MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sun Jan 31 12:57:07 2010
Length of input sequence	640 amino acids
Number of nanomers from input sequence	632
Number of nanomers with obligatory P1 anchor residue	199
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	64

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	IVNANAAHL	243	2.1000	35.00
2	LLNLPAARV	89	1.7000	28.33
3	FGRLKALGR	462	1.4000	23.33
4	LLRSHAVTL	266	1.2000	20.00
5	VVMIGMLSS	493	1.2000	20.00
6	IGMLSSVVG	496	1.1000	18.33
7	LVLAAGPDG	119	1.0700	17.83
8	VRVVIAGLL	70	1.0500	17.50
9	LQRQLGILS	609	1.0000	16.67
10	LGLFNPLSV	505	0.9800	16.33
11	FVRQAHQIC	216	0.9000	15.00
12	LRVEVGAPS	155	0.7000	11.67
13	LGRMESKPL	468	0.7000	11.67
14	MIGMLSSVV	495	0.6000	10.00

15	WREIVNANA	240	0.4000	6.67
16	IVKFLSEQV	288	0.2800	4.67
17	WAYQRSEAL	424	0.2000	3.33
18	LNSLLNLPA	86	0.1000	1.67
19	VVSYSAQPS	108	0.1000	1.67
20	VKFLSEQVL	289	0.1000	1.67
21	VENAIATAV	410	-0.0100	0
22	LRRGHKMII	476	-0.0100	0
23	VITVVSYSA	105	-0.0500	0
24	ICPVGAVVA	223	-0.0500	0
25	YRDLRRKRA	8	-0.2000	0
26	IIGMRGSYG	483	-0.2000	0
27	LAGLEPTLT	623	-0.2100	0
28	YSAQPSARL	111	-0.3000	0
29	MPIIAVSSL	258	-0.3000	0
30	YQRSEALAD	426	-0.4000	0
31	MRGSYGGVV	486	-0.4000	0
32	YGGVVMIGM	490	-0.4700	0
33	LKQGKSQLL	78	-0.5000	0
34	LKMIQRLLR	562	-0.5000	0
35	LAFIDTPGV	170	-0.5300	0
36	VVGLGLFNP	502	-0.6000	0
37	VGGLGQPHL	178	-0.6300	0
38	LSSVVGLGL	499	-0.6500	0
39	VGAVVATKT	226	-0.6600	0
40	VVIAGLLKQ	72	-0.7000	0
41	VRSEAKANV	535	-0.7000	0
42	IRSATEQLA	312	-0.8000	0
43	LRGGLAFID	166	-0.9000	0
44	VEVGAPSPL	157	-1.0000	0
45	LGLLPEADA	190	-1.0000	0
46	FLSEQVLSR	291	-1.0000	0
47	VMIGMLSSV	494	-1.0000	0
48	FNPLSVGAG	508	-1.0000	0
49	LSVGAGLIL	511	-1.0000	0
50	LKALGRMES	465	-1.0100	0
51	IVELIDHTI	35	-1.1000	0
52	VRRAPHAGG	143	-1.1000	0
53	VRQAHQICP	217	-1.1000	0
54	LGILSQVND	613	-1.1000	0
55	LAVSLGSEL	319	-1.2000	0

56	LQRARVPMP	251	-1.2300	0
57	IIAVSSLLR	260	-1.2500	0
58	LLRGGLAFI	165	-1.3000	0
59	MVPAGLCAY	0	-1.5000	0
60	LFNPLSVGA	507	-1.5000	0
61	IRELQRQLG	606	-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	IVNANAAHL	243	3.1000	51.67
2	LLNLPAARV	89	2.7000	45.00
3	LLRSHAVTL	266	2.2000	36.67
4	VVMIGMLSS	493	2.2000	36.67
5	IGMLSSVVG	496	2.1000	35.00
6	LVLAAGPDG	119	2.0700	34.50
7	VRVVIAGLL	70	2.0500	34.17
8	LQRQLGILS	609	2.0000	33.33
9	LGLFNPLSV	505	1.9800	33.00
10	LRVEVGAPS	155	1.7000	28.33
11	LGRMESKPL	468	1.7000	28.33
12	MIGMLSSVV	495	1.6000	26.67
13	FGRLKALGR	462	1.4000	23.33
14	IVKFLSEQV	288	1.2800	21.33
15	LNSLLNLPA	86	1.1000	18.33
16	VVSYSAQPS	108	1.1000	18.33
17	VKFLSEQVL	289	1.1000	18.33
18	VVITVVSYS	104	1.0000	16.67
19	VENAIATAV	410	0.9900	16.50
20	LRRGHKMII	476	0.9900	16.50
21	VITVVSYSA	105	0.9500	15.83
22	ICPVGAVVA	223	0.9500	15.83
23	FVRQAHQIC	216	0.9000	15.00
24	IIGMRGSYG	483	0.8000	13.33
25	LAGLEPTLT	623	0.7900	13.17
26	MPIIAVSSL	258	0.7000	11.67
27	MRGSYGGVV	486	0.6000	10.00

28	LKQGKSQLL	78	0.5000	8.33
29	LKMIQRLLR	562	0.5000	8.33
30	LAFIDTPGV	170	0.4700	7.83
31	VVGLGLFNP	502	0.4000	6.67
32	VGGLGQPHL	178	0.3700	6.17
33	LSSVVGLGL	499	0.3500	5.83
34	VGAVVATKT	226	0.3400	5.67
35	VVIAGLLKQ	72	0.3000	5.00
36	VRSEAKANV	535	0.3000	5.00
37	IRSATEQLA	312	0.2000	3.33
38	LRGGLAFID	166	0.1000	1.67
39	LKALGRMES	465	-0.0100	0
40	IVELIDHTI	35	-0.1000	0
41	VRRAPHAGG	143	-0.1000	0
42	VRQAHQICP	217	-0.1000	0
43	LGILSQVND	613	-0.1000	0
44	LAVSLGSEL	319	-0.2000	0
45	LQRARVPMP	251	-0.2300	0
46	IIAVSSLLR	260	-0.2500	0
47	LLRGGLAFI	165	-0.3000	0
48	MVPAGLCAY	0	-0.5000	0
49	LFNPLSVGA	507	-0.5000	0
50	IRELQRQLG	606	-0.5000	0
51	LRRKRARKW	11	-0.5100	0
52	VELIDHTIA	36	-0.5100	0
53	LRSHAVTLN	267	-0.5100	0
54	VQRLTRARQ	55	-0.6000	0
55	LLKQGKSQL	77	-0.6000	0
56	WREIVNANA	240	-0.6000	0
57	ISFVVSKQS	550	-0.6500	0
58	VNANAAHLQ	244	-0.6600	0
59	LPEADAVLV	193	-0.7000	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	LRRGHKMII	476	6.4000	67.37

2	VVSDTSQEF	201	5.3000	55.79
3	VVITVVSYS	104	4.9700	52.32
4	LKMIQRLLR	562	4.7000	49.47
5	MIIGMRGSY	482	4.5000	47.37
6	VVMIGMLSS	493	4.4000	46.32
7	LKALGRMES	465	4.3000	45.26
8	VVNDPNLRD	329	3.9000	41.05
9	LVVSDTSQE	200	3.8700	40.74
10	VVIAGLLKQ	72	3.8000	40.00
11	VMIGMLSSV	494	3.6700	38.63
12	VRAGVLGEI	304	3.6000	37.89
13	MLSSVVGLG	498	3.6000	37.89
14	LVLAAGPDG	119	3.5000	36.84
15	LQRARVPMP	251	3.5000	36.84
16	VRRAPHAGG	143	3.2000	33.68
17	LAFIDTPGV	170	3.1000	32.63
18	LLRGGLAFI	165	3.0000	31.58
19	VDHDLRTRF	375	3.0000	31.58
20	VRSEAKANV	535	3.0000	31.58
21	MVPAGLCAY	0	2.9000	30.53
22	LRSHAVTLN	267	2.9000	30.53
23	LRGGLAFID	166	2.8000	29.47
24	MRGSYGGVV	486	2.8000	29.47
25	FVDDISFVV	546	2.8000	29.47
26	VRVVIAGLL	70	2.7600	29.05
27	MPIIAVSSL	258	2.7300	28.74
28	VQRLTRARQ	55	2.7000	28.42
29	VLRVEVGAP	154	2.7000	28.42
30	IAVSSLLRS	261	2.7000	28.42
31	VVGLGLFNP	502	2.7000	28.42
32	LQRQLGILS	609	2.7000	28.42
33	IQRLLRDHY	565	2.6000	27.37
34	IVNANAAHL	243	2.5600	26.95
35	LLRSHAVTL	266	2.5600	26.95
36	IPVDDISTD	134	2.4700	26.00
37	IGNDVENAI	406	2.4100	25.37
38	IGMLSSVVG	496	2.4000	25.26
39	VGAGLILGR	513	2.4000	25.26
40	LLKQGKSQL	77	2.3300	24.53
41	VVSYSAQPS	108	2.3000	24.21
42	LLRDHYREI	568	2.3000	24.21

43	IRELQRQLG	606	2.3000	24.21
44	IAIAKLNER	43	2.1100	22.21
45	LRVEVGAPS	155	2.1000	22.11
46	LLNSLLNLP	85	2.0100	21.16
47	VRQAHQICP	217	2.0000	21.05
48	VLGDGFNDL	363	1.9700	20.74
49	ITRSLTESL	580	1.9600	20.63
50	FPAIVKFLS	285	1.9000	20.00
51	LLNLPAARV	89	1.8000	18.95
52	ISTDVRRAP	139	1.8000	18.95
53	FNPLSVGAG	508	1.8000	18.95
54	VGDDEATVV	97	1.7000	17.89
55	VPMPIIAVS	256	1.7000	17.89
56	IIAVSSLLR	260	1.7000	17.89
57	VTLNDKELN	272	1.7000	17.89
58	LRDHYREIA	569	1.7000	17.89
59	VEVGAPSPL	157	1.6300	17.16
60	VSYSAQPSA	109	1.6000	16.84
61	FVRQAHQIC	216	1.6000	16.84
62	VVATKTDLY	229	1.6000	16.84
63	LRTRFRTVT	379	1.6000	16.84
64	MIGMLSSVV	495	1.5700	16.53

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	LRRGHKMII	476	4.5000	49.45
2	VVITVVSYS	104	3.5700	39.23
3	VVIAGLLKQ	72	3.5000	38.46
4	VVMIGMLSS	493	3.0000	32.97
5	LKALGRMES	465	2.9000	31.87
6	FVDDISFVV	546	2.8000	30.77
7	FVRQAHQIC	216	2.6000	28.57
8	FPAIVKFLS	285	2.5000	27.47
9	VQRLTRARQ	55	2.4000	26.37
10	VVSDTSQEF	201	2.4000	26.37
11	MIIGMRGSY	482	2.2000	24.18

12	LKMIQRLLR	562	2.2000	24.18
13	VVNDPNLRD	329	1.8000	19.78
14	VRAGVLGEI	304	1.7000	18.68
15	VMIGMLSSV	494	1.6700	18.35
16	LQRARVPMP	251	1.5000	16.48
17	LVVSDTSQE	200	1.4700	16.15
18	FNPLSVGAG	508	1.4000	15.38
19	FVVSKQSRD	552	1.3700	15.05
20	IAVSSLLRS	261	1.3000	14.29
21	LQRQLGILS	609	1.3000	14.29
22	MLSSVVGLG	498	1.2000	13.19
23	LVLAAGPDG	119	1.1000	12.09
24	LLRGGLAFI	165	1.1000	12.09
25	LAFIDTPGV	170	1.1000	12.09
26	LRSHAVTLN	267	1.1000	12.09
27	YQRSEALAD	426	1.1000	12.09
28	YRDLRRKRA	8	1.0000	10.99
29	VRSEAKANV	535	1.0000	10.99
30	VVSYSAQPS	108	0.9000	9.89
31	WREIVNANA	240	0.9000	9.89
32	YKEDKQNRL	524	0.8100	8.90
33	VRVVIAGLL	70	0.8000	8.79
34	VRRAPHAGG	143	0.8000	8.79
35	MRGSYGGVV	486	0.8000	8.79
36	MPIIAVSSL	258	0.7700	8.46
37	VLRVEVGAP	154	0.7000	7.69
38	LRVEVGAPS	155	0.7000	7.69
39	LRGGLAFID	166	0.7000	7.69
40	VVGLGLFNP	502	0.7000	7.69
41	LRDHYREIA	569	0.7000	7.69
42	MVPAGLCAY	0	0.6000	6.59
43	VSYSAQPSA	109	0.6000	6.59
44	IVNANAAHL	243	0.6000	6.59
45	LLRSHAVTL	266	0.6000	6.59
46	FLSEQVLSR	291	0.6000	6.59
47	VLSAELSPH	448	0.5500	6.04
48	IGNDVENAI	406	0.5100	5.60
49	VELIDHTIA	36	0.4000	4.40
50	FGRLKALGR	462	0.4000	4.40
51	LILGRMAYK	517	0.4000	4.40
52	LLRDHYREI	568	0.4000	4.40

53	LLKQGKSQL	77	0.3700	4.07
54	IPVDDISTD	134	0.3700	4.07
55	VPMPIIAVS	256	0.3000	3.30
56	IQRLLRDHY	565	0.3000	3.30
57	IAGLLKQGK	74	0.1000	1.10
58	LERRKREAQ	343	0.1000	1.10
59	VDHDLRTRF	375	0.1000	1.10
60	LLRVRSEAK	532	0.1000	1.10
61	LLNSLLNLP	85	0.0100	0.11
62	VLGDGFNDL	363	0.0100	0.11

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	LRRGHKMII	476	5.2000	59.09
2	VVIAGLLKQ	72	5.0000	56.82
3	VVMIGMLSS	493	4.5000	51.14
4	VVITVVSYS	104	4.3000	48.86
5	LKMIQRLLR	562	3.7000	42.05
6	LKALGRMES	465	3.6000	40.91
7	VVSDTSQEF	201	3.5000	39.77
8	VQRLTRARQ	55	3.4000	38.64
9	VVNDPNLRD	329	3.3000	37.50
10	IAVSSLLRS	261	2.8000	31.82
11	VMIGMLSSV	494	2.4000	27.27
12	LVVSDTSQE	200	2.2000	25.00
13	IGNDVENAI	406	2.2000	25.00
14	LLRGGLAFI	165	2.1000	23.86
15	LRSHAVTLN	267	2.1000	23.86
16	LRDHYREIA	569	2.1000	23.86
17	VVSYSAQPS	108	2.0000	22.73
18	VRSEAKANV	535	2.0000	22.73
19	LQRQLGILS	609	1.9800	22.50
20	VRRAPHAGG	143	1.8000	20.45
21	MIIGMRGSY	482	1.8000	20.45
22	LLNSLLNLP	85	1.7000	19.32
23	LRVEVGAPS	155	1.7000	19.32

24	FVRQAHQIC	216	1.7000	19.32
25	VLGDGFNDL	363	1.7000	19.32
26	MVPAGLCAY	0	1.6000	18.18
27	IVNANAAHL	243	1.6000	18.18
28	IQRLLRDHY	565	1.6000	18.18
29	VNANAAHLQ	244	1.5000	17.05
30	MPIIAVSSL	258	1.5000	17.05
31	LERRKREAQ	343	1.5000	17.05
32	LLRVRSEAK	532	1.5000	17.05
33	LLRSHAVTL	266	1.4800	16.82
34	VELIDHTIA	36	1.4000	15.91
35	VGAGLILGR	513	1.4000	15.91
36	LILGRMAYK	517	1.4000	15.91
37	ITRSLTESL	580	1.4000	15.91
38	IAIAKLNER	43	1.3000	14.77
39	VPMPIIAVS	256	1.3000	14.77
40	VTLNDKELN	272	1.3000	14.77
41	VRAGVLGEI	304	1.3000	14.77
42	VLSAELSPH	448	1.2800	14.55
43	IAGLLKQGK	74	1.2000	13.64
44	LLKQGKSQL	77	1.1000	12.50
45	LNSLLNLPA	86	1.1000	12.50
46	IPVDDISTD	134	1.1000	12.50
47	LQRARVPMP	251	1.1000	12.50
48	VDHDLRTRF	375	1.1000	12.50
49	LLRDHYREI	568	1.1000	12.50
50	IRSATEQLA	312	1.0000	11.36
51	LGLFNPLSV	505	1.0000	11.36
52	IRELQRQLG	606	1.0000	11.36
53	MWFVRQAHQ	214	0.9000	10.23
54	LRTRFRTVT	379	0.9000	10.23
55	IGMLSSVVG	496	0.8800	10.00
56	LLNLPAARV	89	0.8000	9.09
57	MLSSVVGLG	498	0.8000	9.09
58	ISFVVSKQS	550	0.8000	9.09
59	VGDDEATVV	97	0.7000	7.95
60	LVLAAGPDG	119	0.7000	7.95
61	LAFIDTPGV	170	0.7000	7.95
62	LYPRWREIV	236	0.7000	7.95
63	IIAVSSLLR	260	0.7000	7.95
64	VSSLLRSHA	263	0.7000	7.95

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	LRRGHKMII	476	5.2000	59.09
2	VVIAGLLKQ	72	5.0000	56.82
3	VVMIGMLSS	493	4.5000	51.14
4	VVITVVSYS	104	4.3000	48.86
5	LKMIQRLLR	562	3.7000	42.05
6	LKALGRMES	465	3.6000	40.91
7	VVSDTSQEF	201	3.5000	39.77
8	VQRLTRARQ	55	3.4000	38.64
9	VVNDPNLRD	329	3.3000	37.50
10	IAVSSLLRS	261	2.8000	31.82
11	VMIGMLSSV	494	2.4000	27.27
12	LVVSDTSQE	200	2.2000	25.00
13	IGNDVENAI	406	2.2000	25.00
14	LLRGGLAFI	165	2.1000	23.86
15	LRSHAVTLN	267	2.1000	23.86
16	LRDHYREIA	569	2.1000	23.86
17	VVSYSAQPS	108	2.0000	22.73
18	VRSEAKANV	535	2.0000	22.73
19	LQRQLGILS	609	1.9800	22.50
20	VRRAPHAGG	143	1.8000	20.45
21	MIIGMRGSY	482	1.8000	20.45
22	LLNSLLNLP	85	1.7000	19.32
23	LRVEVGAPS	155	1.7000	19.32
24	FVRQAHQIC	216	1.7000	19.32
25	VLGDGFNDL	363	1.7000	19.32
26	MVPAGLCAY	0	1.6000	18.18
27	IVNANAAHL	243	1.6000	18.18
28	IQRLLRDHY	565	1.6000	18.18
29	VNANAAHLQ	244	1.5000	17.05
30	MPIIAVSSL	258	1.5000	17.05
31	LERRKREAQ	343	1.5000	17.05
32	LLRVRSEAK	532	1.5000	17.05
33	LLRSHAVTL	266	1.4800	16.82
34	VELIDHTIA	36	1.4000	15.91

35	VGAGLILGR	513	1.4000	15.91
36	LILGRMAYK	517	1.4000	15.91
37	ITRSLTESL	580	1.4000	15.91
38	IAIAKLNER	43	1.3000	14.77
39	VPMPIIAVS	256	1.3000	14.77
40	VTLNDKELN	272	1.3000	14.77
41	VRAGVLGEI	304	1.3000	14.77
42	VLSAELSPH	448	1.2800	14.55
43	IAGLLKQGK	74	1.2000	13.64
44	LLKQGKSQL	77	1.1000	12.50
45	LNSLLNLPA	86	1.1000	12.50
46	IPVDDISTD	134	1.1000	12.50
47	LQRARVPMP	251	1.1000	12.50
48	VDHDLRTRF	375	1.1000	12.50
49	LLRDHYREI	568	1.1000	12.50
50	IRSATEQLA	312	1.0000	11.36
51	LGLFNPLSV	505	1.0000	11.36
52	IRELQRQLG	606	1.0000	11.36
53	MWFVRQAHQ	214	0.9000	10.23
54	LRTRFRTVT	379	0.9000	10.23
55	IGMLSSVVG	496	0.8800	10.00
56	LLNLPAARV	89	0.8000	9.09
57	MLSSVVGLG	498	0.8000	9.09
58	ISFVVSKQS	550	0.8000	9.09
59	VGDDEATVV	97	0.7000	7.95
60	LVLAAGPDG	119	0.7000	7.95
61	LAFIDTPGV	170	0.7000	7.95
62	LYPRWREIV	236	0.7000	7.95
63	IIAVSSLLR	260	0.7000	7.95
64	VSSLLRSHA	263	0.7000	7.95

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	LRRGHKMII	476	5.2000	59.09
2	VVIAGLLKQ	72	5.0000	56.82
3	VVMIGMLSS	493	4.5000	51.14

4	VVITVVSYS	104	4.3000	48.86
5	LKMIQRLLR	562	3.7000	42.05
6	LKALGRMES	465	3.6000	40.91
7	VVSDTSQEF	201	3.5000	39.77
8	VQRLTRARQ	55	3.4000	38.64
9	VVNDPNLRD	329	3.3000	37.50
10	IAVSSLLRS	261	2.8000	31.82
11	VMIGMLSSV	494	2.4000	27.27
12	LVVSDTSQE	200	2.2000	25.00
13	IGNDVENAI	406	2.2000	25.00
14	LLRGGLAFI	165	2.1000	23.86
15	LRSHAVTLN	267	2.1000	23.86
16	LRDHYREIA	569	2.1000	23.86
17	VVSYSAQPS	108	2.0000	22.73
18	VRSEAKANV	535	2.0000	22.73
19	LQRQLGILS	609	1.9800	22.50
20	VRRAPHAGG	143	1.8000	20.45
21	MIIGMRGSY	482	1.8000	20.45
22	LLNSLLNLP	85	1.7000	19.32
23	LRVEVGAPS	155	1.7000	19.32
24	FVRQAHQIC	216	1.7000	19.32
25	VLGDGFNDL	363	1.7000	19.32
26	MVPAGLCAY	0	1.6000	18.18
27	IVNANAAHL	243	1.6000	18.18
28	IQRLLRDHY	565	1.6000	18.18
29	VNANAAHLQ	244	1.5000	17.05
30	MPIIAVSSL	258	1.5000	17.05
31	LERRKREAQ	343	1.5000	17.05
32	LLRVRSEAK	532	1.5000	17.05
33	LLRSHAVTL	266	1.4800	16.82
34	VELIDHTIA	36	1.4000	15.91
35	VGAGLILGR	513	1.4000	15.91
36	LILGRMAYK	517	1.4000	15.91
37	ITRSLTESL	580	1.4000	15.91
38	IAIAKLNER	43	1.3000	14.77
39	VPMPIIAVS	256	1.3000	14.77
40	VTLNDKELN	272	1.3000	14.77
41	VRAGVLGEI	304	1.3000	14.77
42	VLSAELSPH	448	1.2800	14.55
43	IAGLLKQGK	74	1.2000	13.64
44	LLKQGKSQL	77	1.1000	12.50

