	0
36	VEASAASGA	179	-0.1000	0
37	LVLSKGAAY	220	-0.1000	0
38	IYGVVGIPI	30	-0.1200	0
39	LKANDVDTI	22	-0.2000	0
40	VDALKANDV	19	-0.3000	0
41	VLSKGAAYA	221	-0.3000	0
42	VIREFVEHT	234	-0.3000	0
43	YRGDEATIF	483	-0.3000	0
44	LASNGPSLI	541	-0.3000	0
45	VTVVILNNG	472	-0.4000	0
46	IIDMHLPRH	410	-0.4200	0

47	IGMGYAIAA	430	-0.4200	0
48	LAMARADVV	270	-0.5000	0
49	VMSALLEAA	330	-0.5000	0
50	WGVMGIGMG	425	-0.5000	0
51	YVVNEGANA	395	-0.6000	0
52	MRRRLADDH	364	-0.6200	0
53	LDLARNIID	404	-0.6200	0
54	LNWLLGNGE	285	-0.7000	0
55	LLEAAADRS	334	-0.7000	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	FRHEASAGN	55	3.5000	40.70
2	YRLPVTVVI	468	3.2800	38.14
3	VLGQAVEAS	174	2.8000	32.56
4	YRIGQVQDI	139	2.7000	31.40
5	VVNEGANAL	396	2.7000	31.40
6	VVILNNGGV	474	2.7000	31.40
7	YRGDEATIF	483	2.7000	31.40
8	WRHDPAPTV	498	2.4000	27.91
9	YNALGAIRS	378	2.3800	27.67
10	IQISGSSSR	104	2.3000	26.74
11	VIREFVEHT	234	2.2000	25.58
12	FPMIQISGS	101	2.1000	24.42
13	YVVNEGANA	395	2.0000	23.26
14	LGAIRSVLQ	381	1.8800	21.86
15	LAKLNTTSA	564	1.6000	18.60
16	FRSAAPVWR	491	1.4800	17.21
17	LKANDVDTI	22	1.3000	15.12
18	WTGELADRK	349	1.1000	12.79
19	MRFYNALGA	375	1.1000	12.79
20	VGIPITDLA	34	1.0000	11.63

21	LANATTNCF	93	1.0000	11.63
22	FIQVDIEAS	303	1.0000	11.63
23	YHVSTPTEL	525	1.0000	11.63
24	VVGIPITDL	33	0.9000	10.47
25	VLTDGCHLV	10	0.7000	8.14
26	WRPVDPAPR	189	0.6000	6.98
27	LVLSKGAAY	220	0.4000	4.65
28	VVLLVGARL	277	0.4000	4.65
29	YAQADNVIR	228	0.3800	4.42
30	YAIAAAVET	434	0.3800	4.42
31	VYLDIPGDV	166	0.3000	3.49
32	LLPDSHPQS	255	0.3000	3.49
33	MEFETICRY	460	0.3000	3.49
34	LARNIIDMH	406	0.2800	3.26
35	LVVDALKAN	17	0.2000	2.33
36	VDIEASEFD	306	0.2000	2.33
37	LNGLPALAN	87	0.1000	1.16
38	FLPMSMAKG	246	0.1000	1.16
39	VVAIEGDSA	446	0.1000	1.16
40	LQRNPDVYV	388	0.0800	0.93
41	YIGFRHEAS	52	-0.1000	0
42	FLNGLPALA	86	-0.1000	0
43	MIQISGSSS	103	-0.1000	0
44	YQDLDQLNA	122	-0.1000	0
45	LESALTDAL	533	-0.1000	0
46	FDSNRPIVA	313	-0.1200	0
47	LVGARLNWL	280	-0.2000	0
48	IVAPLTGDI	319	-0.2000	0
49	MRRRLADDH	364	-0.2200	0
50	FLTARPGVC	70	-0.3000	0
51	VEASAASGA	179	-0.3000	0
52	VAIEGDSAF	447	-0.3000	0
53	MARADVVLL	272	-0.3200	0
54	IPITDLARA	36	-0.4000	0

55	IRTATSGRP	155	-0.4000	0
56	MGYAIAAAV	432	-0.4000	0
57	FSGMEFETI	457	-0.4000	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	YRIGQVQDI	139	7.2000	62.07
2	YRLPVTVVI	468	6.9200	59.66
3	YHVSTPTEL	525	6.6000	56.90
4	IYGVVGIPI	30	6.2000	53.45
5	VVGIPITDL	33	6.2000	53.45
6	LPMSMAKGL	247	5.3000	45.69
7	LVGARLNWL	280	5.2000	44.83
8	FETICRYRL	462	5.2000	44.83
9	VVNEGANAL	396	5.0000	43.10
10	FVEHTGIPF	238	4.9000	42.24
11	MARADVVLL	272	4.8000	41.38
12	IGSVMSALL	327	4.6000	39.66
13	MGIGMGYAI	428	4.4000	37.93
14	LVLSKGAAY	220	4.1000	35.34
15	VVLLVGARL	277	4.1000	35.34
16	YRGDEATIF	483	3.8000	32.76
17	ISGSSSRPM	106	3.7000	31.90
18	YAIAAAVET	434	3.5000	30.17
19	LTTSGPGFL	79	3.4000	29.31
20	IQISGSSSR	104	3.4000	29.31
21	VEHTGIPFL	239	3.4000	29.31
22	LQRGDYQDL	117	3.3000	28.45
23	MRFYNALGA	375	3.3000	28.45
24	IVAPLTGDI	319	3.2200	27.76
25	IGRGVARAI	147	3.2000	27.59
26	VVILNNGGV	474	3.2000	27.59

27	LNAHARHEL	507	3.1000	26.72
28	FSGMEFETI	457	3.0000	25.86
29	LANATTNCF	93	2.9200	25.17
30	IRYIGFRHE	50	2.7000	23.28
31	FRSAAPVWR	491	2.7000	23.28
32	VGARLNWLL	281	2.6000	22.41
33	FGFSGMEFE	455	2.6000	22.41
34	IFRSAAPVW	490	2.6000	22.41
35	WRHDPAPTV	498	2.6000	22.41
36	LPVTVVILN	470	2.4000	20.69
37	LTARPGVCL	71	2.3000	19.83
38	YLDIPGDVL	167	2.3000	19.83
39	MGYAIAAAV	432	2.3000	19.83
40	IGMGYAIAA	430	2.2000	18.97
41	WRPVDPAPR	189	2.1000	18.10
42	VLLVGARLN	278	2.1000	18.10
43	FIQVDIEAS	303	2.1000	18.10
44	YNALGAIRS	378	2.1000	18.10
45	LGAIRSVLQ	381	1.9000	16.38
46	IEGDSAFGF	449	1.9000	16.38
47	YGVVGIPIT	31	1.6000	13.79
48	FPMIQISGS	101	1.6000	13.79
49	VLAQAQRPL	211	1.5000	12.93
50	VCLTTSGPG	77	1.4000	12.07
51	LASNGPSLI	541	1.4000	12.07
52	LESALTDAL	533	1.3200	11.38
53	VLTDGCHLV	10	1.3000	11.21
54	YIGFRHEAS	52	1.3000	11.21
55	LLVGARLNW	279	1.3000	11.21
56	IRSVLQRNP	384	1.3000	11.21
57	LKANDVDTI	22	1.2000	10.34
58	FVKAAYRIG	134	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	YRIGQVQDI	139	7.2000	62.07
2	YRLPVTVVI	468	6.9200	59.66
3	YHVSTPTEL	525	6.6000	56.90
4	IYGVVGIPI	30	6.2000	53.45
5	VVGIPITDL	33	6.2000	53.45
6	LPMSMAKGL	247	5.3000	45.69
7	LVGARLNWL	280	5.2000	44.83
8	FETICRYRL	462	5.2000	44.83
9	VVNEGANAL	396	5.0000	43.10
10	FVEHTGIPF	238	4.9000	42.24
11	MARADVVLL	272	4.8000	41.38
12	IGSVMSALL	327	4.6000	39.66
13	MGIGMGYAI	428	4.4000	37.93
14	LVLSKGAAY	220	4.1000	35.34
15	VVLLVGARL	277	4.1000	35.34
16	YRGDEATIF	483	3.8000	32.76
17	ISGSSSRPM	106	3.7000	31.90
18	YAIAAAVET	434	3.5000	30.17
19	LTTSGPGFL	79	3.4000	29.31
20	IQISGSSSR	104	3.4000	29.31
21	VEHTGIPFL	239	3.4000	29.31
22	LQRGDYQDL	117	3.3000	28.45
23	MRFYNALGA	375	3.3000	28.45
24	IVAPLTGDI	319	3.2200	27.76
25	IGRGVARAI	147	3.2000	27.59
26	VVILNNGGV	474	3.2000	27.59
27	LNAHARHEL	507	3.1000	26.72
28	FSGMEFETI	457	3.0000	25.86
29	LANATTNCF	93	2.9200	25.17
30	IRYIGFRHE	50	2.7000	23.28
31	FRSAAPVWR	491	2.7000	23.28

32	VGARLNWLL	281	2.6000	22.41
33	FGFSGMEFE	455	2.6000	22.41
34	IFRSAAPVW	490	2.6000	22.41
35	WRHDPAPTV	498	2.6000	22.41
36	LPVTVVILN	470	2.4000	20.69
37	LTARPGVCL	71	2.3000	19.83
38	YLDIPGDVL	167	2.3000	19.83
39	MGYAIAAAV	432	2.3000	19.83
40	IGMGYAIAA	430	2.2000	18.97
41	WRPVDPAPR	189	2.1000	18.10
42	VLLVGARLN	278	2.1000	18.10
43	FIQVDIEAS	303	2.1000	18.10
44	YNALGAIRS	378	2.1000	18.10
45	LGAIRSVLQ	381	1.9000	16.38
46	IEGDSAFGF	449	1.9000	16.38
47	YGVVGIPIT	31	1.6000	13.79
48	FPMIQISGS	101	1.6000	13.79
49	VLAQAQRPL	211	1.5000	12.93
50	VCLTTSGPG	77	1.4000	12.07
51	LASNGPSLI	541	1.4000	12.07
52	LESALTDAL	533	1.3200	11.38
53	VLTDGCHLV	10	1.3000	11.21
54	YIGFRHEAS	52	1.3000	11.21
55	LLVGARLNW	279	1.3000	11.21
56	IRSVLQRNP	384	1.3000	11.21
57	LKANDVDTI	22	1.2000	10.34
58	FVKAAYRIG	134	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	MRFYNALGA	375	3.9000	45.35
2	MRRRLADDH	364	3.1000	36.05

3	WGVMGIGMG	425	2.9000	33.72
4	YRIGQVQDI	139	2.6000	30.23
5	VLSKGAAYA	221	2.5000	29.07
6	WRPVDPAPR	189	2.3000	26.74
7	VVDALKAND	18	2.1000	24.42
8	FLPMSMAKG	246	2.1000	24.42
9	VVLLVGARL	277	2.1000	24.42
10	LLVLSKGAA	219	2.0000	23.26
11	FRHEASAGN	55	1.9000	22.09
12	YVVNEGANA	395	1.9000	22.09
13	YRLPVTVVI	468	1.8000	20.93
14	VVILNNGGV	474	1.8000	20.93
15	IRYIGFRHE	50	1.6000	18.60
16	VKAAYRIGQ	135	1.6000	18.60
17	YNALGAIRS	378	1.4000	16.28
18	FGGKGYHVS	520	1.4000	16.28
19	FPMIQISGS	101	1.3000	15.12
20	VLLVGARLN	278	1.3000	15.12
21	IGFRHEASA	53	1.2000	13.95
22	VLNAHARHE	506	1.2000	13.95
23	MVDLQRGDY	114	1.1000	12.79
24	FLTARPGVC	70	1.0000	11.63
25	FLNGLPALA	86	1.0000	11.63
26	LNGLPALAN	87	1.0000	11.63
27	FRSAAPVWR	491	0.8000	9.30
28	ITDLARAAQ	38	0.7000	8.14
29	LVVDALKAN	17	0.6000	6.98
30	ICRYRLPVT	465	0.6000	6.98
31	YGVVGIPIT	31	0.5000	5.81
32	LVLSKGAAY	220	0.5000	5.81
33	VLQRNPDVY	387	0.5000	5.81
34	IIDMHLPRH	410	0.5000	5.81
35	FVKAAYRIG	134	0.4000	4.65
36	WSADAKFIQ	297	0.4000	4.65

