MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Mar 22 23:50:38 2010
Length of input sequence	524 amino acids
Number of nanomers from input sequence	516
Number of nanomers with obligatory P1 anchor residue	180
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	52

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	FHLIIAVAA	56	3.0000	50.00
2	LRLLTATTT	351	2.9900	49.83
3	IVMLVLVLV	130	2.4000	40.00
4	WVIFGKQVL	90	2.3800	39.67
5	LIIAVAALL	58	2.1000	35.00
6	LVLVLVPGI	133	1.7200	28.67
7	IMVLSASAV	72	1.6000	26.67
8	LVPAAVVAL	194	1.5000	25.00
9	VVVSAAILA	242	1.5000	25.00

10	WVLGQAFIN	361	1.5000	25.00
11	LIPLVPAAV	191	1.4000	23.33
12	WFVVAGFSM	151	1.3300	22.17
13	LGLVGALGL	320	1.2500	20.83
14	VGLIGGYVC	102	1.2000	20.00
15	VRFMRRIAF	115	1.2000	20.00
16	FLRLLTATT	350	1.2000	20.00
17	LVGLIGGYV	101	1.1000	18.33
18	LLGLFGLFA	328	1.1000	18.33
19	VRALEGQRY	514	1.1000	18.33
20	LRVFLSSLA	232	0.9800	16.33
21	VIGLLPVTG	373	0.9000	15.00
22	LIGIIANAA	400	0.9000	15.00
23	IGLLPVTGL	374	0.8900	14.83
24	LIMVLSASA	71	0.8500	14.17
25	FLSSLAAVV	235	0.8000	13.33
26	LSSLAAVVV	236	0.8000	13.33
27	YVIGLLPVT	372	0.7700	12.83
28	LLPVTGLQL	376	0.7500	12.50
29	LVLVPGIGK	135	0.6500	10.83
30	VLSASAVRS	74	0.6000	10.00
31	VVALALIVA	199	0.6000	10.00
32	WYAGLPLRV	226	0.6000	10.00
33	LFGLFAYTG	331	0.6000	10.00
34	INIGYVIGL	368	0.6000	10.00
35	LVGALGLLG	322	0.5000	8.33
36	VNRLLRLPL	426	0.4000	6.67
37	FAIWGAHLL	169	0.3000	5.00
38	LGLIMVLSA	69	0.2000	3.33
39	LVPGIGKEA	137	0.2000	3.33
40	WNYLPNAHN	301	0.2000	3.33
41	LGLLGLFGL	326	0.2000	3.33
42	IIAVAALLT	59	0.1500	2.50
43	LGLLWYAGL	222	-0.1000	0

44	IFAIIGEEL	312	-0.1000	0
45	LISAGGTST	386	-0.1100	0
46	MVLSASAVR	73	-0.2000	0
47	FAITIVMLV	126	-0.2100	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	LRLLTATTT	351	3.9900	66.50
2	IVMLVLVLV	130	3.4000	56.67
3	LIIAVAALL	58	3.1000	51.67
4	FHLIIAVAA	56	3.0000	50.00
5	LVLVLVPGI	133	2.7200	45.33
6	IMVLSASAV	72	2.6000	43.33
7	LVPAAVVAL	194	2.5000	41.67
8	VVVSAAILA	242	2.5000	41.67
9	LIPLVPAAV	191	2.4000	40.00
10	LGLVGALGL	320	2.2500	37.50
11	VGLIGGYVC	102	2.2000	36.67
12	VRFMRRIAF	115	2.2000	36.67
13	LVGLIGGYV	101	2.1000	35.00
14	LLGLFGLFA	328	2.1000	35.00
15	VRALEGQRY	514	2.1000	35.00
16	LRVFLSSLA	232	1.9800	33.00
17	VIGLLPVTG	373	1.9000	31.67
18	LIGIIANAA	400	1.9000	31.67
19	IGLLPVTGL	374	1.8900	31.50
20	LIMVLSASA	71	1.8500	30.83
21	LSSLAAVVV	236	1.8000	30.00
22	LLPVTGLQL	376	1.7500	29.17
23	LVLVPGIGK	135	1.6500	27.50
24	VLSASAVRS	74	1.6000	26.67
25	VVALALIVA	199	1.6000	26.67

26	LFGLFAYTG	331	1.6000	26.67
27	INIGYVIGL	368	1.6000	26.67
28	LVGALGLLG	322	1.5000	25.00
29	VNRLLRLPL	426	1.4000	23.33
30	WVIFGKQVL	90	1.3800	23.00
31	LGLIMVLSA	69	1.2000	20.00
32	LVPGIGKEA	137	1.2000	20.00
33	LGLLGLFGL	326	1.2000	20.00
34	FLRLLTATT	350	1.2000	20.00
35	IIAVAALLT	59	1.1500	19.17
36	VVSAAILAV	243	1.0000	16.67
37	LGLLWYAGL	222	0.9000	15.00
38	IFAIIGEEL	312	0.9000	15.00
39	LISAGGTST	386	0.8900	14.83
40	MVLSASAVR	73	0.8000	13.33
41	FLSSLAAVV	235	0.8000	13.33
42	IPLVPAAVV	192	0.7500	12.50
43	MRRIAFSGF	118	0.7000	11.67
44	WVLGQAFIN	361	0.5000	8.33
45	VLGQAFINI	362	0.5000	8.33
46	ITIVMLVLV	128	0.4500	7.50
47	LRMSVRFMR	111	0.4000	6.67
48	IILLGLLWY	219	0.4000	6.67
49	LLWYAGLPL	224	0.4000	6.67
50	IGIIANAAR	401	0.4000	6.67
51	WFVVAGFSM	151	0.3300	5.50
52	MLVLVLVPG	132	0.3000	5.00

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	LRMSVRFMR	111	6.3000	66.32
2	LVLVLVPGI	133	5.6000	58.95

3	VRFMRRIAF	115	5.3000	55.79
4	INIGYVIGL	368	4.3600	45.89
5	MVLSASAVR	73	4.2000	44.21
6	IVMLVLVLV	130	4.2000	44.21
7	MRIASRSAD	340	4.1700	43.89
8	IFGDGLGQG	289	4.0000	42.11
9	LVPAAVVAL	194	3.7600	39.58
10	VVVSAAILA	242	3.7000	38.95
11	LLAARRMER	176	3.6000	37.89
12	LIGGYVCLR	104	3.5000	36.84
13	MQPSELAKM	159	3.5000	36.84
14	VVSAAILAV	243	3.5000	36.84
15	YVIGLLPVT	372	3.5000	36.84
16	LGLIMVLSA	69	3.4000	35.79
17	MLIPLVPAA	190	3.4000	35.79
18	VVAGFSMQP	153	3.3000	34.74
19	MGLPPRPGS	477	3.3000	34.74
20	VMLVLVLVP	131	3.2000	33.68
21	VFLSSLAAV	234	3.0000	31.58
22	YRSDRVRSW	255	3.0000	31.58
23	MRRIAFSGF	118	2.9700	31.26
24	VSMGIILLG	215	2.9000	30.53
25	IILLGLLWY	219	2.8000	29.47
26	LRLPLPEPY	430	2.8000	29.47
27	WVIFGKQVL	90	2.7600	29.05
28	MGIILLGLL	217	2.7600	29.05
29	LREMLIPLV	187	2.7000	28.42
30	VVALALIVA	199	2.7000	28.42
31	VRRSVHHGA	493	2.7000	28.42
32	VNRLLRLPL	426	2.6600	28.00
33	LVLVPGIGK	135	2.6000	27.37
34	LRLLTATTT	351	2.6000	27.37
35	LIIAVAALL	58	2.5600	26.95
36	IGLLPVTGL	374	2.5600	26.95

37	VLSASAVRS	74	2.5000	26.32
38	VLVLVPGIG	134	2.5000	26.32
39	WVLGQAFIN	361	2.5000	26.32
40	LIMVLSASA	71	2.4000	25.26
41	VIGLLPVTG	373	2.4000	25.26
42	IGIIANAAR	401	2.4000	25.26
43	LQLPLISAG	382	2.3700	24.95
44	MLVLVLVPG	132	2.3000	24.21
45	LLRLPLPEP	429	2.3000	24.21
46	ITIVMLVLV	128	2.2000	23.16
47	LIPLVPAAV	191	2.2000	23.16
48	LVGALGLLG	322	2.2000	23.16
49	LGLLGLFGL	326	2.1600	22.74
50	LRRGTSDTD	5	2.1000	22.11
51	FAITIVMLV	126	2.1000	22.11
52	ILLGLLWYA	220	2.1000	22.11

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	YRSDRVRSW	255	4.0000	43.96
2	LRMSVRFMR	111	3.8000	41.76
3	YVIGLLPVT	372	3.8000	41.76
4	LVLVLVPGI	133	3.7000	40.66
5	WVIFGKQVL	90	2.8000	30.77
6	VVVSAAILA	242	2.7000	29.67
7	WVLGQAFIN	361	2.7000	29.67
8	FHLIIAVAA	56	2.5000	27.47
9	LGLIMVLSA	69	2.4000	26.37
10	VRFMRRIAF	115	2.4000	26.37
11	MLIPLVPAA	190	2.4000	26.37
12	INIGYVIGL	368	2.4000	26.37
13	IVMLVLVLV	130	2.2000	24.18

14	FAITIVMLV	126	2.1000	23.08
15	MRIASRSAD	340	2.0700	22.75
16	MGLPPRPGS	477	1.9000	20.88
17	LVPAAVVAL	194	1.8000	19.78
18	FVVAGFSMQ	152	1.7700	19.45
19	MVLSASAVR	73	1.7000	18.68
20	VVALALIVA	199	1.7000	18.68
21	VRRSVHHGA	493	1.7000	18.68
22	IFGDGLGQG	289	1.6000	17.58
23	LVLVPGIGK	135	1.5000	16.48
24	VVSAAILAV	243	1.5000	16.48
25	LIMVLSASA	71	1.4000	15.38
26	VALALIVAQ	200	1.4000	15.38
27	WYAGLPLRV	226	1.4000	15.38
28	VVAGFSMQP	153	1.3000	14.29
29	FLRLLTATT	350	1.3000	14.29
30	VMLVLVLVP	131	1.2000	13.19
31	FLSSLAAVV	235	1.2000	13.19
32	VLSASAVRS	74	1.1000	12.09
33	LLAARRMER	176	1.1000	12.09
34	ILLGLLWYA	220	1.1000	12.09
35	LIGGYVCLR	104	1.0000	10.99
36	MQPSELAKM	159	1.0000	10.99
37	VFLSSLAAV	234	1.0000	10.99
38	FIFAIIGEE	311	1.0000	10.99
39	LRLLTATTT	351	0.9000	9.89
40	FSMQPSELA	157	0.8000	8.79
41	MGIILLGLL	217	0.8000	8.79
42	LIGIIANAA	400	0.7100	7.80
43	WFVVAGFSM	151	0.7000	7.69
44	LREMLIPLV	187	0.7000	7.69
45	VNRLLRLPL	426	0.7000	7.69
46	LRVFLSSLA	232	0.6700	7.36
47	LIIAVAALL	58	0.6000	6.59