45	LNSLLNLPA	86	1.1000	12.50
46	IPVDDISTD	134	1.1000	12.50
47	LQRARVPMP	251	1.1000	12.50
48	VDHDLRTRF	375	1.1000	12.50
49	LLRDHYREI	568	1.1000	12.50
50	IRSATEQLA	312	1.0000	11.36
51	LGLFNPLSV	505	1.0000	11.36
52	IRELQRQLG	606	1.0000	11.36
53	MWFVRQAHQ	214	0.9000	10.23
54	LRTRFRTVT	379	0.9000	10.23
55	IGMLSSVVG	496	0.8800	10.00
56	LLNLPAARV	89	0.8000	9.09
57	MLSSVVGLG	498	0.8000	9.09
58	ISFVVSKQS	550	0.8000	9.09
59	VGDDEATVV	97	0.7000	7.95
60	LVLAAGPDG	119	0.7000	7.95
61	LAFIDTPGV	170	0.7000	7.95
62	LYPRWREIV	236	0.7000	7.95
63	IIAVSSLLR	260	0.7000	7.95
64	VSSLLRSHA	263	0.7000	7.95

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	LRRGHKMII	476	5.4000	56.84
2	VVSDTSQEF	201	4.3000	45.26
3	VVITVVSYS	104	3.9700	41.79
4	FVDDISFVV	546	3.8000	40.00
5	LKMIQRLLR	562	3.7000	38.95
6	MIIGMRGSY	482	3.5000	36.84
7	VVMIGMLSS	493	3.4000	35.79
8	LKALGRMES	465	3.3000	34.74
9	FPAIVKFLS	285	2.9000	30.53
10	VVNDPNLRD	329	2.9000	30.53
11	LVVSDTSQE	200	2.8700	30.21
12	VVIAGLLKQ	72	2.8000	29.47
13	FNPLSVGAG	508	2.8000	29.47

14	VMIGMLSSV	494	2.6700	28.11
15	FVRQAHQIC	216	2.6000	27.37
16	VRAGVLGEI	304	2.6000	27.37
17	MLSSVVGLG	498	2.6000	27.37
18	LVLAAGPDG	119	2.5000	26.32
19	LQRARVPMP	251	2.5000	26.32
20	FVVSKQSRD	552	2.4700	26.00
21	VRRAPHAGG	143	2.2000	23.16
22	YQRSEALAD	426	2.2000	23.16
23	LAFIDTPGV	170	2.1000	22.11
24	FLSEQVLSR	291	2.1000	22.11
25	LLRGGLAFI	165	2.0000	21.05
26	VDHDLRTRF	375	2.0000	21.05
27	VRSEAKANV	535	2.0000	21.05
28	MVPAGLCAY	0	1.9000	20.00
29	LRSHAVTLN	267	1.9000	20.00
30	FGRLKALGR	462	1.9000	20.00
31	LRGGLAFID	166	1.8000	18.95
32	MRGSYGGVV	486	1.8000	18.95
33	YKEDKQNRL	524	1.7700	18.63
34	VRVVIAGLL	70	1.7600	18.53
35	MPIIAVSSL	258	1.7300	18.21
36	VQRLTRARQ	55	1.7000	17.89
37	VLRVEVGAP	154	1.7000	17.89
38	IAVSSLLRS	261	1.7000	17.89
39	VVGLGLFNP	502	1.7000	17.89
40	LQRQLGILS	609	1.7000	17.89
41	IQRLLRDHY	565	1.6000	16.84
42	IVNANAAHL	243	1.5600	16.42
43	LLRSHAVTL	266	1.5600	16.42
44	IPVDDISTD	134	1.4700	15.47
45	IGNDVENAI	406	1.4100	14.84
46	IGMLSSVVG	496	1.4000	14.74
47	VGAGLILGR	513	1.4000	14.74
48	LLKQGKSQL	77	1.3300	14.00
49	VVSYSAQPS	108	1.3000	13.68
50	YGGVVMIGM	490	1.3000	13.68
51	LLRDHYREI	568	1.3000	13.68
52	IRELQRQLG	606	1.3000	13.68
53	IAIAKLNER	43	1.1100	11.68
54	LRVEVGAPS	155	1.1000	11.58

55	LLNSLLNLP	85	1.0100	10.63
56	YRDLRRKRA	8	1.0000	10.53
57	VRQAHQICP	217	1.0000	10.53
58	VLGDGFNDL	363	0.9700	10.21
59	ITRSLTESL	580	0.9600	10.11
60	WREIVNANA	240	0.9000	9.47
61	LLNLPAARV	89	0.8000	8.42
62	ISTDVRRAP	139	0.8000	8.42
63	WQQVLGDGF	360	0.8000	8.42
64	VGDDEATVV	97	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	LRRGHKMII	476	5.2000	59.09
2	VVIAGLLKQ	72	5.0000	56.82
3	VVMIGMLSS	493	4.5000	51.14
4	VVITVVSYS	104	4.3000	48.86
5	LKMIQRLLR	562	3.7000	42.05
6	LKALGRMES	465	3.6000	40.91
7	VVSDTSQEF	201	3.5000	39.77
8	VQRLTRARQ	55	3.4000	38.64
9	VVNDPNLRD	329	3.3000	37.50
10	IAVSSLLRS	261	2.8000	31.82
11	VMIGMLSSV	494	2.4000	27.27
12	LVVSDTSQE	200	2.2000	25.00
13	IGNDVENAI	406	2.2000	25.00
14	LLRGGLAFI	165	2.1000	23.86
15	LRSHAVTLN	267	2.1000	23.86
16	LRDHYREIA	569	2.1000	23.86
17	VVSYSAQPS	108	2.0000	22.73
18	VRSEAKANV	535	2.0000	22.73
19	LQRQLGILS	609	1.9800	22.50
20	VRRAPHAGG	143	1.8000	20.45
21	MIIGMRGSY	482	1.8000	20.45
22	LLNSLLNLP	85	1.7000	19.32
23	LRVEVGAPS	155	1.7000	19.32

24	FVRQAHQIC	216	1.7000	19.32
25	VLGDGFNDL	363	1.7000	19.32
26	MVPAGLCAY	0	1.6000	18.18
27	IVNANAAHL	243	1.6000	18.18
28	IQRLLRDHY	565	1.6000	18.18
29	VNANAAHLQ	244	1.5000	17.05
30	MPIIAVSSL	258	1.5000	17.05
31	LERRKREAQ	343	1.5000	17.05
32	LLRVRSEAK	532	1.5000	17.05
33	LLRSHAVTL	266	1.4800	16.82
34	VELIDHTIA	36	1.4000	15.91
35	VGAGLILGR	513	1.4000	15.91
36	LILGRMAYK	517	1.4000	15.91
37	ITRSLTESL	580	1.4000	15.91
38	IAIAKLNER	43	1.3000	14.77
39	VPMPIIAVS	256	1.3000	14.77
40	VTLNDKELN	272	1.3000	14.77
41	VRAGVLGEI	304	1.3000	14.77
42	VLSAELSPH	448	1.2800	14.55
43	IAGLLKQGK	74	1.2000	13.64
44	LLKQGKSQL	77	1.1000	12.50
45	LNSLLNLPA	86	1.1000	12.50
46	IPVDDISTD	134	1.1000	12.50
47	LQRARVPMP	251	1.1000	12.50
48	VDHDLRTRF	375	1.1000	12.50
49	LLRDHYREI	568	1.1000	12.50
50	IRSATEQLA	312	1.0000	11.36
51	LGLFNPLSV	505	1.0000	11.36
52	IRELQRQLG	606	1.0000	11.36
53	MWFVRQAHQ	214	0.9000	10.23
54	LRTRFRTVT	379	0.9000	10.23
55	IGMLSSVVG	496	0.8800	10.00
56	LLNLPAARV	89	0.8000	9.09
57	MLSSVVGLG	498	0.8000	9.09
58	ISFVVSKQS	550	0.8000	9.09
59	VGDDEATVV	97	0.7000	7.95
60	LVLAAGPDG	119	0.7000	7.95
61	LAFIDTPGV	170	0.7000	7.95
62	LYPRWREIV	236	0.7000	7.95
63	IIAVSSLLR	260	0.7000	7.95
64	VSSLLRSHA	263	0.7000	7.95

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	VVITVVSYS	104	4.7000	54.65
2	VVMIGMLSS	493	3.6000	41.86
3	FLSEQVLSR	291	3.3000	38.37
4	VVNDPNLRD	329	3.3000	38.37
5	WREIVNANA	240	3.1000	36.05
6	LNSLLNLPA	86	2.8000	32.56
7	VVIAGLLKQ	72	2.7000	31.40
8	VVSDTSQEF	201	2.7000	31.40
9	LRVEVGAPS	155	2.4000	27.91
10	LVVSDTSQE	200	2.4000	27.91
11	VVATKTDLY	229	2.4000	27.91
12	FVRQAHQIC	216	2.2000	25.58
13	LRSHAVTLN	267	1.9000	22.09
14	WAYQRSEAL	424	1.8000	20.93
15	IGMLSSVVG	496	1.7800	20.70
16	YQRSEALAD	426	1.7000	19.77
17	FGRLKALGR	462	1.7000	19.77
18	ITRSLTESL	580	1.6000	18.60
19	FVDDISFVV	546	1.5000	17.44
20	LQATIAAAQ	588	1.4000	16.28
21	MIGMLSSVV	495	1.3000	15.12
22	LEPTLTPRA	626	1.3000	15.12
23	VNANAAHLQ	244	1.2000	13.95
24	LAFIDTPGV	170	1.1000	12.79
25	ILSQVNDNL	615	1.0000	11.63
26	LQRQLGILS	609	0.9800	11.40
27	LGSELSVVN	323	0.8800	10.23
28	LGRMESKPL	468	0.8000	9.30
29	IVKFLSEQV	288	0.7000	8.14
30	LLRVRSEAK	532	0.7000	8.14
31	LLNLPAARV	89	0.6000	6.98
32	IVNANAAHL	243	0.6000	6.98
33	IAVSSLLRS	261	0.6000	6.98
34	LLRSHAVTL	266	0.5800	6.74

35	VIVELIDHT	34	0.5000	5.81
36	YSAQPSARL	111	0.5000	5.81
37	MPIIAVSSL	258	0.5000	5.81
38	FNPLSVGAG	508	0.5000	5.81
39	VVSYSAQPS	108	0.4000	4.65
40	LNEESNFPA	279	0.4000	4.65
41	VRRFVDDIS	543	0.3000	3.49
42	WGDTVTQPD	19	0.1000	1.16
43	VLGDGFNDL	363	0.1000	1.16
44	IIAVSSLLR	260	-0.1000	0
45	LIDHTIAIA	38	-0.2000	0
46	VQRLTRARQ	55	-0.2000	0
47	LQRARVPMP	251	-0.2000	0
48	LSAELSPHV	449	-0.2000	0
49	VRSEAKANV	535	-0.2000	0
50	LFNPLSVGA	507	-0.2200	0
51	LLPEADAVL	192	-0.3000	0
52	VLSRATERV	296	-0.3000	0
53	MLSSVVGLG	498	-0.4000	0
54	LGLFNPLSV	505	-0.4000	0
55	LKMIQRLLR	562	-0.4000	0
56	LLNSLLNLP	85	-0.5000	0
57	VRRAPHAGG	143	-0.5000	0
58	VELIDHTIA	36	-0.6000	0
59	YKEDKQNRL	524	-0.6000	0
60	MVPAGLCAY	0	-0.7000	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	LVQRLTRAR	54	5.7000	59.38
2	VVITVVSYS	104	4.3000	44.79
3	VVMIGMLSS	493	4.1800	43.54
4	VVSKQSRDR	553	4.1000	42.71
5	VVIAGLLKQ	72	4.0000	41.67
6	IGMRGSYGG	484	3.8000	39.58
7	LRRKRARKW	11	3.7000	38.54

8	VVSYSAQPS	108	3.7000	38.54
9	LRSHAVTLN	267	3.2000	33.33
10	MIQRLLRDH	564	2.7800	28.96
11	LNSLLNLPA	86	2.7000	28.13
12	VITVVSYSA	105	2.3000	23.96
13	LTPRASLGR	630	2.3000	23.96
14	VLSRATERV	296	2.2000	22.92
15	LGLFNPLSV	505	2.1000	21.88
16	LGRMESKPL	468	1.8000	18.75
17	MIGMLSSVV	495	1.8000	18.75
18	IVNANAAHL	243	1.6000	16.67
19	LKQGKSQLL	78	1.5000	15.62
20	WFVRQAHQI	215	1.5000	15.62
21	IVKFLSEQV	288	1.5000	15.62
22	VQQTALWQQ	354	1.5000	15.62
23	IGMLSSVVG	496	1.5000	15.62
24	ISFVVSKQS	550	1.5000	15.62
25	LVVSDTSQE	200	1.4000	14.58
26	VNANAAHLQ	244	1.4000	14.58
27	IIAVSSLLR	260	1.4000	14.58
28	ILGRMAYKE	518	1.4000	14.58
29	WREIVNANA	240	1.3800	14.37
30	LRVRSEAKA	533	1.3000	13.54
31	LNLPAARVG	90	1.2000	12.50
32	LFNPLSVGA	507	1.2000	12.50
33	LQATIAAAQ	588	1.2000	12.50
34	LQRQLGILS	609	1.2000	12.50
35	VVSDTSQEF	201	1.1000	11.46
36	FVRQAHQIC	216	1.1000	11.46
37	IRSATEQLA	312	1.1000	11.46
38	LAFIDTPGV	170	1.0800	11.25
39	LNERGDLVQ	48	1.0000	10.42
40	LIDHTIAIA	38	0.9000	9.38
41	VVNDPNLRD	329	0.9000	9.38
42	LEPTLTPRA	626	0.8000	8.33
43	VRRFVDDIS	543	0.7000	7.29
44	MPIIAVSSL	258	0.5800	6.04
45	VRRAPHAGG	143	0.5000	5.21
46	LRGGLAFID	166	0.5000	5.21
47	LQRARVPMP	251	0.5000	5.21
48	LRDRLASDL	335	0.5000	5.21

49	LLRVRSEAK	532	0.5000	5.21
50	VVATKTDLY	229	0.4000	4.17
51	MVPAGLCAY	0	0.3000	3.12
52	VLVVSDTSQ	199	0.3000	3.12
53	LRRGHKMII	476	0.3000	3.12
54	LLNLPAARV	89	0.2000	2.08
55	VPMPIIAVS	256	0.2000	2.08
56	LKMIQRLLR	562	0.1800	1.88
57	IAVSSLLRS	261	0.1000	1.04
58	VGDNFVWAY	418	0.1000	1.04
59	VRQAHQICP	217	-0.1000	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	VVITVVSYS	104	4.8000	54.55
2	VVMIGMLSS	493	4.5000	51.14
3	MIGMLSSVV	495	3.9000	44.32
4	LNSLLNLPA	86	3.6000	40.91
5	VVIAGLLKQ	72	3.3000	37.50
6	IGMLSSVVG	496	2.8000	31.82
7	IVKFLSEQV	288	2.7000	30.68
8	LVVSDTSQE	200	2.6000	29.55
9	MPIIAVSSL	258	2.5000	28.41
10	VITVVSYSA	105	2.4000	27.27
11	VVSYSAQPS	108	2.4000	27.27
12	WREIVNANA	240	2.4000	27.27
13	VRRFVDDIS	543	2.3000	26.14
14	LLRVRSEAK	532	2.2000	25.00
15	LAFIDTPGV	170	2.1000	23.86
16	LGLFNPLSV	505	2.1000	23.86
17	IIAVSSLLR	260	1.9000	21.59
18	LLNLPAARV	89	1.8000	20.45
19	VLVVSDTSQ	199	1.8000	20.45
20	LGRMESKPL	468	1.7000	19.32
21	IVNANAAHL	243	1.6000	18.18
22	VVNDPNLRD	329	1.4000	15.91

23	ISFVVSKQS	550	1.4000	15.91
24	LRSHAVTLN	267	1.3000	14.77
25	VELIDHTIA	36	1.2000	13.64
26	LQRQLGILS	609	1.1800	13.41
27	LKALGRMES	465	1.1000	12.50
28	IIGMRGSYG	483	1.1000	12.50
29	VQRLTRARQ	55	1.0000	11.36
30	VRVVIAGLL	70	1.0000	11.36
31	VVSDTSQEF	201	1.0000	11.36
32	VVATKTDLY	229	0.9000	10.23
33	LFNPLSVGA	507	0.9000	10.23
34	VVGLGLFNP	502	0.8500	9.66
35	LRVEVGAPS	155	0.8000	9.09
36	LQATIAAAQ	588	0.8000	9.09
37	ICPVGAVVA	223	0.7000	7.95
38	VLSAELSPH	448	0.6800	7.73
39	VLRVEVGAP	154	0.6000	6.82
40	ITVVSYSAQ	106	0.5000	5.68
41	VRRAPHAGG	143	0.5000	5.68
42	LQRARVPMP	251	0.5000	5.68
43	FGRLKALGR	462	0.5000	5.68
44	LKMIQRLLR	562	0.5000	5.68
45	LAGLEPTLT	623	0.4000	4.55
46	LEPTLTPRA	626	0.4000	4.55
47	MVPAGLCAY	0	0.3000	3.41
48	VENAIATAV	410	0.3000	3.41
49	ILSQVNDNL	615	0.3000	3.41
50	MWFVRQAHQ	214	0.2000	2.27
51	FVRQAHQIC	216	0.2000	2.27
52	VGAVVATKT	226	0.2000	2.27
53	VNANAAHLQ	244	0.2000	2.27
54	VPMPIIAVS	256	0.2000	2.27
55	ITRSLTESL	580	0.2000	2.27
56	IVELIDHTI	35	0.1000	1.14
57	IAIAKLNER	43	0.1000	1.14
58	LGLLPEADA	190	0.1000	1.14
59	LLRSHAVTL	266	-0.1000	0
60	VVSKQSRDR	553	-0.1000	0
61	IRSATEQLA	312	-0.2000	0
62	FNPLSVGAG	508	-0.2000	0
63	LSQVNDNLA	616	-0.2000	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	LVVSDTSQE	200	4.6000	48.94
2	VVITVVSYS	104	3.8000	40.43
3	VVMIGMLSS	493	3.5000	37.23
4	WREIVNANA	240	3.4000	36.17
5	MIGMLSSVV	495	3.2000	34.04
6	VVIAGLLKQ	72	3.1000	32.98
7	VVNDPNLRD	329	3.1000	32.98
8	IGMLSSVVG	496	3.1000	32.98
9	LNSLLNLPA	86	2.6000	27.66
10	MPIIAVSSL	258	2.5000	26.60
11	YQRSEALAD	426	2.5000	26.60
12	LRSHAVTLN	267	2.3000	24.47
13	FNPLSVGAG	508	2.1000	22.34
14	IVKFLSEQV	288	2.0000	21.28
15	FVVSKQSRD	552	1.9000	20.21
16	LGEIRSATE	309	1.7000	18.09
17	LGRMESKPL	468	1.7000	18.09
18	VLVVSDTSQ	199	1.6000	17.02
19	IVNANAAHL	243	1.6000	17.02
20	FGRLKALGR	462	1.5000	15.96
21	VITVVSYSA	105	1.4000	14.89
22	VVSYSAQPS	108	1.4000	14.89
23	LAFIDTPGV	170	1.4000	14.89
24	IIGMRGSYG	483	1.4000	14.89
25	LGLFNPLSV	505	1.4000	14.89
26	LGILSQVND	613	1.4000	14.89
27	WAEIGNDVE	403	1.3000	13.83
28	VRRFVDDIS	543	1.3000	13.83
29	FVRQAHQIC	216	1.2000	12.77
30	LLNLPAARV	89	1.1000	11.70
31	WAYQRSEAL	424	1.1000	11.70
32	WGDTVTQPD	19	1.0000	10.64
33	VRVVIAGLL	70	1.0000	10.64
34	VVATKTDLY	229	1.0000	10.64

35	FVWAYQRSE	422	1.0000	10.64
36	VVSDTSQEF	201	0.9000	9.57
37	IIAVSSLLR	260	0.9000	9.57
38	VLSAELSPH	448	0.9000	9.57
39	YGGVVMIGM	490	0.8800	9.36
40	VQRLTRARQ	55	0.8000	8.51
41	VRRAPHAGG	143	0.8000	8.51
42	YSAQPSARL	111	0.7000	7.45
43	LQATIAAAQ	588	0.6000	6.38
44	LLRVRSEAK	532	0.5000	5.32
45	MVPAGLCAY	0	0.4000	4.26
46	FRTVTEDAE	383	0.4000	4.26
47	ISFVVSKQS	550	0.4000	4.26
48	ITVVSYSAQ	106	0.3000	3.19
49	FLSEQVLSR	291	0.3000	3.19
50	FNDLTADVD	368	0.3000	3.19
51	ILSQVNDNL	615	0.3000	3.19
52	LAGLEPTLT	623	0.3000	3.19
53	VVGLGLFNP	502	0.2500	2.66
54	FVDDISFVV	546	0.2500	2.66
55	VELIDHTIA	36	0.2000	2.13
56	LGRMAYKED	519	0.2000	2.13
57	ITRSLTESL	580	0.2000	2.13
58	LQRQLGILS	609	0.1800	1.91
59	VGAVVATKT	226	0.1000	1.06
60	LGSELSVVN	323	0.1000	1.06
61	LKALGRMES	465	0.1000	1.06