37	FIQVDIEAS	303	0.4000	4.65
38	IVAPLTGDI	319	0.3000	3.49
39	FETICRYRL	462	0.3000	3.49
40	LVGARLNWL	280	0.2000	2.33
41	LLVGARLNW	279	0.1000	1.16
42	LADRKARNS	353	0.1000	1.16
43	MHLPRHRLD	413	0.1000	1.16
44	YAIAAAVET	434	0.1000	1.16
45	VVGIPITDL	33	-0.1000	0
46	LLPAPEAID	198	-0.1000	0
47	IGSVMSALL	327	-0.1000	0
48	LGAIRSVLQ	381	-0.1000	0
49	IRSVLQRNP	384	-0.1000	0
50	MGYAIAAAV	432	-0.1000	0
51	MARADVVLL	272	-0.2000	0
52	LNWLLGNGE	285	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	3.9000	48.75
2	VLSKGAAYA	221	2.5000	31.25
3	YRIGQVQDI	139	2.4000	30.00
4	WRPVDPAPR	189	2.3000	28.75
5	LLVLSKGAA	219	2.0000	25.00
6	YVVNEGANA	395	1.9000	23.75
7	MRRRLADDH	364	1.8800	23.50
8	WGVMGIGMG	425	1.6000	20.00
9	YRLPVTVVI	468	1.6000	20.00
10	VVILNNGGV	474	1.5000	18.75
11	YNALGAIRS	378	1.4000	17.50
12	FGGKGYHVS	520	1.4000	17.50
13	FPMIQISGS	101	1.3000	16.25

14	IGFRHEASA	53	1.2000	15.00
15	VVLLVGARL	277	1.1000	13.75
16	FLTARPGVC	70	1.0000	12.50
17	FLNGLPALA	86	1.0000	12.50
18	VKAAYRIGQ	135	0.8000	10.00
19	FLPMSMAKG	246	0.8000	10.00
20	FRSAAPVWR	491	0.8000	10.00
21	FIQVDIEAS	303	0.4000	5.00
22	IVAPLTGDI	319	0.1000	1.25
23	LADRKARNS	353	0.1000	1.25
24	ITDLARAAQ	38	-0.1000	0
25	FRHEASAGN	55	-0.1000	0
26	VQDIGRGVA	144	-0.3000	0
27	FYNALGAIR	377	-0.3000	0
28	ICRYRLPVT	465	-0.3000	0
29	YGVVGIPIT	31	-0.4000	0
30	WSADAKFIQ	297	-0.4000	0
31	MGYAIAAAV	432	-0.4000	0
32	IRSVLQRNP	384	-0.5000	0
33	WRHDPAPTV	498	-0.5000	0
34	VVDALKAND	18	-0.6000	0
35	LVLSKGAAY	220	-0.6000	0
36	VLQRNPDVY	387	-0.6000	0
37	IRTATSGRP	155	-0.7000	0
38	VLLVGARLN	278	-0.7000	0
39	FETICRYRL	462	-0.7000	0
40	IIDMHLPRH	410	-0.7200	0
41	IPITDLARA	36	-0.8000	0
42	VYLDIPGDV	166	-0.8000	0
43	LLVGARLNW	279	-0.8000	0
44	LVGARLNWL	280	-0.8000	0
45	VMGIGMGYA	427	-0.8000	0
46	YAIAAAVET	434	-0.8000	0
47	MIQISGSSS	103	-0.9000	0

48	LNAARPFVK	128	-0.9000	0
49	FVKAAYRIG	134	-0.9000	0
50	LGAIRSVLQ	381	-0.9000	0
51	IGMGYAIAA	430	-0.9000	0
52	LNGLPALAN	87	-1.0000	0
53	VGARLNWLL	281	-1.0000	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	MRFYNALGA	375	4.9000	61.25
2	VLSKGAAYA	221	3.5000	43.75
3	LLVLSKGAA	219	3.0000	37.50
4	MRRRLADDH	364	2.8800	36.00
5	VVILNNGGV	474	2.5000	31.25
6	IGFRHEASA	53	2.2000	27.50
7	VVLLVGARL	277	2.1000	26.25
8	VKAAYRIGQ	135	1.8000	22.50
9	YRIGQVQDI	139	1.4000	17.50
10	WRPVDPAPR	189	1.3000	16.25
11	IVAPLTGDI	319	1.1000	13.75
12	LADRKARNS	353	1.1000	13.75
13	MTTRSASPC	0	1.0000	12.50
14	MVDLQRGDY	114	1.0000	12.50
15	ITDLARAAQ	38	0.9000	11.25
16	YVVNEGANA	395	0.9000	11.25
17	VQDIGRGVA	144	0.7000	8.75
18	ICRYRLPVT	465	0.7000	8.75
19	WGVMGIGMG	425	0.6000	7.50
20	MGYAIAAAV	432	0.6000	7.50
21	YRLPVTVVI	468	0.6000	7.50
22	IRSVLQRNP	384	0.5000	6.25
23	VVDALKAND	18	0.4000	5.00

24	LVLSKGAAY	220	0.4000	5.00
25	YNALGAIRS	378	0.4000	5.00
26	VLQRNPDVY	387	0.4000	5.00
27	FGGKGYHVS	520	0.4000	5.00
28	FPMIQISGS	101	0.3000	3.75
29	IRTATSGRP	155	0.3000	3.75
30	VLLVGARLN	278	0.3000	3.75
31	IIDMHLPRH	410	0.2800	3.50
32	IPITDLARA	36	0.2000	2.50
33	VYLDIPGDV	166	0.2000	2.50
34	LLVGARLNW	279	0.2000	2.50
35	LVGARLNWL	280	0.2000	2.50
36	VMGIGMGYA	427	0.2000	2.50
37	MIQISGSSS	103	0.1000	1.25
38	LNAARPFVK	128	0.1000	1.25
39	LGAIRSVLQ	381	0.1000	1.25
40	IGMGYAIAA	430	0.1000	1.25
41	VVGIPITDL	33	-0.1000	0
42	IGSVMSALL	327	-0.1000	0
43	VILNNGGVY	475	-0.1000	0
44	FLPMSMAKG	246	-0.2000	0
45	MARADVVLL	272	-0.2000	0
46	FRSAAPVWR	491	-0.2000	0
47	VLGQAVEAS	174	-0.3000	0
48	LLPDSHPQS	255	-0.3000	0
49	LVVDALKAN	17	-0.4000	0
50	LKANDVDTI	22	-0.4000	0
51	IYGVVGIPI	30	-0.4000	0
52	IRYIGFRHE	50	-0.4000	0
53	MEFETICRY	460	-0.4000	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	MRFYNALGA	375	4.9000	56.98
2	MRRRLADDH	364	4.1000	47.67
3	VLSKGAAYA	221	3.5000	40.70
4	VVDALKAND	18	3.1000	36.05
5	VVLLVGARL	277	3.1000	36.05
6	LLVLSKGAA	219	3.0000	34.88
7	VVILNNGGV	474	2.8000	32.56
8	IRYIGFRHE	50	2.6000	30.23
9	VKAAYRIGQ	135	2.6000	30.23
10	VLLVGARLN	278	2.3000	26.74
11	IGFRHEASA	53	2.2000	25.58
12	VLNAHARHE	506	2.2000	25.58
13	MVDLQRGDY	114	2.1000	24.42
14	LNGLPALAN	87	2.0000	23.26
15	WGVMGIGMG	425	1.9000	22.09
16	ITDLARAAQ	38	1.7000	19.77
17	LVVDALKAN	17	1.6000	18.60
18	YRIGQVQDI	139	1.6000	18.60
19	ICRYRLPVT	465	1.6000	18.60
20	LVLSKGAAY	220	1.5000	17.44
21	VLQRNPDVY	387	1.5000	17.44
22	IIDMHLPRH	410	1.5000	17.44
23	WRPVDPAPR	189	1.3000	15.12
24	IVAPLTGDI	319	1.3000	15.12
25	LVGARLNWL	280	1.2000	13.95
26	FLPMSMAKG	246	1.1000	12.79
27	LLVGARLNW	279	1.1000	12.79
28	LADRKARNS	353	1.1000	12.79
29	MHLPRHRLD	413	1.1000	12.79
30	MTTRSASPC	0	1.0000	11.63
31	VGARLNWLL	281	1.0000	11.63
32	VILNNGGVY	475	1.0000	11.63
33	VVGIPITDL	33	0.9000	10.47

34	FRHEASAGN	55	0.9000	10.47
35	LLPAPEAID	198	0.9000	10.47
36	IGSVMSALL	327	0.9000	10.47
37	LGAIRSVLQ	381	0.9000	10.47
38	IRSVLQRNP	384	0.9000	10.47
39	YVVNEGANA	395	0.9000	10.47
40	MGYAIAAAV	432	0.9000	10.47
41	MARADVVLL	272	0.8000	9.30
42	LNWLLGNGE	285	0.8000	9.30
43	YRLPVTVVI	468	0.8000	9.30
44	LARAAQASG	41	0.7000	8.14
45	VQDIGRGVA	144	0.7000	8.14
46	IRTATSGRP	155	0.7000	8.14
47	MEFETICRY	460	0.7000	8.14
48	LNNGGVYRG	477	0.7000	8.14
49	IQVDIEASE	304	0.6000	6.98
50	LTARPGVCL	71	0.5000	5.81
51	VYLDIPGDV	166	0.5000	5.81
52	YNALGAIRS	378	0.4000	4.65
53	VYVVNEGAN	394	0.4000	4.65
54	FGGKGYHVS	520	0.4000	4.65
55	FPMIQISGS	101	0.3000	3.49
56	VVNEGANAL	396	0.3000	3.49
57	LARNIIDMH	406	0.3000	3.49
58	IPITDLARA	36	0.2000	2.33

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	MRFYNALGA	375	4.5000	51.72
2	YRIGQVQDI	139	3.4000	39.08
3	FPMIQISGS	101	3.1000	35.63
4	MRRRLADDH	364	3.0800	35.40

5	YRLPVTVVI	468	2.6000	29.89
6	VLSKGAAYA	221	2.5000	28.74
7	WRPVDPAPR	189	2.3000	26.44
8	YNALGAIRS	378	2.2800	26.21
9	FIQVDIEAS	303	2.1000	24.14
10	YVVNEGANA	395	1.9000	21.84
11	FGGKGYHVS	520	1.9000	21.84
12	MTTRSASPC	0	1.8000	20.69
13	FRSAAPVWR	491	1.8000	20.69
14	VVGIPITDL	33	1.7000	19.54
15	YIGFRHEAS	52	1.7000	19.54
16	VKAAYRIGQ	135	1.6800	19.31
17	LLVLSKGAA	219	1.3000	14.94
18	IGFRHEASA	53	1.2000	13.79
19	LVGARLNWL	280	1.2000	13.79
20	VVLLVGARL	277	1.1000	12.64
21	FLNGLPALA	86	1.0000	11.49
22	MIQISGSSS	103	0.9000	10.34
23	WGVMGIGMG	425	0.9000	10.34
24	LAKLNTTSA	564	0.9000	10.34
25	FLPMSMAKG	246	0.8000	9.20
26	VVILNNGGV	474	0.8000	9.20
27	YRGDEATIF	483	0.8000	9.20
28	YQDLDQLNA	122	0.6000	6.90
29	VLQRNPDVY	387	0.6000	6.90
30	WSADAKFIQ	297	0.4500	5.17
31	VLGQAVEAS	174	0.4000	4.60
32	FLTARPGVC	70	0.3000	3.45
33	VVNEGANAL	396	0.3000	3.45
34	YAIAAAVET	434	0.2000	2.30
35	FETICRYRL	462	0.2000	2.30
36	YHVSTPTEL	525	0.2000	2.30
37	IQISGSSSR	104	0.1000	1.15
38	LGAIRSVLQ	381	0.1000	1.15

39	IGMGYAIAA	430	-0.0200	0
40	LNAARPFVK	128	-0.0500	0
41	ITDLARAAQ	38	-0.1000	0
42	FRHEASAGN	55	-0.1000	0
43	VARAIRTAT	151	-0.1000	0
44	ICRYRLPVT	465	-0.1000	0
45	LASNGPSLI	541	-0.1000	0
46	LKANDVDTI	22	-0.2000	0
47	YGVVGIPIT	31	-0.2000	0
48	MARADVVLL	272	-0.2000	0
49	LLVGARLNW	279	-0.2000	0
50	LLGNGESPQ	288	-0.2000	0
51	VMSALLEAA	330	-0.2000	0
52	LADRKARNS	353	-0.2000	0
53	FYNALGAIR	377	-0.3000	0
54	VTVVILNNG	472	-0.3000	0
55	WRHDPAPTV	498	-0.3000	0
56	VGIPITDLA	34	-0.4000	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	MRFYNALGA	375	5.7000	56.44
2	VKAAYRIGQ	135	3.2000	31.68
3	YNALGAIRS	378	3.0000	29.70
4	WGVMGIGMG	425	3.0000	29.70
5	LNGLPALAN	87	2.8000	27.72
6	MRRRLADDH	364	2.8000	27.72
7	YRIGQVQDI	139	2.7000	26.73
8	VLSKGAAYA	221	2.5000	24.75
9	WRPVDPAPR	189	2.3000	22.77
10	YRLPVTVVI	468	2.3000	22.77
11	VVDALKAND	18	2.1000	20.79