48	WTLVGLIGG	99	0.6000	6.59
49	IGLLPVTGL	374	0.6000	6.59
50	VSMGIILLG	215	0.5000	5.49
51	IILLGLLWY	219	0.5000	5.49
52	LRLPLPEPY	430	0.5000	5.49

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	LGLIMVLSA	69	3.9000	44.32
2	VRRSVHHGA	493	3.5000	39.77
3	VVVSAAILA	242	3.3800	38.41
4	LRMSVRFMR	111	3.3000	37.50
5	LVLVLVPGI	133	3.3000	37.50
6	VRFMRRIAF	115	3.0800	35.00
7	IVMLVLVLV	130	3.0800	35.00
8	INIGYVIGL	368	3.0800	35.00
9	VVSAAILAV	243	3.0000	34.09
10	MRIASRSAD	340	2.8000	31.82
11	MVLSASAVR	73	2.7000	30.68
12	VMLVLVLVP	131	2.7000	30.68
13	YRSDRVRSW	255	2.7000	30.68
14	LVPAAVVAL	194	2.6800	30.45
15	LIMVLSASA	71	2.4000	27.27
16	LIGIIANAA	400	2.4000	27.27
17	VVALALIVA	199	2.3800	27.05
18	VALALIVAQ	200	2.2800	25.91
19	VNRLLRLPL	426	2.2000	25.00
20	LVLVPGIGK	135	2.1800	24.77
21	LIGGYVCLR	104	2.0000	22.73
22	VVAGFSMQP	153	2.0000	22.73
23	MQPSELAKM	159	2.0000	22.73
24	MLIPLVPAA	190	2.0000	22.73

25	VSMGIILLG	215	2.0000	22.73
26	IILLGLLWY	219	2.0000	22.73
27	VFLSSLAAV	234	2.0000	22.73
28	VLSASAVRS	74	1.9800	22.50
29	WVIFGKQVL	90	1.9000	21.59
30	LVPGIGKEA	137	1.9000	21.59
31	LRLLTATTT	351	1.9000	21.59
32	LRLPLPEPY	430	1.9000	21.59
33	LLAARRMER	176	1.8000	20.45
34	LIIAVAALL	58	1.6000	18.18
35	IGLLPVTGL	374	1.6000	18.18
36	MGLPPRPGS	477	1.5000	17.05
37	LRVFLSSLA	232	1.4000	15.91
38	YVIGLLPVT	372	1.4000	15.91
39	FHLIIAVAA	56	1.3800	15.68
40	LRRGTSDTD	5	1.3000	14.77
41	ILLGLLWYA	220	1.3000	14.77
42	LVGALGLLG	322	1.3000	14.77
43	LIPLVPAAV	191	1.2000	13.64
44	IFGDGLGQG	289	1.2000	13.64
45	LGLVGALGL	320	1.2000	13.64
46	LLGLFGLFA	328	1.2000	13.64
47	VIFGKQVLW	91	1.1800	13.41
48	ITIVMLVLV	128	1.0800	12.27
49	IWGAHLLAA	171	1.0000	11.36
50	LAAVVVSAA	239	1.0000	11.36
51	IVAQPDLGQ	205	0.9000	10.23
52	WYAGLPLRV	226	0.9000	10.23

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	LGLIMVLSA	69	3.9000	44.32

2	VRRSVHHGA	493	3.5000	39.77
3	VVVSAAILA	242	3.3800	38.41
4	LRMSVRFMR	111	3.3000	37.50
5	LVLVLVPGI	133	3.3000	37.50
6	VRFMRRIAF	115	3.0800	35.00
7	IVMLVLVLV	130	3.0800	35.00
8	INIGYVIGL	368	3.0800	35.00
9	VVSAAILAV	243	3.0000	34.09
10	MRIASRSAD	340	2.8000	31.82
11	MVLSASAVR	73	2.7000	30.68
12	VMLVLVLVP	131	2.7000	30.68
13	YRSDRVRSW	255	2.7000	30.68
14	LVPAAVVAL	194	2.6800	30.45
15	LIMVLSASA	71	2.4000	27.27
16	LIGIIANAA	400	2.4000	27.27
17	VVALALIVA	199	2.3800	27.05
18	VALALIVAQ	200	2.2800	25.91
19	VNRLLRLPL	426	2.2000	25.00
20	LVLVPGIGK	135	2.1800	24.77
21	LIGGYVCLR	104	2.0000	22.73
22	VVAGFSMQP	153	2.0000	22.73
23	MQPSELAKM	159	2.0000	22.73
24	MLIPLVPAA	190	2.0000	22.73
25	VSMGIILLG	215	2.0000	22.73
26	IILLGLLWY	219	2.0000	22.73
27	VFLSSLAAV	234	2.0000	22.73
28	VLSASAVRS	74	1.9800	22.50
29	WVIFGKQVL	90	1.9000	21.59
30	LVPGIGKEA	137	1.9000	21.59
31	LRLLTATTT	351	1.9000	21.59
32	LRLPLPEPY	430	1.9000	21.59
33	LLAARRMER	176	1.8000	20.45
34	LIIAVAALL	58	1.6000	18.18
35	IGLLPVTGL	374	1.6000	18.18

36	MGLPPRPGS	477	1.5000	17.05
37	LRVFLSSLA	232	1.4000	15.91
38	YVIGLLPVT	372	1.4000	15.91
39	FHLIIAVAA	56	1.3800	15.68
40	LRRGTSDTD	5	1.3000	14.77
41	ILLGLLWYA	220	1.3000	14.77
42	LVGALGLLG	322	1.3000	14.77
43	LIPLVPAAV	191	1.2000	13.64
44	IFGDGLGQG	289	1.2000	13.64
45	LGLVGALGL	320	1.2000	13.64
46	LLGLFGLFA	328	1.2000	13.64
47	VIFGKQVLW	91	1.1800	13.41
48	ITIVMLVLV	128	1.0800	12.27
49	IWGAHLLAA	171	1.0000	11.36
50	LAAVVVSAA	239	1.0000	11.36
51	IVAQPDLGQ	205	0.9000	10.23
52	WYAGLPLRV	226	0.9000	10.23

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	LGLIMVLSA	69	3.9000	44.32
2	VRRSVHHGA	493	3.5000	39.77
3	VVVSAAILA	242	3.3800	38.41
4	LRMSVRFMR	111	3.3000	37.50
5	LVLVLVPGI	133	3.3000	37.50
6	VRFMRRIAF	115	3.0800	35.00
7	IVMLVLVLV	130	3.0800	35.00
8	INIGYVIGL	368	3.0800	35.00
9	VVSAAILAV	243	3.0000	34.09
10	MRIASRSAD	340	2.8000	31.82
11	MVLSASAVR	73	2.7000	30.68
12	VMLVLVLVP	131	2.7000	30.68

13	YRSDRVRSW	255	2.7000	30.68
14	LVPAAVVAL	194	2.6800	30.45
15	LIMVLSASA	71	2.4000	27.27
16	LIGIIANAA	400	2.4000	27.27
17	VVALALIVA	199	2.3800	27.05
18	VALALIVAQ	200	2.2800	25.91
19	VNRLLRLPL	426	2.2000	25.00
20	LVLVPGIGK	135	2.1800	24.77
21	LIGGYVCLR	104	2.0000	22.73
22	VVAGFSMQP	153	2.0000	22.73
23	MQPSELAKM	159	2.0000	22.73
24	MLIPLVPAA	190	2.0000	22.73
25	VSMGIILLG	215	2.0000	22.73
26	IILLGLLWY	219	2.0000	22.73
27	VFLSSLAAV	234	2.0000	22.73
28	VLSASAVRS	74	1.9800	22.50
29	WVIFGKQVL	90	1.9000	21.59
30	LVPGIGKEA	137	1.9000	21.59
31	LRLLTATTT	351	1.9000	21.59
32	LRLPLPEPY	430	1.9000	21.59
33	LLAARRMER	176	1.8000	20.45
34	LIIAVAALL	58	1.6000	18.18
35	IGLLPVTGL	374	1.6000	18.18
36	MGLPPRPGS	477	1.5000	17.05
37	LRVFLSSLA	232	1.4000	15.91
38	YVIGLLPVT	372	1.4000	15.91
39	FHLIIAVAA	56	1.3800	15.68
40	LRRGTSDTD	5	1.3000	14.77
41	ILLGLLWYA	220	1.3000	14.77
42	LVGALGLLG	322	1.3000	14.77
43	LIPLVPAAV	191	1.2000	13.64
44	IFGDGLGQG	289	1.2000	13.64
45	LGLVGALGL	320	1.2000	13.64
46	LLGLFGLFA	328	1.2000	13.64

47	VIFGKQVLW	91	1.1800	13.41
48	ITIVMLVLV	128	1.0800	12.27
49	IWGAHLLAA	171	1.0000	11.36
50	LAAVVVSAA	239	1.0000	11.36
51	IVAQPDLGQ	205	0.9000	10.23
52	WYAGLPLRV	226	0.9000	10.23

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	LRMSVRFMR	111	5.3000	55.79
2	LVLVLVPGI	133	4.6000	48.42
3	YVIGLLPVT	372	4.5000	47.37
4	VRFMRRIAF	115	4.3000	45.26
5	YRSDRVRSW	255	4.0000	42.11
6	WVIFGKQVL	90	3.7600	39.58
7	WVLGQAFIN	361	3.5000	36.84
8	INIGYVIGL	368	3.3600	35.37
9	MVLSASAVR	73	3.2000	33.68
10	IVMLVLVLV	130	3.2000	33.68
11	MRIASRSAD	340	3.1700	33.37
12	FAITIVMLV	126	3.1000	32.63
13	IFGDGLGQG	289	3.0000	31.58
14	LVPAAVVAL	194	2.7600	29.05
15	VVVSAAILA	242	2.7000	28.42
16	LLAARRMER	176	2.6000	27.37
17	FHLIIAVAA	56	2.5000	26.32
18	LIGGYVCLR	104	2.5000	26.32
19	MQPSELAKM	159	2.5000	26.32
20	VVSAAILAV	243	2.5000	26.32
21	LGLIMVLSA	69	2.4000	25.26
22	MLIPLVPAA	190	2.4000	25.26
23	WYAGLPLRV	226	2.4000	25.26