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	VVITVVSYS	104	3.8000	43.18
2	VVMIGMLSS	493	3.5000	39.77
3	WREIVNANA	240	3.4000	38.64
4	MIGMLSSVV	495	2.9000	32.95
5	LNSLLNLPA	86	2.6000	29.55
6	VVIAGLLKQ	72	2.3000	26.14

7	IGMLSSVVG	496	1.8000	20.45
8	IVKFLSEQV	288	1.7000	19.32
9	LVVSDTSQE	200	1.6000	18.18
10	MPIIAVSSL	258	1.5000	17.05
11	FGRLKALGR	462	1.5000	17.05
12	VITVVSYSA	105	1.4000	15.91
13	VVSYSAQPS	108	1.4000	15.91
14	VRRFVDDIS	543	1.3000	14.77
15	FVRQAHQIC	216	1.2000	13.64
16	LLRVRSEAK	532	1.2000	13.64
17	LAFIDTPGV	170	1.1000	12.50
18	LGLFNPLSV	505	1.1000	12.50
19	IIAVSSLLR	260	0.9000	10.23
20	LLNLPAARV	89	0.8000	9.09
21	VLVVSDTSQ	199	0.8000	9.09
22	FNPLSVGAG	508	0.8000	9.09
23	LGRMESKPL	468	0.7000	7.95
24	IVNANAAHL	243	0.6000	6.82
25	VVNDPNLRD	329	0.4000	4.55
26	ISFVVSKQS	550	0.4000	4.55
27	LRSHAVTLN	267	0.3000	3.41
28	FLSEQVLSR	291	0.3000	3.41
29	VELIDHTIA	36	0.2000	2.27
30	LQRQLGILS	609	0.1800	2.05
31	WAYQRSEAL	424	0.1000	1.14
32	LKALGRMES	465	0.1000	1.14
33	IIGMRGSYG	483	0.1000	1.14
34	FVDDISFVV	546	-0.0500	0
35	VVATKTDLY	229	-0.1000	0
36	LFNPLSVGA	507	-0.1000	0
37	VVGLGLFNP	502	-0.1500	0
38	LRVEVGAPS	155	-0.2000	0
39	YQRSEALAD	426	-0.2000	0
40	LQATIAAAQ	588	-0.2000	0
41	YGGVVMIGM	490	-0.2200	0
42	YSAQPSARL	111	-0.3000	0
43	ICPVGAVVA	223	-0.3000	0
44	VLSAELSPH	448	-0.3200	0
45	VLRVEVGAP	154	-0.4000	0
46	ITVVSYSAQ	106	-0.5000	0
47	VRRAPHAGG	143	-0.5000	0

48	LQRARVPMP	251	-0.5000	0
49	LKMIQRLLR	562	-0.5000	0
50	LAGLEPTLT	623	-0.6000	0
51	LEPTLTPRA	626	-0.6000	0
52	MVPAGLCAY	0	-0.7000	0
53	VENAIATAV	410	-0.7000	0
54	ILSQVNDNL	615	-0.7000	0
55	MWFVRQAHQ	214	-0.8000	0
56	VGAVVATKT	226	-0.8000	0
57	VNANAAHLQ	244	-0.8000	0
58	VPMPIIAVS	256	-0.8000	0
59	FVVSKQSRD	552	-0.8000	0
60	ITRSLTESL	580	-0.8000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVSDTSQE	200	5.6000	59.57
2	VVITVVSYS	104	4.8000	51.06
3	VVMIGMLSS	493	4.5000	47.87
4	MIGMLSSVV	495	4.2000	44.68
5	VVIAGLLKQ	72	4.1000	43.62
6	VVNDPNLRD	329	4.1000	43.62
7	IGMLSSVVG	496	4.1000	43.62
8	LNSLLNLPA	86	3.6000	38.30
9	MPIIAVSSL	258	3.5000	37.23
10	LRSHAVTLN	267	3.3000	35.11
11	IVKFLSEQV	288	3.0000	31.91
12	LGEIRSATE	309	2.7000	28.72
13	LGRMESKPL	468	2.7000	28.72
14	VLVVSDTSQ	199	2.6000	27.66
15	IVNANAAHL	243	2.6000	27.66
16	VITVVSYSA	105	2.4000	25.53
17	VVSYSAQPS	108	2.4000	25.53
18	LAFIDTPGV	170	2.4000	25.53
19	WREIVNANA	240	2.4000	25.53
20	IIGMRGSYG	483	2.4000	25.53

21	LGLFNPLSV	505	2.4000	25.53
22	LGILSQVND	613	2.4000	25.53
23	VRRFVDDIS	543	2.3000	24.47
24	LLNLPAARV	89	2.1000	22.34
25	VRVVIAGLL	70	2.0000	21.28
26	VVATKTDLY	229	2.0000	21.28
27	VVSDTSQEF	201	1.9000	20.21
28	IIAVSSLLR	260	1.9000	20.21
29	VLSAELSPH	448	1.9000	20.21
30	VQRLTRARQ	55	1.8000	19.15
31	VRRAPHAGG	143	1.8000	19.15
32	LQATIAAAQ	588	1.6000	17.02
33	YQRSEALAD	426	1.5000	15.96
34	LLRVRSEAK	532	1.5000	15.96
35	MVPAGLCAY	0	1.4000	14.89
36	ISFVVSKQS	550	1.4000	14.89
37	ITVVSYSAQ	106	1.3000	13.83
38	ILSQVNDNL	615	1.3000	13.83
39	LAGLEPTLT	623	1.3000	13.83
40	VVGLGLFNP	502	1.2500	13.30
41	VELIDHTIA	36	1.2000	12.77
42	LGRMAYKED	519	1.2000	12.77
43	ITRSLTESL	580	1.2000	12.77
44	LQRQLGILS	609	1.1800	12.55
45	VGAVVATKT	226	1.1000	11.70
46	LGSELSVVN	323	1.1000	11.70
47	LKALGRMES	465	1.1000	11.70
48	FNPLSVGAG	508	1.1000	11.70
49	VGVIVELID	32	1.0000	10.64
50	VLRVEVGAP	154	1.0000	10.64
51	MWFVRQAHQ	214	1.0000	10.64
52	VNANAAHLQ	244	1.0000	10.64
53	LRGGLAFID	166	0.9500	10.11
54	LVLAAGPDG	119	0.9000	9.57
55	LQRARVPMP	251	0.9000	9.57
56	LLRSHAVTL	266	0.9000	9.57
57	LFNPLSVGA	507	0.9000	9.57
58	FVVSKQSRD	552	0.9000	9.57
59	LRVEVGAPS	155	0.8000	8.51
60	ICPVGAVVA	223	0.7000	7.45
61	IDSCDPTAH	394	0.6000	6.38

62	VENAIATAV	410	0.6000	6.38
63	IGMRGSYGG	484	0.6000	6.38
64	IAAAQVAET	592	0.6000	6.38

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	VVITVVSYS	104	5.1000	56.67
2	FLSEQVLSR	291	4.8000	53.33
3	VVSDTSQEF	201	4.6000	51.11
4	VVNDPNLRD	329	4.4000	48.89
5	VVMIGMLSS	493	4.0000	44.44
6	LVVSDTSQE	200	3.8000	42.22
7	VVATKTDLY	229	3.7000	41.11
8	FGRLKALGR	462	3.2000	35.56
9	IGMLSSVVG	496	3.1800	35.33
10	WREIVNANA	240	3.1000	34.44
11	LNSLLNLPA	86	2.8000	31.11
12	LRVEVGAPS	155	2.8000	31.11
13	YQRSEALAD	426	2.8000	31.11
14	WAYQRSEAL	424	2.7600	30.67
15	LRSHAVTLN	267	2.7000	30.00
16	ITRSLTESL	580	2.5600	28.44
17	FVDDISFVV	546	2.5000	27.78
18	MIGMLSSVV	495	2.3000	25.56
19	FVRQAHQIC	216	2.2000	24.44
20	LAFIDTPGV	170	2.1000	23.33
21	VVIAGLLKQ	72	2.0000	22.22
22	ILSQVNDNL	615	1.9600	21.78
23	FNPLSVGAG	508	1.9000	21.11
24	LGRMESKPL	468	1.7600	19.56
25	IVKFLSEQV	288	1.7000	18.89
26	LGSELSVVN	323	1.6800	18.67
27	LLNLPAARV	89	1.6000	17.78
28	IVNANAAHL	243	1.5600	17.33
29	LLRSHAVTL	266	1.5400	17.11
30	YSAQPSARL	111	1.4600	16.22

31	MPIIAVSSL	258	1.4600	16.22
32	IIAVSSLLR	260	1.4000	15.56
33	LQRQLGILS	609	1.3800	15.33
34	LEPTLTPRA	626	1.3000	14.44
35	WGDTVTQPD	19	1.2000	13.33
36	VIVELIDHT	34	1.2000	13.33
37	FVVSKQSRD	552	1.1000	12.22
38	LKMIQRLLR	562	1.1000	12.22
39	VLGDGFNDL	363	1.0600	11.78
40	IAVSSLLRS	261	1.0000	11.11
41	MLSSVVGLG	498	1.0000	11.11
42	VRRAPHAGG	143	0.9000	10.00
43	VVSYSAQPS	108	0.8000	8.89
44	LQRARVPMP	251	0.8000	8.89
45	LSAELSPHV	449	0.8000	8.89
46	LLRVRSEAK	532	0.8000	8.89
47	VRSEAKANV	535	0.8000	8.89
48	VLSRATERV	296	0.7000	7.78
49	VRRFVDDIS	543	0.7000	7.78
50	LQATIAAAQ	588	0.7000	7.78
51	LLPEADAVL	192	0.6600	7.33
52	MVPAGLCAY	0	0.6000	6.67
53	VARSFADAG	436	0.6000	6.67
54	LGLFNPLSV	505	0.6000	6.67
55	IAIAKLNER	43	0.5000	5.56
56	LLNSLLNLP	85	0.5000	5.56
57	VNANAAHLQ	244	0.5000	5.56
58	LVQRLTRAR	54	0.4000	4.44
59	LNEESNFPA	279	0.4000	4.44
60	LKALGRMES	465	0.4000	4.44
61	ISFVVSKQS	550	0.4000	4.44
62	YKEDKQNRL	524	0.3600	4.00
63	LVLAAGPDG	119	0.3000	3.33
64	WAEIGNDVE	403	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	VVITVVSYS	104	4.8000	54.55
2	VVMIGMLSS	493	4.5000	51.14
3	MIGMLSSVV	495	3.9000	44.32
4	LNSLLNLPA	86	3.6000	40.91
5	VVIAGLLKQ	72	3.3000	37.50
6	IGMLSSVVG	496	2.8000	31.82
7	IVKFLSEQV	288	2.7000	30.68
8	LVVSDTSQE	200	2.6000	29.55
9	MPIIAVSSL	258	2.5000	28.41
10	VITVVSYSA	105	2.4000	27.27
11	VVSYSAQPS	108	2.4000	27.27
12	WREIVNANA	240	2.4000	27.27
13	VRRFVDDIS	543	2.3000	26.14
14	LLRVRSEAK	532	2.2000	25.00
15	LAFIDTPGV	170	2.1000	23.86
16	LGLFNPLSV	505	2.1000	23.86
17	IIAVSSLLR	260	1.9000	21.59
18	LLNLPAARV	89	1.8000	20.45
19	VLVVSDTSQ	199	1.8000	20.45
20	LGRMESKPL	468	1.7000	19.32
21	IVNANAAHL	243	1.6000	18.18
22	VVNDPNLRD	329	1.4000	15.91
23	ISFVVSKQS	550	1.4000	15.91
24	LRSHAVTLN	267	1.3000	14.77
25	VELIDHTIA	36	1.2000	13.64
26	LQRQLGILS	609	1.1800	13.41
27	LKALGRMES	465	1.1000	12.50
28	IIGMRGSYG	483	1.1000	12.50
29	VQRLTRARQ	55	1.0000	11.36
30	VRVVIAGLL	70	1.0000	11.36
31	VVSDTSQEF	201	1.0000	11.36
32	VVATKTDLY	229	0.9000	10.23
33	LFNPLSVGA	507	0.9000	10.23
34	VVGLGLFNP	502	0.8500	9.66
35	LRVEVGAPS	155	0.8000	9.09
36	LQATIAAAQ	588	0.8000	9.09
37	ICPVGAVVA	223	0.7000	7.95
38	VLSAELSPH	448	0.6800	7.73
39	VLRVEVGAP	154	0.6000	6.82
40	ITVVSYSAQ	106	0.5000	5.68

41	VRRAPHAGG	143	0.5000	5.68
42	LQRARVPMP	251	0.5000	5.68
43	FGRLKALGR	462	0.5000	5.68
44	LKMIQRLLR	562	0.5000	5.68
45	LAGLEPTLT	623	0.4000	4.55
46	LEPTLTPRA	626	0.4000	4.55
47	MVPAGLCAY	0	0.3000	3.41
48	VENAIATAV	410	0.3000	3.41
49	ILSQVNDNL	615	0.3000	3.41
50	MWFVRQAHQ	214	0.2000	2.27
51	FVRQAHQIC	216	0.2000	2.27
52	VGAVVATKT	226	0.2000	2.27
53	VNANAAHLQ	244	0.2000	2.27
54	VPMPIIAVS	256	0.2000	2.27
55	ITRSLTESL	580	0.2000	2.27
56	IVELIDHTI	35	0.1000	1.14
57	IAIAKLNER	43	0.1000	1.14
58	LGLLPEADA	190	0.1000	1.14
59	LLRSHAVTL	266	-0.1000	0
60	VVSKQSRDR	553	-0.1000	0
61	IRSATEQLA	312	-0.2000	0
62	FNPLSVGAG	508	-0.2000	0
63	LSQVNDNLA	616	-0.2000	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	VVITVVSYS	104	4.7000	54.65
2	VVMIGMLSS	493	3.6000	41.86
3	FLSEQVLSR	291	3.3000	38.37
4	VVNDPNLRD	329	3.3000	38.37
5	WREIVNANA	240	3.1000	36.05
6	LNSLLNLPA	86	2.8000	32.56
7	VVIAGLLKQ	72	2.7000	31.40
8	VVSDTSQEF	201	2.7000	31.40
9	LRVEVGAPS	155	2.4000	27.91
10	LVVSDTSQE	200	2.4000	27.91

11	VVATKTDLY	229	2.4000	27.91
12	FVRQAHQIC	216	2.2000	25.58
13	LRSHAVTLN	267	1.9000	22.09
14	WAYQRSEAL	424	1.8000	20.93
15	IGMLSSVVG	496	1.7800	20.70
16	YQRSEALAD	426	1.7000	19.77
17	FGRLKALGR	462	1.7000	19.77
18	ITRSLTESL	580	1.6000	18.60
19	FVDDISFVV	546	1.5000	17.44
20	LQATIAAAQ	588	1.4000	16.28
21	MIGMLSSVV	495	1.3000	15.12
22	LEPTLTPRA	626	1.3000	15.12
23	VNANAAHLQ	244	1.2000	13.95
24	LAFIDTPGV	170	1.1000	12.79
25	ILSQVNDNL	615	1.0000	11.63
26	LQRQLGILS	609	0.9800	11.40
27	LGSELSVVN	323	0.8800	10.23
28	LGRMESKPL	468	0.8000	9.30
29	IVKFLSEQV	288	0.7000	8.14
30	LLRVRSEAK	532	0.7000	8.14
31	LLNLPAARV	89	0.6000	6.98
32	IVNANAAHL	243	0.6000	6.98
33	IAVSSLLRS	261	0.6000	6.98
34	LLRSHAVTL	266	0.5800	6.74
35	VIVELIDHT	34	0.5000	5.81
36	YSAQPSARL	111	0.5000	5.81
37	MPIIAVSSL	258	0.5000	5.81
38	FNPLSVGAG	508	0.5000	5.81
39	VVSYSAQPS	108	0.4000	4.65
40	LNEESNFPA	279	0.4000	4.65
41	VRRFVDDIS	543	0.3000	3.49
42	WGDTVTQPD	19	0.1000	1.16
43	VLGDGFNDL	363	0.1000	1.16
44	IIAVSSLLR	260	-0.1000	0
45	LIDHTIAIA	38	-0.2000	0
46	VQRLTRARQ	55	-0.2000	0
47	LQRARVPMP	251	-0.2000	0
48	LSAELSPHV	449	-0.2000	0
49	VRSEAKANV	535	-0.2000	0
50	LFNPLSVGA	507	-0.2200	0
51	LLPEADAVL	192	-0.3000	0

52	VLSRATERV	296	-0.3000	0
53	MLSSVVGLG	498	-0.4000	0
54	LGLFNPLSV	505	-0.4000	0
55	LKMIQRLLR	562	-0.4000	0
56	LLNSLLNLP	85	-0.5000	0
57	VRRAPHAGG	143	-0.5000	0
58	VELIDHTIA	36	-0.6000	0
59	YKEDKQNRL	524	-0.6000	0
60	MVPAGLCAY	0	-0.7000	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	LLRSHAVTL	266	7.2000	62.07
2	VRVVIAGLL	70	6.0000	51.72
3	ITRSLTESL	580	5.4200	46.72
4	YGGVVMIGM	490	5.2000	44.83
5	IVNANAAHL	243	5.0000	43.10
6	MPIIAVSSL	258	5.0000	43.10
7	LRRGHKMII	476	4.9000	42.24
8	IVKFLSEQV	288	4.8000	41.38
9	LSSVVGLGL	499	4.8000	41.38
10	VVMIGMLSS	493	4.7000	40.52
11	WFVRQAHQI	215	4.5000	38.79
12	YQRSEALAD	426	4.4000	37.93
13	LGLFNPLSV	505	4.4000	37.93
14	VMGTDFGRL	457	4.3000	37.07
15	LGRMESKPL	468	4.3000	37.07
16	MRGSYGGVV	486	4.3000	37.07
17	VVITVVSYS	104	4.2000	36.21
18	LAVSLGSEL	319	4.2000	36.21
19	WAYQRSEAL	424	4.2000	36.21
20	LKQGKSQLL	78	4.1000	35.34
21	FVDDISFVV	546	3.9000	33.62
22	VVSDTSQEF	201	3.5000	30.17
23	VGLGLFNPL	503	3.4000	29.31
24	VITVVSYSA	105	3.3000	28.45

25	LVVSDTSQE	200	3.1200	26.90
26	LSVGAGLIL	511	3.1000	26.72
27	VVIAGLLKQ	72	3.0000	25.86
28	IIAVSSLLR	260	3.0000	25.86
29	MIGMLSSVV	495	2.9000	25.00
30	LKMIQRLLR	562	2.9000	25.00
31	LDSVLSAEL	445	2.8000	24.14
32	LAFIDTPGV	170	2.6200	22.59
33	VRAGVLGEI	304	2.6000	22.41
34	LRDRLASDL	335	2.6000	22.41
35	VLGDGFNDL	363	2.6000	22.41
36	VENAIATAV	410	2.5000	21.55
37	WQQVLGDGF	360	2.3000	19.83
38	VVATKTDLY	229	2.2200	19.14
39	YSAQPSARL	111	2.2000	18.97
40	FVVSKQSRD	552	2.2000	18.97
41	LLRDHYREI	568	2.2000	18.97
42	LRRKRARKW	11	2.1000	18.10
43	LLRGGLAFI	165	2.1000	18.10
44	VKFLSEQVL	289	2.1000	18.10
45	IAVSSLLRS	261	2.0000	17.24
46	LRSHAVTLN	267	2.0000	17.24
47	VMIGMLSSV	494	2.0000	17.24
48	YKEDKQNRL	524	2.0000	17.24
49	LLRVRSEAK	532	2.0000	17.24
50	VLSRATERV	296	1.9200	16.55
51	LLNSLLNLP	85	1.9000	16.38
52	VRQAHQICP	217	1.9000	16.38
53	VEVGAPSPL	157	1.8000	15.52
54	ICPVGAVVA	223	1.8000	15.52
55	FGRLKALGR	462	1.8000	15.52
56	LLNLPAARV	89	1.7000	14.66
57	VGAVVATKT	226	1.7000	14.66
58	IGMLSSVVG	496	1.7000	14.66
59	MVPAGLCAY	0	1.6000	13.79
60	FIDTPGVGG	172	1.6000	13.79
61	FVRQAHQIC	216	1.6000	13.79
62	LTESLQATI	584	1.6000	13.79
63	WREIVNANA	240	1.5000	12.93
64	IGMRGSYGG	484	1.5000	12.93

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	LLRSHAVTL	266	7.2000	62.07
2	VRVVIAGLL	70	6.0000	51.72
3	ITRSLTESL	580	5.4200	46.72
4	YGGVVMIGM	490	5.2000	44.83
5	IVNANAAHL	243	5.0000	43.10
6	MPIIAVSSL	258	5.0000	43.10
7	LRRGHKMII	476	4.9000	42.24
8	IVKFLSEQV	288	4.8000	41.38
9	LSSVVGLGL	499	4.8000	41.38
10	VVMIGMLSS	493	4.7000	40.52
11	WFVRQAHQI	215	4.5000	38.79
12	YQRSEALAD	426	4.4000	37.93
13	LGLFNPLSV	505	4.4000	37.93
14	VMGTDFGRL	457	4.3000	37.07
15	LGRMESKPL	468	4.3000	37.07
16	MRGSYGGVV	486	4.3000	37.07
17	VVITVVSYS	104	4.2000	36.21
18	LAVSLGSEL	319	4.2000	36.21
19	WAYQRSEAL	424	4.2000	36.21
20	LKQGKSQLL	78	4.1000	35.34
21	FVDDISFVV	546	3.9000	33.62
22	VVSDTSQEF	201	3.5000	30.17
23	VGLGLFNPL	503	3.4000	29.31
24	VITVVSYSA	105	3.3000	28.45
25	LVVSDTSQE	200	3.1200	26.90
26	LSVGAGLIL	511	3.1000	26.72
27	VVIAGLLKQ	72	3.0000	25.86
28	IIAVSSLLR	260	3.0000	25.86
29	MIGMLSSVV	495	2.9000	25.00
30	LKMIQRLLR	562	2.9000	25.00
31	LDSVLSAEL	445	2.8000	24.14
32	LAFIDTPGV	170	2.6200	22.59
33	VRAGVLGEI	304	2.6000	22.41
34	LRDRLASDL	335	2.6000	22.41
35	VLGDGFNDL	363	2.6000	22.41