12	LLVLSKGAA	219	2.1000	20.79
13	FLPMSMAKG	246	2.1000	20.79
14	VVLLVGARL	277	2.1000	20.79
15	FGGKGYHVS	520	2.1000	20.79
16	FRHEASAGN	55	1.9000	18.81
17	LLVGARLNW	279	1.9000	18.81
18	YVVNEGANA	395	1.9000	18.81
19	VVILNNGGV	474	1.9000	18.81
20	IRYIGFRHE	50	1.8000	17.82
21	YQDLDQLNA	122	1.8000	17.82
22	ICRYRLPVT	465	1.7500	17.33
23	YGVVGIPIT	31	1.6500	16.34
24	IIDMHLPRH	410	1.6500	16.34
25	VLLVGARLN	278	1.5000	14.85
26	FIQVDIEAS	303	1.5000	14.85
27	VLNAHARHE	506	1.4000	13.86
28	FPMIQISGS	101	1.3000	12.87
29	FRSAAPVWR	491	1.3000	12.87
30	LVVDALKAN	17	1.2000	11.88
31	IGFRHEASA	53	1.2000	11.88
32	MVDLQRGDY	114	1.2000	11.88
33	YIGFRHEAS	52	1.1000	10.89
34	FLTARPGVC	70	1.1000	10.89
35	VVGIPITDL	33	1.0000	9.90
36	FLNGLPALA	86	1.0000	9.90
37	FETICRYRL	462	1.0000	9.90
38	WRHDPAPTV	498	0.9500	9.41
39	WSADAKFIQ	297	0.9000	8.91
40	VGARLNWLL	281	0.8000	7.92
41	ITDLARAAQ	38	0.7000	6.93
42	IGMGYAIAA	430	0.7000	6.93
43	FVKAAYRIG	134	0.6000	5.94
44	YAIAAAVET	434	0.6000	5.94
45	LPVTVVILN	470	0.6000	5.94

46	LVLSKGAAY	220	0.5000	4.95
47	LVGARLNWL	280	0.5000	4.95
48	IYGVVGIPI	30	0.4000	3.96
49	IVAPLTGDI	319	0.4000	3.96
50	LGAIRSVLQ	381	0.4000	3.96
51	LNNGGVYRG	477	0.4000	3.96
52	MARADVVLL	272	0.3000	2.97
53	LADRKARNS	353	0.3000	2.97
54	MHLPRHRLD	413	0.3000	2.97
55	FDSNRPIVA	313	0.2000	1.98
56	VLQRNPDVY	387	0.2000	1.98
57	LNWLLGNGE	285	0.1000	0.99
58	IRSVLQRNP	384	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	YNALGAIRS	378	3.4000	40.96
2	MRFYNALGA	375	2.8000	33.73
3	LLVLSKGAA	219	2.5000	30.12
4	VKAAYRIGQ	135	2.4000	28.92
5	WRPVDPAPR	189	2.4000	28.92
6	YQDLDQLNA	122	2.2000	26.51
7	VVILNNGGV	474	2.0000	24.10
8	FPMIQISGS	101	1.9000	22.89
9	YVVNEGANA	395	1.9000	22.89
10	YRIGQVQDI	139	1.8000	21.69
11	FIQVDIEAS	303	1.6000	19.28
12	VVLLVGARL	277	1.5000	18.07
13	YRLPVTVVI	468	1.4000	16.87
14	WGVMGIGMG	425	1.3000	15.66
15	FRSAAPVWR	491	1.3000	15.66
16	LNGLPALAN	87	1.2000	14.46

17	FLTARPGVC	70	1.1000	13.25
18	YIGFRHEAS	52	1.0000	12.05
19	YGVVGIPIT	31	0.8500	10.24
20	VVGIPITDL	33	0.6000	7.23
21	FETICRYRL	462	0.6000	7.23
22	MVDLQRGDY	114	0.5000	6.02
23	VQDIGRGVA	144	0.4000	4.82
24	VLGQAVEAS	174	0.4000	4.82
25	FLPMSMAKG	246	0.4000	4.82
26	IYGVVGIPI	30	0.3000	3.61
27	ITDLARAAQ	38	0.3000	3.61
28	FLNGLPALA	86	0.3000	3.61
29	LLVGARLNW	279	0.3000	3.61
30	FDSNRPIVA	313	0.2000	2.41
31	LGAIRSVLQ	381	0.2000	2.41
32	IIDMHLPRH	410	0.0300	0.36
33	WRHDPAPTV	498	-0.0500	0
34	VMGIGMGYA	427	-0.1000	0
35	IRSVLQRNP	384	-0.2000	0
36	MIQISGSSS	103	-0.3000	0
37	LVLSKGAAY	220	-0.3000	0
38	VLSKGAAYA	221	-0.3000	0
39	FYNALGAIR	377	-0.3000	0
40	YAIAAAVET	434	-0.3000	0
41	IPITDLARA	36	-0.4000	0
42	LNAARPFVK	128	-0.4000	0
43	MSMAKGLLP	249	-0.4000	0
44	VLLVGARLN	278	-0.4000	0
45	MGYAIAAAV	432	-0.4000	0
46	LAKLNTTSA	564	-0.4000	0
47	LVGARLNWL	280	-0.5000	0
48	IVAPLTGDI	319	-0.5000	0
49	VVDALKAND	18	-0.6000	0
50	IRYIGFRHE	50	-0.6000	0

51	IRTATSGRP	155	-0.6000	0
52	FVEHTGIPF	238	-0.6000	0
53	WSADAKFIQ	297	-0.6000	0
54	FVKAAYRIG	134	-0.7000	0
55	MARADVVLL	272	-0.7000	0
56	FGGKGYHVS	520	-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	MRFYNALGA	375	3.8000	45.24
2	VLGQAVEAS	174	2.7000	32.14
3	LNAHARHEL	507	2.6000	30.95
4	IDMHLPRHR	411	2.3000	27.38
5	VKAAYRIGQ	135	2.1000	25.00
6	VLSKGAAYA	221	2.0000	23.81
7	VVLLVGARL	277	1.8000	21.43
8	YRIGQVQDI	139	1.7000	20.24
9	LLVLSKGAA	219	1.7000	20.24
10	MRRRLADDH	364	1.6800	20.00
11	LNAARPFVK	128	1.6000	19.05
12	LVGARLNWL	280	1.6000	19.05
13	VLAQAQRPL	211	1.5000	17.86
14	VWRHDPAPT	497	1.4000	16.67
15	VVILNNGGV	474	1.2000	14.29
16	IRSVLQRNP	384	1.1000	13.10
17	YRLPVTVVI	468	1.1000	13.10
18	YVVNEGANA	395	1.0000	11.90
19	VLNAHARHE	506	1.0000	11.90
20	VLLVGARLN	278	0.9000	10.71
21	LVLSKGAAY	220	0.8000	9.52
22	MARADVVLL	272	0.8000	9.52
23	LADRKARNS	353	0.8000	9.52

24	FRSAAPVWR	491	0.8000	9.52
25	YIGFRHEAS	52	0.7000	8.33
26	LKANDVDTI	22	0.6000	7.14
27	ITDLARAAQ	38	0.6000	7.14
28	IGRGVARAI	147	0.6000	7.14
29	VVNEGANAL	396	0.6000	7.14
30	MGYAIAAAV	432	0.6000	7.14
31	VVGIPITDL	33	0.5000	5.95
32	IRYIGFRHE	50	0.5000	5.95
33	VMSALLEAA	330	0.5000	5.95
34	VVDALKAND	18	0.4000	4.76
35	LNGLPALAN	87	0.4000	4.76
36	LANATTNCF	93	0.4000	4.76
37	LLVGARLNW	279	0.4000	4.76
38	YNALGAIRS	378	0.4000	4.76
39	IIDMHLPRH	410	0.3800	4.52
40	LAKLNTTSA	564	0.3000	3.57
41	LGAIRSVLQ	381	0.2000	2.38
42	IPITDLARA	36	0.1000	1.19
43	IGFRHEASA	53	0.1000	1.19
44	IQISGSSSR	104	0.1000	1.19
45	WRPVDPAPR	189	0.1000	1.19
46	FGGKGYHVS	520	0.1000	1.19
47	LARNIIDMH	406	0.0800	0.95
48	FVKAAYRIG	134	-0.1000	0
49	IGMGYAIAA	430	-0.1000	0
50	VGIPITDLA	34	-0.2000	0
51	FPMIQISGS	101	-0.2000	0
52	ILNNGGVYR	476	-0.2000	0
53	LNNGGVYRG	477	-0.2000	0
54	MVDLQRGDY	114	-0.3000	0

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

	2.0	

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	3.8000	45.78
2	LLVLSKGAA	219	3.5000	42.17
3	VKAAYRIGQ	135	3.4000	40.96
4	VVILNNGGV	474	3.0000	36.14
5	VVLLVGARL	277	2.5000	30.12
6	YNALGAIRS	378	2.4000	28.92
7	LNGLPALAN	87	2.2000	26.51
8	VVGIPITDL	33	1.6000	19.28
9	MVDLQRGDY	114	1.5000	18.07
10	VQDIGRGVA	144	1.4000	16.87
11	VLGQAVEAS	174	1.4000	16.87
12	WRPVDPAPR	189	1.4000	16.87
13	IYGVVGIPI	30	1.3000	15.66
14	ITDLARAAQ	38	1.3000	15.66
15	LLVGARLNW	279	1.3000	15.66
16	YQDLDQLNA	122	1.2000	14.46
17	LGAIRSVLQ	381	1.2000	14.46
18	IIDMHLPRH	410	1.0300	12.41
19	IGMGYAIAA	430	1.0000	12.05
20	FPMIQISGS	101	0.9000	10.84
21	YVVNEGANA	395	0.9000	10.84
22	VMGIGMGYA	427	0.9000	10.84
23	YRIGQVQDI	139	0.8000	9.64
24	IRSVLQRNP	384	0.8000	9.64
25	MIQISGSSS	103	0.7000	8.43
26	LVLSKGAAY	220	0.7000	8.43
27	VLSKGAAYA	221	0.7000	8.43
28	IPITDLARA	36	0.6000	7.23
29	LNAARPFVK	128	0.6000	7.23
30	MSMAKGLLP	249	0.6000	7.23
31	VLLVGARLN	278	0.6000	7.23
32	FIQVDIEAS	303	0.6000	7.23

33	MGYAIAAAV	432	0.6000	7.23
34	LAKLNTTSA	564	0.6000	7.23
35	LVGARLNWL	280	0.5000	6.02
36	IVAPLTGDI	319	0.5000	6.02
37	VVDALKAND	18	0.4000	4.82
38	IRYIGFRHE	50	0.4000	4.82
39	IRTATSGRP	155	0.4000	4.82
40	YRLPVTVVI	468	0.4000	4.82
41	MARADVVLL	272	0.3000	3.61
42	WGVMGIGMG	425	0.3000	3.61
43	FRSAAPVWR	491	0.3000	3.61
44	VDPAPRLLP	192	0.2000	2.41
45	VMSALLEAA	330	0.2000	2.41
46	LLPDSHPQS	255	0.1500	1.81
47	FLTARPGVC	70	0.1000	1.20
48	LAQAQRPLL	212	-0.0500	0
49	YGVVGIPIT	31	-0.1500	0
50	IFRSAAPVW	490	-0.2500	0
51	IQISGSSSR	104	-0.4000	0
52	VYLDIPGDV	166	-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	MRFYNALGA	375	3.8000	45.78
2	LLVLSKGAA	219	3.5000	42.17
3	VKAAYRIGQ	135	3.4000	40.96
4	VVILNNGGV	474	3.0000	36.14
5	VVLLVGARL	277	2.5000	30.12
6	YNALGAIRS	378	2.4000	28.92
7	LNGLPALAN	87	2.2000	26.51
8	VVGIPITDL	33	1.6000	19.28
9	MVDLQRGDY	114	1.5000	18.07

10	VQDIGRGVA	144	1.4000	16.87
11	VLGQAVEAS	174	1.4000	16.87
12	WRPVDPAPR	189	1.4000	16.87
13	IYGVVGIPI	30	1.3000	15.66
14	ITDLARAAQ	38	1.3000	15.66
15	LLVGARLNW	279	1.3000	15.66
16	YQDLDQLNA	122	1.2000	14.46
17	LGAIRSVLQ	381	1.2000	14.46
18	IIDMHLPRH	410	1.0300	12.41
19	IGMGYAIAA	430	1.0000	12.05
20	FPMIQISGS	101	0.9000	10.84
21	YVVNEGANA	395	0.9000	10.84
22	VMGIGMGYA	427	0.9000	10.84
23	YRIGQVQDI	139	0.8000	9.64
24	IRSVLQRNP	384	0.8000	9.64
25	MIQISGSSS	103	0.7000	8.43
26	LVLSKGAAY	220	0.7000	8.43
27	VLSKGAAYA	221	0.7000	8.43
28	IPITDLARA	36	0.6000	7.23
29	LNAARPFVK	128	0.6000	7.23
30	MSMAKGLLP	249	0.6000	7.23
31	VLLVGARLN	278	0.6000	7.23
32	FIQVDIEAS	303	0.6000	7.23
33	MGYAIAAAV	432	0.6000	7.23
34	LAKLNTTSA	564	0.6000	7.23
35	LVGARLNWL	280	0.5000	6.02
36	IVAPLTGDI	319	0.5000	6.02
37	VVDALKAND	18	0.4000	4.82
38	IRYIGFRHE	50	0.4000	4.82
39	IRTATSGRP	155	0.4000	4.82
40	YRLPVTVVI	468	0.4000	4.82
41	MARADVVLL	272	0.3000	3.61
42	WGVMGIGMG	425	0.3000	3.61
43	FRSAAPVWR	491	0.3000	3.61