24	FIFAIIGEE	311	2.4000	25.26
25	VVAGFSMQP	153	2.3000	24.21
26	MGLPPRPGS	477	2.3000	24.21
27	YLPNAHNDF	303	2.2100	23.26
28	VMLVLVLVP	131	2.2000	23.16
29	WFVVAGFSM	151	2.2000	23.16
30	FLSSLAAVV	235	2.2000	23.16
31	WTLVGLIGG	99	2.0000	21.05
32	VFLSSLAAV	234	2.0000	21.05
33	FLRLLTATT	350	2.0000	21.05
34	MRRIAFSGF	118	1.9700	20.74
35	VSMGIILLG	215	1.9000	20.00
36	IILLGLLWY	219	1.8000	18.95
37	LRLPLPEPY	430	1.8000	18.95
38	YVCLRMSVR	108	1.7700	18.63
39	MGIILLGLL	217	1.7600	18.53
40	FMRRIAFSG	117	1.7000	17.89
41	LREMLIPLV	187	1.7000	17.89
42	VVALALIVA	199	1.7000	17.89
43	VRRSVHHGA	493	1.7000	17.89
44	VNRLLRLPL	426	1.6600	17.47
45	LVLVPGIGK	135	1.6000	16.84
46	LRLLTATTT	351	1.6000	16.84
47	YAGQRRTRR	505	1.6000	16.84
48	LIIAVAALL	58	1.5600	16.42
49	IGLLPVTGL	374	1.5600	16.42
50	VLSASAVRS	74	1.5000	15.79
51	VLVLVPGIG	134	1.5000	15.79
52	LIMVLSASA	71	1.4000	14.74

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	LGLIMVLSA	69	3.9000	44.32
2	VRRSVHHGA	493	3.5000	39.77
3	VVVSAAILA	242	3.3800	38.41
4	LRMSVRFMR	111	3.3000	37.50
5	LVLVLVPGI	133	3.3000	37.50
6	VRFMRRIAF	115	3.0800	35.00
7	IVMLVLVLV	130	3.0800	35.00
8	INIGYVIGL	368	3.0800	35.00
9	VVSAAILAV	243	3.0000	34.09
10	MRIASRSAD	340	2.8000	31.82
11	MVLSASAVR	73	2.7000	30.68
12	VMLVLVLVP	131	2.7000	30.68
13	YRSDRVRSW	255	2.7000	30.68
14	LVPAAVVAL	194	2.6800	30.45
15	LIMVLSASA	71	2.4000	27.27
16	LIGIIANAA	400	2.4000	27.27
17	VVALALIVA	199	2.3800	27.05
18	VALALIVAQ	200	2.2800	25.91
19	VNRLLRLPL	426	2.2000	25.00
20	LVLVPGIGK	135	2.1800	24.77
21	LIGGYVCLR	104	2.0000	22.73
22	VVAGFSMQP	153	2.0000	22.73
23	MQPSELAKM	159	2.0000	22.73
24	MLIPLVPAA	190	2.0000	22.73
25	VSMGIILLG	215	2.0000	22.73
26	IILLGLLWY	219	2.0000	22.73
27	VFLSSLAAV	234	2.0000	22.73
28	VLSASAVRS	74	1.9800	22.50
29	WVIFGKQVL	90	1.9000	21.59
30	LVPGIGKEA	137	1.9000	21.59
31	LRLLTATTT	351	1.9000	21.59
32	LRLPLPEPY	430	1.9000	21.59
33	LLAARRMER	176	1.8000	20.45
34	LIIAVAALL	58	1.6000	18.18

35	IGLLPVTGL	374	1.6000	18.18
36	MGLPPRPGS	477	1.5000	17.05
37	LRVFLSSLA	232	1.4000	15.91
38	YVIGLLPVT	372	1.4000	15.91
39	FHLIIAVAA	56	1.3800	15.68
40	LRRGTSDTD	5	1.3000	14.77
41	ILLGLLWYA	220	1.3000	14.77
42	LVGALGLLG	322	1.3000	14.77
43	LIPLVPAAV	191	1.2000	13.64
44	IFGDGLGQG	289	1.2000	13.64
45	LGLVGALGL	320	1.2000	13.64
46	LLGLFGLFA	328	1.2000	13.64
47	VIFGKQVLW	91	1.1800	13.41
48	ITIVMLVLV	128	1.0800	12.27
49	IWGAHLLAA	171	1.0000	11.36
50	LAAVVVSAA	239	1.0000	11.36
51	IVAQPDLGQ	205	0.9000	10.23
52	WYAGLPLRV	226	0.9000	10.23

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	FAITIVMLV	126	3.2000	37.21
2	FLRLLTATT	350	3.2000	37.21
3	FSMQPSELA	157	3.1000	36.05
4	LGLIMVLSA	69	2.9000	33.72
5	MVLSASAVR	73	2.9000	33.72
6	FHLIIAVAA	56	2.6800	31.16
7	YRSDRVRSW	255	2.5000	29.07
8	VVVSAAILA	242	2.4800	28.84
9	WNYLPNAHN	301	2.3000	26.74
10	IGIIANAAR	401	2.1000	24.42
11	IVAQPDLGQ	205	2.0000	23.26

12	FVVAGFSMQ	152	1.8000	20.93
13	LGQTVSMGI	211	1.7000	19.77
14	LRLLTATTT	351	1.7000	19.77
15	LIGIIANAA	400	1.7000	19.77
16	LIMVLSASA	71	1.6000	18.60
17	LRVFLSSLA	232	1.6000	18.60
18	LTATTTLWV	354	1.6000	18.60
19	IVMLVLVLV	130	1.5800	18.37
20	WLNPENDPQ	263	1.4000	16.28
21	LVPAAVVAL	194	1.3800	16.05
22	FLSSLAAVV	235	1.3000	15.12
23	VRRSVHHGA	493	1.3000	15.12
24	VVSAAILAV	243	1.2000	13.95
25	LVLVLVPGI	133	1.1000	12.79
26	IGLLPVTGL	374	1.1000	12.79
27	VLSASAVRS	74	0.9800	11.40
28	VVALALIVA	199	0.8800	10.23
29	LLTATTTLW	353	0.8000	9.30
30	LIIAVAALL	58	0.6000	6.98
31	VAALLTTLG	62	0.6000	6.98
32	YVCLRMSVR	108	0.6000	6.98
33	IMVLSASAV	72	0.5000	5.81
34	VMLVLVLVP	131	0.5000	5.81
35	LIPLVPAAV	191	0.5000	5.81
36	IILLGLLWY	219	0.5000	5.81
37	VALALIVAQ	200	0.4800	5.58
38	MRRIAFSGF	118	0.4000	4.65
39	YLPNAHNDF	303	0.4000	4.65
40	LGRPMTSFH	49	0.3800	4.42
41	LLGLFGLFA	328	0.2000	2.33
42	VIGLLPVTG	373	0.1800	2.09
43	MLIPLVPAA	190	0.1000	1.16
44	FINIGYVIG	367	-0.0200	0
45	MQPSELAKM	159	-0.2000	0

46	VFLSSLAAV	234	-0.2000	0
47	LRLPLPEPY	430	-0.2000	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	LRVFLSSLA	232	3.6000	37.50
2	LGLIMVLSA	69	3.4800	36.25
3	LLRRGTSDT	4	3.0000	31.25
4	VRSWLNPEN	260	2.9000	30.21
5	LIMVLSASA	71	2.8000	29.17
6	LVPAAVVAL	194	2.5000	26.04
7	VVSAAILAV	243	2.5000	26.04
8	IGIIANAAR	401	2.3800	24.79
9	VCLRMSVRF	109	2.2000	22.92
10	MVLSASAVR	73	2.1000	21.88
11	VLSASAVRS	74	2.1000	21.88
12	IVAQPDLGQ	205	2.1000	21.88
13	LPLRVFLSS	230	2.1000	21.88
14	VVVSAAILA	242	2.1000	21.88
15	VMLVLVLVP	131	2.0000	20.83
16	LVLVLVPGI	133	2.0000	20.83
17	LLTATTTLW	353	2.0000	20.83
18	INIGYVIGL	368	2.0000	20.83
19	LIGIIANAA	400	1.9800	20.62
20	VVAGFSMQP	153	1.9000	19.79
21	IFGKQVLWT	92	1.8000	18.75
22	LTATTTLWV	354	1.7000	17.71
23	VLTRLLRRG	0	1.6000	16.67
24	LIIAVAALL	58	1.6000	16.67
25	FAIWGAHLL	169	1.6000	16.67
26	VALALIVAQ	200	1.6000	16.67
27	ILLGLLWYA	220	1.6000	16.67

28	MSVRFMRRI	113	1.5000	15.62
29	LGQTVSMGI	211	1.5000	15.62
30	LRLLTATTT	351	1.5000	15.62
31	LGRPMTSFH	49	1.4800	15.42
32	FMRRIAFSG	117	1.3000	13.54
33	IVMLVLVLV	130	1.3000	13.54
34	VAGFSMQPS	154	1.2000	12.50
35	YQARQAKFA	275	1.2000	12.50
36	LVLVPGIGK	135	1.1000	11.46
37	MLIPLVPAA	190	1.1000	11.46
38	FHLIIAVAA	56	1.0800	11.25
39	FAITIVMLV	126	1.0000	10.42
40	MERASLREM	182	1.0000	10.42
41	VRRSVHHGA	493	1.0000	10.42
42	VGLIGGYVC	102	0.9800	10.21
43	FGAWLGRPM	45	0.9000	9.38
44	IGGYVCLRM	105	0.9000	9.38
45	VVALALIVA	199	0.9000	9.38
46	IGLLPVTGL	374	0.9000	9.38
47	LGLVGALGL	320	0.8000	8.33
48	LVGALGLLG	322	0.8000	8.33
49	FLRLLTATT	350	0.8000	8.33
50	VRFMRRIAF	115	0.7000	7.29
51	YRSDRVRSW	255	0.7000	7.29
52	IIANAARHE	403	0.7000	7.29

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	LRVFLSSLA	232	5.2000	59.09
2	LIMVLSASA	71	4.0000	45.45
3	LGLIMVLSA	69	3.8000	43.18
4	LRLLTATTT	351	3.4000	38.64