36	VENAIATAV	410	2.5000	21.55
37	WQQVLGDGF	360	2.3000	19.83
38	VVATKTDLY	229	2.2200	19.14
39	YSAQPSARL	111	2.2000	18.97
40	FVVSKQSRD	552	2.2000	18.97
41	LLRDHYREI	568	2.2000	18.97
42	LRRKRARKW	11	2.1000	18.10
43	LLRGGLAFI	165	2.1000	18.10
44	VKFLSEQVL	289	2.1000	18.10
45	IAVSSLLRS	261	2.0000	17.24
46	LRSHAVTLN	267	2.0000	17.24
47	VMIGMLSSV	494	2.0000	17.24
48	YKEDKQNRL	524	2.0000	17.24
49	LLRVRSEAK	532	2.0000	17.24
50	VLSRATERV	296	1.9200	16.55
51	LLNSLLNLP	85	1.9000	16.38
52	VRQAHQICP	217	1.9000	16.38
53	VEVGAPSPL	157	1.8000	15.52
54	ICPVGAVVA	223	1.8000	15.52
55	FGRLKALGR	462	1.8000	15.52
56	LLNLPAARV	89	1.7000	14.66
57	VGAVVATKT	226	1.7000	14.66
58	IGMLSSVVG	496	1.7000	14.66
59	MVPAGLCAY	0	1.6000	13.79
60	FIDTPGVGG	172	1.6000	13.79
61	FVRQAHQIC	216	1.6000	13.79
62	LTESLQATI	584	1.6000	13.79
63	WREIVNANA	240	1.5000	12.93
64	IGMRGSYGG	484	1.5000	12.93

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	VQRLTRARQ	55	3.9000	45.35
2	VVIAGLLKQ	72	3.8000	44.19
3	LRRKRARKW	11	3.5000	40.70
4	MIQRLLRDH	564	3.3000	38.37

5	VVSYSAQPS	108	3.0000	34.88
6	FNPLSVGAG	508	2.8000	32.56
7	ILGRMAYKE	518	2.7000	31.40
8	LVQRLTRAR	54	2.6000	30.23
9	WFVRQAHQI	215	2.6000	30.23
10	LRVRSEAKA	533	2.6000	30.23
11	FVWAYQRSE	422	2.5000	29.07
12	IGMRGSYGG	484	2.3000	26.74
13	VVMIGMLSS	493	2.3000	26.74
14	VVITVVSYS	104	2.2000	25.58
15	LKALGRMES	465	2.2000	25.58
16	VRRAPHAGG	143	2.1000	24.42
17	LERRKREAQ	343	2.0000	23.26
18	VVSKQSRDR	553	1.9000	22.09
19	YRDLRRKRA	8	1.8000	20.93
20	LRTRFRTVT	379	1.8000	20.93
21	LRRGHKMII	476	1.8000	20.93
22	MVPAGLCAY	0	1.7000	19.77
23	IVNANAAHL	243	1.6000	18.60
24	YQRSEALAD	426	1.6000	18.60
25	VRVVIAGLL	70	1.5000	17.44
26	MESKPLRRG	471	1.5000	17.44
27	LKMIQRLLR	562	1.5000	17.44
28	LVVSDTSQE	200	1.4000	16.28
29	VRSEAKANV	535	1.3000	15.12
30	LGILSQVND	613	1.3000	15.12
31	MIIGMRGSY	482	1.2000	13.95
32	MWFVRQAHQ	214	1.0000	11.63
33	LNDKELNEE	274	1.0000	11.63
34	FVVSKQSRD	552	1.0000	11.63
35	FPAIVKFLS	285	0.9000	10.47
36	LRDRLASDL	335	0.9000	10.47
37	LLNLPAARV	89	0.8000	9.30
38	VLRVEVGAP	154	0.8000	9.30
39	VWAYQRSEA	423	0.8000	9.30
40	LGLFNPLSV	505	0.8000	9.30
41	IRELQRQLG	606	0.8000	9.30
42	LRVEVGAPS	155	0.7000	8.14
43	LYPRWREIV	236	0.7000	8.14
44	WREIVNANA	240	0.7000	8.14
45	VVNDPNLRD	329	0.7000	8.14

46	LGRMESKPL	468	0.7000	8.14
47	IGMLSSVVG	496	0.7000	8.14
48	FGRLKALGR	462	0.6000	6.98
49	LVLAAGPDG	119	0.5000	5.81
50	LRGGLAFID	166	0.5000	5.81
51	FVRQAHQIC	216	0.5000	5.81
52	VLSRATERV	296	0.5000	5.81
53	LQATIAAAQ	588	0.5000	5.81
54	VLSAELSPH	448	0.4000	4.65
55	VVGLGLFNP	502	0.4000	4.65
56	LGRMAYKED	519	0.4000	4.65
57	VPMPIIAVS	256	0.3000	3.49
58	IQRLLRDHY	565	0.3000	3.49
59	LPAARVGDD	92	0.2000	2.33
60	VNANAAHLQ	244	0.2000	2.33
61	MPIIAVSSL	258	0.2000	2.33
62	MLSSVVGLG	498	0.2000	2.33
63	LTPRASLGR	630	0.2000	2.33
64	FLSEQVLSR	291	0.1000	1.16

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VQRLTRARQ	55	3.1000	38.75
2	VVIAGLLKQ	72	3.0000	37.50
3	VVSYSAQPS	108	3.0000	37.50
4	LRRKRARKW	11	2.6000	32.50
5	LVQRLTRAR	54	2.6000	32.50
6	LRVRSEAKA	533	2.6000	32.50
7	WFVRQAHQI	215	2.4000	30.00
8	VVMIGMLSS	493	2.3000	28.75
9	VVITVVSYS	104	2.2000	27.50
10	LKALGRMES	465	2.2000	27.50
11	MIQRLLRDH	564	2.0800	26.00
12	VVSKQSRDR	553	1.9000	23.75
13	YRDLRRKRA	8	1.8000	22.50
14	LRRGHKMII	476	1.6000	20.00

15	FNPLSVGAG	508	1.5000	18.75
16	LKMIQRLLR	562	1.5000	18.75
17	LERRKREAQ	343	1.2000	15.00
18	IGMRGSYGG	484	1.0000	12.50
19	VRSEAKANV	535	1.0000	12.50
20	FPAIVKFLS	285	0.9000	11.25
21	LRTRFRTVT	379	0.9000	11.25
22	VRRAPHAGG	143	0.8000	10.00
23	VWAYQRSEA	423	0.8000	10.00
24	LRVEVGAPS	155	0.7000	8.75
25	WREIVNANA	240	0.7000	8.75
26	MVPAGLCAY	0	0.6000	7.50
27	IVNANAAHL	243	0.6000	7.50
28	FGRLKALGR	462	0.6000	7.50
29	VRVVIAGLL	70	0.5000	6.25
30	LLNLPAARV	89	0.5000	6.25
31	FVRQAHQIC	216	0.5000	6.25
32	LGLFNPLSV	505	0.5000	6.25
33	VLRVEVGAP	154	0.4000	5.00
34	LYPRWREIV	236	0.4000	5.00
35	VPMPIIAVS	256	0.3000	3.75
36	MWFVRQAHQ	214	0.2000	2.50
37	VLSRATERV	296	0.2000	2.50
38	MESKPLRRG	471	0.2000	2.50
39	LTPRASLGR	630	0.2000	2.50
40	FLSEQVLSR	291	0.1000	1.25
41	MIIGMRGSY	482	0.1000	1.25
42	LRDRLASDL	335	-0.1000	0
43	LNSLLNLPA	86	-0.2000	0
44	LGLLPEADA	190	-0.2000	0
45	IAGLLKQGK	74	-0.3000	0
46	LGRMESKPL	468	-0.3000	0
47	ILGRMAYKE	518	-0.3000	0
48	LQATIAAAQ	588	-0.3000	0
49	LLRGGLAFI	165	-0.4000	0
50	LQRARVPMP	251	-0.4000	0
51	VRAGVLGEI	304	-0.4000	0
52	MIGMLSSVV	495	-0.4000	0
53	ISFVVSKQS	550	-0.4000	0
54	FVWAYQRSE	422	-0.5000	0
55	IRELQRQLG	606	-0.5000	0

56	VNANAAHLQ	244	-0.6000	0
57	IGMLSSVVG	496	-0.6000	0
58	VSSLLRSHA	263	-0.7000	0
59	VITVVSYSA	105	-0.8000	0
60	LVLAAGPDG	119	-0.8000	0
61	MPIIAVSSL	258	-0.8000	0
62	IQRLLRDHY	565	-0.8000	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	VQRLTRARQ	55	4.1000	51.25
2	VVIAGLLKQ	72	4.0000	50.00
3	VVSYSAQPS	108	4.0000	50.00
4	LRRKRARKW	11	3.6000	45.00
5	LVQRLTRAR	54	3.6000	45.00
6	LRVRSEAKA	533	3.6000	45.00
7	VVMIGMLSS	493	3.3000	41.25
8	VVITVVSYS	104	3.2000	40.00
9	LKALGRMES	465	3.2000	40.00
10	MIQRLLRDH	564	3.0800	38.50
11	VVSKQSRDR	553	2.9000	36.25
12	LRRGHKMII	476	2.6000	32.50
13	LKMIQRLLR	562	2.5000	31.25
14	LERRKREAQ	343	2.2000	27.50
15	IGMRGSYGG	484	2.0000	25.00
16	VRSEAKANV	535	2.0000	25.00
17	LRTRFRTVT	379	1.9000	23.75
18	VRRAPHAGG	143	1.8000	22.50
19	VWAYQRSEA	423	1.8000	22.50
20	LRVEVGAPS	155	1.7000	21.25
21	MVPAGLCAY	0	1.6000	20.00
22	IVNANAAHL	243	1.6000	20.00
23	VRVVIAGLL	70	1.5000	18.75
24	LLNLPAARV	89	1.5000	18.75
25	LGLFNPLSV	505	1.5000	18.75
26	VLRVEVGAP	154	1.4000	17.50

27	WFVRQAHQI	215	1.4000	17.50
28	LYPRWREIV	236	1.4000	17.50
29	VPMPIIAVS	256	1.3000	16.25
30	MWFVRQAHQ	214	1.2000	15.00
31	VLSRATERV	296	1.2000	15.00
32	MESKPLRRG	471	1.2000	15.00
33	LTPRASLGR	630	1.2000	15.00
34	MIIGMRGSY	482	1.1000	13.75
35	VVGLGLFNP	502	1.0000	12.50
36	LRDRLASDL	335	0.9000	11.25
37	YRDLRRKRA	8	0.8000	10.00
38	LNSLLNLPA	86	0.8000	10.00
39	LGLLPEADA	190	0.8000	10.00
40	IAGLLKQGK	74	0.7000	8.75
41	LGRMESKPL	468	0.7000	8.75
42	ILGRMAYKE	518	0.7000	8.75
43	LQATIAAAQ	588	0.7000	8.75
44	LLRGGLAFI	165	0.6000	7.50
45	LQRARVPMP	251	0.6000	7.50
46	VRAGVLGEI	304	0.6000	7.50
47	MIGMLSSVV	495	0.6000	7.50
48	ISFVVSKQS	550	0.6000	7.50
49	FNPLSVGAG	508	0.5000	6.25
50	IRELQRQLG	606	0.5000	6.25
51	VNANAAHLQ	244	0.4000	5.00
52	IGMLSSVVG	496	0.4000	5.00
53	VSSLLRSHA	263	0.3000	3.75
54	VITVVSYSA	105	0.2000	2.50
55	LVLAAGPDG	119	0.2000	2.50
56	MPIIAVSSL	258	0.2000	2.50
57	IQRLLRDHY	565	0.2000	2.50
58	VLSAELSPH	448	0.1800	2.25
59	IAVSSLLRS	261	0.1000	1.25
60	LQRQLGILS	609	0.1000	1.25

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	VQRLTRARQ	55	4.9000	56.98
2	VVIAGLLKQ	72	4.8000	55.81
3	LRRKRARKW	11	4.5000	52.33
4	MIQRLLRDH	564	4.3000	50.00
5	VVSYSAQPS	108	4.0000	46.51
6	ILGRMAYKE	518	3.7000	43.02
7	LVQRLTRAR	54	3.6000	41.86
8	LRVRSEAKA	533	3.6000	41.86
9	IGMRGSYGG	484	3.3000	38.37
10	VVMIGMLSS	493	3.3000	38.37
11	VVITVVSYS	104	3.2000	37.21
12	LKALGRMES	465	3.2000	37.21
13	VRRAPHAGG	143	3.1000	36.05
14	LERRKREAQ	343	3.0000	34.88
15	VVSKQSRDR	553	2.9000	33.72
16	LRTRFRTVT	379	2.8000	32.56
17	LRRGHKMII	476	2.8000	32.56
18	MVPAGLCAY	0	2.7000	31.40
19	IVNANAAHL	243	2.6000	30.23
20	VRVVIAGLL	70	2.5000	29.07
21	MESKPLRRG	471	2.5000	29.07
22	LKMIQRLLR	562	2.5000	29.07
23	LVVSDTSQE	200	2.4000	27.91
24	VRSEAKANV	535	2.3000	26.74
25	LGILSQVND	613	2.3000	26.74
26	MIIGMRGSY	482	2.2000	25.58
27	MWFVRQAHQ	214	2.0000	23.26
28	LNDKELNEE	274	2.0000	23.26
29	LRDRLASDL	335	1.9000	22.09
30	LLNLPAARV	89	1.8000	20.93
31	VLRVEVGAP	154	1.8000	20.93
32	VWAYQRSEA	423	1.8000	20.93
33	LGLFNPLSV	505	1.8000	20.93
34	FNPLSVGAG	508	1.8000	20.93
35	IRELQRQLG	606	1.8000	20.93
36	LRVEVGAPS	155	1.7000	19.77
37	LYPRWREIV	236	1.7000	19.77
38	VVNDPNLRD	329	1.7000	19.77
39	LGRMESKPL	468	1.7000	19.77
40	IGMLSSVVG	496	1.7000	19.77

41	WFVRQAHQI	215	1.6000	18.60
42	LVLAAGPDG	119	1.5000	17.44
43	LRGGLAFID	166	1.5000	17.44
44	VLSRATERV	296	1.5000	17.44
45	FVWAYQRSE	422	1.5000	17.44
46	LQATIAAAQ	588	1.5000	17.44
47	VLSAELSPH	448	1.4000	16.28
48	VVGLGLFNP	502	1.4000	16.28
49	LGRMAYKED	519	1.4000	16.28
50	VPMPIIAVS	256	1.3000	15.12
51	IQRLLRDHY	565	1.3000	15.12
52	LPAARVGDD	92	1.2000	13.95
53	VNANAAHLQ	244	1.2000	13.95
54	MPIIAVSSL	258	1.2000	13.95
55	MLSSVVGLG	498	1.2000	13.95
56	LTPRASLGR	630	1.2000	13.95
57	LQRARVPMP	251	1.0000	11.63
58	IIGMRGSYG	483	1.0000	11.63
59	MIGMLSSVV	495	0.9000	10.47
60	IAAAQVAET	592	0.9000	10.47
61	YRDLRRKRA	8	0.8000	9.30
62	LNSLLNLPA	86	0.8000	9.30
63	LLRGGLAFI	165	0.8000	9.30
64	LGLLPEADA	190	0.8000	9.30

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	VVITVVSYS	104	4.0000	45.98
2	VVSYSAQPS	108	4.0000	45.98
3	LRTRFRTVT	379	3.7000	42.53
4	VVIAGLLKQ	72	3.6000	41.38
5	LKALGRMES	465	3.2000	36.78
6	VQRLTRARQ	55	3.1000	35.63
7	WFVRQAHQI	215	2.9000	33.33
8	LERRKREAQ	343	2.9000	33.33
9	VVMIGMLSS	493	2.9000	33.33

10	VWAYQRSEA	423	2.6000	29.89
11	LRRGHKMII	476	2.6000	29.89
12	LRVRSEAKA	533	2.6000	29.89
13	LRRKRARKW	11	2.3000	26.44
14	LVQRLTRAR	54	2.3000	26.44
15	LYPRWREIV	236	2.1000	24.14
16	LKMIQRLLR	562	2.1000	24.14
17	VLSRATERV	296	1.9000	21.84
18	IGMRGSYGG	484	1.9000	21.84
19	MIQRLLRDH	564	1.7800	20.46
20	FPAIVKFLS	285	1.7500	20.11
21	LRDRLASDL	335	1.7000	19.54
22	VVSKQSRDR	553	1.6000	18.39
23	FVRQAHQIC	216	1.5000	17.24
24	MIGMLSSVV	495	1.4000	16.09
25	YRDLRRKRA	8	1.3000	14.94
26	FGRLKALGR	462	1.2000	13.79
27	VSSLLRSHA	263	1.1000	12.64
28	LGLFNPLSV	505	1.1000	12.64
29	MPIIAVSSL	258	1.0000	11.49
30	VRSEAKANV	535	1.0000	11.49
31	VLSAELSPH	448	0.9800	11.26
32	VVGLGLFNP	502	0.8500	9.77
33	VRRAPHAGG	143	0.8000	9.20
34	FNPLSVGAG	508	0.8000	9.20
35	LTPRASLGR	630	0.8000	9.20
36	VELIDHTIA	36	0.7000	8.05
37	IAGLLKQGK	74	0.7000	8.05
38	LRVEVGAPS	155	0.7000	8.05
39	WREIVNANA	240	0.7000	8.05
40	FLSEQVLSR	291	0.7000	8.05
41	MVPAGLCAY	0	0.6000	6.90
42	IVNANAAHL	243	0.6000	6.90
43	LRSHAVTLN	267	0.6000	6.90
44	VMIGMLSSV	494	0.6000	6.90
45	ILGRMAYKE	518	0.6000	6.90
46	LLNLPAARV	89	0.5000	5.75
47	IIGMRGSYG	483	0.5000	5.75
48	IRELQRQLG	606	0.5000	5.75
49	IAIAKLNER	43	0.4000	4.60
50	LNSLLNLPA	86	0.4000	4.60

51	IGMLSSVVG	496	0.4000	4.60
52	IQRLLRDHY	565	0.4000	4.60
53	VPMPIIAVS	256	0.3000	3.45
54	LVVSDTSQE	200	0.2000	2.30
55	MWFVRQAHQ	214	0.2000	2.30
56	VITVVSYSA	105	0.1000	1.15
57	IVKFLSEQV	288	0.1000	1.15
58	FVVSKQSRD	552	0.1000	1.15
59	LQRQLGILS	609	-0.0200	0
60	VNANAAHLQ	244	-0.1000	0
61	MESKPLRRG	471	-0.1000	0
62	LLRVRSEAK	532	-0.1000	0

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1

Rank	Sequence	At Position	Score	% of Highest Score
1	VVIAGLLKQ	72	5.6000	55.45
2	VVMIGMLSS	493	4.1000	40.59
3	VQRLTRARQ	55	3.9000	38.61
4	LKALGRMES	465	3.8000	37.62
5	LRRKRARKW	11	3.7000	36.63
6	MIQRLLRDH	564	3.5000	34.65
7	YQRSEALAD	426	3.4000	33.66
8	LRRGHKMII	476	3.4000	33.66
9	ILGRMAYKE	518	3.4000	33.66
10	WFVRQAHQI	215	3.3000	32.67
11	LKMIQRLLR	562	3.3000	32.67
12	VVSYSAQPS	108	3.1000	30.69
13	LERRKREAQ	343	3.1000	30.69
14	IGMRGSYGG	484	3.0000	29.70
15	LRTRFRTVT	379	2.9000	28.71
16	FNPLSVGAG	508	2.9000	28.71
17	LVQRLTRAR	54	2.8000	27.72
18	FVWAYQRSE	422	2.7000	26.73
19	LGLFNPLSV	505	2.6000	25.74
20	LRVRSEAKA	533	2.6000	25.74
21	VVNDPNLRD	329	2.5000	24.75

22	YRDLRRKRA	8	2.4000	23.76
23	FGRLKALGR	462	2.4000	23.76
24	VVITVVSYS	104	2.2000	21.78
25	VRRAPHAGG	143	2.1000	20.79
26	VVSKQSRDR	553	2.1000	20.79
27	LTPRASLGR	630	2.0000	19.80
28	FLSEQVLSR	291	1.9000	18.81
29	LYPRWREIV	236	1.8000	17.82
30	LGILSQVND	613	1.8000	17.82
31	MVPAGLCAY	0	1.7000	16.83
32	MESKPLRRG	471	1.7000	16.83
33	LVLAAGPDG	119	1.6500	16.34
34	VRVVIAGLL	70	1.6000	15.84
35	LNSLLNLPA	86	1.6000	15.84
36	IVNANAAHL	243	1.6000	15.84
37	VLSRATERV	296	1.6000	15.84
38	YGGVVMIGM	490	1.6000	15.84
39	VGVIVELID	32	1.4000	13.86
40	LVVSDTSQE	200	1.4000	13.86
41	FPAIVKFLS	285	1.4000	13.86
42	LNERGDLVQ	48	1.3000	12.87
43	LNDKELNEE	274	1.3000	12.87
44	LGRMESKPL	468	1.3000	12.87
45	MIIGMRGSY	482	1.3000	12.87
46	VRSEAKANV	535	1.3000	12.87
47	IGMLSSVVG	496	1.2000	11.88
48	LQRARVPMP	251	1.1500	11.39
49	LRGGLAFID	166	1.0000	9.90
50	MWFVRQAHQ	214	1.0000	9.90
51	LGRMAYKED	519	1.0000	9.90
52	FVVSKQSRD	552	1.0000	9.90
53	VLRVEVGAP	154	0.9000	8.91
54	VNANAAHLQ	244	0.9000	8.91
55	IAVSSLLRS	261	0.9000	8.91
56	LRSHAVTLN	267	0.9000	8.91
57	LRDRLASDL	335	0.9000	8.91
58	VVGLGLFNP	502	0.9000	8.91
59	IRELQRQLG	606	0.9000	8.91
60	LLNLPAARV	89	0.8000	7.92
61	VRQAHQICP	217	0.8000	7.92
62	IIAVSSLLR	260	0.8000	7.92