44	VDPAPRLLP	192	0.2000	2.41
45	VMSALLEAA	330	0.2000	2.41
46	LLPDSHPQS	255	0.1500	1.81
47	FLTARPGVC	70	0.1000	1.20
48	LAQAQRPLL	212	-0.0500	0
49	YGVVGIPIT	31	-0.1500	0
50	IFRSAAPVW	490	-0.2500	0
51	IQISGSSSR	104	-0.4000	0
52	VYLDIPGDV	166	-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	LLPDSHPQS	255	4.9000	53.85
2	VYLDIPGDV	166	4.1000	45.05
3	YRIGQVQDI	139	4.0000	43.96
4	WRHDPAPTV	498	3.7000	40.66
5	WSADAKFIQ	297	3.3000	36.26
6	VKAAYRIGQ	135	3.0000	32.97
7	VLGQAVEAS	174	2.9000	31.87
8	LLVLSKGAA	219	2.9000	31.87
9	LVVDALKAN	17	2.8000	30.77
10	IGMGYAIAA	430	2.8000	30.77
11	YRGDEATIF	483	2.6000	28.57
12	VVGIPITDL	33	2.4000	26.37
13	VVILNNGGV	474	2.4000	26.37
14	IQISGSSSR	104	2.3700	26.04
15	IPGDVLGQA	170	2.3000	25.27
16	LLVGARLNW	279	2.2000	24.18
17	MRFYNALGA	375	2.2000	24.18
18	LVLSKGAAY	220	2.1000	23.08
19	MAKGLLPDS	251	2.1000	23.08
20	IEGDSAFGF	449	2.1000	23.08

21	LNNGGVYRG	477	1.9500	21.43
22	YRLPVTVVI	468	1.9000	20.88
23	IFRSAAPVW	490	1.9000	20.88
24	FPMIQISGS	101	1.8700	20.55
25	VLTDGCHLV	10	1.8000	19.78
26	IVAPLTGDI	319	1.7000	18.68
27	MIQISGSSS	103	1.6700	18.35
28	LKANDVDTI	22	1.6000	17.58
29	LGAIRSVLQ	381	1.6000	17.58
30	FLNGLPALA	86	1.5000	16.48
31	LNAARPFVK	128	1.5000	16.48
32	VQDIGRGVA	144	1.5000	16.48
33	LTGDIGSVM	323	1.4700	16.15
34	MGIGMGYAI	428	1.4500	15.93
35	LVGARLNWL	280	1.4100	15.49
36	VVLLVGARL	277	1.4000	15.38
37	MRRRLADDH	364	1.3800	15.16
38	FIQVDIEAS	303	1.3000	14.29
39	VMSALLEAA	330	1.3000	14.29
40	VETGRPVVA	440	1.3000	14.29
41	VVAIEGDSA	446	1.3000	14.29
42	VGIPITDLA	34	1.2000	13.19
43	MARADVVLL	272	1.1000	12.09
44	LGNGESPQW	289	1.1000	12.09
45	YVVNEGANA	395	1.1000	12.09
46	FRSAAPVWR	491	1.1000	12.09
47	LARNIIDMH	406	1.0800	11.87
48	WRPVDPAPR	189	1.0000	10.99
49	VMGIGMGYA	427	1.0000	10.99
50	MVDLQRGDY	114	0.9000	9.89
51	IRTATSGRP	155	0.9000	9.89
52	IQVDIEASE	304	0.9000	9.89
53	YNALGAIRS	378	0.9000	9.89
54	VEASAASGA	179	0.8700	9.56

55	IIDMHLPRH	410	0.7800	8.57
56	LAQAQRPLL	212	0.7000	7.69
57	VILNNGGVY	475	0.7000	7.69
58	LAKLNTTSA	564	0.7000	7.69

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	MRFYNALGA	375	2.8000	33.33
2	YRIGQVQDI	139	2.7000	32.14
3	YRLPVTVVI	468	2.1000	25.00
4	YVVNEGANA	395	2.0000	23.81
5	FRSAAPVWR	491	1.8000	21.43
6	YIGFRHEAS	52	1.7000	20.24
7	VLGQAVEAS	174	1.7000	20.24
8	LNAHARHEL	507	1.6000	19.05
9	YNALGAIRS	378	1.4000	16.67
10	IDMHLPRHR	411	1.3000	15.48
11	VKAAYRIGQ	135	1.1000	13.10
12	WRPVDPAPR	189	1.1000	13.10
13	FGGKGYHVS	520	1.1000	13.10
14	VLSKGAAYA	221	1.0000	11.90
15	FVKAAYRIG	134	0.9000	10.71
16	FPMIQISGS	101	0.8000	9.52
17	VVLLVGARL	277	0.8000	9.52
18	LLVLSKGAA	219	0.7000	8.33
19	WSADAKFIQ	297	0.7000	8.33
20	MRRRLADDH	364	0.6800	8.10
21	LNAARPFVK	128	0.6000	7.14
22	LVGARLNWL	280	0.6000	7.14
23	FIQVDIEAS	303	0.6000	7.14
24	FLNGLPALA	86	0.5000	5.95
25	VLAQAQRPL	211	0.5000	5.95

26	YQDLDQLNA	122	0.4000	4.76
27	VWRHDPAPT	497	0.4000	4.76
28	FVEHTGIPF	238	0.2000	2.38
29	FLPMSMAKG	246	0.2000	2.38
30	YAIAAAVET	434	0.2000	2.38
31	VVILNNGGV	474	0.2000	2.38
32	IRSVLQRNP	384	0.1000	1.19
33	VLLVGARLN	278	-0.1000	0
34	FRHEASAGN	55	-0.2000	0
35	LVLSKGAAY	220	-0.2000	0
36	MARADVVLL	272	-0.2000	0
37	LADRKARNS	353	-0.2000	0
38	WRHDPAPTV	498	-0.2000	0
39	FYNALGAIR	377	-0.3000	0
40	LKANDVDTI	22	-0.4000	0
41	ITDLARAAQ	38	-0.4000	0
42	IGRGVARAI	147	-0.4000	0
43	VVNEGANAL	396	-0.4000	0
44	MGYAIAAAV	432	-0.4000	0
45	VVGIPITDL	33	-0.5000	0
46	IRYIGFRHE	50	-0.5000	0
47	VMSALLEAA	330	-0.5000	0
48	VVDALKAND	18	-0.6000	0
49	LNGLPALAN	87	-0.6000	0
50	LANATTNCF	93	-0.6000	0
51	LLVGARLNW	279	-0.6000	0
52	IIDMHLPRH	410	-0.6200	0
53	FETICRYRL	462	-0.7000	0
54	YHVSTPTEL	525	-0.7000	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	YRIGQVQDI	139	3.6000	40.91
2	FRSAAPVWR	491	3.3000	37.50
3	YRLPVTVVI	468	3.0000	34.09
4	MRFYNALGA	375	2.8000	31.82
5	IDMHLPRHR	411	2.8000	31.82
6	WRPVDPAPR	189	2.6000	29.55
7	LNAHARHEL	507	2.5600	29.09
8	FVKAAYRIG	134	2.3000	26.14
9	YIGFRHEAS	52	2.1000	23.86
10	VLGQAVEAS	174	2.1000	23.86
11	FVEHTGIPF	238	2.1000	23.86
12	YVVNEGANA	395	2.0000	22.73
13	YNALGAIRS	378	1.8000	20.45
14	VVLLVGARL	277	1.7600	20.00
15	FLPMSMAKG	246	1.6000	18.18
16	LVGARLNWL	280	1.5600	17.73
17	FGGKGYHVS	520	1.5000	17.05
18	VLAQAQRPL	211	1.4600	16.59
19	WGVMGIGMG	425	1.4000	15.91
20	VLNAHARHE	506	1.4000	15.91
21	LANATTNCF	93	1.3000	14.77
22	FPMIQISGS	101	1.2000	13.64
23	FYNALGAIR	377	1.2000	13.64
24	VVILNNGGV	474	1.2000	13.64
25	LVLSKGAAY	220	1.1000	12.50
26	IRSVLQRNP	384	1.1000	12.50
27	VWRHDPAPT	497	1.1000	12.50
28	VLSKGAAYA	221	1.0000	11.36
29	FIQVDIEAS	303	1.0000	11.36
30	YRGDEATIF	483	1.0000	11.36
31	IRYIGFRHE	50	0.9000	10.23
32	YAIAAAVET	434	0.9000	10.23
33	WRHDPAPTV	498	0.8000	9.09
34	MARADVVLL	272	0.7600	8.64

35	LNAARPFVK	128	0.7000	7.95
36	LLVLSKGAA	219	0.7000	7.95
37	VLLVGARLN	278	0.7000	7.95
38	FRHEASAGN	55	0.6000	6.82
39	IQISGSSSR	104	0.6000	6.82
40	MGYAIAAAV	432	0.6000	6.82
41	VVNEGANAL	396	0.5600	6.36
42	VVDALKAND	18	0.5000	5.68
43	LKANDVDTI	22	0.5000	5.68
44	FLNGLPALA	86	0.5000	5.68
45	ISGSSSRPM	106	0.5000	5.68
46	IGRGVARAI	147	0.5000	5.68
47	VVGIPITDL	33	0.4600	5.23
48	YQDLDQLNA	122	0.4000	4.55
49	VKAAYRIGQ	135	0.4000	4.55
50	ILNNGGVYR	476	0.3000	3.41
51	FETICRYRL	462	0.2600	2.95
52	YHVSTPTEL	525	0.2600	2.95
53	LNGLPALAN	87	0.2000	2.27
54	LADRKARNS	353	0.2000	2.27
55	LNNGGVYRG	477	0.2000	2.27
56	IREFVEHTG	235	0.1000	1.14
57	MRRRLADDH	364	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	3.8000	45.24
2	VLGQAVEAS	174	2.7000	32.14
3	LNAHARHEL	507	2.6000	30.95
4	IDMHLPRHR	411	2.3000	27.38
5	VKAAYRIGQ	135	2.1000	25.00
6	VLSKGAAYA	221	2.0000	23.81

7	VVLLVGARL	277	1.8000	21.43
8	YRIGQVQDI	139	1.7000	20.24
9	LLVLSKGAA	219	1.7000	20.24
10	MRRRLADDH	364	1.6800	20.00
11	LNAARPFVK	128	1.6000	19.05
12	LVGARLNWL	280	1.6000	19.05
13	VLAQAQRPL	211	1.5000	17.86
14	VWRHDPAPT	497	1.4000	16.67
15	VVILNNGGV	474	1.2000	14.29
16	IRSVLQRNP	384	1.1000	13.10
17	YRLPVTVVI	468	1.1000	13.10
18	YVVNEGANA	395	1.0000	11.90
19	VLNAHARHE	506	1.0000	11.90
20	VLLVGARLN	278	0.9000	10.71
21	LVLSKGAAY	220	0.8000	9.52
22	MARADVVLL	272	0.8000	9.52
23	LADRKARNS	353	0.8000	9.52
24	FRSAAPVWR	491	0.8000	9.52
25	YIGFRHEAS	52	0.7000	8.33
26	LKANDVDTI	22	0.6000	7.14
27	ITDLARAAQ	38	0.6000	7.14
28	IGRGVARAI	147	0.6000	7.14
29	VVNEGANAL	396	0.6000	7.14
30	MGYAIAAAV	432	0.6000	7.14
31	VVGIPITDL	33	0.5000	5.95
32	IRYIGFRHE	50	0.5000	5.95
33	VMSALLEAA	330	0.5000	5.95
34	VVDALKAND	18	0.4000	4.76
35	LNGLPALAN	87	0.4000	4.76
36	LANATTNCF	93	0.4000	4.76
37	LLVGARLNW	279	0.4000	4.76
38	YNALGAIRS	378	0.4000	4.76
39	IIDMHLPRH	410	0.3800	4.52
40	LAKLNTTSA	564	0.3000	3.57

41	LGAIRSVLQ	381	0.2000	2.38
42	IPITDLARA	36	0.1000	1.19
43	IGFRHEASA	53	0.1000	1.19
44	IQISGSSSR	104	0.1000	1.19
45	WRPVDPAPR	189	0.1000	1.19
46	FGGKGYHVS	520	0.1000	1.19
47	LARNIIDMH	406	0.0800	0.95
48	FVKAAYRIG	134	-0.1000	0
49	IGMGYAIAA	430	-0.1000	0
50	VGIPITDLA	34	-0.2000	0
51	FPMIQISGS	101	-0.2000	0
52	ILNNGGVYR	476	-0.2000	0
53	LNNGGVYRG	477	-0.2000	0
54	MVDLQRGDY	114	-0.3000	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	WRPVDPAPR	189	3.9000	44.83
2	YNALGAIRS	378	3.8000	43.68
3	VVILNNGGV	474	3.0000	34.48
4	MRFYNALGA	375	2.8000	32.18
5	FRSAAPVWR	491	2.8000	32.18
6	YRIGQVQDI	139	2.7000	31.03
7	WGVMGIGMG	425	2.7000	31.03
8	LLVLSKGAA	219	2.5000	28.74
9	VVLLVGARL	277	2.4600	28.28
10	FPMIQISGS	101	2.3000	26.44
11	YRLPVTVVI	468	2.3000	26.44
12	YQDLDQLNA	122	2.2000	25.29
13	LNGLPALAN	87	2.0000	22.99
14	FIQVDIEAS	303	2.0000	22.99
15	YVVNEGANA	395	1.9000	21.84