5	IGIIANAAR	401	3.4000	38.64
6	LVLVLVPGI	133	3.2000	36.36
7	LIGIIANAA	400	3.1000	35.23
8	IGLLPVTGL	374	2.8000	31.82
9	IVMLVLVLV	130	2.6000	29.55
10	VMLVLVLVP	131	2.5000	28.41
11	IMVLSASAV	72	2.4000	27.27
12	MVLSASAVR	73	2.4000	27.27
13	MRRIAFSGF	118	2.4000	27.27
14	FLRLLTATT	350	2.4000	27.27
15	LGRPMTSFH	49	2.3800	27.05
16	VAALLTTLG	62	2.3000	26.14
17	LLTATTTLW	353	2.3000	26.14
18	LVPAAVVAL	194	2.2000	25.00
19	VVALALIVA	199	2.0800	23.64
20	VVVSAAILA	242	1.9800	22.50
21	LAAVVVSAA	239	1.9000	21.59
22	LVLVPGIGK	135	1.8800	21.36
23	FHLIIAVAA	56	1.8000	20.45
24	VLSASAVRS	74	1.8000	20.45
25	IVAQPDLGQ	205	1.8000	20.45
26	VVSAAILAV	243	1.8000	20.45
27	LIPLVPAAV	191	1.7000	19.32
28	LIIAVAALL	58	1.6000	18.18
29	FVVAGFSMQ	152	1.5000	17.05
30	WNYLPNAHN	301	1.5000	17.05
31	VRFMRRIAF	115	1.4800	16.82
32	VALALIVAQ	200	1.3000	14.77
33	IILLGLLWY	219	1.3000	14.77
34	LGLVGALGL	320	1.3000	14.77
35	VRSWLNPEN	260	1.2500	14.20
36	VIGLLPVTG	373	1.2000	13.64
37	MLIPLVPAA	190	1.1000	12.50
38	LREMLIPLV	187	1.0000	11.36

39	LGQTVSMGI	211	1.0000	11.36
40	LLGLFGLFA	328	1.0000	11.36
41	VGLIGGYVC	102	0.9000	10.23
42	LFGLFAYTG	331	0.8000	9.09
43	IIAVAALLT	59	0.7000	7.95
44	VAGFSMQPS	154	0.6000	6.82
45	LTATTTLWV	354	0.6000	6.82
46	LLRRGTSDT	4	0.5000	5.68
47	YVCLRMSVR	108	0.5000	5.68
48	FAITIVMLV	126	0.5000	5.68
49	VRALEGQRY	514	0.5000	5.68
50	VRSYDDDGS	80	0.4000	4.55
51	FSMQPSELA	157	0.4000	4.55
52	VPAAVVALA	195	0.4000	4.55

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	WNYLPNAHN	301	4.5000	47.87
2	FLRLLTATT	350	4.3000	45.74
3	LRVFLSSLA	232	4.2000	44.68
4	FVVAGFSMQ	152	3.3000	35.11
5	LRLLTATTT	351	3.3000	35.11
6	LIMVLSASA	71	3.0000	31.91
7	FHLIIAVAA	56	2.8000	29.79
8	LGLIMVLSA	69	2.8000	29.79
9	IGLLPVTGL	374	2.8000	29.79
10	LGRPMTSFH	49	2.6000	27.66
11	VAALLTTLG	62	2.6000	27.66
12	LVLVLVPGI	133	2.4000	25.53
13	IGIIANAAR	401	2.4000	25.53
14	MRRIAFSGF	118	2.3000	24.47
15	VRSWLNPEN	260	2.2500	23.94

16	LVPAAVVAL	194	2.2000	23.40
17	LLTATTTLW	353	2.2000	23.40
18	FGLFAYTGM	332	2.1000	22.34
19	LIGIIANAA	400	2.1000	22.34
20	WVIFGKQVL	90	2.0000	21.28
21	IVMLVLVLV	130	1.9000	20.21
22	VMLVLVLVP	131	1.9000	20.21
23	LALIVAQPD	202	1.9000	20.21
24	FIFAIIGEE	311	1.9000	20.21
25	FAITIVMLV	126	1.8000	19.15
26	MRIASRSAD	340	1.8000	19.15
27	IMVLSASAV	72	1.7000	18.09
28	LIIAVAALL	58	1.6000	17.02
29	IVAQPDLGQ	205	1.6000	17.02
30	WLNPENDPQ	263	1.6000	17.02
31	YVCLRMSVR	108	1.5000	15.96
32	VIGLLPVTG	373	1.5000	15.96
33	MVLSASAVR	73	1.4000	14.89
34	FSMQPSELA	157	1.4000	14.89
35	IILLGLLWY	219	1.4000	14.89
36	FINIGYVIG	367	1.4000	14.89
37	VRFMRRIAF	115	1.3800	14.68
38	LSLIGIIAN	398	1.3800	14.68
39	VEGQRTGPE	23	1.3000	13.83
40	LGLVGALGL	320	1.3000	13.83
41	WVLGQAFIN	361	1.2500	13.30
42	YRSDRVRSW	255	1.2000	12.77
43	VALALIVAQ	200	1.1000	11.70
44	VVSAAILAV	243	1.1000	11.70
45	LFGLFAYTG	331	1.1000	11.70
46	VVALALIVA	199	1.0800	11.49
47	FAIWGAHLL	169	1.0500	11.17
48	LIPLVPAAV	191	1.0000	10.64
49	VVVSAAILA	242	0.9800	10.43

50	WFVVAGFSM	151	0.9500	10.11
51	LAAVVVSAA	239	0.9000	9.57
52	YTGMRIASR	337	0.9000	9.57

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	LRVFLSSLA	232	4.2000	47.73
2	FLRLLTATT	350	3.4000	38.64
3	LIMVLSASA	71	3.0000	34.09
4	FHLIIAVAA	56	2.8000	31.82
5	LGLIMVLSA	69	2.8000	31.82
6	FVVAGFSMQ	152	2.5000	28.41
7	WNYLPNAHN	301	2.5000	28.41
8	LRLLTATTT	351	2.4000	27.27
9	IGIIANAAR	401	2.4000	27.27
10	LVLVLVPGI	133	2.2000	25.00
11	LIGIIANAA	400	2.1000	23.86
12	IGLLPVTGL	374	1.8000	20.45
13	IVMLVLVLV	130	1.6000	18.18
14	YVCLRMSVR	108	1.5000	17.05
15	FAITIVMLV	126	1.5000	17.05
16	VMLVLVLVP	131	1.5000	17.05
17	IMVLSASAV	72	1.4000	15.91
18	MVLSASAVR	73	1.4000	15.91
19	MRRIAFSGF	118	1.4000	15.91
20	FSMQPSELA	157	1.4000	15.91
21	LGRPMTSFH	49	1.3800	15.68
22	VAALLTTLG	62	1.3000	14.77
23	LLTATTTLW	353	1.3000	14.77
24	LVPAAVVAL	194	1.2000	13.64
25	VVALALIVA	199	1.0800	12.27
26	WVIFGKQVL	90	1.0000	11.36

27	FGLFAYTGM	332	1.0000	11.36
28	VVVSAAILA	242	0.9800	11.14
29	LAAVVVSAA	239	0.9000	10.23
30	YTGMRIASR	337	0.9000	10.23
31	LVLVPGIGK	135	0.8800	10.00
32	VLSASAVRS	74	0.8000	9.09
33	IVAQPDLGQ	205	0.8000	9.09
34	VVSAAILAV	243	0.8000	9.09
35	WLNPENDPQ	263	0.8000	9.09
36	LIPLVPAAV	191	0.7000	7.95
37	LIIAVAALL	58	0.6000	6.82
38	FSGFAITIV	123	0.5000	5.68
39	VRFMRRIAF	115	0.4800	5.45
40	VALALIVAQ	200	0.3000	3.41
41	IILLGLLWY	219	0.3000	3.41
42	YRSDRVRSW	255	0.3000	3.41
43	LGLVGALGL	320	0.3000	3.41
44	VRSWLNPEN	260	0.2500	2.84
45	VIGLLPVTG	373	0.2000	2.27
46	MLIPLVPAA	190	0.1000	1.14
47	FINIGYVIG	367	0.1000	1.14
48	FAIWGAHLL	169	0.0500	0.57

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	LRVFLSSLA	232	5.2000	55.32
2	LRLLTATTT	351	4.3000	45.74
3	LIMVLSASA	71	4.0000	42.55
4	LGLIMVLSA	69	3.8000	40.43
5	IGLLPVTGL	374	3.8000	40.43
6	LGRPMTSFH	49	3.6000	38.30
7	VAALLTTLG	62	3.6000	38.30

8	WNYLPNAHN	301	3.5000	37.23
9	LVLVLVPGI	133	3.4000	36.17
10	IGIIANAAR	401	3.4000	36.17
11	MRRIAFSGF	118	3.3000	35.11
12	FLRLLTATT	350	3.3000	35.11
13	VRSWLNPEN	260	3.2500	34.57
14	LVPAAVVAL	194	3.2000	34.04
15	LLTATTTLW	353	3.2000	34.04
16	LIGIIANAA	400	3.1000	32.98
17	IVMLVLVLV	130	2.9000	30.85
18	VMLVLVLVP	131	2.9000	30.85
19	LALIVAQPD	202	2.9000	30.85
20	MRIASRSAD	340	2.8000	29.79
21	IMVLSASAV	72	2.7000	28.72
22	LIIAVAALL	58	2.6000	27.66
23	IVAQPDLGQ	205	2.6000	27.66
24	VIGLLPVTG	373	2.5000	26.60
25	MVLSASAVR	73	2.4000	25.53
26	IILLGLLWY	219	2.4000	25.53
27	VRFMRRIAF	115	2.3800	25.32
28	LSLIGIIAN	398	2.3800	25.32
29	VEGQRTGPE	23	2.3000	24.47
30	FVVAGFSMQ	152	2.3000	24.47
31	LGLVGALGL	320	2.3000	24.47
32	VALALIVAQ	200	2.1000	22.34
33	VVSAAILAV	243	2.1000	22.34
34	LFGLFAYTG	331	2.1000	22.34
35	VVALALIVA	199	2.0800	22.13
36	LIPLVPAAV	191	2.0000	21.28
37	VVVSAAILA	242	1.9800	21.06
38	LAAVVVSAA	239	1.9000	20.21
39	FHLIIAVAA	56	1.8000	19.15
40	VLSASAVRS	74	1.8000	19.15
41	IIAVAALLT	59	1.6000	17.02

42	MLVLVLVPG	132	1.6000	17.02
43	VLVLVPGIG	134	1.6000	17.02
44	LQLPLISAG	382	1.6000	17.02
45	VRALEGQRY	514	1.6000	17.02
46	LGLFGLFAY	329	1.4500	15.43
47	LLRRGTSDT	4	1.4000	14.89
48	LVGALGLLG	322	1.4000	14.89
49	LGQAFINIG	363	1.4000	14.89
50	LGLLGLFGL	326	1.3500	14.36
51	LRRGTSDTD	5	1.3000	13.83
52	IGGYVCLRM	105	1.3000	13.83