63	VWAYQRSEA	423	0.8000	7.92
64	LRVEVGAPS	155	0.7000	6.93

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	VVIAGLLKQ	72	4.8000	57.83
2	VVMIGMLSS	493	4.7000	56.63
3	LKALGRMES	465	4.2000	50.60
4	LKMIQRLLR	562	3.9000	46.99
5	VQRLTRARQ	55	3.5000	42.17
6	YRDLRRKRA	8	2.8000	33.73
7	FGRLKALGR	462	2.8000	33.73
8	VVITVVSYS	104	2.6000	31.33
9	LRRGHKMII	476	2.5000	30.12
10	LGLFNPLSV	505	2.2000	26.51
11	LNSLLNLPA	86	2.0000	24.10
12	FPAIVKFLS	285	2.0000	24.10
13	FNPLSVGAG	508	2.0000	24.10
14	WREIVNANA	240	1.3000	15.66
15	LQRQLGILS	609	1.3000	15.66
16	FVRQAHQIC	216	1.2000	14.46
17	IAVSSLLRS	261	1.2000	14.46
18	FLSEQVLSR	291	1.2000	14.46
19	YQRSEALAD	426	1.0000	12.05
20	LLNLPAARV	89	0.9000	10.84
21	IIAVSSLLR	260	0.9000	10.84
22	VVGLGLFNP	502	0.9000	10.84
23	VRRAPHAGG	143	0.8000	9.64
24	LAFIDTPGV	170	0.7500	9.04
25	LQRARVPMP	251	0.7500	9.04
26	VRVVIAGLL	70	0.7000	8.43
27	MVPAGLCAY	0	0.6000	7.23
28	VLRVEVGAP	154	0.6000	7.23
29	IVNANAAHL	243	0.6000	7.23
30	YGGVVMIGM	490	0.6000	7.23
31	VRQAHQICP	217	0.4000	4.82

32	LVLAAGPDG	119	0.3500	4.22
33	MWFVRQAHQ	214	0.3000	3.61
34	IGMLSSVVG	496	0.3000	3.61
35	VRSEAKANV	535	0.3000	3.61
36	ISFVVSKQS	550	0.3000	3.61
37	IAGLLKQGK	74	0.2000	2.41
38	VVSYSAQPS	108	0.2000	2.41
39	LGLLPEADA	190	0.2000	2.41
40	WFVRQAHQI	215	0.1000	1.20
41	VNANAAHLQ	244	0.1000	1.20
42	LQATIAAAQ	588	0.1000	1.20
43	VQQTALWQQ	354	-0.1000	0
44	LGRMESKPL	468	-0.1000	0
45	LVQRLTRAR	54	-0.2000	0
46	MPIIAVSSL	258	-0.2000	0
47	VSSLLRSHA	263	-0.3000	0
48	FVWAYQRSE	422	-0.3000	0
49	VELIDHTIA	36	-0.4000	0
50	VPMPIIAVS	256	-0.4000	0
51	LRVRSEAKA	533	-0.4000	0
52	LEPTLTPRA	626	-0.4500	0
53	MIIGMRGSY	482	-0.5000	0
54	LGILSQVND	613	-0.5000	0
55	VGGLGQPHL	178	-0.5500	0
56	IVKFLSEQV	288	-0.6000	0
57	LLRVRSEAK	532	-0.6000	0
58	VGVIVELID	32	-0.7000	0
59	LRSHAVTLN	267	-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	VVIAGLLKQ	72	4.7000	55.95
2	LRRKRARKW	11	3.9000	46.43
3	VQRLTRARQ	55	3.8000	45.24
4	VVITVVSYS	104	3.5000	41.67
5	LVQRLTRAR	54	3.3000	39.29

6	LKALGRMES	465	3.2000	38.10
7	VVSKQSRDR	553	3.2000	38.10
8	VVMIGMLSS	493	3.1000	36.90
9	VVSYSAQPS	108	3.0000	35.71
10	LRSHAVTLN	267	2.8000	33.33
11	MIQRLLRDH	564	2.7800	33.10
12	LGLFNPLSV	505	2.5000	29.76
13	LRRGHKMII	476	2.4000	28.57
14	LRDHYREIA	569	2.4000	28.57
15	LKMIQRLLR	562	2.3000	27.38
16	VVGLGLFNP	502	2.2000	26.19
17	LIDHTIAIA	38	2.0000	23.81
18	LQRQLGILS	609	2.0000	23.81
19	FVRQAHQIC	216	1.9000	22.62
20	VRSEAKANV	535	1.9000	22.62
21	VRRAPHAGG	143	1.8000	21.43
22	VNANAAHLQ	244	1.7000	20.24
23	MVPAGLCAY	0	1.6000	19.05
24	LRVEVGAPS	155	1.6000	19.05
25	IVNANAAHL	243	1.6000	19.05
26	LERRKREAQ	343	1.5000	17.86
27	MESKPLRRG	471	1.5000	17.86
28	LRVRSEAKA	533	1.5000	17.86
29	YRDLRRKRA	8	1.3000	15.48
30	LQRARVPMP	251	1.3000	15.48
31	LRTRFRTVT	379	1.3000	15.48
32	IAGLLKQGK	74	1.2000	14.29
33	LNSLLNLPA	86	1.2000	14.29
34	LLNLPAARV	89	1.2000	14.29
35	IAVSSLLRS	261	1.2000	14.29
36	VQQTALWQQ	354	1.2000	14.29
37	IVKFLSEQV	288	1.1000	13.10
38	IGMLSSVVG	496	1.1000	13.10
39	LLKQGKSQL	77	1.0000	11.90
40	IRELQRQLG	606	1.0000	11.90
41	LVLAAGPDG	119	0.9000	10.71
42	LGRMESKPL	468	0.9000	10.71
43	IAIAKLNER	43	0.8000	9.52
44	VPMPIIAVS	256	0.8000	9.52
45	IGMRGSYGG	484	0.8000	9.52
46	IQRLLRDHY	565	0.8000	9.52

47	LYPRWREIV	236	0.7000	8.33
48	IRSATEQLA	312	0.6000	7.14
49	LQATIAAAQ	588	0.6000	7.14
50	VLSAELSPH	448	0.5800	6.90
51	LNLPAARVG	90	0.5000	5.95
52	LGLLPEADA	190	0.5000	5.95
53	WFVRQAHQI	215	0.5000	5.95
54	FPAIVKFLS	285	0.5000	5.95
55	VLSRATERV	296	0.5000	5.95
56	VRRFVDDIS	543	0.5000	5.95
57	LTRARQRIT	58	0.4000	4.76
58	VSSLLRSHA	263	0.4000	4.76
59	VWAYQRSEA	423	0.4000	4.76
60	MIGMLSSVV	495	0.4000	4.76
61	FVWAYQRSE	422	0.3000	3.57
62	LGILSQVND	613	0.3000	3.57
63	LVVSDTSQE	200	0.2000	2.38
64	ISFVVSKQS	550	0.2000	2.38

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	VVIAGLLKQ	72	5.8000	69.88
2	VVMIGMLSS	493	5.7000	68.67
3	LKALGRMES	465	5.2000	62.65
4	LKMIQRLLR	562	4.9000	59.04
5	VQRLTRARQ	55	4.5000	54.22
6	VVITVVSYS	104	3.6000	43.37
7	LRRGHKMII	476	3.5000	42.17
8	LGLFNPLSV	505	3.2000	38.55
9	LNSLLNLPA	86	3.0000	36.14
10	LQRQLGILS	609	2.3000	27.71
11	IAVSSLLRS	261	2.2000	26.51
12	LLNLPAARV	89	1.9000	22.89
13	IIAVSSLLR	260	1.9000	22.89
14	VVGLGLFNP	502	1.9000	22.89
15	YRDLRRKRA	8	1.8000	21.69

16	VRRAPHAGG	143	1.8000	21.69
17	FGRLKALGR	462	1.8000	21.69
18	LAFIDTPGV	170	1.7500	21.08
19	LQRARVPMP	251	1.7500	21.08
20	VRVVIAGLL	70	1.7000	20.48
21	MVPAGLCAY	0	1.6000	19.28
22	VLRVEVGAP	154	1.6000	19.28
23	IVNANAAHL	243	1.6000	19.28
24	VRQAHQICP	217	1.4000	16.87
25	LVLAAGPDG	119	1.3500	16.27
26	MWFVRQAHQ	214	1.3000	15.66
27	IGMLSSVVG	496	1.3000	15.66
28	VRSEAKANV	535	1.3000	15.66
29	ISFVVSKQS	550	1.3000	15.66
30	IAGLLKQGK	74	1.2000	14.46
31	VVSYSAQPS	108	1.2000	14.46
32	LGLLPEADA	190	1.2000	14.46
33	VNANAAHLQ	244	1.1000	13.25
34	LQATIAAAQ	588	1.1000	13.25
35	LRRKRARKW	11	1.0000	12.05
36	VITVVSYSA	105	1.0000	12.05
37	LRVEVGAPS	155	1.0000	12.05
38	FPAIVKFLS	285	1.0000	12.05
39	FNPLSVGAG	508	1.0000	12.05
40	IRELQRQLG	606	1.0000	12.05
41	VQQTALWQQ	354	0.9000	10.84
42	LGRMESKPL	468	0.9000	10.84
43	LVQRLTRAR	54	0.8000	9.64
44	MPIIAVSSL	258	0.8000	9.64
45	VSSLLRSHA	263	0.7000	8.43
46	VELIDHTIA	36	0.6000	7.23
47	VPMPIIAVS	256	0.6000	7.23
48	LRVRSEAKA	533	0.6000	7.23
49	LEPTLTPRA	626	0.5500	6.63
50	MIIGMRGSY	482	0.5000	6.02
51	LGILSQVND	613	0.5000	6.02
52	VGGLGQPHL	178	0.4500	5.42
53	IVKFLSEQV	288	0.4000	4.82
54	LLRVRSEAK	532	0.4000	4.82
55	VGVIVELID	32	0.3000	3.61
56	WREIVNANA	240	0.3000	3.61

57	LRSHAVTLN	267	0.3000	3.61
58	LERRKREAQ	343	0.3000	3.61
59	MLSSVVGLG	498	0.3000	3.61
60	VVSKQSRDR	553	0.3000	3.61
61	IQRLLRDHY	565	0.3000	3.61
62	MIQRLLRDH	564	0.2800	3.37
63	FVRQAHQIC	216	0.2000	2.41
64	FLSEQVLSR	291	0.2000	2.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVIAGLLKQ	72	5.8000	69.88
2	VVMIGMLSS	493	5.7000	68.67
3	LKALGRMES	465	5.2000	62.65
4	LKMIQRLLR	562	4.9000	59.04
5	VQRLTRARQ	55	4.5000	54.22
6	VVITVVSYS	104	3.6000	43.37
7	LRRGHKMII	476	3.5000	42.17
8	LGLFNPLSV	505	3.2000	38.55
9	LNSLLNLPA	86	3.0000	36.14
10	LQRQLGILS	609	2.3000	27.71
11	IAVSSLLRS	261	2.2000	26.51
12	LLNLPAARV	89	1.9000	22.89
13	IIAVSSLLR	260	1.9000	22.89
14	VVGLGLFNP	502	1.9000	22.89
15	YRDLRRKRA	8	1.8000	21.69
16	VRRAPHAGG	143	1.8000	21.69
17	FGRLKALGR	462	1.8000	21.69
18	LAFIDTPGV	170	1.7500	21.08
19	LQRARVPMP	251	1.7500	21.08
20	VRVVIAGLL	70	1.7000	20.48
21	MVPAGLCAY	0	1.6000	19.28
22	VLRVEVGAP	154	1.6000	19.28
23	IVNANAAHL	243	1.6000	19.28
24	VRQAHQICP	217	1.4000	16.87
25	LVLAAGPDG	119	1.3500	16.27

26	MWFVRQAHQ	214	1.3000	15.66
27	IGMLSSVVG	496	1.3000	15.66
28	VRSEAKANV	535	1.3000	15.66
29	ISFVVSKQS	550	1.3000	15.66
30	IAGLLKQGK	74	1.2000	14.46
31	VVSYSAQPS	108	1.2000	14.46
32	LGLLPEADA	190	1.2000	14.46
33	VNANAAHLQ	244	1.1000	13.25
34	LQATIAAAQ	588	1.1000	13.25
35	LRRKRARKW	11	1.0000	12.05
36	VITVVSYSA	105	1.0000	12.05
37	LRVEVGAPS	155	1.0000	12.05
38	FPAIVKFLS	285	1.0000	12.05
39	FNPLSVGAG	508	1.0000	12.05
40	IRELQRQLG	606	1.0000	12.05
41	VQQTALWQQ	354	0.9000	10.84
42	LGRMESKPL	468	0.9000	10.84
43	LVQRLTRAR	54	0.8000	9.64
44	MPIIAVSSL	258	0.8000	9.64
45	VSSLLRSHA	263	0.7000	8.43
46	VELIDHTIA	36	0.6000	7.23
47	VPMPIIAVS	256	0.6000	7.23
48	LRVRSEAKA	533	0.6000	7.23
49	LEPTLTPRA	626	0.5500	6.63
50	MIIGMRGSY	482	0.5000	6.02
51	LGILSQVND	613	0.5000	6.02
52	VGGLGQPHL	178	0.4500	5.42
53	IVKFLSEQV	288	0.4000	4.82
54	LLRVRSEAK	532	0.4000	4.82
55	VGVIVELID	32	0.3000	3.61
56	WREIVNANA	240	0.3000	3.61
57	LRSHAVTLN	267	0.3000	3.61
58	LERRKREAQ	343	0.3000	3.61
59	MLSSVVGLG	498	0.3000	3.61
60	VVSKQSRDR	553	0.3000	3.61
61	IQRLLRDHY	565	0.3000	3.61
62	MIQRLLRDH	564	0.2800	3.37
63	FVRQAHQIC	216	0.2000	2.41
64	FLSEQVLSR	291	0.2000	2.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGHKMII	476	5.5000	60.44
2	VVITVVSYS	104	4.5700	50.22
3	VVIAGLLKQ	72	4.5000	49.45
4	VVMIGMLSS	493	4.0000	43.96
5	LKALGRMES	465	3.9000	42.86
6	VQRLTRARQ	55	3.4000	37.36
7	VVSDTSQEF	201	3.4000	37.36
8	MIIGMRGSY	482	3.2000	35.16
9	LKMIQRLLR	562	3.2000	35.16
10	VVNDPNLRD	329	2.8000	30.77
11	VRAGVLGEI	304	2.7000	29.67
12	VMIGMLSSV	494	2.6700	29.34
13	LQRARVPMP	251	2.5000	27.47
14	LVVSDTSQE	200	2.4700	27.14
15	IAVSSLLRS	261	2.3000	25.27
16	LQRQLGILS	609	2.3000	25.27
17	MLSSVVGLG	498	2.2000	24.18
18	LVLAAGPDG	119	2.1000	23.08
19	LLRGGLAFI	165	2.1000	23.08
20	LAFIDTPGV	170	2.1000	23.08
21	LRSHAVTLN	267	2.1000	23.08
22	VRSEAKANV	535	2.0000	21.98
23	VVSYSAQPS	108	1.9000	20.88
24	VRVVIAGLL	70	1.8000	19.78
25	VRRAPHAGG	143	1.8000	19.78
26	MRGSYGGVV	486	1.8000	19.78
27	FVDDISFVV	546	1.8000	19.78
28	MPIIAVSSL	258	1.7700	19.45
29	VLRVEVGAP	154	1.7000	18.68
30	LRVEVGAPS	155	1.7000	18.68
31	LRGGLAFID	166	1.7000	18.68
32	VVGLGLFNP	502	1.7000	18.68
33	LRDHYREIA	569	1.7000	18.68
34	MVPAGLCAY	0	1.6000	17.58
35	VSYSAQPSA	109	1.6000	17.58
36	FVRQAHQIC	216	1.6000	17.58

37	IVNANAAHL	243	1.6000	17.58
38	LLRSHAVTL	266	1.6000	17.58
39	VLSAELSPH	448	1.5500	17.03
40	IGNDVENAI	406	1.5100	16.59
41	FPAIVKFLS	285	1.5000	16.48
42	VELIDHTIA	36	1.4000	15.38
43	LILGRMAYK	517	1.4000	15.38
44	LLRDHYREI	568	1.4000	15.38
45	LLKQGKSQL	77	1.3700	15.05
46	IPVDDISTD	134	1.3700	15.05
47	VPMPIIAVS	256	1.3000	14.29
48	IQRLLRDHY	565	1.3000	14.29
49	IAGLLKQGK	74	1.1000	12.09
50	LERRKREAQ	343	1.1000	12.09
51	VDHDLRTRF	375	1.1000	12.09
52	LLRVRSEAK	532	1.1000	12.09
53	LLNSLLNLP	85	1.0100	11.10
54	VLGDGFNDL	363	1.0100	11.10
55	VRQAHQICP	217	1.0000	10.99
56	IGMLSSVVG	496	1.0000	10.99
57	ITRSLTESL	580	1.0000	10.99
58	VSSLLRSHA	263	0.9700	10.66
59	VITVVSYSA	105	0.9500	10.44
60	MWFVRQAHQ	214	0.9000	9.89
61	VTLNDKELN	272	0.9000	9.89
62	IRSATEQLA	312	0.9000	9.89
63	LRTRFRTVT	379	0.9000	9.89
64	MGTDFGRLK	458	0.9000	9.89

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVIAGLLKQ	72	3.7000	44.05
2	LRRKRARKW	11	2.9000	34.52
3	FVRQAHQIC	216	2.9000	34.52
4	VQRLTRARQ	55	2.8000	33.33
5	VVITVVSYS	104	2.5000	29.76

6	YRDLRRKRA	8	2.3000	27.38
7	LVQRLTRAR	54	2.3000	27.38
8	LKALGRMES	465	2.2000	26.19
9	VVSKQSRDR	553	2.2000	26.19
10	VVMIGMLSS	493	2.1000	25.00
11	VVSYSAQPS	108	2.0000	23.81
12	LRSHAVTLN	267	1.8000	21.43
13	MIQRLLRDH	564	1.7800	21.19
14	WFVRQAHQI	215	1.5000	17.86
15	FPAIVKFLS	285	1.5000	17.86
16	LGLFNPLSV	505	1.5000	17.86
17	LRRGHKMII	476	1.4000	16.67
18	LRDHYREIA	569	1.4000	16.67
19	FVWAYQRSE	422	1.3000	15.48
20	LKMIQRLLR	562	1.3000	15.48
21	VVGLGLFNP	502	1.2000	14.29
22	LIDHTIAIA	38	1.0000	11.90
23	FGRLKALGR	462	1.0000	11.90
24	LQRQLGILS	609	1.0000	11.90
25	VRSEAKANV	535	0.9000	10.71
26	VRRAPHAGG	143	0.8000	9.52
27	VNANAAHLQ	244	0.7000	8.33
28	FLSEQVLSR	291	0.7000	8.33
29	MVPAGLCAY	0	0.6000	7.14
30	LRVEVGAPS	155	0.6000	7.14
31	IVNANAAHL	243	0.6000	7.14
32	LERRKREAQ	343	0.5000	5.95
33	MESKPLRRG	471	0.5000	5.95
34	LRVRSEAKA	533	0.5000	5.95
35	LQRARVPMP	251	0.3000	3.57
36	LRTRFRTVT	379	0.3000	3.57
37	IAGLLKQGK	74	0.2000	2.38
38	LNSLLNLPA	86	0.2000	2.38
39	LLNLPAARV	89	0.2000	2.38
40	IAVSSLLRS	261	0.2000	2.38
41	VQQTALWQQ	354	0.2000	2.38
42	FNPLSVGAG	508	0.2000	2.38
43	IVKFLSEQV	288	0.1000	1.19
44	IGMLSSVVG	496	0.1000	1.19
45	LVLAAGPDG	119	-0.1000	0
46	LGRMESKPL	468	-0.1000	0

47	IAIAKLNER	43	-0.2000	0
48	WREIVNANA	240	-0.2000	0
49	VPMPIIAVS	256	-0.2000	0
50	IGMRGSYGG	484	-0.2000	0
51	IQRLLRDHY	565	-0.2000	0
52	LYPRWREIV	236	-0.3000	0
53	IRSATEQLA	312	-0.4000	0
54	LQATIAAAQ	588	-0.4000	0
55	VLSAELSPH	448	-0.4200	0
56	LNLPAARVG	90	-0.5000	0
57	LGLLPEADA	190	-0.5000	0
58	VLSRATERV	296	-0.5000	0
59	VRRFVDDIS	543	-0.5000	0
60	LTRARQRIT	58	-0.6000	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	LVQRLTRAR	54	3.8000	43.18
2	VVSKQSRDR	553	3.7000	42.05
3	VVIAGLLKQ	72	3.0000	34.09
4	LRRKRARKW	11	2.9000	32.95
5	VVITVVSYS	104	2.9000	32.95
6	FVRQAHQIC	216	2.9000	32.95
7	LKMIQRLLR	562	2.8000	31.82
8	FVWAYQRSE	422	2.7000	30.68
9	LRSHAVTLN	267	2.6000	29.55
10	LKALGRMES	465	2.6000	29.55
11	FGRLKALGR	462	2.5000	28.41
12	VVMIGMLSS	493	2.5000	28.41
13	LGLFNPLSV	505	2.5000	28.41
14	VVSYSAQPS	108	2.4000	27.27
15	WFVRQAHQI	215	2.4000	27.27
16	YRDLRRKRA	8	2.3000	26.14
17	LRRGHKMII	476	2.3000	26.14
18	VRRAPHAGG	143	2.2000	25.00
19	FLSEQVLSR	291	2.2000	25.00