16	MVDLQRGDY	114	1.8000	20.69
17	FLPMSMAKG	246	1.8000	20.69
18	VKAAYRIGQ	135	1.7000	19.54
19	VVGIPITDL	33	1.5600	17.93
20	FETICRYRL	462	1.5600	17.93
21	YGVVGIPIT	31	1.5500	17.82
22	YIGFRHEAS	52	1.4000	16.09
23	FVEHTGIPF	238	1.3000	14.94
24	IYGVVGIPI	30	1.2000	13.79
25	FYNALGAIR	377	1.2000	13.79
26	FLTARPGVC	70	1.1000	12.64
27	LVLSKGAAY	220	1.0000	11.49
28	WRHDPAPTV	498	0.9500	10.92
29	IRYIGFRHE	50	0.8000	9.20
30	VLGQAVEAS	174	0.8000	9.20
31	IRSVLQRNP	384	0.8000	9.20
32	FVKAAYRIG	134	0.7000	8.05
33	MSMAKGLLP	249	0.6000	6.90
34	MGYAIAAAV	432	0.6000	6.90
35	VVDALKAND	18	0.5000	5.75
36	LVGARLNWL	280	0.4600	5.29
37	VQDIGRGVA	144	0.4000	4.60
38	IRTATSGRP	155	0.4000	4.60
39	VLLVGARLN	278	0.4000	4.60
40	IVAPLTGDI	319	0.4000	4.60
41	YAIAAAVET	434	0.4000	4.60
42	FLNGLPALA	86	0.3000	3.45
43	LLVGARLNW	279	0.3000	3.45
44	VILNNGGVY	475	0.3000	3.45
45	YRGDEATIF	483	0.3000	3.45
46	MARADVVLL	272	0.2600	2.99
47	LANATTNCF	93	0.2000	2.30
48	VDPAPRLLP	192	0.2000	2.30
49	FDSNRPIVA	313	0.2000	2.30

50	MIQISGSSS	103	0.1000	1.15
51	IQISGSSSR	104	0.1000	1.15
52	IGSVMSALL	327	-0.0400	0
53	LNAHARHEL	507	-0.0400	0
54	LAQAQRPLL	212	-0.0900	0
55	VMGIGMGYA	427	-0.1000	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	MRFYNALGA	375	3.8000	43.18
2	IDMHLPRHR	411	3.8000	43.18
3	LNAHARHEL	507	3.5600	40.45
4	VLGQAVEAS	174	3.1000	35.23
5	VVLLVGARL	277	2.7600	31.36
6	YRIGQVQDI	139	2.6000	29.55
7	LVGARLNWL	280	2.5600	29.09
8	VLAQAQRPL	211	2.4600	27.95
9	VLNAHARHE	506	2.4000	27.27
10	LANATTNCF	93	2.3000	26.14
11	FRSAAPVWR	491	2.3000	26.14
12	VVILNNGGV	474	2.2000	25.00
13	LVLSKGAAY	220	2.1000	23.86
14	IRSVLQRNP	384	2.1000	23.86
15	VWRHDPAPT	497	2.1000	23.86
16	VLSKGAAYA	221	2.0000	22.73
17	YRLPVTVVI	468	2.0000	22.73
18	IRYIGFRHE	50	1.9000	21.59
19	MARADVVLL	272	1.7600	20.00
20	LNAARPFVK	128	1.7000	19.32
21	LLVLSKGAA	219	1.7000	19.32
22	VLLVGARLN	278	1.7000	19.32
23	IQISGSSSR	104	1.6000	18.18

24	WRPVDPAPR	189	1.6000	18.18
25	MGYAIAAAV	432	1.6000	18.18
26	VVNEGANAL	396	1.5600	17.73
27	VVDALKAND	18	1.5000	17.05
28	LKANDVDTI	22	1.5000	17.05
29	ISGSSSRPM	106	1.5000	17.05
30	IGRGVARAI	147	1.5000	17.05
31	VVGIPITDL	33	1.4600	16.59
32	VKAAYRIGQ	135	1.4000	15.91
33	FVKAAYRIG	134	1.3000	14.77
34	ILNNGGVYR	476	1.3000	14.77
35	LNGLPALAN	87	1.2000	13.64
36	LADRKARNS	353	1.2000	13.64
37	LNNGGVYRG	477	1.2000	13.64
38	YIGFRHEAS	52	1.1000	12.50
39	IREFVEHTG	235	1.1000	12.50
40	FVEHTGIPF	238	1.1000	12.50
41	MRRRLADDH	364	1.1000	12.50
42	MVDLQRGDY	114	1.0000	11.36
43	YVVNEGANA	395	1.0000	11.36
44	LVVDALKAN	17	0.8000	9.09
45	LARAAQASG	41	0.8000	9.09
46	YNALGAIRS	378	0.8000	9.09
47	MHLPRHRLD	413	0.8000	9.09
48	LPRHRLDSG	415	0.8000	9.09
49	MEFETICRY	460	0.8000	9.09
50	FLPMSMAKG	246	0.6000	6.82
51	MSMAKGLLP	249	0.5000	5.68
52	IVAPLTGDI	319	0.5000	5.68
53	VMSALLEAA	330	0.5000	5.68
54	VLQRNPDVY	387	0.5000	5.68
55	FGGKGYHVS	520	0.5000	5.68
56	LASNGPSLI	541	0.5000	5.68
57	LAQAQRPLL	212	0.4600	5.23

58	VGARLNWLL	281	0.4600	5.23

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	YRIGQVQDI	139	3.6000	40.91
2	FRSAAPVWR	491	3.3000	37.50
3	YRLPVTVVI	468	3.0000	34.09
4	MRFYNALGA	375	2.8000	31.82
5	IDMHLPRHR	411	2.8000	31.82
6	WRPVDPAPR	189	2.6000	29.55
7	LNAHARHEL	507	2.5600	29.09
8	FVKAAYRIG	134	2.3000	26.14
9	YIGFRHEAS	52	2.1000	23.86
10	VLGQAVEAS	174	2.1000	23.86
11	FVEHTGIPF	238	2.1000	23.86
12	YVVNEGANA	395	2.0000	22.73
13	YNALGAIRS	378	1.8000	20.45
14	VVLLVGARL	277	1.7600	20.00
15	FLPMSMAKG	246	1.6000	18.18
16	LVGARLNWL	280	1.5600	17.73
17	FGGKGYHVS	520	1.5000	17.05
18	VLAQAQRPL	211	1.4600	16.59
19	WGVMGIGMG	425	1.4000	15.91
20	VLNAHARHE	506	1.4000	15.91
21	LANATTNCF	93	1.3000	14.77
22	FPMIQISGS	101	1.2000	13.64
23	FYNALGAIR	377	1.2000	13.64
24	VVILNNGGV	474	1.2000	13.64
25	LVLSKGAAY	220	1.1000	12.50
26	IRSVLQRNP	384	1.1000	12.50
27	VWRHDPAPT	497	1.1000	12.50
28	VLSKGAAYA	221	1.0000	11.36

29	FIQVDIEAS	303	1.0000	11.36
30	YRGDEATIF	483	1.0000	11.36
31	IRYIGFRHE	50	0.9000	10.23
32	YAIAAAVET	434	0.9000	10.23
33	WRHDPAPTV	498	0.8000	9.09
34	MARADVVLL	272	0.7600	8.64
35	LNAARPFVK	128	0.7000	7.95
36	LLVLSKGAA	219	0.7000	7.95
37	VLLVGARLN	278	0.7000	7.95
38	FRHEASAGN	55	0.6000	6.82
39	IQISGSSSR	104	0.6000	6.82
40	MGYAIAAAV	432	0.6000	6.82
41	VVNEGANAL	396	0.5600	6.36
42	VVDALKAND	18	0.5000	5.68
43	LKANDVDTI	22	0.5000	5.68
44	FLNGLPALA	86	0.5000	5.68
45	ISGSSSRPM	106	0.5000	5.68
46	IGRGVARAI	147	0.5000	5.68
47	VVGIPITDL	33	0.4600	5.23
48	YQDLDQLNA	122	0.4000	4.55
49	VKAAYRIGQ	135	0.4000	4.55
50	ILNNGGVYR	476	0.3000	3.41
51	FETICRYRL	462	0.2600	2.95
52	YHVSTPTEL	525	0.2600	2.95
53	LNGLPALAN	87	0.2000	2.27
54	LADRKARNS	353	0.2000	2.27
55	LNNGGVYRG	477	0.2000	2.27
56	IREFVEHTG	235	0.1000	1.14
57	MRRRLADDH	364	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score

1	VLNAHARHE	506	4.0000	44.44
2	MRFYNALGA	375	3.8000	42.22
3	LNAHARHEL	507	3.6000	40.00
4	IRYIGFRHE	50	3.5000	38.89
5	VVDALKAND	18	3.1000	34.44
6	VKAAYRIGQ	135	2.9000	32.22
7	VLLVGARLN	278	2.9000	32.22
8	MRRRLADDH	364	2.9000	32.22
9	VVLLVGARL	277	2.8000	31.11
10	VLGQAVEAS	174	2.7000	30.00
11	LVGARLNWL	280	2.6000	28.89
12	VLAQAQRPL	211	2.5000	27.78
13	LNGLPALAN	87	2.4000	26.67
14	MHLPRHRLD	413	2.4000	26.67
15	IDMHLPRHR	411	2.3000	25.56
16	VWRHDPAPT	497	2.3000	25.56
17	LVVDALKAN	17	2.0000	22.22
18	VLSKGAAYA	221	2.0000	22.22
19	YRIGQVQDI	139	1.9000	21.11
20	LVLSKGAAY	220	1.9000	21.11
21	LNWLLGNGE	285	1.9000	21.11
22	MARADVVLL	272	1.8000	20.00
23	LLVLSKGAA	219	1.7000	18.89
24	VVNEGANAL	396	1.6000	17.78
25	IIDMHLPRH	410	1.6000	17.78
26	VVGIPITDL	33	1.5000	16.67
27	IRSVLQRNP	384	1.5000	16.67
28	VVILNNGGV	474	1.5000	16.67
29	ITDLARAAQ	38	1.4000	15.56
30	LANATTNCF	93	1.3000	14.44
31	LLVGARLNW	279	1.3000	14.44
32	LARNIIDMH	406	1.3000	14.44
33	YRLPVTVVI	468	1.3000	14.44
34	FVKAAYRIG	134	1.2000	13.33

35	ISGSSSRPM	106	1.1000	12.22
36	LNNGGVYRG	477	1.1000	12.22
37	IREFVEHTG	235	1.0000	11.11
38	LGAIRSVLQ	381	1.0000	11.11
39	YVVNEGANA	395	1.0000	11.11
40	LNAARPFVK	128	0.9000	10.00
41	LLPAPEAID	198	0.9000	10.00
42	MGYAIAAAV	432	0.9000	10.00
43	LKANDVDTI	22	0.8000	8.89
44	FRHEASAGN	55	0.8000	8.89
45	MVDLQRGDY	114	0.8000	8.89
46	IGRGVARAI	147	0.8000	8.89
47	LADRKARNS	353	0.8000	8.89
48	FRSAAPVWR	491	0.8000	8.89
49	LARAAQASG	41	0.7000	7.78
50	YIGFRHEAS	52	0.7000	7.78
51	LPRHRLDSG	415	0.7000	7.78
52	VIREFVEHT	234	0.6000	6.67
53	MEFETICRY	460	0.6000	6.67
54	VARAIRTAT	151	0.5000	5.56
55	LAQAQRPLL	212	0.5000	5.56
56	FLPMSMAKG	246	0.5000	5.56
57	VGARLNWLL	281	0.5000	5.56
58	WSADAKFIQ	297	0.5000	5.56

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	WRPVDPAPR	189	3.9000	44.83
2	YNALGAIRS	378	3.8000	43.68
3	VVILNNGGV	474	3.0000	34.48
4	MRFYNALGA	375	2.8000	32.18
5	FRSAAPVWR	491	2.8000	32.18