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	MVLSASAVR	73	4.4000	48.89
2	FAITIVMLV	126	4.2000	46.67
3	FLRLLTATT	350	3.9000	43.33
4	IGIIANAAR	401	3.6000	40.00
5	FSMQPSELA	157	3.1000	34.44
6	WNYLPNAHN	301	3.1000	34.44
7	LGLIMVLSA	69	2.9000	32.22
8	FHLIIAVAA	56	2.6800	29.78
9	LGQTVSMGI	211	2.6000	28.89
10	LTATTTLWV	354	2.6000	28.89
11	IVMLVLVLV	130	2.5800	28.67
12	YRSDRVRSW	255	2.5000	27.78
13	VVVSAAILA	242	2.4800	27.56
14	LRLLTATTT	351	2.4000	26.67
15	LVPAAVVAL	194	2.3400	26.00
16	MRRIAFSGF	118	2.3000	25.56
17	FLSSLAAVV	235	2.3000	25.56
18	YLPNAHNDF	303	2.3000	25.56

19	VVSAAILAV	243	2.2000	24.44
20	YVCLRMSVR	108	2.1000	23.33
21	IGLLPVTGL	374	2.0600	22.89
22	VAALLTTLG	62	2.0000	22.22
23	LVLVLVPGI	133	2.0000	22.22
24	IILLGLLWY	219	1.8000	20.00
25	LIGIIANAA	400	1.7000	18.89
26	LIMVLSASA	71	1.6000	17.78
27	LRVFLSSLA	232	1.6000	17.78
28	VIGLLPVTG	373	1.5800	17.56
29	LIIAVAALL	58	1.5600	17.33
30	IMVLSASAV	72	1.5000	16.67
31	VMLVLVLVP	131	1.5000	16.67
32	IGKEANGSR	141	1.5000	16.67
33	LIPLVPAAV	191	1.5000	16.67
34	YTGMRIASR	337	1.5000	16.67
35	VRFMRRIAF	115	1.4800	16.44
36	VLSASAVRS	74	1.3800	15.33
37	FINIGYVIG	367	1.3800	15.33
38	MQPSELAKM	159	1.3000	14.44
39	IVAQPDLGQ	205	1.3000	14.44
40	VRRSVHHGA	493	1.3000	14.44
41	FVVAGFSMQ	152	1.1000	12.22
42	LRLPLPEPY	430	1.1000	12.22
43	LLTTLGLIM	65	1.0000	11.11
44	VVAGFSMQP	153	1.0000	11.11
45	WGAHLLAAR	172	1.0000	11.11
46	VLWTLVGLI	97	0.9000	10.00
47	LVGALGLLG	322	0.9000	10.00
48	VVALALIVA	199	0.8800	9.78
49	VFLSSLAAV	234	0.8000	8.89
50	LLTATTTLW	353	0.8000	8.89
51	VRALEGQRY	514	0.8000	8.89
52	LIVAQPDLG	204	0.7000	7.78

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	LRVFLSSLA	232	5.2000	59.09
2	LIMVLSASA	71	4.0000	45.45
3	LGLIMVLSA	69	3.8000	43.18
4	LRLLTATTT	351	3.4000	38.64
5	IGIIANAAR	401	3.4000	38.64
6	LVLVLVPGI	133	3.2000	36.36
7	LIGIIANAA	400	3.1000	35.23
8	IGLLPVTGL	374	2.8000	31.82
9	IVMLVLVLV	130	2.6000	29.55
10	VMLVLVLVP	131	2.5000	28.41
11	IMVLSASAV	72	2.4000	27.27
12	MVLSASAVR	73	2.4000	27.27
13	MRRIAFSGF	118	2.4000	27.27
14	FLRLLTATT	350	2.4000	27.27
15	LGRPMTSFH	49	2.3800	27.05
16	VAALLTTLG	62	2.3000	26.14
17	LLTATTTLW	353	2.3000	26.14
18	LVPAAVVAL	194	2.2000	25.00
19	VVALALIVA	199	2.0800	23.64
20	VVVSAAILA	242	1.9800	22.50
21	LAAVVVSAA	239	1.9000	21.59
22	LVLVPGIGK	135	1.8800	21.36
23	FHLIIAVAA	56	1.8000	20.45
24	VLSASAVRS	74	1.8000	20.45
25	IVAQPDLGQ	205	1.8000	20.45
26	VVSAAILAV	243	1.8000	20.45
27	LIPLVPAAV	191	1.7000	19.32
28	LIIAVAALL	58	1.6000	18.18
29	FVVAGFSMQ	152	1.5000	17.05
30	WNYLPNAHN	301	1.5000	17.05

31	VRFMRRIAF	115	1.4800	16.82
32	VALALIVAQ	200	1.3000	14.77
33	IILLGLLWY	219	1.3000	14.77
34	LGLVGALGL	320	1.3000	14.77
35	VRSWLNPEN	260	1.2500	14.20
36	VIGLLPVTG	373	1.2000	13.64
37	MLIPLVPAA	190	1.1000	12.50
38	LREMLIPLV	187	1.0000	11.36
39	LGQTVSMGI	211	1.0000	11.36
40	LLGLFGLFA	328	1.0000	11.36
41	VGLIGGYVC	102	0.9000	10.23
42	LFGLFAYTG	331	0.8000	9.09
43	IIAVAALLT	59	0.7000	7.95
44	VAGFSMQPS	154	0.6000	6.82
45	LTATTTLWV	354	0.6000	6.82
46	LLRRGTSDT	4	0.5000	5.68
47	YVCLRMSVR	108	0.5000	5.68
48	FAITIVMLV	126	0.5000	5.68
49	VRALEGQRY	514	0.5000	5.68
50	VRSYDDDGS	80	0.4000	4.55
51	FSMQPSELA	157	0.4000	4.55
52	VPAAVVALA	195	0.4000	4.55

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	FAITIVMLV	126	3.2000	37.21
2	FLRLLTATT	350	3.2000	37.21
3	FSMQPSELA	157	3.1000	36.05
4	LGLIMVLSA	69	2.9000	33.72
5	MVLSASAVR	73	2.9000	33.72
6	FHLIIAVAA	56	2.6800	31.16
7	YRSDRVRSW	255	2.5000	29.07

8	VVVSAAILA	242	2.4800	28.84
9	WNYLPNAHN	301	2.3000	26.74
10	IGIIANAAR	401	2.1000	24.42
11	IVAQPDLGQ	205	2.0000	23.26
12	FVVAGFSMQ	152	1.8000	20.93
13	LGQTVSMGI	211	1.7000	19.77
14	LRLLTATTT	351	1.7000	19.77
15	LIGIIANAA	400	1.7000	19.77
16	LIMVLSASA	71	1.6000	18.60
17	LRVFLSSLA	232	1.6000	18.60
18	LTATTTLWV	354	1.6000	18.60
19	IVMLVLVLV	130	1.5800	18.37
20	WLNPENDPQ	263	1.4000	16.28
21	LVPAAVVAL	194	1.3800	16.05
22	FLSSLAAVV	235	1.3000	15.12
23	VRRSVHHGA	493	1.3000	15.12
24	VVSAAILAV	243	1.2000	13.95
25	LVLVLVPGI	133	1.1000	12.79
26	IGLLPVTGL	374	1.1000	12.79
27	VLSASAVRS	74	0.9800	11.40
28	VVALALIVA	199	0.8800	10.23
29	LLTATTTLW	353	0.8000	9.30
30	LIIAVAALL	58	0.6000	6.98
31	VAALLTTLG	62	0.6000	6.98
32	YVCLRMSVR	108	0.6000	6.98
33	IMVLSASAV	72	0.5000	5.81
34	VMLVLVLVP	131	0.5000	5.81
35	LIPLVPAAV	191	0.5000	5.81
36	IILLGLLWY	219	0.5000	5.81
37	VALALIVAQ	200	0.4800	5.58
38	MRRIAFSGF	118	0.4000	4.65
39	YLPNAHNDF	303	0.4000	4.65
40	LGRPMTSFH	49	0.3800	4.42
41	LLGLFGLFA	328	0.2000	2.33

42	VIGLLPVTG	373	0.1800	2.09
43	MLIPLVPAA	190	0.1000	1.16
44	FINIGYVIG	367	-0.0200	0
45	MQPSELAKM	159	-0.2000	0
46	VFLSSLAAV	234	-0.2000	0
47	LRLPLPEPY	430	-0.2000	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	WVIFGKQVL	90	7.2000	62.07
2	LGLVGALGL	320	7.0000	60.34
3	FAITIVMLV	126	6.8000	58.62
4	LGQTVSMGI	211	6.7000	57.76
5	LVPAAVVAL	194	6.5000	56.03
6	LVLVLVPGI	133	6.3000	54.31
7	LLPVTGLQL	376	6.2000	53.45
8	INIGYVIGL	368	6.1000	52.59
9	WFVVAGFSM	151	5.7000	49.14
10	VVVSAAILA	242	5.5000	47.41
11	LIIAVAALL	58	5.0000	43.10
12	LLTTLGLIM	65	5.0000	43.10
13	VRFMRRIAF	115	5.0000	43.10
14	VVSAAILAV	243	5.0000	43.10
15	VLWTLVGLI	97	4.9000	42.24
16	MRRIAFSGF	118	4.7000	40.52
17	FAIWGAHLL	169	4.7000	40.52
18	FLSSLAAVV	235	4.7000	40.52
19	MGIILLGLL	217	4.6000	39.66
20	IFAIIGEEL	312	4.6000	39.66
21	LTATTTLWV	354	4.5200	38.97
22	FHLIIAVAA	56	4.5000	38.79
23	IVMLVLVLV	130	4.4000	37.93

24	LRMSVRFMR	111	4.3000	37.07
25	LGLLGLFGL	326	4.3000	37.07
26	VNRLLRLPL	426	4.2000	36.21
27	ITIVMLVLV	128	4.1000	35.34
28	LLWYAGLPL	224	4.1000	35.34
29	IGLLPVTGL	374	4.1000	35.34
30	LGLIMVLSA	69	3.9000	33.62
31	VMLVLVLVP	131	3.7000	31.90
32	LVLVPGIGK	135	3.7000	31.90
33	VLGQAFINI	362	3.7000	31.90
34	IIAVAALLT	59	3.6000	31.03
35	FGLFAYTGM	332	3.6000	31.03
36	WVLGQAFIN	361	3.6000	31.03
37	WYAGLPLRV	226	3.5000	30.17
38	LFAYTGMRI	334	3.5000	30.17
39	VRRSVHHGA	493	3.5000	30.17
40	MVLSASAVR	73	3.4000	29.31
41	VFLSSLAAV	234	3.4000	29.31
42	VGALGLLGL	323	3.4000	29.31
43	VCLRMSVRF	109	3.2000	27.59
44	MQPSELAKM	159	3.1000	26.72
45	LIMVLSASA	71	3.0000	25.86
46	IGGYVCLRM	105	3.0000	25.86
47	LGLFGLFAY	329	3.0000	25.86
48	FGKQVLWTL	93	2.9000	25.00
49	LRVFLSSLA	232	2.9000	25.00
50	YLPNAHNDF	303	2.9000	25.00
51	WTLVGLIGG	99	2.8000	24.14
52	LIGIIANAA	400	2.8000	24.14