20	VVGLGLFNP	502	2.2000	25.00
21	VQRLTRARQ	55	2.1000	23.86
22	MVPAGLCAY	0	1.9000	21.59
23	FPAIVKFLS	285	1.9000	21.59
24	MESKPLRRG	471	1.9000	21.59
25	VRSEAKANV	535	1.9000	21.59
26	FNPLSVGAG	508	1.6000	18.18
27	IVNANAAHL	243	1.5600	17.73
28	IGMLSSVVG	496	1.5000	17.05
29	LRDHYREIA	569	1.4000	15.91
30	IRELQRQLG	606	1.4000	15.91
31	LQRQLGILS	609	1.4000	15.91
32	IAIAKLNER	43	1.3000	14.77
33	LVLAAGPDG	119	1.3000	14.77
34	LQRARVPMP	251	1.3000	14.77
35	LLNLPAARV	89	1.2000	13.64
36	IGMRGSYGG	484	1.2000	13.64
37	MIQRLLRDH	564	1.2000	13.64
38	IVKFLSEQV	288	1.1000	12.50
39	YQRSEALAD	426	1.1000	12.50
40	IQRLLRDHY	565	1.1000	12.50
41	LIDHTIAIA	38	1.0000	11.36
42	LRVEVGAPS	155	1.0000	11.36
43	LRTRFRTVT	379	1.0000	11.36
44	LLKQGKSQL	77	0.9600	10.91
45	LNLPAARVG	90	0.9000	10.23
46	LGRMESKPL	468	0.8600	9.77
47	LYPRWREIV	236	0.7000	7.95
48	LVVSDTSQE	200	0.6000	6.82
49	IAVSSLLRS	261	0.6000	6.82
50	VLSRATERV	296	0.5000	5.68
51	LRVRSEAKA	533	0.5000	5.68
52	MIGMLSSVV	495	0.4000	4.55
53	LGILSQVND	613	0.4000	4.55
54	IAGLLKQGK	74	0.3000	3.41
55	VVSDTSQEF	201	0.3000	3.41
56	LTPRASLGR	630	0.3000	3.41
57	WAYQRSEAL	424	0.2600	2.95
58	LNSLLNLPA	86	0.2000	2.27
59	VPMPIIAVS	256	0.2000	2.27
60	VGDNFVWAY	418	0.2000	2.27

61	FVDDISFVV	546	0.2000	2.27
62	FVVSKQSRD	552	0.2000	2.27
63	YSAQPSARL	111	0.1600	1.82
64	LTRARQRIT	58	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	VVIAGLLKQ	72	4.7000	55.95
2	LRRKRARKW	11	3.9000	46.43
3	VQRLTRARQ	55	3.8000	45.24
4	VVITVVSYS	104	3.5000	41.67
5	LVQRLTRAR	54	3.3000	39.29
6	LKALGRMES	465	3.2000	38.10
7	VVSKQSRDR	553	3.2000	38.10
8	VVMIGMLSS	493	3.1000	36.90
9	VVSYSAQPS	108	3.0000	35.71
10	LRSHAVTLN	267	2.8000	33.33
11	MIQRLLRDH	564	2.7800	33.10
12	LGLFNPLSV	505	2.5000	29.76
13	LRRGHKMII	476	2.4000	28.57
14	LRDHYREIA	569	2.4000	28.57
15	LKMIQRLLR	562	2.3000	27.38
16	VVGLGLFNP	502	2.2000	26.19
17	LIDHTIAIA	38	2.0000	23.81
18	LQRQLGILS	609	2.0000	23.81
19	FVRQAHQIC	216	1.9000	22.62
20	VRSEAKANV	535	1.9000	22.62
21	VRRAPHAGG	143	1.8000	21.43
22	VNANAAHLQ	244	1.7000	20.24
23	MVPAGLCAY	0	1.6000	19.05
24	LRVEVGAPS	155	1.6000	19.05
25	IVNANAAHL	243	1.6000	19.05
26	LERRKREAQ	343	1.5000	17.86
27	MESKPLRRG	471	1.5000	17.86
28	LRVRSEAKA	533	1.5000	17.86
29	YRDLRRKRA	8	1.3000	15.48

30	LQRARVPMP	251	1.3000	15.48
31	LRTRFRTVT	379	1.3000	15.48
32	IAGLLKQGK	74	1.2000	14.29
33	LNSLLNLPA	86	1.2000	14.29
34	LLNLPAARV	89	1.2000	14.29
35	IAVSSLLRS	261	1.2000	14.29
36	VQQTALWQQ	354	1.2000	14.29
37	IVKFLSEQV	288	1.1000	13.10
38	IGMLSSVVG	496	1.1000	13.10
39	LLKQGKSQL	77	1.0000	11.90
40	IRELQRQLG	606	1.0000	11.90
41	LVLAAGPDG	119	0.9000	10.71
42	LGRMESKPL	468	0.9000	10.71
43	IAIAKLNER	43	0.8000	9.52
44	VPMPIIAVS	256	0.8000	9.52
45	IGMRGSYGG	484	0.8000	9.52
46	IQRLLRDHY	565	0.8000	9.52
47	LYPRWREIV	236	0.7000	8.33
48	IRSATEQLA	312	0.6000	7.14
49	LQATIAAAQ	588	0.6000	7.14
50	VLSAELSPH	448	0.5800	6.90
51	LNLPAARVG	90	0.5000	5.95
52	LGLLPEADA	190	0.5000	5.95
53	WFVRQAHQI	215	0.5000	5.95
54	FPAIVKFLS	285	0.5000	5.95
55	VLSRATERV	296	0.5000	5.95
56	VRRFVDDIS	543	0.5000	5.95
57	LTRARQRIT	58	0.4000	4.76
58	VSSLLRSHA	263	0.4000	4.76
59	VWAYQRSEA	423	0.4000	4.76
60	MIGMLSSVV	495	0.4000	4.76
61	FVWAYQRSE	422	0.3000	3.57
62	LGILSQVND	613	0.3000	3.57
63	LVVSDTSQE	200	0.2000	2.38
64	ISFVVSKQS	550	0.2000	2.38

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	LKMIQRLLR	562	5.4000	62.07
2	VVMIGMLSS	493	5.1000	58.62
3	LKALGRMES	465	4.6000	52.87
4	FGRLKALGR	462	4.3000	49.43
5	VVIAGLLKQ	72	4.1000	47.13
6	LRRGHKMII	476	3.4000	39.08
7	FNPLSVGAG	508	3.4000	39.08
8	LGLFNPLSV	505	3.2000	36.78
9	VVITVVSYS	104	3.0000	34.48
10	YRDLRRKRA	8	2.8000	32.18
11	VQRLTRARQ	55	2.8000	32.18
12	FLSEQVLSR	291	2.7000	31.03
13	IIAVSSLLR	260	2.4000	27.59
14	FPAIVKFLS	285	2.4000	27.59
15	VRRAPHAGG	143	2.2000	25.29
16	YQRSEALAD	426	2.1000	24.14
17	YGGVVMIGM	490	2.1000	24.14
18	LNSLLNLPA	86	2.0000	22.99
19	MVPAGLCAY	0	1.9000	21.84
20	LLNLPAARV	89	1.9000	21.84
21	VVGLGLFNP	502	1.9000	21.84
22	LVLAAGPDG	119	1.7500	20.11
23	LAFIDTPGV	170	1.7500	20.11
24	LQRARVPMP	251	1.7500	20.11
25	IGMLSSVVG	496	1.7000	19.54
26	LQRQLGILS	609	1.7000	19.54
27	VRVVIAGLL	70	1.6600	19.08
28	VLRVEVGAP	154	1.6000	18.39
29	IAVSSLLRS	261	1.6000	18.39
30	IVNANAAHL	243	1.5600	17.93
31	VRQAHQICP	217	1.4000	16.09
32	IRELQRQLG	606	1.4000	16.09
33	LVQRLTRAR	54	1.3000	14.94
34	WREIVNANA	240	1.3000	14.94
35	VRSEAKANV	535	1.3000	14.94
36	FVRQAHQIC	216	1.2000	13.79
37	FVWAYQRSE	422	1.1000	12.64
38	WFVRQAHQI	215	1.0000	11.49
39	LGRMESKPL	468	0.8600	9.89
40	MIIGMRGSY	482	0.8000	9.20

41	VVSKQSRDR	553	0.8000	9.20
42	MPIIAVSSL	258	0.7600	8.74
43	MLSSVVGLG	498	0.7000	8.05
44	ISFVVSKQS	550	0.7000	8.05
45	VVSYSAQPS	108	0.6000	6.90
46	IQRLLRDHY	565	0.6000	6.90
47	LGILSQVND	613	0.6000	6.90
48	VGAGLILGR	513	0.5000	5.75
49	LTPRASLGR	630	0.5000	5.75
50	VGGLGQPHL	178	0.4100	4.71
51	VGVIVELID	32	0.4000	4.60
52	LRVEVGAPS	155	0.4000	4.60
53	IVKFLSEQV	288	0.4000	4.60
54	IAGLLKQGK	74	0.3000	3.45
55	VGAPSPLLR	159	0.3000	3.45
56	IAIAKLNER	43	0.2000	2.30
57	LGLLPEADA	190	0.2000	2.30
58	VVNDPNLRD	329	0.2000	2.30
59	MIGMLSSVV	495	0.2000	2.30
60	LVVSDTSQE	200	0.1000	1.15
61	LRSHAVTLN	267	0.1000	1.15
62	IGMRGSYGG	484	0.1000	1.15
63	LSSVVGLGL	499	0.0600	0.69

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	LVQRLTRAR	54	4.8000	54.55
2	VVSKQSRDR	553	4.7000	53.41
3	VVIAGLLKQ	72	4.0000	45.45
4	LRRKRARKW	11	3.9000	44.32
5	VVITVVSYS	104	3.9000	44.32
6	LKMIQRLLR	562	3.8000	43.18
7	LRSHAVTLN	267	3.6000	40.91
8	LKALGRMES	465	3.6000	40.91
9	VVMIGMLSS	493	3.5000	39.77
10	LGLFNPLSV	505	3.5000	39.77

11	VVSYSAQPS	108	3.4000	38.64
12	LRRGHKMII	476	3.3000	37.50
13	VRRAPHAGG	143	3.2000	36.36
14	VVGLGLFNP	502	3.2000	36.36
15	VQRLTRARQ	55	3.1000	35.23
16	MVPAGLCAY	0	2.9000	32.95
17	MESKPLRRG	471	2.9000	32.95
18	VRSEAKANV	535	2.9000	32.95
19	IVNANAAHL	243	2.5600	29.09
20	IGMLSSVVG	496	2.5000	28.41
21	LRDHYREIA	569	2.4000	27.27
22	IRELQRQLG	606	2.4000	27.27
23	LQRQLGILS	609	2.4000	27.27
24	IAIAKLNER	43	2.3000	26.14
25	LVLAAGPDG	119	2.3000	26.14
26	LQRARVPMP	251	2.3000	26.14
27	LLNLPAARV	89	2.2000	25.00
28	IGMRGSYGG	484	2.2000	25.00
29	MIQRLLRDH	564	2.2000	25.00
30	IVKFLSEQV	288	2.1000	23.86
31	IQRLLRDHY	565	2.1000	23.86
32	LIDHTIAIA	38	2.0000	22.73
33	LRVEVGAPS	155	2.0000	22.73
34	LRTRFRTVT	379	2.0000	22.73
35	LLKQGKSQL	77	1.9600	22.27
36	LNLPAARVG	90	1.9000	21.59
37	FVRQAHQIC	216	1.9000	21.59
38	LGRMESKPL	468	1.8600	21.14
39	LYPRWREIV	236	1.7000	19.32
40	FVWAYQRSE	422	1.7000	19.32
41	LVVSDTSQE	200	1.6000	18.18
42	IAVSSLLRS	261	1.6000	18.18
43	VLSRATERV	296	1.5000	17.05
44	FGRLKALGR	462	1.5000	17.05
45	LRVRSEAKA	533	1.5000	17.05
46	WFVRQAHQI	215	1.4000	15.91
47	MIGMLSSVV	495	1.4000	15.91
48	LGILSQVND	613	1.4000	15.91
49	YRDLRRKRA	8	1.3000	14.77
50	IAGLLKQGK	74	1.3000	14.77
51	VVSDTSQEF	201	1.3000	14.77

52	LTPRASLGR	630	1.3000	14.77
53	LNSLLNLPA	86	1.2000	13.64
54	VPMPIIAVS	256	1.2000	13.64
55	FLSEQVLSR	291	1.2000	13.64
56	VGDNFVWAY	418	1.2000	13.64
57	LTRARQRIT	58	1.1000	12.50
58	VRQAHQICP	217	1.1000	12.50
59	LLRGGLAFI	165	1.0000	11.36
60	VNANAAHLQ	244	1.0000	11.36
61	IIAVSSLLR	260	1.0000	11.36
62	LLRSHAVTL	266	0.9600	10.91
63	LLNSLLNLP	85	0.9000	10.23
64	LRGGLAFID	166	0.9000	10.23

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVQRLTRAR	54	3.8000	43.18
2	VVSKQSRDR	553	3.7000	42.05
3	VVIAGLLKQ	72	3.0000	34.09
4	LRRKRARKW	11	2.9000	32.95
5	VVITVVSYS	104	2.9000	32.95
6	FVRQAHQIC	216	2.9000	32.95
7	LKMIQRLLR	562	2.8000	31.82
8	FVWAYQRSE	422	2.7000	30.68
9	LRSHAVTLN	267	2.6000	29.55
10	LKALGRMES	465	2.6000	29.55
11	FGRLKALGR	462	2.5000	28.41
12	VVMIGMLSS	493	2.5000	28.41
13	LGLFNPLSV	505	2.5000	28.41
14	VVSYSAQPS	108	2.4000	27.27
15	WFVRQAHQI	215	2.4000	27.27
16	YRDLRRKRA	8	2.3000	26.14
17	LRRGHKMII	476	2.3000	26.14
18	VRRAPHAGG	143	2.2000	25.00
19	FLSEQVLSR	291	2.2000	25.00
20	VVGLGLFNP	502	2.2000	25.00

21	VQRLTRARQ	55	2.1000	23.86
22	MVPAGLCAY	0	1.9000	21.59
23	FPAIVKFLS	285	1.9000	21.59
24	MESKPLRRG	471	1.9000	21.59
25	VRSEAKANV	535	1.9000	21.59
26	FNPLSVGAG	508	1.6000	18.18
27	IVNANAAHL	243	1.5600	17.73
28	IGMLSSVVG	496	1.5000	17.05
29	LRDHYREIA	569	1.4000	15.91
30	IRELQRQLG	606	1.4000	15.91
31	LQRQLGILS	609	1.4000	15.91
32	IAIAKLNER	43	1.3000	14.77
33	LVLAAGPDG	119	1.3000	14.77
34	LQRARVPMP	251	1.3000	14.77
35	LLNLPAARV	89	1.2000	13.64
36	IGMRGSYGG	484	1.2000	13.64
37	MIQRLLRDH	564	1.2000	13.64
38	IVKFLSEQV	288	1.1000	12.50
39	YQRSEALAD	426	1.1000	12.50
40	IQRLLRDHY	565	1.1000	12.50
41	LIDHTIAIA	38	1.0000	11.36
42	LRVEVGAPS	155	1.0000	11.36
43	LRTRFRTVT	379	1.0000	11.36
44	LLKQGKSQL	77	0.9600	10.91
45	LNLPAARVG	90	0.9000	10.23
46	LGRMESKPL	468	0.8600	9.77
47	LYPRWREIV	236	0.7000	7.95
48	LVVSDTSQE	200	0.6000	6.82
49	IAVSSLLRS	261	0.6000	6.82
50	VLSRATERV	296	0.5000	5.68
51	LRVRSEAKA	533	0.5000	5.68
52	MIGMLSSVV	495	0.4000	4.55
53	LGILSQVND	613	0.4000	4.55
54	IAGLLKQGK	74	0.3000	3.41
55	VVSDTSQEF	201	0.3000	3.41
56	LTPRASLGR	630	0.3000	3.41
57	WAYQRSEAL	424	0.2600	2.95
58	LNSLLNLPA	86	0.2000	2.27
59	VPMPIIAVS	256	0.2000	2.27
60	VGDNFVWAY	418	0.2000	2.27
61	FVDDISFVV	546	0.2000	2.27

62	FVVSKQSRD	552	0.2000	2.27
63	YSAQPSARL	111	0.1600	1.82
64	LTRARQRIT	58	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	VVIAGLLKQ	72	5.5000	61.11
2	LRRKRARKW	11	4.8000	53.33
3	LRSHAVTLN	267	4.8000	53.33
4	VQRLTRARQ	55	4.6000	51.11
5	MIQRLLRDH	564	4.0000	44.44
6	VVITVVSYS	104	3.5000	38.89
7	LVQRLTRAR	54	3.3000	36.67
8	FVWAYQRSE	422	3.3000	36.67
9	LVVSDTSQE	200	3.2000	35.56
10	LKALGRMES	465	3.2000	35.56
11	VVSKQSRDR	553	3.2000	35.56
12	VRRAPHAGG	143	3.1000	34.44
13	VVMIGMLSS	493	3.1000	34.44
14	VVSYSAQPS	108	3.0000	33.33
15	LGILSQVND	613	3.0000	33.33
16	MESKPLRRG	471	2.8000	31.11
17	LGLFNPLSV	505	2.8000	31.11
18	MVPAGLCAY	0	2.7000	30.00
19	IVNANAAHL	243	2.6000	28.89
20	LRRGHKMII	476	2.6000	28.89
21	VVGLGLFNP	502	2.6000	28.89
22	LRGGLAFID	166	2.5000	27.78
23	VNANAAHLQ	244	2.5000	27.78
24	ILGRMAYKE	518	2.5000	27.78
25	IGMLSSVVG	496	2.4000	26.67
26	LRDHYREIA	569	2.4000	26.67
27	LERRKREAQ	343	2.3000	25.56
28	LKMIQRLLR	562	2.3000	25.56
29	IRELQRQLG	606	2.3000	25.56
30	LVLAAGPDG	119	2.2000	24.44

31	LRTRFRTVT	379	2.2000	24.44
32	VRSEAKANV	535	2.2000	24.44
33	IGMRGSYGG	484	2.1000	23.33
34	LIDHTIAIA	38	2.0000	22.22
35	LLKQGKSQL	77	2.0000	22.22
36	VTLNDKELN	272	2.0000	22.22
37	VVNDPNLRD	329	2.0000	22.22
38	VQQTALWQQ	354	2.0000	22.22
39	LQRQLGILS	609	2.0000	22.22
40	FVRQAHQIC	216	1.9000	21.11
41	LNDKELNEE	274	1.9000	21.11
42	LGRMESKPL	468	1.9000	21.11
43	IQRLLRDHY	565	1.9000	21.11
44	LNLPAARVG	90	1.8000	20.00
45	VLSAELSPH	448	1.8000	20.00
46	LQRARVPMP	251	1.7000	18.89
47	YQRSEALAD	426	1.7000	18.89
48	LRVEVGAPS	155	1.6000	17.78
49	LGRMAYKED	519	1.6000	17.78
50	LLNLPAARV	89	1.5000	16.67
51	LRVRSEAKA	533	1.5000	16.67
52	IVKFLSEQV	288	1.4000	15.56
53	LQATIAAAQ	588	1.4000	15.56
54	YRDLRRKRA	8	1.3000	14.44
55	LTRARQRIT	58	1.3000	14.44
56	IAKLNERGD	45	1.2000	13.33
57	LNSLLNLPA	86	1.2000	13.33
58	IAVSSLLRS	261	1.2000	13.33
59	LYPRWREIV	236	1.0000	11.11
60	LLRSHAVTL	266	1.0000	11.11
61	VGDNFVWAY	418	1.0000	11.11
62	IAAAQVAET	592	0.9000	10.00
63	IAIAKLNER	43	0.8000	8.89
64	MWFVRQAHQ	214	0.8000	8.89

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	LKMIQRLLR	562	5.4000	62.07
2	VVMIGMLSS	493	5.1000	58.62
3	LKALGRMES	465	4.6000	52.87
4	FGRLKALGR	462	4.3000	49.43
5	VVIAGLLKQ	72	4.1000	47.13
6	LRRGHKMII	476	3.4000	39.08
7	FNPLSVGAG	508	3.4000	39.08
8	LGLFNPLSV	505	3.2000	36.78
9	VVITVVSYS	104	3.0000	34.48
10	YRDLRRKRA	8	2.8000	32.18
11	VQRLTRARQ	55	2.8000	32.18
12	FLSEQVLSR	291	2.7000	31.03
13	IIAVSSLLR	260	2.4000	27.59
14	FPAIVKFLS	285	2.4000	27.59
15	VRRAPHAGG	143	2.2000	25.29
16	YQRSEALAD	426	2.1000	24.14
17	YGGVVMIGM	490	2.1000	24.14
18	LNSLLNLPA	86	2.0000	22.99
19	MVPAGLCAY	0	1.9000	21.84
20	LLNLPAARV	89	1.9000	21.84
21	VVGLGLFNP	502	1.9000	21.84
22	LVLAAGPDG	119	1.7500	20.11
23	LAFIDTPGV	170	1.7500	20.11
24	LQRARVPMP	251	1.7500	20.11
25	IGMLSSVVG	496	1.7000	19.54
26	LQRQLGILS	609	1.7000	19.54
27	VRVVIAGLL	70	1.6600	19.08
28	VLRVEVGAP	154	1.6000	18.39
29	IAVSSLLRS	261	1.6000	18.39
30	IVNANAAHL	243	1.5600	17.93
31	VRQAHQICP	217	1.4000	16.09
32	IRELQRQLG	606	1.4000	16.09
33	LVQRLTRAR	54	1.3000	14.94
34	WREIVNANA	240	1.3000	14.94
35	VRSEAKANV	535	1.3000	14.94
36	FVRQAHQIC	216	1.2000	13.79
37	FVWAYQRSE	422	1.1000	12.64
38	WFVRQAHQI	215	1.0000	11.49
39	LGRMESKPL	468	0.8600	9.89
40	MIIGMRGSY	482	0.8000	9.20