6	YRIGQVQDI	139	2.7000	31.03
7	WGVMGIGMG	425	2.7000	31.03
8	LLVLSKGAA	219	2.5000	28.74
9	VVLLVGARL	277	2.4600	28.28
10	FPMIQISGS	101	2.3000	26.44
11	YRLPVTVVI	468	2.3000	26.44
12	YQDLDQLNA	122	2.2000	25.29
13	LNGLPALAN	87	2.0000	22.99
14	FIQVDIEAS	303	2.0000	22.99
15	YVVNEGANA	395	1.9000	21.84
16	MVDLQRGDY	114	1.8000	20.69
17	FLPMSMAKG	246	1.8000	20.69
18	VKAAYRIGQ	135	1.7000	19.54
19	VVGIPITDL	33	1.5600	17.93
20	FETICRYRL	462	1.5600	17.93
21	YGVVGIPIT	31	1.5500	17.82
22	YIGFRHEAS	52	1.4000	16.09
23	FVEHTGIPF	238	1.3000	14.94
24	IYGVVGIPI	30	1.2000	13.79
25	FYNALGAIR	377	1.2000	13.79
26	FLTARPGVC	70	1.1000	12.64
27	LVLSKGAAY	220	1.0000	11.49
28	WRHDPAPTV	498	0.9500	10.92
29	IRYIGFRHE	50	0.8000	9.20
30	VLGQAVEAS	174	0.8000	9.20
31	IRSVLQRNP	384	0.8000	9.20
32	FVKAAYRIG	134	0.7000	8.05
33	MSMAKGLLP	249	0.6000	6.90
34	MGYAIAAAV	432	0.6000	6.90
35	VVDALKAND	18	0.5000	5.75
36	LVGARLNWL	280	0.4600	5.29
37	VQDIGRGVA	144	0.4000	4.60
38	IRTATSGRP	155	0.4000	4.60
39	VLLVGARLN	278	0.4000	4.60

40	IVAPLTGDI	319	0.4000	4.60
41	YAIAAAVET	434	0.4000	4.60
42	FLNGLPALA	86	0.3000	3.45
43	LLVGARLNW	279	0.3000	3.45
44	VILNNGGVY	475	0.3000	3.45
45	YRGDEATIF	483	0.3000	3.45
46	MARADVVLL	272	0.2600	2.99
47	LANATTNCF	93	0.2000	2.30
48	VDPAPRLLP	192	0.2000	2.30
49	FDSNRPIVA	313	0.2000	2.30
50	MIQISGSSS	103	0.1000	1.15
51	IQISGSSSR	104	0.1000	1.15
52	IGSVMSALL	327	-0.0400	0
53	LNAHARHEL	507	-0.0400	0
54	LAQAQRPLL	212	-0.0900	0
55	VMGIGMGYA	427	-0.1000	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	WRPVDPAPR	189	2.4000	35.29
2	LLVLSKGAA	219	2.4000	35.29
3	FPMIQISGS	101	1.9000	27.94
4	YVVNEGANA	395	1.9000	27.94
5	VVILNNGGV	474	1.9000	27.94
6	YNALGAIRS	378	1.8000	26.47
7	YRIGQVQDI	139	1.7000	25.00
8	VVLLVGARL	277	1.5000	22.06
9	WGVMGIGMG	425	1.2000	17.65
10	FLTARPGVC	70	1.0000	14.71
11	MRFYNALGA	375	1.0000	14.71
12	YRLPVTVVI	468	0.9000	13.24
13	VKAAYRIGQ	135	0.8000	11.76

14	FRSAAPVWR	491	0.8000	11.76
15	FIQVDIEAS	303	0.5000	7.35
16	MVDLQRGDY	114	0.4000	5.88
17	YQDLDQLNA	122	0.4000	5.88
18	FLPMSMAKG	246	0.4000	5.88
19	ITDLARAAQ	38	0.3000	4.41
20	FLNGLPALA	86	0.3000	4.41
21	VQDIGRGVA	144	0.3000	4.41
22	YIGFRHEAS	52	-0.1000	0
23	FETICRYRL	462	-0.1000	0
24	VMGIGMGYA	427	-0.2000	0
25	YGVVGIPIT	31	-0.3000	0
26	MIQISGSSS	103	-0.3000	0
27	LVLSKGAAY	220	-0.3000	0
28	VLSKGAAYA	221	-0.3000	0
29	FYNALGAIR	377	-0.3000	0
30	LGAIRSVLQ	381	-0.3000	0
31	IPITDLARA	36	-0.4000	0
32	IRSVLQRNP	384	-0.4000	0
33	MGYAIAAAV	432	-0.4000	0
34	VVGIPITDL	33	-0.5000	0
35	VVDALKAND	18	-0.6000	0
36	LNGLPALAN	87	-0.6000	0
37	VLLVGARLN	278	-0.6000	0
38	IVAPLTGDI	319	-0.6000	0
39	IRTATSGRP	155	-0.7000	0
40	VLGQAVEAS	174	-0.7000	0
41	IRYIGFRHE	50	-0.8000	0
42	FRHEASAGN	55	-0.8000	0
43	LVGARLNWL	280	-0.8000	0
44	YAIAAAVET	434	-0.8000	0
45	LNAARPFVK	128	-0.9000	0
46	FVKAAYRIG	134	-0.9000	0
47	IGSVMSALL	327	-1.0000	0

48	WSADAKFIQ	297	-1.1000	0
49	VVAIEGDSA	446	-1.1000	0
50	VILNNGGVY	475	-1.1000	0
51	MRRRLADDH	364	-1.1200	0
52	IIDMHLPRH	410	-1.1200	0
53	MARADVVLL	272	-1.2000	0
54	WRHDPAPTV	498	-1.2000	0
55	IYGVVGIPI	30	-1.3000	0
56	LKANDVDTI	22	-1.4000	0
57	IQISGSSSR	104	-1.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	3.8000	45.78
2	LLVLSKGAA	219	3.5000	42.17
3	VKAAYRIGQ	135	3.4000	40.96
4	VVILNNGGV	474	3.0000	36.14
5	VVLLVGARL	277	2.5000	30.12
6	YNALGAIRS	378	2.4000	28.92
7	LNGLPALAN	87	2.2000	26.51
8	VVGIPITDL	33	1.6000	19.28
9	MVDLQRGDY	114	1.5000	18.07
10	VQDIGRGVA	144	1.4000	16.87
11	VLGQAVEAS	174	1.4000	16.87
12	WRPVDPAPR	189	1.4000	16.87
13	IYGVVGIPI	30	1.3000	15.66
14	ITDLARAAQ	38	1.3000	15.66
15	LLVGARLNW	279	1.3000	15.66
16	YQDLDQLNA	122	1.2000	14.46
17	LGAIRSVLQ	381	1.2000	14.46
18	IIDMHLPRH	410	1.0300	12.41
19	IGMGYAIAA	430	1.0000	12.05

20	FPMIQISGS	101	0.9000	10.84
21	YVVNEGANA	395	0.9000	10.84
22	VMGIGMGYA	427	0.9000	10.84
23	YRIGQVQDI	139	0.8000	9.64
24	IRSVLQRNP	384	0.8000	9.64
25	MIQISGSSS	103	0.7000	8.43
26	LVLSKGAAY	220	0.7000	8.43
27	VLSKGAAYA	221	0.7000	8.43
28	IPITDLARA	36	0.6000	7.23
29	LNAARPFVK	128	0.6000	7.23
30	MSMAKGLLP	249	0.6000	7.23
31	VLLVGARLN	278	0.6000	7.23
32	FIQVDIEAS	303	0.6000	7.23
33	MGYAIAAAV	432	0.6000	7.23
34	LAKLNTTSA	564	0.6000	7.23
35	LVGARLNWL	280	0.5000	6.02
36	IVAPLTGDI	319	0.5000	6.02
37	VVDALKAND	18	0.4000	4.82
38	IRYIGFRHE	50	0.4000	4.82
39	IRTATSGRP	155	0.4000	4.82
40	YRLPVTVVI	468	0.4000	4.82
41	MARADVVLL	272	0.3000	3.61
42	WGVMGIGMG	425	0.3000	3.61
43	FRSAAPVWR	491	0.3000	3.61
44	VDPAPRLLP	192	0.2000	2.41
45	VMSALLEAA	330	0.2000	2.41
46	LLPDSHPQS	255	0.1500	1.81
47	FLTARPGVC	70	0.1000	1.20
48	LAQAQRPLL	212	-0.0500	0
49	YGVVGIPIT	31	-0.1500	0
50	IFRSAAPVW	490	-0.2500	0
51	IQISGSSSR	104	-0.4000	0
52	VYLDIPGDV	166	-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	YNALGAIRS	378	3.4000	38.20
2	LNGLPALAN	87	3.2000	35.96
3	VKAAYRIGQ	135	3.2000	35.96
4	MRFYNALGA	375	2.8000	31.46
5	WGVMGIGMG	425	2.6000	29.21
6	LLVLSKGAA	219	2.5000	28.09
7	VVLLVGARL	277	2.5000	28.09
8	IRYIGFRHE	50	2.4000	26.97
9	WRPVDPAPR	189	2.4000	26.97
10	VVILNNGGV	474	2.3000	25.84
11	YQDLDQLNA	122	2.2000	24.72
12	VVDALKAND	18	2.1000	23.60
13	YRIGQVQDI	139	2.0000	22.47
14	FPMIQISGS	101	1.9000	21.35
15	YVVNEGANA	395	1.9000	21.35
16	YGVVGIPIT	31	1.7500	19.66
17	FLPMSMAKG	246	1.7000	19.10
18	VVGIPITDL	33	1.6000	17.98
19	MVDLQRGDY	114	1.6000	17.98
20	VLLVGARLN	278	1.6000	17.98
21	FIQVDIEAS	303	1.6000	17.98
22	FETICRYRL	462	1.6000	17.98
23	YRLPVTVVI	468	1.6000	17.98
24	VLNAHARHE	506	1.4000	15.73
25	FRSAAPVWR	491	1.3000	14.61
26	IIDMHLPRH	410	1.2500	14.04
27	FRHEASAGN	55	1.2000	13.48
28	LLVGARLNW	279	1.2000	13.48
29	ITDLARAAQ	38	1.1000	12.36
30	FLTARPGVC	70	1.1000	12.36

31	YIGFRHEAS	52	1.0000	11.24
32	LGAIRSVLQ	381	1.0000	11.24
33	LPVTVVILN	470	1.0000	11.24
34	LVLSKGAAY	220	0.8000	8.99
35	FVKAAYRIG	134	0.6000	6.74
36	YAIAAAVET	434	0.6000	6.74
37	LVVDALKAN	17	0.5000	5.62
38	IYGVVGIPI	30	0.5000	5.62
39	LVGARLNWL	280	0.5000	5.62
40	LNWLLGNGE	285	0.5000	5.62
41	VQDIGRGVA	144	0.4000	4.49
42	VLGQAVEAS	174	0.4000	4.49
43	FLNGLPALA	86	0.3000	3.37
44	FVEHTGIPF	238	0.3000	3.37
45	MARADVVLL	272	0.3000	3.37
46	WRHDPAPTV	498	0.2500	2.81
47	WSADAKFIQ	297	0.2000	2.25
48	FDSNRPIVA	313	0.2000	2.25
49	IRSVLQRNP	384	0.2000	2.25
50	VILNNGGVY	475	0.1000	1.12
51	LAQAQRPLL	212	-0.0500	0
52	LLPAPEAID	198	-0.1000	0
53	LDLARNIID	404	-0.1000	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	MRFYNALGA	375	3.8000	45.24
2	VLGQAVEAS	174	2.7000	32.14
3	LNAHARHEL	507	2.6000	30.95
4	IDMHLPRHR	411	2.3000	27.38
5	VKAAYRIGQ	135	2.1000	25.00
6	VLSKGAAYA	221	2.0000	23.81

7	VVLLVGARL	277	1.8000	21.43
8	YRIGQVQDI	139	1.7000	20.24
9	LLVLSKGAA	219	1.7000	20.24
10	MRRRLADDH	364	1.6800	20.00
11	LNAARPFVK	128	1.6000	19.05
12	LVGARLNWL	280	1.6000	19.05
13	VLAQAQRPL	211	1.5000	17.86
14	VWRHDPAPT	497	1.4000	16.67
15	VVILNNGGV	474	1.2000	14.29
16	IRSVLQRNP	384	1.1000	13.10
17	YRLPVTVVI	468	1.1000	13.10
18	YVVNEGANA	395	1.0000	11.90
19	VLNAHARHE	506	1.0000	11.90
20	VLLVGARLN	278	0.9000	10.71
21	LVLSKGAAY	220	0.8000	9.52
22	MARADVVLL	272	0.8000	9.52
23	LADRKARNS	353	0.8000	9.52
24	FRSAAPVWR	491	0.8000	9.52
25	YIGFRHEAS	52	0.7000	8.33
26	LKANDVDTI	22	0.6000	7.14
27	ITDLARAAQ	38	0.6000	7.14
28	IGRGVARAI	147	0.6000	7.14
29	VVNEGANAL	396	0.6000	7.14
30	MGYAIAAAV	432	0.6000	7.14
31	VVGIPITDL	33	0.5000	5.95
32	IRYIGFRHE	50	0.5000	5.95
33	VMSALLEAA	330	0.5000	5.95
34	VVDALKAND	18	0.4000	4.76
35	LNGLPALAN	87	0.4000	4.76
36	LANATTNCF	93	0.4000	4.76
37	LLVGARLNW	279	0.4000	4.76
38	YNALGAIRS	378	0.4000	4.76
39	IIDMHLPRH	410	0.3800	4.52
40	LAKLNTTSA	564	0.3000	3.57