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	WVIFGKQVL	90	7.2000	62.07
2	LGLVGALGL	320	7.0000	60.34
3	FAITIVMLV	126	6.8000	58.62
4	LGQTVSMGI	211	6.7000	57.76
5	LVPAAVVAL	194	6.5000	56.03
6	LVLVLVPGI	133	6.3000	54.31
7	LLPVTGLQL	376	6.2000	53.45
8	INIGYVIGL	368	6.1000	52.59
9	WFVVAGFSM	151	5.7000	49.14
10	VVVSAAILA	242	5.5000	47.41
11	LIIAVAALL	58	5.0000	43.10
12	LLTTLGLIM	65	5.0000	43.10
13	VRFMRRIAF	115	5.0000	43.10
14	VVSAAILAV	243	5.0000	43.10
15	VLWTLVGLI	97	4.9000	42.24
16	MRRIAFSGF	118	4.7000	40.52
17	FAIWGAHLL	169	4.7000	40.52
18	FLSSLAAVV	235	4.7000	40.52
19	MGIILLGLL	217	4.6000	39.66
20	IFAIIGEEL	312	4.6000	39.66
21	LTATTTLWV	354	4.5200	38.97
22	FHLIIAVAA	56	4.5000	38.79
23	IVMLVLVLV	130	4.4000	37.93
24	LRMSVRFMR	111	4.3000	37.07
25	LGLLGLFGL	326	4.3000	37.07
26	VNRLLRLPL	426	4.2000	36.21
27	ITIVMLVLV	128	4.1000	35.34
28	LLWYAGLPL	224	4.1000	35.34
29	IGLLPVTGL	374	4.1000	35.34
30	LGLIMVLSA	69	3.9000	33.62
31	VMLVLVLVP	131	3.7000	31.90
32	LVLVPGIGK	135	3.7000	31.90
33	VLGQAFINI	362	3.7000	31.90
34	IIAVAALLT	59	3.6000	31.03

35	FGLFAYTGM	332	3.6000	31.03
36	WVLGQAFIN	361	3.6000	31.03
37	WYAGLPLRV	226	3.5000	30.17
38	LFAYTGMRI	334	3.5000	30.17
39	VRRSVHHGA	493	3.5000	30.17
40	MVLSASAVR	73	3.4000	29.31
41	VFLSSLAAV	234	3.4000	29.31
42	VGALGLLGL	323	3.4000	29.31
43	VCLRMSVRF	109	3.2000	27.59
44	MQPSELAKM	159	3.1000	26.72
45	LIMVLSASA	71	3.0000	25.86
46	IGGYVCLRM	105	3.0000	25.86
47	LGLFGLFAY	329	3.0000	25.86
48	FGKQVLWTL	93	2.9000	25.00
49	LRVFLSSLA	232	2.9000	25.00
50	YLPNAHNDF	303	2.9000	25.00
51	WTLVGLIGG	99	2.8000	24.14
52	LIGIIANAA	400	2.8000	24.14

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	WVIFGKQVL	90	4.2000	48.84
2	VRFMRRIAF	115	3.5000	40.70
3	FMRRIAFSG	117	3.5000	40.70
4	FIFAIIGEE	311	3.4000	39.53
5	MRIASRSAD	340	3.4000	39.53
6	FRDRKRANP	446	3.3000	38.37
7	IFGKQVLWT	92	2.9000	33.72
8	FLRLLTATT	350	2.9000	33.72
9	YQARQAKFA	275	2.7000	31.40
10	IGGYVCLRM	105	2.3000	26.74
11	LVLVLVPGI	133	2.3000	26.74

12	WNYLPNAHN	301	2.3000	26.74
13	VLTRLLRRG	0	2.2000	25.58
14	LLRRGTSDT	4	2.2000	25.58
15	IVMLVLVLV	130	1.9000	22.09
16	YRSDRVRSW	255	1.9000	22.09
17	VNRLLRLPL	426	1.9000	22.09
18	IILLGLLWY	219	1.8000	20.93
19	WVLGQAFIN	361	1.8000	20.93
20	LGLIMVLSA	69	1.7000	19.77
21	LIMVLSASA	71	1.7000	19.77
22	LIIAVAALL	58	1.6000	18.60
23	VLVLVPGIG	134	1.5000	17.44
24	LVPAAVVAL	194	1.5000	17.44
25	VMLVLVLVP	131	1.4000	16.28
26	VVSAAILAV	243	1.3000	15.12
27	YTGMRIASR	337	1.3000	15.12
28	YVIGLLPVT	372	1.3000	15.12
29	FVVAGFSMQ	152	1.2000	13.95
30	LIPLVPAAV	191	1.2000	13.95
31	VVALALIVA	199	1.2000	13.95
32	LLWYAGLPL	224	1.2000	13.95
33	FHLIIAVAA	56	1.0000	11.63
34	WTLVGLIGG	99	1.0000	11.63
35	VCLRMSVRF	109	1.0000	11.63
36	FAITIVMLV	126	1.0000	11.63
37	VLVPGIGKE	136	1.0000	11.63
38	MGIILLGLL	217	1.0000	11.63
39	VALALIVAQ	200	0.9000	10.47
40	LFAYTGMRI	334	0.9000	10.47
41	LPLRVFLSS	230	0.8000	9.30
42	LRVFLSSLA	232	0.8000	9.30
43	IIANAARHE	403	0.8000	9.30
44	LRMSVRFMR	111	0.7000	8.14
45	WFVVAGFSM	151	0.7000	8.14

46	INIGYVIGL	368	0.7000	8.14
47	VIGLLPVTG	373	0.7000	8.14
48	MLVLVLVPG	132	0.6000	6.98
49	FAIWGAHLL	169	0.6000	6.98
50	LVGALGLLG	322	0.6000	6.98
51	LTRLLRRGT	1	0.5000	5.81
52	LREMLIPLV	187	0.5000	5.81

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	WVIFGKQVL	90	3.2000	40.00
2	FRDRKRANP	446	2.9000	36.25
3	YQARQAKFA	275	2.7000	33.75
4	VRFMRRIAF	115	2.6000	32.50
5	FMRRIAFSG	117	2.2000	27.50
6	LVLVLVPGI	133	2.1000	26.25
7	IFGKQVLWT	92	2.0000	25.00
8	FLRLLTATT	350	2.0000	25.00
9	LGLIMVLSA	69	1.7000	21.25
10	LIMVLSASA	71	1.7000	21.25
11	IVMLVLVLV	130	1.6000	20.00
12	LLRRGTSDT	4	1.3000	16.25
13	YTGMRIASR	337	1.3000	16.25
14	IGGYVCLRM	105	1.2000	15.00
15	VVALALIVA	199	1.2000	15.00
16	FHLIIAVAA	56	1.0000	12.50
17	VMLVLVLVP	131	1.0000	12.50
18	VVSAAILAV	243	1.0000	12.50
19	YRSDRVRSW	255	1.0000	12.50
20	VLTRLLRRG	0	0.9000	11.25
21	LIPLVPAAV	191	0.9000	11.25
22	VNRLLRLPL	426	0.9000	11.25

23	LPLRVFLSS	230	0.8000	10.00
24	LRVFLSSLA	232	0.8000	10.00
25	LRMSVRFMR	111	0.7000	8.75
26	FAITIVMLV	126	0.7000	8.75
27	IILLGLLWY	219	0.7000	8.75
28	LFAYTGMRI	334	0.7000	8.75
29	MRIASRSAD	340	0.7000	8.75
30	LIIAVAALL	58	0.6000	7.50
31	LVLVPGIGK	135	0.6000	7.50
32	MLIPLVPAA	190	0.5000	6.25
33	LVPAAVVAL	194	0.5000	6.25
34	FVVAGFSMQ	152	0.4000	5.00
35	FIFAIIGEE	311	0.4000	5.00
36	YVIGLLPVT	372	0.4000	5.00
37	WNYLPNAHN	301	0.3000	3.75
38	VLVLVPGIG	134	0.2000	2.50
39	LREMLIPLV	187	0.2000	2.50
40	LLWYAGLPL	224	0.2000	2.50
41	LVGLIGGYV	101	0.1000	1.25
42	VCLRMSVRF	109	0.1000	1.25
43	VALALIVAQ	200	0.1000	1.25
44	LLGLFGLFA	328	-0.1000	0
45	VRRSVHHGA	493	-0.1000	0
46	VLSASAVRS	74	-0.2000	0
47	VVVSAAILA	242	-0.2000	0
48	WVLGQAFIN	361	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFMRRIAF	115	3.6000	45.00
2	LVLVLVPGI	133	3.1000	38.75
3	IFGKQVLWT	92	3.0000	37.50

4	LGLIMVLSA	69	2.7000	33.75
5	LIMVLSASA	71	2.7000	33.75
6	IVMLVLVLV	130	2.6000	32.50
7	LLRRGTSDT	4	2.3000	28.75
8	WVIFGKQVL	90	2.2000	27.50
9	IGGYVCLRM	105	2.2000	27.50
10	VVALALIVA	199	2.2000	27.50
11	VMLVLVLVP	131	2.0000	25.00
12	VVSAAILAV	243	2.0000	25.00
13	VLTRLLRRG	0	1.9000	23.75
14	LIPLVPAAV	191	1.9000	23.75
15	VNRLLRLPL	426	1.9000	23.75
16	FRDRKRANP	446	1.9000	23.75
17	LPLRVFLSS	230	1.8000	22.50
18	LRVFLSSLA	232	1.8000	22.50
19	LRMSVRFMR	111	1.7000	21.25
20	IILLGLLWY	219	1.7000	21.25
21	YQARQAKFA	275	1.7000	21.25
22	LFAYTGMRI	334	1.7000	21.25
23	MRIASRSAD	340	1.7000	21.25
24	LIIAVAALL	58	1.6000	20.00
25	LVLVPGIGK	135	1.6000	20.00
26	MLIPLVPAA	190	1.5000	18.75
27	LVPAAVVAL	194	1.5000	18.75
28	FMRRIAFSG	117	1.2000	15.00
29	VLVLVPGIG	134	1.2000	15.00
30	LREMLIPLV	187	1.2000	15.00
31	LLWYAGLPL	224	1.2000	15.00
32	LVGLIGGYV	101	1.1000	13.75
33	VCLRMSVRF	109	1.1000	13.75
34	VALALIVAQ	200	1.1000	13.75
35	MVLSASAVR	73	1.0000	12.50
36	MGIILLGLL	217	1.0000	12.50
37	FLRLLTATT	350	1.0000	12.50