41	VVSKQSRDR	553	0.8000	9.20
42	MPIIAVSSL	258	0.7600	8.74
43	MLSSVVGLG	498	0.7000	8.05
44	ISFVVSKQS	550	0.7000	8.05
45	VVSYSAQPS	108	0.6000	6.90
46	IQRLLRDHY	565	0.6000	6.90
47	LGILSQVND	613	0.6000	6.90
48	VGAGLILGR	513	0.5000	5.75
49	LTPRASLGR	630	0.5000	5.75
50	VGGLGQPHL	178	0.4100	4.71
51	VGVIVELID	32	0.4000	4.60
52	LRVEVGAPS	155	0.4000	4.60
53	IVKFLSEQV	288	0.4000	4.60
54	IAGLLKQGK	74	0.3000	3.45
55	VGAPSPLLR	159	0.3000	3.45
56	IAIAKLNER	43	0.2000	2.30
57	LGLLPEADA	190	0.2000	2.30
58	VVNDPNLRD	329	0.2000	2.30
59	MIGMLSSVV	495	0.2000	2.30
60	LVVSDTSQE	200	0.1000	1.15
61	LRSHAVTLN	267	0.1000	1.15
62	IGMRGSYGG	484	0.1000	1.15
63	LSSVVGLGL	499	0.0600	0.69

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	VQRLTRARQ	55	3.5000	51.47
2	VVIAGLLKQ	72	3.0000	44.12
3	VVMIGMLSS	493	2.9000	42.65
4	VVITVVSYS	104	2.6000	38.24
5	LKALGRMES	465	2.6000	38.24
6	YRDLRRKRA	8	2.2000	32.35
7	LKMIQRLLR	562	2.1000	30.88
8	FNPLSVGAG	508	1.9000	27.94
9	FPAIVKFLS	285	1.5000	22.06
10	WREIVNANA	240	1.3000	19.12

11	FVRQAHQIC	216	1.1000	16.18
12	FGRLKALGR	462	1.0000	14.71
13	LLNLPAARV	89	0.9000	13.24
14	LRRGHKMII	476	0.9000	13.24
15	VRRAPHAGG	143	0.8000	11.76
16	MVPAGLCAY	0	0.6000	8.82
17	VRVVIAGLL	70	0.6000	8.82
18	IVNANAAHL	243	0.6000	8.82
19	VLRVEVGAP	154	0.5000	7.35
20	VVGLGLFNP	502	0.4000	5.88
21	LGLFNPLSV	505	0.4000	5.88
22	MWFVRQAHQ	214	0.3000	4.41
23	VRSEAKANV	535	0.3000	4.41
24	LNSLLNLPA	86	0.2000	2.94
25	LGLLPEADA	190	0.2000	2.94
26	IAGLLKQGK	74	0.1000	1.47
27	VVSYSAQPS	108	0.1000	1.47
28	LQATIAAAQ	588	0.1000	1.47
29	IRELQRQLG	606	-0.1000	0
30	LRRKRARKW	11	-0.2000	0
31	MPIIAVSSL	258	-0.2000	0
32	IGMLSSVVG	496	-0.2000	0
33	VSSLLRSHA	263	-0.3000	0
34	ISFVVSKQS	550	-0.3000	0
35	LQRQLGILS	609	-0.3000	0
36	LVQRLTRAR	54	-0.4000	0
37	LAFIDTPGV	170	-0.4000	0
38	LQRARVPMP	251	-0.4000	0
39	VPMPIIAVS	256	-0.4000	0
40	LRVRSEAKA	533	-0.4000	0
41	IQRLLRDHY	565	-0.4000	0
42	FVWAYQRSE	422	-0.5000	0
43	WFVRQAHQI	215	-0.6000	0
44	VNANAAHLQ	244	-0.6000	0
45	IAVSSLLRS	261	-0.6000	0
46	FLSEQVLSR	291	-0.6000	0
47	MIIGMRGSY	482	-0.6000	0
48	VITVVSYSA	105	-0.7000	0
49	LGRMESKPL	468	-0.7000	0
50	LVLAAGPDG	119	-0.8000	0
51	YQRSEALAD	426	-0.8000	0

52	MIGMLSSVV	495	-0.8000	0
53	MLSSVVGLG	498	-0.8000	0
54	VLSAELSPH	448	-0.8200	0
55	IIAVSSLLR	260	-0.9000	0
56	VQQTALWQQ	354	-0.9000	0
57	VVSKQSRDR	553	-0.9000	0
58	MIQRLLRDH	564	-0.9200	0
59	YGGVVMIGM	490	-1.0000	0
60	IAAAQVAET	592	-1.0000	0
61	LGILSQVND	613	-1.0000	0
62	LIDHTIAIA	38	-1.1000	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	VVIAGLLKQ	72	5.8000	69.88
2	VVMIGMLSS	493	5.7000	68.67
3	LKALGRMES	465	5.2000	62.65
4	LKMIQRLLR	562	4.9000	59.04
5	VQRLTRARQ	55	4.5000	54.22
6	VVITVVSYS	104	3.6000	43.37
7	LRRGHKMII	476	3.5000	42.17
8	LGLFNPLSV	505	3.2000	38.55
9	LNSLLNLPA	86	3.0000	36.14
10	LQRQLGILS	609	2.3000	27.71
11	IAVSSLLRS	261	2.2000	26.51
12	LLNLPAARV	89	1.9000	22.89
13	IIAVSSLLR	260	1.9000	22.89
14	VVGLGLFNP	502	1.9000	22.89
15	YRDLRRKRA	8	1.8000	21.69
16	VRRAPHAGG	143	1.8000	21.69
17	FGRLKALGR	462	1.8000	21.69
18	LAFIDTPGV	170	1.7500	21.08
19	LQRARVPMP	251	1.7500	21.08
20	VRVVIAGLL	70	1.7000	20.48
21	MVPAGLCAY	0	1.6000	19.28
22	VLRVEVGAP	154	1.6000	19.28

23	IVNANAAHL	243	1.6000	19.28
24	VRQAHQICP	217	1.4000	16.87
25	LVLAAGPDG	119	1.3500	16.27
26	MWFVRQAHQ	214	1.3000	15.66
27	IGMLSSVVG	496	1.3000	15.66
28	VRSEAKANV	535	1.3000	15.66
29	ISFVVSKQS	550	1.3000	15.66
30	IAGLLKQGK	74	1.2000	14.46
31	VVSYSAQPS	108	1.2000	14.46
32	LGLLPEADA	190	1.2000	14.46
33	VNANAAHLQ	244	1.1000	13.25
34	LQATIAAAQ	588	1.1000	13.25
35	LRRKRARKW	11	1.0000	12.05
36	VITVVSYSA	105	1.0000	12.05
37	LRVEVGAPS	155	1.0000	12.05
38	FPAIVKFLS	285	1.0000	12.05
39	FNPLSVGAG	508	1.0000	12.05
40	IRELQRQLG	606	1.0000	12.05
41	VQQTALWQQ	354	0.9000	10.84
42	LGRMESKPL	468	0.9000	10.84
43	LVQRLTRAR	54	0.8000	9.64
44	MPIIAVSSL	258	0.8000	9.64
45	VSSLLRSHA	263	0.7000	8.43
46	VELIDHTIA	36	0.6000	7.23
47	VPMPIIAVS	256	0.6000	7.23
48	LRVRSEAKA	533	0.6000	7.23
49	LEPTLTPRA	626	0.5500	6.63
50	MIIGMRGSY	482	0.5000	6.02
51	LGILSQVND	613	0.5000	6.02
52	VGGLGQPHL	178	0.4500	5.42
53	IVKFLSEQV	288	0.4000	4.82
54	LLRVRSEAK	532	0.4000	4.82
55	VGVIVELID	32	0.3000	3.61
56	WREIVNANA	240	0.3000	3.61
57	LRSHAVTLN	267	0.3000	3.61
58	LERRKREAQ	343	0.3000	3.61
59	MLSSVVGLG	498	0.3000	3.61
60	VVSKQSRDR	553	0.3000	3.61
61	IQRLLRDHY	565	0.3000	3.61
62	MIQRLLRDH	564	0.2800	3.37
63	FVRQAHQIC	216	0.2000	2.41

64	FLSEQVLSR	291	0.2000	2.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVIAGLLKQ	72	5.6000	62.92
2	VVMIGMLSS	493	4.7000	52.81
3	VQRLTRARQ	55	4.3000	48.31
4	LKALGRMES	465	4.2000	47.19
5	LKMIQRLLR	562	3.9000	43.82
6	YQRSEALAD	426	3.7000	41.57
7	FNPLSVGAG	508	3.3000	37.08
8	YRDLRRKRA	8	2.8000	31.46
9	FGRLKALGR	462	2.8000	31.46
10	FVWAYQRSE	422	2.7000	30.34
11	LRRGHKMII	476	2.7000	30.34
12	VVITVVSYS	104	2.6000	29.21
13	LGLFNPLSV	505	2.5000	28.09
14	LGILSQVND	613	2.2000	24.72
15	VRRAPHAGG	143	2.1000	23.60
16	VGVIVELID	32	2.0000	22.47
17	LNSLLNLPA	86	2.0000	22.47
18	FPAIVKFLS	285	2.0000	22.47
19	VVNDPNLRD	329	1.8000	20.22
20	MVPAGLCAY	0	1.7000	19.10
21	VRVVIAGLL	70	1.7000	19.10
22	LVVSDTSQE	200	1.7000	19.10
23	YGGVVMIGM	490	1.7000	19.10
24	LVLAAGPDG	119	1.6500	18.54
25	IVNANAAHL	243	1.6000	17.98
26	IGMLSSVVG	496	1.6000	17.98
27	WREIVNANA	240	1.3000	14.61
28	LRSHAVTLN	267	1.3000	14.61
29	VVGLGLFNP	502	1.3000	14.61
30	FVVSKQSRD	552	1.3000	14.61
31	IRELQRQLG	606	1.3000	14.61
32	LQRQLGILS	609	1.3000	14.61

33	LLNLPAARV	89	1.2000	13.48
34	FVRQAHQIC	216	1.2000	13.48
35	IAVSSLLRS	261	1.2000	13.48
36	FLSEQVLSR	291	1.2000	13.48
37	LQRARVPMP	251	1.1500	12.92
38	MWFVRQAHQ	214	1.1000	12.36
39	LAFIDTPGV	170	1.0500	11.80
40	VLRVEVGAP	154	1.0000	11.24
41	LRRKRARKW	11	0.9000	10.11
42	VNANAAHLQ	244	0.9000	10.11
43	IIAVSSLLR	260	0.9000	10.11
44	LGRMESKPL	468	0.9000	10.11
45	LQATIAAAQ	588	0.9000	10.11
46	VRQAHQICP	217	0.8000	8.99
47	MPIIAVSSL	258	0.8000	8.99
48	VQQTALWQQ	354	0.7000	7.87
49	VTLNDKELN	272	0.6000	6.74
50	MIIGMRGSY	482	0.6000	6.74
51	MLSSVVGLG	498	0.6000	6.74
52	LGRMAYKED	519	0.6000	6.74
53	VRSEAKANV	535	0.6000	6.74
54	MIQRLLRDH	564	0.5000	5.62
55	VGGLGQPHL	178	0.4500	5.06
56	LGEIRSATE	309	0.4000	4.49
57	VLSAELSPH	448	0.4000	4.49
58	ILGRMAYKE	518	0.4000	4.49
59	IQRLLRDHY	565	0.4000	4.49
60	LPAARVGDD	92	0.3000	3.37
61	LRGGLAFID	166	0.3000	3.37
62	WFVRQAHQI	215	0.3000	3.37
63	ISFVVSKQS	550	0.3000	3.37
64	VVSYSAQPS	108	0.2000	2.25

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	VVIAGLLKQ	72	4.7000	55.95

2	LRRKRARKW	11	3.9000	46.43
3	VQRLTRARQ	55	3.8000	45.24
4	VVITVVSYS	104	3.5000	41.67
5	LVQRLTRAR	54	3.3000	39.29
6	LKALGRMES	465	3.2000	38.10
7	VVSKQSRDR	553	3.2000	38.10
8	VVMIGMLSS	493	3.1000	36.90
9	VVSYSAQPS	108	3.0000	35.71
10	LRSHAVTLN	267	2.8000	33.33
11	MIQRLLRDH	564	2.7800	33.10
12	LGLFNPLSV	505	2.5000	29.76
13	LRRGHKMII	476	2.4000	28.57
14	LRDHYREIA	569	2.4000	28.57
15	LKMIQRLLR	562	2.3000	27.38
16	VVGLGLFNP	502	2.2000	26.19
17	LIDHTIAIA	38	2.0000	23.81
18	LQRQLGILS	609	2.0000	23.81
19	FVRQAHQIC	216	1.9000	22.62
20	VRSEAKANV	535	1.9000	22.62
21	VRRAPHAGG	143	1.8000	21.43
22	VNANAAHLQ	244	1.7000	20.24
23	MVPAGLCAY	0	1.6000	19.05
24	LRVEVGAPS	155	1.6000	19.05
25	IVNANAAHL	243	1.6000	19.05
26	LERRKREAQ	343	1.5000	17.86
27	MESKPLRRG	471	1.5000	17.86
28	LRVRSEAKA	533	1.5000	17.86
29	YRDLRRKRA	8	1.3000	15.48
30	LQRARVPMP	251	1.3000	15.48
31	LRTRFRTVT	379	1.3000	15.48
32	IAGLLKQGK	74	1.2000	14.29
33	LNSLLNLPA	86	1.2000	14.29
34	LLNLPAARV	89	1.2000	14.29
35	IAVSSLLRS	261	1.2000	14.29
36	VQQTALWQQ	354	1.2000	14.29
37	IVKFLSEQV	288	1.1000	13.10
38	IGMLSSVVG	496	1.1000	13.10
39	LLKQGKSQL	77	1.0000	11.90
40	IRELQRQLG	606	1.0000	11.90
41	LVLAAGPDG	119	0.9000	10.71
42	LGRMESKPL	468	0.9000	10.71

43	IAIAKLNER	43	0.8000	9.52
44	VPMPIIAVS	256	0.8000	9.52
45	IGMRGSYGG	484	0.8000	9.52
46	IQRLLRDHY	565	0.8000	9.52
47	LYPRWREIV	236	0.7000	8.33
48	IRSATEQLA	312	0.6000	7.14
49	LQATIAAAQ	588	0.6000	7.14
50	VLSAELSPH	448	0.5800	6.90
51	LNLPAARVG	90	0.5000	5.95
52	LGLLPEADA	190	0.5000	5.95
53	WFVRQAHQI	215	0.5000	5.95
54	FPAIVKFLS	285	0.5000	5.95
55	VLSRATERV	296	0.5000	5.95
56	VRRFVDDIS	543	0.5000	5.95
57	LTRARQRIT	58	0.4000	4.76
58	VSSLLRSHA	263	0.4000	4.76
59	VWAYQRSEA	423	0.4000	4.76
60	MIGMLSSVV	495	0.4000	4.76
61	FVWAYQRSE	422	0.3000	3.57
62	LGILSQVND	613	0.3000	3.57
63	LVVSDTSQE	200	0.2000	2.38
64	ISFVVSKQS	550	0.2000	2.38

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	VVIAGLLKQ	72	3.7000	44.05
2	LRRKRARKW	11	2.9000	34.52
3	FVRQAHQIC	216	2.9000	34.52
4	VQRLTRARQ	55	2.8000	33.33
5	VVITVVSYS	104	2.5000	29.76
6	YRDLRRKRA	8	2.3000	27.38
7	LVQRLTRAR	54	2.3000	27.38
8	LKALGRMES	465	2.2000	26.19
9	VVSKQSRDR	553	2.2000	26.19
10	VVMIGMLSS	493	2.1000	25.00
11	VVSYSAQPS	108	2.0000	23.81

12	LRSHAVTLN	267	1.8000	21.43
13	MIQRLLRDH	564	1.7800	21.19
14	WFVRQAHQI	215	1.5000	17.86
15	FPAIVKFLS	285	1.5000	17.86
16	LGLFNPLSV	505	1.5000	17.86
17	LRRGHKMII	476	1.4000	16.67
18	LRDHYREIA	569	1.4000	16.67
19	FVWAYQRSE	422	1.3000	15.48
20	LKMIQRLLR	562	1.3000	15.48
21	VVGLGLFNP	502	1.2000	14.29
22	LIDHTIAIA	38	1.0000	11.90
23	FGRLKALGR	462	1.0000	11.90
24	LQRQLGILS	609	1.0000	11.90
25	VRSEAKANV	535	0.9000	10.71
26	VRRAPHAGG	143	0.8000	9.52
27	VNANAAHLQ	244	0.7000	8.33
28	FLSEQVLSR	291	0.7000	8.33
29	MVPAGLCAY	0	0.6000	7.14
30	LRVEVGAPS	155	0.6000	7.14
31	IVNANAAHL	243	0.6000	7.14
32	LERRKREAQ	343	0.5000	5.95
33	MESKPLRRG	471	0.5000	5.95
34	LRVRSEAKA	533	0.5000	5.95
35	LQRARVPMP	251	0.3000	3.57
36	LRTRFRTVT	379	0.3000	3.57
37	IAGLLKQGK	74	0.2000	2.38
38	LNSLLNLPA	86	0.2000	2.38
39	LLNLPAARV	89	0.2000	2.38
40	IAVSSLLRS	261	0.2000	2.38
41	VQQTALWQQ	354	0.2000	2.38
42	FNPLSVGAG	508	0.2000	2.38
43	IVKFLSEQV	288	0.1000	1.19
44	IGMLSSVVG	496	0.1000	1.19
45	LVLAAGPDG	119	-0.1000	0
46	LGRMESKPL	468	-0.1000	0
47	IAIAKLNER	43	-0.2000	0
48	WREIVNANA	240	-0.2000	0
49	VPMPIIAVS	256	-0.2000	0
50	IGMRGSYGG	484	-0.2000	0
51	IQRLLRDHY	565	-0.2000	0
52	LYPRWREIV	236	-0.3000	0

53	IRSATEQLA	312	-0.4000	0
54	LQATIAAAQ	588	-0.4000	0
55	VLSAELSPH	448	-0.4200	0
56	LNLPAARVG	90	-0.5000	0
57	LGLLPEADA	190	-0.5000	0
58	VLSRATERV	296	-0.5000	0
59	VRRFVDDIS	543	-0.5000	0
60	LTRARQRIT	58	-0.6000	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	LVQRLTRAR	54	4.8000	54.55
2	VVSKQSRDR	553	4.7000	53.41
3	VVIAGLLKQ	72	4.0000	45.45
4	LRRKRARKW	11	3.9000	44.32
5	VVITVVSYS	104	3.9000	44.32
6	LKMIQRLLR	562	3.8000	43.18
7	LRSHAVTLN	267	3.6000	40.91
8	LKALGRMES	465	3.6000	40.91
9	VVMIGMLSS	493	3.5000	39.77
10	LGLFNPLSV	505	3.5000	39.77
11	VVSYSAQPS	108	3.4000	38.64
12	LRRGHKMII	476	3.3000	37.50
13	VRRAPHAGG	143	3.2000	36.36
14	VVGLGLFNP	502	3.2000	36.36
15	VQRLTRARQ	55	3.1000	35.23
16	MVPAGLCAY	0	2.9000	32.95
17	MESKPLRRG	471	2.9000	32.95
18	VRSEAKANV	535	2.9000	32.95
19	IVNANAAHL	243	2.5600	29.09
20	IGMLSSVVG	496	2.5000	28.41
21	LRDHYREIA	569	2.4000	27.27
22	IRELQRQLG	606	2.4000	27.27
23	LQRQLGILS	609	2.4000	27.27
24	IAIAKLNER	43	2.3000	26.14
25	LVLAAGPDG	119	2.3000	26.14

26	LQRARVPMP	251	2.3000	26.14
27	LLNLPAARV	89	2.2000	25.00
28	IGMRGSYGG	484	2.2000	25.00
29	MIQRLLRDH	564	2.2000	25.00
30	IVKFLSEQV	288	2.1000	23.86
31	IQRLLRDHY	565	2.1000	23.86
32	LIDHTIAIA	38	2.0000	22.73
33	LRVEVGAPS	155	2.0000	22.73
34	LRTRFRTVT	379	2.0000	22.73
35	LLKQGKSQL	77	1.9600	22.27
36	LNLPAARVG	90	1.9000	21.59
37	FVRQAHQIC	216	1.9000	21.59
38	LGRMESKPL	468	1.8600	21.14
39	LYPRWREIV	236	1.7000	19.32
40	FVWAYQRSE	422	1.7000	19.32
41	LVVSDTSQE	200	1.6000	18.18
42	IAVSSLLRS	261	1.6000	18.18
43	VLSRATERV	296	1.5000	17.05
44	FGRLKALGR	462	1.5000	17.05
45	LRVRSEAKA	533	1.5000	17.05
46	WFVRQAHQI	215	1.4000	15.91
47	MIGMLSSVV	495	1.4000	15.91
48	LGILSQVND	613	1.4000	15.91
49	YRDLRRKRA	8	1.3000	14.77
50	IAGLLKQGK	74	1.3000	14.77
51	VVSDTSQEF	201	1.3000	14.77
52	LTPRASLGR	630	1.3000	14.77
53	LNSLLNLPA	86	1.2000	13.64
54	VPMPIIAVS	256	1.2000	13.64
55	FLSEQVLSR	291	1.2000	13.64
56	VGDNFVWAY	418	1.2000	13.64
57	LTRARQRIT	58	1.1000	12.50
58	VRQAHQICP	217	1.1000	12.50
59	LLRGGLAFI	165	1.0000	11.36
60	VNANAAHLQ	244	1.0000	11.36
61	IIAVSSLLR	260	1.0000	11.36
62	LLRSHAVTL	266	0.9600	10.91
63	LLNSLLNLP	85	0.9000	10.23
64	LRGGLAFID	166	0.9000	10.23