41	LGAIRSVLQ	381	0.2000	2.38
42	IPITDLARA	36	0.1000	1.19
43	IGFRHEASA	53	0.1000	1.19
44	IQISGSSSR	104	0.1000	1.19
45	WRPVDPAPR	189	0.1000	1.19
46	FGGKGYHVS	520	0.1000	1.19
47	LARNIIDMH	406	0.0800	0.95
48	FVKAAYRIG	134	-0.1000	0
49	IGMGYAIAA	430	-0.1000	0
50	VGIPITDLA	34	-0.2000	0
51	FPMIQISGS	101	-0.2000	0
52	ILNNGGVYR	476	-0.2000	0
53	LNNGGVYRG	477	-0.2000	0
54	MVDLQRGDY	114	-0.3000	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	MRFYNALGA	375	2.8000	33.33
2	YRIGQVQDI	139	2.7000	32.14
3	YRLPVTVVI	468	2.1000	25.00
4	YVVNEGANA	395	2.0000	23.81
5	FRSAAPVWR	491	1.8000	21.43
6	YIGFRHEAS	52	1.7000	20.24
7	VLGQAVEAS	174	1.7000	20.24
8	LNAHARHEL	507	1.6000	19.05
9	YNALGAIRS	378	1.4000	16.67
10	IDMHLPRHR	411	1.3000	15.48
11	VKAAYRIGQ	135	1.1000	13.10
12	WRPVDPAPR	189	1.1000	13.10
13	FGGKGYHVS	520	1.1000	13.10
14	VLSKGAAYA	221	1.0000	11.90
15	FVKAAYRIG	134	0.9000	10.71

16	FPMIQISGS	101	0.8000	9.52
17	VVLLVGARL	277	0.8000	9.52
18	LLVLSKGAA	219	0.7000	8.33
19	WSADAKFIQ	297	0.7000	8.33
20	MRRRLADDH	364	0.6800	8.10
21	LNAARPFVK	128	0.6000	7.14
22	LVGARLNWL	280	0.6000	7.14
23	FIQVDIEAS	303	0.6000	7.14
24	FLNGLPALA	86	0.5000	5.95
25	VLAQAQRPL	211	0.5000	5.95
26	YQDLDQLNA	122	0.4000	4.76
27	VWRHDPAPT	497	0.4000	4.76
28	FVEHTGIPF	238	0.2000	2.38
29	FLPMSMAKG	246	0.2000	2.38
30	YAIAAAVET	434	0.2000	2.38
31	VVILNNGGV	474	0.2000	2.38
32	IRSVLQRNP	384	0.1000	1.19
33	VLLVGARLN	278	-0.1000	0
34	FRHEASAGN	55	-0.2000	0
35	LVLSKGAAY	220	-0.2000	0
36	MARADVVLL	272	-0.2000	0
37	LADRKARNS	353	-0.2000	0
38	WRHDPAPTV	498	-0.2000	0
39	FYNALGAIR	377	-0.3000	0
40	LKANDVDTI	22	-0.4000	0
41	ITDLARAAQ	38	-0.4000	0
42	IGRGVARAI	147	-0.4000	0
43	VVNEGANAL	396	-0.4000	0
44	MGYAIAAAV	432	-0.4000	0
45	VVGIPITDL	33	-0.5000	0
46	IRYIGFRHE	50	-0.5000	0
47	VMSALLEAA	330	-0.5000	0
48	VVDALKAND	18	-0.6000	0
49	LNGLPALAN	87	-0.6000	0

50	LANATTNCF	93	-0.6000	0
51	LLVGARLNW	279	-0.6000	0
52	IIDMHLPRH	410	-0.6200	0
53	FETICRYRL	462	-0.7000	0
54	YHVSTPTEL	525	-0.7000	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	MRFYNALGA	375	3.8000	43.18
2	IDMHLPRHR	411	3.8000	43.18
3	LNAHARHEL	507	3.5600	40.45
4	VLGQAVEAS	174	3.1000	35.23
5	VVLLVGARL	277	2.7600	31.36
6	YRIGQVQDI	139	2.6000	29.55
7	LVGARLNWL	280	2.5600	29.09
8	VLAQAQRPL	211	2.4600	27.95
9	VLNAHARHE	506	2.4000	27.27
10	LANATTNCF	93	2.3000	26.14
11	FRSAAPVWR	491	2.3000	26.14
12	VVILNNGGV	474	2.2000	25.00
13	LVLSKGAAY	220	2.1000	23.86
14	IRSVLQRNP	384	2.1000	23.86
15	VWRHDPAPT	497	2.1000	23.86
16	VLSKGAAYA	221	2.0000	22.73
17	YRLPVTVVI	468	2.0000	22.73
18	IRYIGFRHE	50	1.9000	21.59
19	MARADVVLL	272	1.7600	20.00
20	LNAARPFVK	128	1.7000	19.32
21	LLVLSKGAA	219	1.7000	19.32
22	VLLVGARLN	278	1.7000	19.32
23	IQISGSSSR	104	1.6000	18.18
24	WRPVDPAPR	189	1.6000	18.18

25	MGYAIAAAV	432	1.6000	18.18
26	VVNEGANAL	396	1.5600	17.73
27	VVDALKAND	18	1.5000	17.05
28	LKANDVDTI	22	1.5000	17.05
29	ISGSSSRPM	106	1.5000	17.05
30	IGRGVARAI	147	1.5000	17.05
31	VVGIPITDL	33	1.4600	16.59
32	VKAAYRIGQ	135	1.4000	15.91
33	FVKAAYRIG	134	1.3000	14.77
34	ILNNGGVYR	476	1.3000	14.77
35	LNGLPALAN	87	1.2000	13.64
36	LADRKARNS	353	1.2000	13.64
37	LNNGGVYRG	477	1.2000	13.64
38	YIGFRHEAS	52	1.1000	12.50
39	IREFVEHTG	235	1.1000	12.50
40	FVEHTGIPF	238	1.1000	12.50
41	MRRRLADDH	364	1.1000	12.50
42	MVDLQRGDY	114	1.0000	11.36
43	YVVNEGANA	395	1.0000	11.36
44	LVVDALKAN	17	0.8000	9.09
45	LARAAQASG	41	0.8000	9.09
46	YNALGAIRS	378	0.8000	9.09
47	MHLPRHRLD	413	0.8000	9.09
48	LPRHRLDSG	415	0.8000	9.09
49	MEFETICRY	460	0.8000	9.09
50	FLPMSMAKG	246	0.6000	6.82
51	MSMAKGLLP	249	0.5000	5.68
52	IVAPLTGDI	319	0.5000	5.68
53	VMSALLEAA	330	0.5000	5.68
54	VLQRNPDVY	387	0.5000	5.68
55	FGGKGYHVS	520	0.5000	5.68
56	LASNGPSLI	541	0.5000	5.68
57	LAQAQRPLL	212	0.4600	5.23
58	VGARLNWLL	281	0.4600	5.23

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	3.8000	43.18
2	IDMHLPRHR	411	3.8000	43.18
3	LNAHARHEL	507	3.5600	40.45
4	VLGQAVEAS	174	3.1000	35.23
5	VVLLVGARL	277	2.7600	31.36
6	YRIGQVQDI	139	2.6000	29.55
7	LVGARLNWL	280	2.5600	29.09
8	VLAQAQRPL	211	2.4600	27.95
9	VLNAHARHE	506	2.4000	27.27
10	LANATTNCF	93	2.3000	26.14
11	FRSAAPVWR	491	2.3000	26.14
12	VVILNNGGV	474	2.2000	25.00
13	LVLSKGAAY	220	2.1000	23.86
14	IRSVLQRNP	384	2.1000	23.86
15	VWRHDPAPT	497	2.1000	23.86
16	VLSKGAAYA	221	2.0000	22.73
17	YRLPVTVVI	468	2.0000	22.73
18	IRYIGFRHE	50	1.9000	21.59
19	MARADVVLL	272	1.7600	20.00
20	LNAARPFVK	128	1.7000	19.32
21	LLVLSKGAA	219	1.7000	19.32
22	VLLVGARLN	278	1.7000	19.32
23	IQISGSSSR	104	1.6000	18.18
24	WRPVDPAPR	189	1.6000	18.18
25	MGYAIAAAV	432	1.6000	18.18
26	VVNEGANAL	396	1.5600	17.73
27	VVDALKAND	18	1.5000	17.05
28	LKANDVDTI	22	1.5000	17.05
29	ISGSSSRPM	106	1.5000	17.05
30	IGRGVARAI	147	1.5000	17.05

31	VVGIPITDL	33	1.4600	16.59
32	VKAAYRIGQ	135	1.4000	15.91
33	FVKAAYRIG	134	1.3000	14.77
34	ILNNGGVYR	476	1.3000	14.77
35	LNGLPALAN	87	1.2000	13.64
36	LADRKARNS	353	1.2000	13.64
37	LNNGGVYRG	477	1.2000	13.64
38	YIGFRHEAS	52	1.1000	12.50
39	IREFVEHTG	235	1.1000	12.50
40	FVEHTGIPF	238	1.1000	12.50
41	MRRRLADDH	364	1.1000	12.50
42	MVDLQRGDY	114	1.0000	11.36
43	YVVNEGANA	395	1.0000	11.36
44	LVVDALKAN	17	0.8000	9.09
45	LARAAQASG	41	0.8000	9.09
46	YNALGAIRS	378	0.8000	9.09
47	MHLPRHRLD	413	0.8000	9.09
48	LPRHRLDSG	415	0.8000	9.09
49	MEFETICRY	460	0.8000	9.09
50	FLPMSMAKG	246	0.6000	6.82
51	MSMAKGLLP	249	0.5000	5.68
52	IVAPLTGDI	319	0.5000	5.68
53	VMSALLEAA	330	0.5000	5.68
54	VLQRNPDVY	387	0.5000	5.68
55	FGGKGYHVS	520	0.5000	5.68
56	LASNGPSLI	541	0.5000	5.68
57	LAQAQRPLL	212	0.4600	5.23
58	VGARLNWLL	281	0.4600	5.23

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	7.4000	75.51

2	VVILNNGGV	474	5.1000	52.04
3	VVLLVGARL	277	4.6000	46.94
4	IYGVVGIPI	30	4.0000	40.82
5	LNAHARHEL	507	4.0000	40.82
6	MGIGMGYAI	428	3.9000	39.80
7	LVGARLNWL	280	3.7000	37.76
8	VVGIPITDL	33	3.6500	37.24
9	ICRYRLPVT	465	3.5000	35.71
10	IGMGYAIAA	430	3.4000	34.69
11	VVNEGANAL	396	3.2000	32.65
12	LLVGARLNW	279	3.0000	30.61
13	YRLPVTVVI	468	2.8600	29.18
14	YRIGQVQDI	139	2.8000	28.57
15	FVEHTGIPF	238	2.6000	26.53
16	LQRGDYQDL	117	2.5000	25.51
17	VGARLNWLL	281	2.5000	25.51
18	VVAIEGDSA	446	2.5000	25.51
19	IVAPLTGDI	319	2.4600	25.10
20	LVLSKGAAY	220	2.4000	24.49
21	MSMAKGLLP	249	2.4000	24.49
22	IQISGSSSR	104	2.3000	23.47
23	LNGLPALAN	87	2.2000	22.45
24	MIQISGSSS	103	2.2000	22.45
25	IREFVEHTG	235	2.2000	22.45
26	VKAAYRIGQ	135	2.0000	20.41
27	IGSVMSALL	327	2.0000	20.41
28	VMGIGMGYA	427	2.0000	20.41
29	LQRNPDVYV	388	1.9000	19.39
30	YVVNEGANA	395	1.9000	19.39
31	FETICRYRL	462	1.9000	19.39
32	LAQAQRPLL	212	1.8000	18.37
33	VARAIRTAT	151	1.7000	17.35
34	IRTATSGRP	155	1.7000	17.35
35	LLVLSKGAA	219	1.7000	17.35

36	VYLDIPGDV	166	1.6000	16.33
37	MGYAIAAAV	432	1.6000	16.33
38	WRHDPAPTV	498	1.6000	16.33
39	VLTDGCHLV	10	1.5000	15.31
40	LTARPGVCL	71	1.5000	15.31
41	VQDIGRGVA	144	1.5000	15.31
42	YNALGAIRS	378	1.5000	15.31
43	VILNNGGVY	475	1.5000	15.31
44	MVDLQRGDY	114	1.4000	14.29
45	IGRGVARAI	147	1.4000	14.29
46	MRRRLADDH	364	1.3000	13.27
47	VYRGDEATI	482	1.3000	13.27
48	VWRHDPAPT	497	1.3000	13.27
49	YIGFRHEAS	52	1.2000	12.24
50	IPFLPMSMA	244	1.2000	12.24
51	MARADVVLL	272	1.2000	12.24
52	ILNNGGVYR	476	1.1000	11.22
53	LAMARADVV	270	1.0000	10.20
54	VESGHLAKL	559	1.0000	10.20
55	VGIPITDLA	34	0.9600	9.80
56	LVVDALKAN	17	0.9000	9.18
57	IPITDLARA	36	0.9000	9.18
58	IRYIGFRHE	50	0.9000	9.18