38	MGLPPRPGS	477	1.0000	12.50
39	LLGLFGLFA	328	0.9000	11.25
40	VRRSVHHGA	493	0.9000	11.25
41	VLSASAVRS	74	0.8000	10.00
42	VVVSAAILA	242	0.8000	10.00
43	MSVRFMRRI	113	0.7000	8.75
44	LLAARRMER	176	0.7000	8.75
45	VPAAVVALA	195	0.7000	8.75
46	INIGYVIGL	368	0.7000	8.75
47	IGIIANAAR	401	0.7000	8.75
48	LTRLLRRGT	1	0.6000	7.50
49	VSAAILAVS	244	0.6000	7.50
50	VRSYDDDGS	80	0.5000	6.25
51	LIGGYVCLR	104	0.5000	6.25
52	LGLVGALGL	320	0.5000	6.25

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	VRFMRRIAF	115	4.5000	52.33
2	MRIASRSAD	340	4.4000	51.16
3	IFGKQVLWT	92	3.9000	45.35
4	IGGYVCLRM	105	3.3000	38.37
5	LVLVLVPGI	133	3.3000	38.37
6	VLTRLLRRG	0	3.2000	37.21
7	LLRRGTSDT	4	3.2000	37.21
8	WVIFGKQVL	90	3.2000	37.21
9	IVMLVLVLV	130	2.9000	33.72
10	VNRLLRLPL	426	2.9000	33.72
11	IILLGLLWY	219	2.8000	32.56
12	LGLIMVLSA	69	2.7000	31.40
13	LIMVLSASA	71	2.7000	31.40
14	LIIAVAALL	58	2.6000	30.23

15	FMRRIAFSG	117	2.5000	29.07
16	VLVLVPGIG	134	2.5000	29.07
17	LVPAAVVAL	194	2.5000	29.07
18	VMLVLVLVP	131	2.4000	27.91
19	FIFAIIGEE	311	2.4000	27.91
20	VVSAAILAV	243	2.3000	26.74
21	FRDRKRANP	446	2.3000	26.74
22	LIPLVPAAV	191	2.2000	25.58
23	VVALALIVA	199	2.2000	25.58
24	LLWYAGLPL	224	2.2000	25.58
25	VCLRMSVRF	109	2.0000	23.26
26	VLVPGIGKE	136	2.0000	23.26
27	MGIILLGLL	217	2.0000	23.26
28	VALALIVAQ	200	1.9000	22.09
29	LFAYTGMRI	334	1.9000	22.09
30	FLRLLTATT	350	1.9000	22.09
31	LPLRVFLSS	230	1.8000	20.93
32	LRVFLSSLA	232	1.8000	20.93
33	IIANAARHE	403	1.8000	20.93
34	LRMSVRFMR	111	1.7000	19.77
35	YQARQAKFA	275	1.7000	19.77
36	INIGYVIGL	368	1.7000	19.77
37	VIGLLPVTG	373	1.7000	19.77
38	MLVLVLVPG	132	1.6000	18.60
39	LVGALGLLG	322	1.6000	18.60
40	LTRLLRRGT	1	1.5000	17.44
41	LREMLIPLV	187	1.5000	17.44
42	MLIPLVPAA	190	1.5000	17.44
43	LGLVGALGL	320	1.5000	17.44
44	LGLLGLFGL	326	1.5000	17.44
45	LSLIGIIAN	398	1.5000	17.44
46	LVGLIGGYV	101	1.4000	16.28
47	MQPSELAKM	159	1.4000	16.28
48	LGLFGLFAY	329	1.4000	16.28

49	WNYLPNAHN	301	1.3000	15.12
50	VRSWLNPEN	260	1.2000	13.95
51	LRLLTATTT	351	1.2000	13.95
52	VAALRAGRD	415	1.2000	13.95

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	WVIFGKQVL	90	4.2000	48.28
2	VRFMRRIAF	115	3.4800	40.00
3	LLRRGTSDT	4	3.1000	35.63
4	FMRRIAFSG	117	3.0500	35.06
5	FRDRKRANP	446	2.9000	33.33
6	IFGKQVLWT	92	2.6000	29.89
7	IVMLVLVLV	130	2.6000	29.89
8	LRVFLSSLA	232	2.6000	29.89
9	MRIASRSAD	340	2.5000	28.74
10	LGLIMVLSA	69	2.3000	26.44
11	LVLVLVPGI	133	2.3000	26.44
12	FVVAGFSMQ	152	2.2000	25.29
13	YQARQAKFA	275	2.2000	25.29
14	LRLLTATTT	351	2.1000	24.14
15	VVALALIVA	199	2.0800	23.91
16	WLGRPMTSF	48	2.0000	22.99
17	FHLIIAVAA	56	2.0000	22.99
18	FLRLLTATT	350	2.0000	22.99
19	IGGYVCLRM	105	1.8000	20.69
20	IGLLPVTGL	374	1.8000	20.69
21	LIMVLSASA	71	1.7000	19.54
22	FAITIVMLV	126	1.7000	19.54
23	LFAYTGMRI	334	1.7000	19.54
24	VMLVLVLVP	131	1.6000	18.39
25	VVSAAILAV	243	1.6000	18.39

26	LRMSVRFMR	111	1.5500	17.82
27	LVPAAVVAL	194	1.5000	17.24
28	VNRLLRLPL	426	1.5000	17.24
29	LVLVPGIGK	135	1.4800	17.01
30	YVCLRMSVR	108	1.4000	16.09
31	LPLRVFLSS	230	1.4000	16.09
32	IILLGLLWY	219	1.3000	14.94
33	YTGMRIASR	337	1.3000	14.94
34	LIGIIANAA	400	1.3000	14.94
35	IMVLSASAV	72	1.1000	12.64
36	VCLRMSVRF	109	1.1000	12.64
37	VALALIVAQ	200	1.1000	12.64
38	LAAVVVSAA	239	1.0000	11.49
39	LIPLVPAAV	191	0.9000	10.34
40	YLPNAHNDF	303	0.9000	10.34
41	VLSASAVRS	74	0.8000	9.20
42	FSGFAITIV	123	0.8000	9.20
43	LLWYAGLPL	224	0.8000	9.20
44	VRSYDDDGS	80	0.7000	8.05
45	LLAARRMER	176	0.7000	8.05
46	MLIPLVPAA	190	0.7000	8.05
47	YRSDRVRSW	255	0.7000	8.05
48	VVVSAAILA	242	0.6800	7.82
49	WVLGQAFIN	361	0.6500	7.47
50	VLTRLLRRG	0	0.6000	6.90
51	LIIAVAALL	58	0.6000	6.90
52	FGLFAYTGM	332	0.6000	6.90

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	VRFMRRIAF	115	5.1000	50.50
2	IFGKQVLWT	92	4.7000	46.53

3	WVIFGKQVL	90	4.3000	42.57
4	IGGYVCLRM	105	4.1000	40.59
5	FMRRIAFSG	117	4.0000	39.60
6	VNRLLRLPL	426	3.7000	36.63
7	IILLGLLWY	219	3.6000	35.64
8	LGLIMVLSA	69	3.5000	34.65
9	FIFAIIGEE	311	3.5000	34.65
10	LVLVLVPGI	133	3.4500	34.16
11	MRIASRSAD	340	3.4000	33.66
12	YQARQAKFA	275	3.3000	32.67
13	FRDRKRANP	446	3.3000	32.67
14	VMLVLVLVP	131	3.2000	31.68
15	VVSAAILAV	243	3.1000	30.69
16	LLWYAGLPL	224	3.0000	29.70
17	FLRLLTATT	350	2.9000	28.71
18	VVALALIVA	199	2.8000	27.72
19	WTLVGLIGG	99	2.6000	25.74
20	FAITIVMLV	126	2.6000	25.74
21	LPLRVFLSS	230	2.6000	25.74
22	LFAYTGMRI	334	2.5000	24.75
23	YVIGLLPVT	372	2.4500	24.26
24	VLTRLLRRG	0	2.4000	23.76
25	IVMLVLVLV	130	2.4000	23.76
26	LVGALGLLG	322	2.4000	23.76
27	WNYLPNAHN	301	2.3000	22.77
28	LGLVGALGL	320	2.3000	22.77
29	WVLGQAFIN	361	2.3000	22.77
30	INIGYVIGL	368	2.3000	22.77
31	LLRRGTSDT	4	2.2000	21.78
32	YRSDRVRSW	255	2.1000	20.79
33	LSLIGIIAN	398	2.1000	20.79
34	LVPAAVVAL	194	2.0000	19.80
35	VGALGLLGL	323	1.9000	18.81
36	LIMVLSASA	71	1.7000	16.83

37	LLGLFGLFA	328	1.7000	16.83
38	LREMLIPLV	187	1.6500	16.34
39	MLIPLVPAA	190	1.6500	16.34
40	LIIAVAALL	58	1.6000	15.84
41	IIAVAALLT	59	1.6000	15.84
42	VLVLVPGIG	134	1.6000	15.84
43	VSMGIILLG	215	1.6000	15.84
44	FHLIIAVAA	56	1.5000	14.85
45	VCLRMSVRF	109	1.5000	14.85
46	LVLVPGIGK	135	1.5000	14.85
47	WYAGLPLRV	226	1.5000	14.85
48	VALALIVAQ	200	1.4000	13.86
49	VVVSAAILA	242	1.4000	13.86
50	LLPVTGLQL	376	1.4000	13.86
51	VRSWLNPEN	260	1.3500	13.37
52	FAIWGAHLL	169	1.3000	12.87

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	LGLIMVLSA	69	4.1000	49.40
2	VRFMRRIAF	115	3.8000	45.78
3	LVLVLVPGI	133	3.3500	40.36
4	WVIFGKQVL	90	3.2000	38.55
5	VVALALIVA	199	3.2000	38.55
6	VNRLLRLPL	426	3.1000	37.35
7	VMLVLVLVP	131	2.9000	34.94
8	IILLGLLWY	219	2.9000	34.94
9	VVSAAILAV	243	2.8000	33.73
10	FAITIVMLV	126	2.7000	32.53
11	IVMLVLVLV	130	2.5000	30.12
12	FLRLLTATT	350	2.4000	28.92
13	LVLVPGIGK	135	2.3000	27.71