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVQRLTRAR	54	4.8000	54.55
2	VVSKQSRDR	553	4.7000	53.41
3	VVIAGLLKQ	72	4.0000	45.45
4	LRRKRARKW	11	3.9000	44.32
5	VVITVVSYS	104	3.9000	44.32
6	LKMIQRLLR	562	3.8000	43.18
7	LRSHAVTLN	267	3.6000	40.91
8	LKALGRMES	465	3.6000	40.91
9	VVMIGMLSS	493	3.5000	39.77
10	LGLFNPLSV	505	3.5000	39.77
11	VVSYSAQPS	108	3.4000	38.64
12	LRRGHKMII	476	3.3000	37.50
13	VRRAPHAGG	143	3.2000	36.36
14	VVGLGLFNP	502	3.2000	36.36
15	VQRLTRARQ	55	3.1000	35.23
16	MVPAGLCAY	0	2.9000	32.95
17	MESKPLRRG	471	2.9000	32.95
18	VRSEAKANV	535	2.9000	32.95
19	IVNANAAHL	243	2.5600	29.09
20	IGMLSSVVG	496	2.5000	28.41
21	LRDHYREIA	569	2.4000	27.27
22	IRELQRQLG	606	2.4000	27.27
23	LQRQLGILS	609	2.4000	27.27
24	IAIAKLNER	43	2.3000	26.14
25	LVLAAGPDG	119	2.3000	26.14
26	LQRARVPMP	251	2.3000	26.14
27	LLNLPAARV	89	2.2000	25.00
28	IGMRGSYGG	484	2.2000	25.00
29	MIQRLLRDH	564	2.2000	25.00
30	IVKFLSEQV	288	2.1000	23.86
31	IQRLLRDHY	565	2.1000	23.86
32	LIDHTIAIA	38	2.0000	22.73
33	LRVEVGAPS	155	2.0000	22.73
34	LRTRFRTVT	379	2.0000	22.73
35	LLKQGKSQL	77	1.9600	22.27
36	LNLPAARVG	90	1.9000	21.59

37	FVRQAHQIC	216	1.9000	21.59
38	LGRMESKPL	468	1.8600	21.14
39	LYPRWREIV	236	1.7000	19.32
40	FVWAYQRSE	422	1.7000	19.32
41	LVVSDTSQE	200	1.6000	18.18
42	IAVSSLLRS	261	1.6000	18.18
43	VLSRATERV	296	1.5000	17.05
44	FGRLKALGR	462	1.5000	17.05
45	LRVRSEAKA	533	1.5000	17.05
46	WFVRQAHQI	215	1.4000	15.91
47	MIGMLSSVV	495	1.4000	15.91
48	LGILSQVND	613	1.4000	15.91
49	YRDLRRKRA	8	1.3000	14.77
50	IAGLLKQGK	74	1.3000	14.77
51	VVSDTSQEF	201	1.3000	14.77
52	LTPRASLGR	630	1.3000	14.77
53	LNSLLNLPA	86	1.2000	13.64
54	VPMPIIAVS	256	1.2000	13.64
55	FLSEQVLSR	291	1.2000	13.64
56	VGDNFVWAY	418	1.2000	13.64
57	LTRARQRIT	58	1.1000	12.50
58	VRQAHQICP	217	1.1000	12.50
59	LLRGGLAFI	165	1.0000	11.36
60	VNANAAHLQ	244	1.0000	11.36
61	IIAVSSLLR	260	1.0000	11.36
62	LLRSHAVTL	266	0.9600	10.91
63	LLNSLLNLP	85	0.9000	10.23
64	LRGGLAFID	166	0.9000	10.23

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LGLFNPLSV	505	5.9000	60.20
2	VVMIGMLSS	493	5.8000	59.18
3	LRRGHKMII	476	5.0000	51.02
4	LKMIQRLLR	562	5.0000	51.02
5	IVKFLSEQV	288	4.7000	47.96

6	VVSYSAQPS	108	4.2000	42.86
7	VVIAGLLKQ	72	4.1000	41.84
8	LNSLLNLPA	86	4.1000	41.84
9	LKALGRMES	465	4.0000	40.82
10	VRRFVDDIS	543	3.9000	39.80
11	VWAYQRSEA	423	3.7000	37.76
12	MIGMLSSVV	495	3.5000	35.71
13	VRVVIAGLL	70	3.4000	34.69
14	LRTRFRTVT	379	3.4000	34.69
15	VMIGMLSSV	494	3.4000	34.69
16	VVGLGLFNP	502	3.3000	33.67
17	LVLAAGPDG	119	3.1000	31.63
18	IVNANAAHL	243	3.1000	31.63
19	VRAGVLGEI	304	3.1000	31.63
20	LSVGAGLIL	511	3.1000	31.63
21	LCAYRDLRR	5	3.0000	30.61
22	VVITVVSYS	104	3.0000	30.61
23	LGRMESKPL	468	3.0000	30.61
24	LSSVVGLGL	499	3.0000	30.61
25	VVNDPNLRD	329	2.9000	29.59
26	MRGSYGGVV	486	2.9000	29.59
27	IIAVSSLLR	260	2.8000	28.57
28	LQRQLGILS	609	2.8000	28.57
29	MIIGMRGSY	482	2.7000	27.55
30	VITVVSYSA	105	2.6000	26.53
31	LLRGGLAFI	165	2.6000	26.53
32	IGMRGSYGG	484	2.6000	26.53
33	IGMLSSVVG	496	2.5000	25.51
34	VGLGLFNPL	503	2.4000	24.49
35	IVELIDHTI	35	2.3000	23.47
36	LLNLPAARV	89	2.3000	23.47
37	LRVEVGAPS	155	2.3000	23.47
38	IIGMRGSYG	483	2.3000	23.47
39	LRDHYREIA	569	2.3000	23.47
40	LLRSHAVTL	266	2.2000	22.45
41	LRSHAVTLN	267	2.2000	22.45
42	MPIIAVSSL	258	2.1000	21.43
43	LYPRWREIV	236	2.0000	20.41
44	IAVSSLLRS	261	2.0000	20.41
45	LTPRASLGR	630	2.0000	20.41
46	LAFIDTPGV	170	1.9600	20.00

47	LKQGKSQLL	78	1.9000	19.39
48	LRGGLAFID	166	1.9000	19.39
49	VSLGSELSV	321	1.9000	19.39
50	LRDRLASDL	335	1.9000	19.39
51	LFNPLSVGA	507	1.9000	19.39
52	LRVRSEAKA	533	1.9000	19.39
53	LLRDHYREI	568	1.9000	19.39
54	VQRLTRARQ	55	1.8000	18.37
55	VVSDTSQEF	201	1.8000	18.37
56	WFVRQAHQI	215	1.8000	18.37
57	VRQAHQICP	217	1.8000	18.37
58	VRSEAKANV	535	1.8000	18.37
59	IQRLLRDHY	565	1.8000	18.37
60	MVPAGLCAY	0	1.7000	17.35
61	VSSLLRSHA	263	1.7000	17.35
62	VLGEIRSAT	308	1.7000	17.35
63	VLGDGFNDL	363	1.7000	17.35
64	FVDDISFVV	546	1.7000	17.35

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	LGLFNPLSV	505	4.9000	50.00
2	VVMIGMLSS	493	4.8000	48.98
3	LRRGHKMII	476	4.0000	40.82
4	LKMIQRLLR	562	4.0000	40.82
5	IVKFLSEQV	288	3.7000	37.76
6	VVSYSAQPS	108	3.2000	32.65
7	VVIAGLLKQ	72	3.1000	31.63
8	LNSLLNLPA	86	3.1000	31.63
9	LKALGRMES	465	3.0000	30.61
10	VRRFVDDIS	543	2.9000	29.59
11	WFVRQAHQI	215	2.8000	28.57
12	VWAYQRSEA	423	2.7000	27.55
13	FVDDISFVV	546	2.7000	27.55
14	FGRLKALGR	462	2.6000	26.53
15	YGGVVMIGM	490	2.5800	26.33

16	MIGMLSSVV	495	2.5000	25.51
17	VRVVIAGLL	70	2.4000	24.49
18	LRTRFRTVT	379	2.4000	24.49
19	VMIGMLSSV	494	2.4000	24.49
20	WREIVNANA	240	2.3000	23.47
21	VVGLGLFNP	502	2.3000	23.47
22	YRDLRRKRA	8	2.1000	21.43
23	LVLAAGPDG	119	2.1000	21.43
24	IVNANAAHL	243	2.1000	21.43
25	VRAGVLGEI	304	2.1000	21.43
26	LSVGAGLIL	511	2.1000	21.43
27	LCAYRDLRR	5	2.0000	20.41
28	VVITVVSYS	104	2.0000	20.41
29	LGRMESKPL	468	2.0000	20.41
30	LSSVVGLGL	499	2.0000	20.41
31	VVNDPNLRD	329	1.9000	19.39
32	MRGSYGGVV	486	1.9000	19.39
33	IIAVSSLLR	260	1.8000	18.37
34	LQRQLGILS	609	1.8000	18.37
35	MIIGMRGSY	482	1.7000	17.35
36	VITVVSYSA	105	1.6000	16.33
37	LLRGGLAFI	165	1.6000	16.33
38	YQRSEALAD	426	1.6000	16.33
39	IGMRGSYGG	484	1.6000	16.33
40	IGMLSSVVG	496	1.5000	15.31
41	VGLGLFNPL	503	1.4000	14.29
42	IVELIDHTI	35	1.3000	13.27
43	LLNLPAARV	89	1.3000	13.27
44	LRVEVGAPS	155	1.3000	13.27
45	IIGMRGSYG	483	1.3000	13.27
46	LRDHYREIA	569	1.3000	13.27
47	FVRQAHQIC	216	1.2000	12.24
48	LLRSHAVTL	266	1.2000	12.24
49	LRSHAVTLN	267	1.2000	12.24
50	FLSEQVLSR	291	1.2000	12.24
51	MPIIAVSSL	258	1.1000	11.22
52	LYPRWREIV	236	1.0000	10.20
53	IAVSSLLRS	261	1.0000	10.20
54	LTPRASLGR	630	1.0000	10.20
55	LAFIDTPGV	170	0.9600	9.80
56	LKQGKSQLL	78	0.9000	9.18

57	LRGGLAFID	166	0.9000	9.18
58	FPAIVKFLS	285	0.9000	9.18
59	VSLGSELSV	321	0.9000	9.18
60	LRDRLASDL	335	0.9000	9.18
61	LFNPLSVGA	507	0.9000	9.18
62	LRVRSEAKA	533	0.9000	9.18
63	LLRDHYREI	568	0.9000	9.18
64	VQRLTRARQ	55	0.8000	8.16

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	LGLFNPLSV	505	5.9000	60.20
2	VVMIGMLSS	493	5.8000	59.18
3	LRRGHKMII	476	5.0000	51.02
4	LKMIQRLLR	562	5.0000	51.02
5	IVKFLSEQV	288	4.7000	47.96
6	VVSYSAQPS	108	4.2000	42.86
7	VVIAGLLKQ	72	4.1000	41.84
8	LNSLLNLPA	86	4.1000	41.84
9	LKALGRMES	465	4.0000	40.82
10	VRRFVDDIS	543	3.9000	39.80
11	VWAYQRSEA	423	3.7000	37.76
12	MIGMLSSVV	495	3.5000	35.71
13	VRVVIAGLL	70	3.4000	34.69
14	LRTRFRTVT	379	3.4000	34.69
15	VMIGMLSSV	494	3.4000	34.69
16	VVGLGLFNP	502	3.3000	33.67
17	LVLAAGPDG	119	3.1000	31.63
18	IVNANAAHL	243	3.1000	31.63
19	VRAGVLGEI	304	3.1000	31.63
20	LSVGAGLIL	511	3.1000	31.63
21	LCAYRDLRR	5	3.0000	30.61
22	VVITVVSYS	104	3.0000	30.61
23	LGRMESKPL	468	3.0000	30.61
24	LSSVVGLGL	499	3.0000	30.61
25	VVNDPNLRD	329	2.9000	29.59

26	MRGSYGGVV	486	2.9000	29.59
27	IIAVSSLLR	260	2.8000	28.57
28	LQRQLGILS	609	2.8000	28.57
29	MIIGMRGSY	482	2.7000	27.55
30	VITVVSYSA	105	2.6000	26.53
31	LLRGGLAFI	165	2.6000	26.53
32	IGMRGSYGG	484	2.6000	26.53
33	IGMLSSVVG	496	2.5000	25.51
34	VGLGLFNPL	503	2.4000	24.49
35	IVELIDHTI	35	2.3000	23.47
36	LLNLPAARV	89	2.3000	23.47
37	LRVEVGAPS	155	2.3000	23.47
38	IIGMRGSYG	483	2.3000	23.47
39	LRDHYREIA	569	2.3000	23.47
40	LLRSHAVTL	266	2.2000	22.45
41	LRSHAVTLN	267	2.2000	22.45
42	MPIIAVSSL	258	2.1000	21.43
43	LYPRWREIV	236	2.0000	20.41
44	IAVSSLLRS	261	2.0000	20.41
45	LTPRASLGR	630	2.0000	20.41
46	LAFIDTPGV	170	1.9600	20.00
47	LKQGKSQLL	78	1.9000	19.39
48	LRGGLAFID	166	1.9000	19.39
49	VSLGSELSV	321	1.9000	19.39
50	LRDRLASDL	335	1.9000	19.39
51	LFNPLSVGA	507	1.9000	19.39
52	LRVRSEAKA	533	1.9000	19.39
53	LLRDHYREI	568	1.9000	19.39
54	VQRLTRARQ	55	1.8000	18.37
55	VVSDTSQEF	201	1.8000	18.37
56	WFVRQAHQI	215	1.8000	18.37
57	VRQAHQICP	217	1.8000	18.37
58	VRSEAKANV	535	1.8000	18.37
59	IQRLLRDHY	565	1.8000	18.37
60	MVPAGLCAY	0	1.7000	17.35
61	VSSLLRSHA	263	1.7000	17.35
62	VLGEIRSAT	308	1.7000	17.35
63	VLGDGFNDL	363	1.7000	17.35
64	FVDDISFVV	546	1.7000	17.35

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	FGRLKALGR	462	4.9000	50.00
2	VRVVIAGLL	70	4.7000	47.96
3	LKMIQRLLR	562	4.6000	46.94
4	IIAVSSLLR	260	3.8000	38.78
5	LGRMESKPL	468	3.6000	36.73
6	VVMIGMLSS	493	3.6000	36.73
7	LLRVRSEAK	532	3.1000	31.63
8	VVIAGLLKQ	72	2.9000	29.59
9	IVNANAAHL	243	2.9000	29.59
10	VVSKQSRDR	553	2.9000	29.59
11	IAIAKLNER	43	2.5000	25.51
12	LVQRLTRAR	54	2.4000	24.49
13	IDHTIAIAK	39	2.1000	21.43
14	VVITVVSYS	104	2.1000	21.43
15	VVSYSAQPS	108	2.1000	21.43
16	WFVRQAHQI	215	2.0000	20.41
17	YGGVVMIGM	490	2.0000	20.41
18	VITVVSYSA	105	1.9000	19.39
19	IIGMRGSYG	483	1.9000	19.39
20	LQRQLGILS	609	1.8000	18.37
21	MVPAGLCAY	0	1.7000	17.35
22	IAGLLKQGK	74	1.7000	17.35
23	FLSEQVLSR	291	1.7000	17.35
24	WQQVLGDGF	360	1.7000	17.35
25	ISFVVSKQS	550	1.7000	17.35
26	LVLAAGPDG	119	1.6000	16.33
27	FVRQAHQIC	216	1.6000	16.33
28	LSSVVGLGL	499	1.6000	16.33
29	VVGLGLFNP	502	1.6000	16.33
30	FPAIVKFLS	285	1.5000	15.31
31	VKFLSEQVL	289	1.5000	15.31
32	FVWAYQRSE	422	1.4000	14.29
33	FNPLSVGAG	508	1.4000	14.29
34	VGAPSPLLR	159	1.3000	13.27
35	MGTDFGRLK	458	1.3000	13.27
36	LLRSHAVTL	266	1.2000	12.24

37	LSRATERVR	297	1.2000	12.24
38	LQATIAAAQ	588	1.2000	12.24
39	YRDLRRKRA	8	1.1000	11.22
40	VRRAPHAGG	143	1.1000	11.22
41	MPIIAVSSL	258	1.1000	11.22
42	MIGMLSSVV	495	1.1000	11.22
43	IGMLSSVVG	496	1.1000	11.22
44	LNLPAARVG	90	1.0000	10.20
45	WREIVNANA	240	1.0000	10.20
46	MRGSYGGVV	486	1.0000	10.20
47	IVELIDHTI	35	0.9000	9.18
48	VQRLTRARQ	55	0.9000	9.18
49	LLNLPAARV	89	0.9000	9.18
50	LRRKRARKW	11	0.8000	8.16
51	LRVEVGAPS	155	0.8000	8.16
52	VVSDTSQEF	201	0.8000	8.16
53	VMGTDFGRL	457	0.8000	8.16
54	VGAVVATKT	226	0.7000	7.14
55	LILGRMAYK	517	0.7000	7.14
56	VLVVSDTSQ	199	0.6000	6.12
57	VQQTALWQQ	354	0.6000	6.12
58	MIIGMRGSY	482	0.6000	6.12
59	VELIDHTIA	36	0.5000	5.10
60	YQRSEALAD	426	0.5000	5.10
61	LKALGRMES	465	0.5000	5.10
62	LGLFNPLSV	505	0.5000	5.10
63	VVATKTDLY	229	0.4000	4.08
64	VRAGVLGEI	304	0.4000	4.08

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	FGRLKALGR	462	4.9000	50.00
2	VRVVIAGLL	70	4.7000	47.96
3	LKMIQRLLR	562	4.6000	46.94
4	IIAVSSLLR	260	3.8000	38.78
5	LGRMESKPL	468	3.6000	36.73

6	VVMIGMLSS	493	3.6000	36.73
7	LLRVRSEAK	532	3.1000	31.63
8	VVIAGLLKQ	72	2.9000	29.59
9	IVNANAAHL	243	2.9000	29.59
10	VVSKQSRDR	553	2.9000	29.59
11	IAIAKLNER	43	2.5000	25.51
12	LVQRLTRAR	54	2.4000	24.49
13	IDHTIAIAK	39	2.1000	21.43
14	VVITVVSYS	104	2.1000	21.43
15	VVSYSAQPS	108	2.1000	21.43
16	WFVRQAHQI	215	2.0000	20.41
17	YGGVVMIGM	490	2.0000	20.41
18	VITVVSYSA	105	1.9000	19.39
19	IIGMRGSYG	483	1.9000	19.39
20	LQRQLGILS	609	1.8000	18.37
21	MVPAGLCAY	0	1.7000	17.35
22	IAGLLKQGK	74	1.7000	17.35
23	FLSEQVLSR	291	1.7000	17.35
24	WQQVLGDGF	360	1.7000	17.35
25	ISFVVSKQS	550	1.7000	17.35
26	LVLAAGPDG	119	1.6000	16.33
27	FVRQAHQIC	216	1.6000	16.33
28	LSSVVGLGL	499	1.6000	16.33
29	VVGLGLFNP	502	1.6000	16.33
30	FPAIVKFLS	285	1.5000	15.31
31	VKFLSEQVL	289	1.5000	15.31
32	FVWAYQRSE	422	1.4000	14.29
33	FNPLSVGAG	508	1.4000	14.29
34	VGAPSPLLR	159	1.3000	13.27
35	MGTDFGRLK	458	1.3000	13.27
36	LLRSHAVTL	266	1.2000	12.24
37	LSRATERVR	297	1.2000	12.24
38	LQATIAAAQ	588	1.2000	12.24
39	YRDLRRKRA	8	1.1000	11.22
40	VRRAPHAGG	143	1.1000	11.22
41	MPIIAVSSL	258	1.1000	11.22
42	MIGMLSSVV	495	1.1000	11.22
43	IGMLSSVVG	496	1.1000	11.22
44	LNLPAARVG	90	1.0000	10.20
45	WREIVNANA	240	1.0000	10.20
46	MRGSYGGVV	486	1.0000	10.20

47	IVELIDHTI	35	0.9000	9.18
48	VQRLTRARQ	55	0.9000	9.18
49	LLNLPAARV	89	0.9000	9.18
50	LRRKRARKW	11	0.8000	8.16
51	LRVEVGAPS	155	0.8000	8.16
52	VVSDTSQEF	201	0.8000	8.16
53	VMGTDFGRL	457	0.8000	8.16
54	VGAVVATKT	226	0.7000	7.14
55	LILGRMAYK	517	0.7000	7.14
56	VLVVSDTSQ	199	0.6000	6.12
57	VQQTALWQQ	354	0.6000	6.12
58	MIIGMRGSY	482	0.6000	6.12
59	VELIDHTIA	36	0.5000	5.10
60	YQRSEALAD	426	0.5000	5.10
61	LKALGRMES	465	0.5000	5.10
62	LGLFNPLSV	505	0.5000	5.10
63	VVATKTDLY	229	0.4000	4.08
64	VRAGVLGEI	304	0.4000	4.08