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	MRFYNALGA	375	6.4000	65.31
2	VVILNNGGV	474	4.1000	41.84
3	YRLPVTVVI	468	3.8600	39.39
4	YRIGQVQDI	139	3.8000	38.78
5	FVEHTGIPF	238	3.6000	36.73
6	VVLLVGARL	277	3.6000	36.73

7	IYGVVGIPI	30	3.0000	30.61
8	LNAHARHEL	507	3.0000	30.61
9	YVVNEGANA	395	2.9000	29.59
10	MGIGMGYAI	428	2.9000	29.59
11	FETICRYRL	462	2.9000	29.59
12	LVGARLNWL	280	2.7000	27.55
13	VVGIPITDL	33	2.6500	27.04
14	WRHDPAPTV	498	2.6000	26.53
15	YNALGAIRS	378	2.5000	25.51
16	ICRYRLPVT	465	2.5000	25.51
17	IGMGYAIAA	430	2.4000	24.49
18	YIGFRHEAS	52	2.2000	22.45
19	VVNEGANAL	396	2.2000	22.45
20	LLVGARLNW	279	2.0000	20.41
21	YRGDEATIF	483	1.8000	18.37
22	FLPMSMAKG	246	1.6000	16.33
23	YAIAAAVET	434	1.6000	16.33
24	FPMIQISGS	101	1.5500	15.82
25	LQRGDYQDL	117	1.5000	15.31
26	YQDLDQLNA	122	1.5000	15.31
27	WRPVDPAPR	189	1.5000	15.31
28	VGARLNWLL	281	1.5000	15.31
29	VVAIEGDSA	446	1.5000	15.31
30	FRSAAPVWR	491	1.5000	15.31
31	YHVSTPTEL	525	1.5000	15.31
32	IVAPLTGDI	319	1.4600	14.90
33	LVLSKGAAY	220	1.4000	14.29
34	MSMAKGLLP	249	1.4000	14.29
35	YGVVGIPIT	31	1.3500	13.78
36	FLNGLPALA	86	1.3000	13.27
37	IQISGSSSR	104	1.3000	13.27
38	WGVMGIGMG	425	1.2500	12.76
39	FRHEASAGN	55	1.2000	12.24
40	LNGLPALAN	87	1.2000	12.24

41	MIQISGSSS	103	1.2000	12.24
42	FVKAAYRIG	134	1.2000	12.24
43	IREFVEHTG	235	1.2000	12.24
44	VKAAYRIGQ	135	1.0000	10.20
45	IGSVMSALL	327	1.0000	10.20
46	VMGIGMGYA	427	1.0000	10.20
47	FYNALGAIR	377	0.9000	9.18
48	LQRNPDVYV	388	0.9000	9.18
49	FLTARPGVC	70	0.8000	8.16
50	LAQAQRPLL	212	0.8000	8.16
51	VARAIRTAT	151	0.7000	7.14
52	IRTATSGRP	155	0.7000	7.14
53	LLVLSKGAA	219	0.7000	7.14
54	WLLGNGESP	287	0.7000	7.14
55	FGGKGYHVS	520	0.7000	7.14
56	VYLDIPGDV	166	0.6000	6.12
57	YLDIPGDVL	167	0.6000	6.12
58	MGYAIAAAV	432	0.6000	6.12

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRFYNALGA	375	7.4000	75.51
2	VVILNNGGV	474	5.1000	52.04
3	VVLLVGARL	277	4.6000	46.94
4	IYGVVGIPI	30	4.0000	40.82
5	LNAHARHEL	507	4.0000	40.82
6	MGIGMGYAI	428	3.9000	39.80
7	LVGARLNWL	280	3.7000	37.76
8	VVGIPITDL	33	3.6500	37.24
9	ICRYRLPVT	465	3.5000	35.71
10	IGMGYAIAA	430	3.4000	34.69
11	VVNEGANAL	396	3.2000	32.65

12	LLVGARLNW	279	3.0000	30.61
13	YRLPVTVVI	468	2.8600	29.18
14	YRIGQVQDI	139	2.8000	28.57
15	FVEHTGIPF	238	2.6000	26.53
16	LQRGDYQDL	117	2.5000	25.51
17	VGARLNWLL	281	2.5000	25.51
18	VVAIEGDSA	446	2.5000	25.51
19	IVAPLTGDI	319	2.4600	25.10
20	LVLSKGAAY	220	2.4000	24.49
21	MSMAKGLLP	249	2.4000	24.49
22	IQISGSSSR	104	2.3000	23.47
23	LNGLPALAN	87	2.2000	22.45
24	MIQISGSSS	103	2.2000	22.45
25	IREFVEHTG	235	2.2000	22.45
26	VKAAYRIGQ	135	2.0000	20.41
27	IGSVMSALL	327	2.0000	20.41
28	VMGIGMGYA	427	2.0000	20.41
29	LQRNPDVYV	388	1.9000	19.39
30	YVVNEGANA	395	1.9000	19.39
31	FETICRYRL	462	1.9000	19.39
32	LAQAQRPLL	212	1.8000	18.37
33	VARAIRTAT	151	1.7000	17.35
34	IRTATSGRP	155	1.7000	17.35
35	LLVLSKGAA	219	1.7000	17.35
36	VYLDIPGDV	166	1.6000	16.33
37	MGYAIAAAV	432	1.6000	16.33
38	WRHDPAPTV	498	1.6000	16.33
39	VLTDGCHLV	10	1.5000	15.31
40	LTARPGVCL	71	1.5000	15.31
41	VQDIGRGVA	144	1.5000	15.31
42	YNALGAIRS	378	1.5000	15.31
43	VILNNGGVY	475	1.5000	15.31
44	MVDLQRGDY	114	1.4000	14.29
45	IGRGVARAI	147	1.4000	14.29

46	MRRRLADDH	364	1.3000	13.27
47	VYRGDEATI	482	1.3000	13.27
48	VWRHDPAPT	497	1.3000	13.27
49	YIGFRHEAS	52	1.2000	12.24
50	IPFLPMSMA	244	1.2000	12.24
51	MARADVVLL	272	1.2000	12.24
52	ILNNGGVYR	476	1.1000	11.22
53	LAMARADVV	270	1.0000	10.20
54	VESGHLAKL	559	1.0000	10.20
55	VGIPITDLA	34	0.9600	9.80
56	LVVDALKAN	17	0.9000	9.18
57	IPITDLARA	36	0.9000	9.18
58	IRYIGFRHE	50	0.9000	9.18

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	WRPVDPAPR	189	6.3000	64.29
2	FRSAAPVWR	491	4.8000	48.98
3	LNAARPFVK	128	4.2000	42.86
4	VVLLVGARL	277	3.7000	37.76
5	FYNALGAIR	377	3.6000	36.73
6	VLLVGARLN	278	3.4000	34.69
7	IYGVVGIPI	30	3.3000	33.67
8	YNALGAIRS	378	3.3000	33.67
9	IQISGSSSR	104	3.0000	30.61
10	VVGIPITDL	33	2.8000	28.57
11	FVKAAYRIG	134	2.8000	28.57
12	YRIGQVQDI	139	2.7000	27.55
13	LVLSKGAAY	220	2.6000	26.53
14	FETICRYRL	462	2.6000	26.53
15	YHVSTPTEL	525	2.6000	26.53
16	IRYIGFRHE	50	2.3000	23.47

17	IGQVQDIGR	141	2.3000	23.47
18	WGVMGIGMG	425	2.3000	23.47
19	VVILNNGGV	474	2.3000	23.47
20	LVGARLNWL	280	2.1000	21.43
21	VVNEGANAL	396	2.1000	21.43
22	MRFYNALGA	375	2.0000	20.41
23	YRGDEATIF	483	2.0000	20.41
24	FLPMSMAKG	246	1.9000	19.39
25	FLTARPGVC	70	1.8000	18.37
26	YRLPVTVVI	468	1.8000	18.37
27	IDMHLPRHR	411	1.7000	17.35
28	MIQISGSSS	103	1.6000	16.33
29	FVEHTGIPF	238	1.6000	16.33
30	LPMSMAKGL	247	1.6000	16.33
31	IGSVMSALL	327	1.6000	16.33
32	IRSVLQRNP	384	1.6000	16.33
33	MGIGMGYAI	428	1.5000	15.31
34	FPMIQISGS	101	1.3000	13.27
35	LNGLPALAN	87	1.2000	12.24
36	VLNAHARHE	506	1.2000	12.24
37	IGRGVARAI	147	1.1000	11.22
38	MVDLQRGDY	114	1.0000	10.20
39	YAIAAAVET	434	1.0000	10.20
40	VILNNGGVY	475	1.0000	10.20
41	YAQADNVIR	228	0.9000	9.18
42	VCLTTSGPG	77	0.8000	8.16
43	VKAAYRIGQ	135	0.7000	7.14
44	LPAPEAIDR	199	0.7000	7.14
45	LGAIRSVLQ	381	0.7000	7.14
46	VMGIGMGYA	427	0.7000	7.14
47	ILNNGGVYR	476	0.7000	7.14
48	FRHEASAGN	55	0.6000	6.12
49	LTTSGPGFL	79	0.6000	6.12
50	FIQVDIEAS	303	0.6000	6.12

51	IVAPLTGDI	319	0.6000	6.12
52	YVVNEGANA	395	0.6000	6.12
53	VVAIEGDSA	446	0.6000	6.12
54	IRTATSGRP	155	0.5000	5.10
55	YLDIPGDVL	167	0.5000	5.10
56	VLAQAQRPL	211	0.5000	5.10
57	IGMGYAIAA	430	0.5000	5.10
58	VTVVILNNG	472	0.5000	5.10

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	WRPVDPAPR	189	6.3000	64.29
2	FRSAAPVWR	491	4.8000	48.98
3	LNAARPFVK	128	4.2000	42.86
4	VVLLVGARL	277	3.7000	37.76
5	FYNALGAIR	377	3.6000	36.73
6	VLLVGARLN	278	3.4000	34.69
7	IYGVVGIPI	30	3.3000	33.67
8	YNALGAIRS	378	3.3000	33.67
9	IQISGSSSR	104	3.0000	30.61
10	VVGIPITDL	33	2.8000	28.57
11	FVKAAYRIG	134	2.8000	28.57
12	YRIGQVQDI	139	2.7000	27.55
13	LVLSKGAAY	220	2.6000	26.53
14	FETICRYRL	462	2.6000	26.53
15	YHVSTPTEL	525	2.6000	26.53
16	IRYIGFRHE	50	2.3000	23.47
17	IGQVQDIGR	141	2.3000	23.47
18	WGVMGIGMG	425	2.3000	23.47
19	VVILNNGGV	474	2.3000	23.47
20	LVGARLNWL	280	2.1000	21.43
21	VVNEGANAL	396	2.1000	21.43

22	MRFYNALGA	375	2.0000	20.41
23	YRGDEATIF	483	2.0000	20.41
24	FLPMSMAKG	246	1.9000	19.39
25	FLTARPGVC	70	1.8000	18.37
26	YRLPVTVVI	468	1.8000	18.37
27	IDMHLPRHR	411	1.7000	17.35
28	MIQISGSSS	103	1.6000	16.33
29	FVEHTGIPF	238	1.6000	16.33
30	LPMSMAKGL	247	1.6000	16.33
31	IGSVMSALL	327	1.6000	16.33
32	IRSVLQRNP	384	1.6000	16.33
33	MGIGMGYAI	428	1.5000	15.31
34	FPMIQISGS	101	1.3000	13.27
35	LNGLPALAN	87	1.2000	12.24
36	VLNAHARHE	506	1.2000	12.24
37	IGRGVARAI	147	1.1000	11.22
38	MVDLQRGDY	114	1.0000	10.20
39	YAIAAAVET	434	1.0000	10.20
40	VILNNGGVY	475	1.0000	10.20
41	YAQADNVIR	228	0.9000	9.18
42	VCLTTSGPG	77	0.8000	8.16
43	VKAAYRIGQ	135	0.7000	7.14
44	LPAPEAIDR	199	0.7000	7.14
45	LGAIRSVLQ	381	0.7000	7.14
46	VMGIGMGYA	427	0.7000	7.14
47	ILNNGGVYR	476	0.7000	7.14
48	FRHEASAGN	55	0.6000	6.12
49	LTTSGPGFL	79	0.6000	6.12
50	FIQVDIEAS	303	0.6000	6.12
51	IVAPLTGDI	319	0.6000	6.12
52	YVVNEGANA	395	0.6000	6.12
53	VVAIEGDSA	446	0.6000	6.12
54	IRTATSGRP	155	0.5000	5.10
55	YLDIPGDVL	167	0.5000	5.10

56	VLAQAQRPL	211	0.5000	5.10
57	IGMGYAIAA	430	0.5000	5.10
58	VTVVILNNG	472	0.5000	5.10