14	FHLIIAVAA	56	2.1000	25.30
15	LLGLFGLFA	328	2.1000	25.30
16	LIMVLSASA	71	1.8000	21.69
17	VVVSAAILA	242	1.7000	20.48
18	LRMSVRFMR	111	1.5000	18.07
19	WTLVGLIGG	99	1.4000	16.87
20	LGLVGALGL	320	1.4000	16.87
21	LLAARRMER	176	1.3000	15.66
22	LIPLVPAAV	191	1.3000	15.66
23	VGALGLLGL	323	1.3000	15.66
24	LVGALGLLG	322	1.1000	13.25
25	IFGKQVLWT	92	1.0000	12.05
26	LVPAAVVAL	194	1.0000	12.05
27	LREMLIPLV	187	0.9500	11.45
28	MLIPLVPAA	190	0.9500	11.45
29	YTGMRIASR	337	0.9000	10.84
30	VRRSVHHGA	493	0.9000	10.84
31	YVIGLLPVT	372	0.8500	10.24
32	IIAVAALLT	59	0.8000	9.64
33	IWGAHLLAA	171	0.8000	9.64
34	LRLLTATTT	351	0.8000	9.64
35	VLVLVPGIG	134	0.7000	8.43
36	MGIILLGLL	217	0.7000	8.43
37	LRVFLSSLA	232	0.7000	8.43
38	WNYLPNAHN	301	0.7000	8.43
39	MRIASRSAD	340	0.7000	8.43
40	LSLIGIIAN	398	0.7000	8.43
41	LLRLPLPEP	429	0.6500	7.83
42	MTSFHLIIA	53	0.6000	7.23
43	LIIAVAALL	58	0.6000	7.23
44	LVGLIGGYV	101	0.6000	7.23
45	VALALIVAQ	200	0.6000	7.23
46	INIGYVIGL	368	0.6000	7.23
47	WYAGLPLRV	226	0.5000	6.02

48	YRSDRVRSW	255	0.5000	6.02
49	FIFAIIGEE	311	0.5000	6.02
50	IGLLPVTGL	374	0.5000	6.02
51	LLPVTGLQL	376	0.5000	6.02
52	MGLPPRPGS	477	0.4500	5.42

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	LRMSVRFMR	111	3.6000	42.86
2	WVIFGKQVL	90	3.3000	39.29
3	VRFMRRIAF	115	3.3000	39.29
4	IVMLVLVLV	130	3.3000	39.29
5	VVSAAILAV	243	2.7000	32.14
6	LVLVLVPGI	133	2.6000	30.95
7	LGLIMVLSA	69	2.5000	29.76
8	LVPAAVVAL	194	2.5000	29.76
9	LRVFLSSLA	232	2.5000	29.76
10	VRRSVHHGA	493	2.5000	29.76
11	VNRLLRLPL	426	2.3000	27.38
12	IFGKQVLWT	92	2.2000	26.19
13	VVALALIVA	199	2.2000	26.19
14	LTRLLRRGT	1	2.1000	25.00
15	VALALIVAQ	200	2.1000	25.00
16	IILLGLLWY	219	2.1000	25.00
17	LGLFGLFAY	329	2.1000	25.00
18	MRIASRSAD	340	2.1000	25.00
19	VLSASAVRS	74	1.8000	21.43
20	MERASLREM	182	1.8000	21.43
21	MLIPLVPAA	190	1.7000	20.24
22	LGLLGLFGL	326	1.7000	20.24
23	VLTRLLRRG	0	1.6000	19.05
24	LIIAVAALL	58	1.6000	19.05

25	LIPLVPAAV	191	1.6000	19.05
26	LIMVLSASA	71	1.5000	17.86
27	VMLVLVLVP	131	1.5000	17.86
28	VVVSAAILA	242	1.5000	17.86
29	LRLLTATTT	351	1.5000	17.86
30	MVLSASAVR	73	1.4000	16.67
31	YRSDRVRSW	255	1.4000	16.67
32	LREMLIPLV	187	1.3000	15.48
33	LLGLFGLFA	328	1.3000	15.48
34	IVAQPDLGQ	205	1.2000	14.29
35	IGLLPVTGL	374	1.2000	14.29
36	MGLPPRPGS	477	1.2000	14.29
37	IGGYVCLRM	105	1.1000	13.10
38	ILLGLLWYA	220	1.1000	13.10
39	VIGLLPVTG	373	1.1000	13.10
40	MLVLVLVPG	132	1.0000	11.90
41	LLAARRMER	176	1.0000	11.90
42	LVGALGLLG	322	1.0000	11.90
43	LIGIIANAA	400	0.8000	9.52
44	MTSFHLIIA	53	0.7000	8.33
45	LVLVPGIGK	135	0.7000	8.33
46	MQPSELAKM	159	0.7000	8.33
47	IWGAHLLAA	171	0.7000	8.33
48	VPAAVVALA	195	0.7000	8.33
49	VFLSSLAAV	234	0.7000	8.33
50	FLRLLTATT	350	0.7000	8.33
51	IIANAARHE	403	0.7000	8.33
52	LLRRGTSDT	4	0.6000	7.14

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	LGLIMVLSA	69	5.1000	61.45

2	VRFMRRIAF	115	4.8000	57.83
3	LVLVLVPGI	133	4.3500	52.41
4	VVALALIVA	199	4.2000	50.60
5	VNRLLRLPL	426	4.1000	49.40
6	VMLVLVLVP	131	3.9000	46.99
7	IILLGLLWY	219	3.9000	46.99
8	VVSAAILAV	243	3.8000	45.78
9	IVMLVLVLV	130	3.5000	42.17
10	LVLVPGIGK	135	3.3000	39.76
11	LLGLFGLFA	328	3.1000	37.35
12	LIMVLSASA	71	2.8000	33.73
13	VVVSAAILA	242	2.7000	32.53
14	LRMSVRFMR	111	2.5000	30.12
15	LGLVGALGL	320	2.4000	28.92
16	LLAARRMER	176	2.3000	27.71
17	LIPLVPAAV	191	2.3000	27.71
18	VGALGLLGL	323	2.3000	27.71
19	WVIFGKQVL	90	2.2000	26.51
20	LVGALGLLG	322	2.1000	25.30
21	IFGKQVLWT	92	2.0000	24.10
22	LVPAAVVAL	194	2.0000	24.10
23	LREMLIPLV	187	1.9500	23.49
24	MLIPLVPAA	190	1.9500	23.49
25	VRRSVHHGA	493	1.9000	22.89
26	IIAVAALLT	59	1.8000	21.69
27	IWGAHLLAA	171	1.8000	21.69
28	LRLLTATTT	351	1.8000	21.69
29	FAITIVMLV	126	1.7000	20.48
30	VLVLVPGIG	134	1.7000	20.48
31	MGIILLGLL	217	1.7000	20.48
32	LRVFLSSLA	232	1.7000	20.48
33	MRIASRSAD	340	1.7000	20.48
34	LSLIGIIAN	398	1.7000	20.48
35	LLRLPLPEP	429	1.6500	19.88

36	MTSFHLIIA	53	1.6000	19.28
37	LIIAVAALL	58	1.6000	19.28
38	LVGLIGGYV	101	1.6000	19.28
39	VALALIVAQ	200	1.6000	19.28
40	INIGYVIGL	368	1.6000	19.28
41	IGLLPVTGL	374	1.5000	18.07
42	LLPVTGLQL	376	1.5000	18.07
43	MGLPPRPGS	477	1.4500	17.47
44	LTTLGLIMV	66	1.4000	16.87
45	LGLLGLFGL	326	1.4000	16.87
46	FLRLLTATT	350	1.4000	16.87
47	MVLSASAVR	73	1.3000	15.66
48	VLSASAVRS	74	1.3000	15.66
49	VGLIGGYVC	102	1.3000	15.66
50	IVAQPDLGQ	205	1.3000	15.66
51	VIGLLPVTG	373	1.3000	15.66
52	IGIIANAAR	401	1.3000	15.66

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	LGLIMVLSA	69	5.1000	61.45
2	VRFMRRIAF	115	4.8000	57.83
3	LVLVLVPGI	133	4.3500	52.41
4	VVALALIVA	199	4.2000	50.60
5	VNRLLRLPL	426	4.1000	49.40
6	VMLVLVLVP	131	3.9000	46.99
7	IILLGLLWY	219	3.9000	46.99
8	VVSAAILAV	243	3.8000	45.78
9	IVMLVLVLV	130	3.5000	42.17
10	LVLVPGIGK	135	3.3000	39.76
11	LLGLFGLFA	328	3.1000	37.35
12	LIMVLSASA	71	2.8000	33.73

13	VVVSAAILA	242	2.7000	32.53
14	LRMSVRFMR	111	2.5000	30.12
15	LGLVGALGL	320	2.4000	28.92
16	LLAARRMER	176	2.3000	27.71
17	LIPLVPAAV	191	2.3000	27.71
18	VGALGLLGL	323	2.3000	27.71
19	WVIFGKQVL	90	2.2000	26.51
20	LVGALGLLG	322	2.1000	25.30
21	IFGKQVLWT	92	2.0000	24.10
22	LVPAAVVAL	194	2.0000	24.10
23	LREMLIPLV	187	1.9500	23.49
24	MLIPLVPAA	190	1.9500	23.49
25	VRRSVHHGA	493	1.9000	22.89
26	IIAVAALLT	59	1.8000	21.69
27	IWGAHLLAA	171	1.8000	21.69
28	LRLLTATTT	351	1.8000	21.69
29	FAITIVMLV	126	1.7000	20.48
30	VLVLVPGIG	134	1.7000	20.48
31	MGIILLGLL	217	1.7000	20.48
32	LRVFLSSLA	232	1.7000	20.48
33	MRIASRSAD	340	1.7000	20.48
34	LSLIGIIAN	398	1.7000	20.48
35	LLRLPLPEP	429	1.6500	19.88
36	MTSFHLIIA	53	1.6000	19.28
37	LIIAVAALL	58	1.6000	19.28
38	LVGLIGGYV	101	1.6000	19.28
39	VALALIVAQ	200	1.6000	19.28
40	INIGYVIGL	368	1.6000	19.28
41	IGLLPVTGL	374	1.5000	18.07
42	LLPVTGLQL	376	1.5000	18.07
43	MGLPPRPGS	477	1.4500	17.47
44	LTTLGLIMV	66	1.4000	16.87
45	LGLLGLFGL	326	1.4000	16.87
46	FLRLLTATT	350	1.4000	16.87

47	MVLSASAVR	73	1.3000	15.66
48	VLSASAVRS	74	1.3000	15.66
49	VGLIGGYVC	102	1.3000	15.66
50	IVAQPDLGQ	205	1.3000	15.66
51	VIGLLPVTG	373	1.3000	15.66
52	IGIIANAAR	401	1.3000	15.66

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	LRMSVRFMR	111	4.8000	52.75
2	LVLVLVPGI	133	4.7000	51.65
3	VVVSAAILA	242	3.7000	40.66
4	LGLIMVLSA	69	3.4000	37.36
5	VRFMRRIAF	115	3.4000	37.36
6	MLIPLVPAA	190	3.4000	37.36
7	INIGYVIGL	368	3.4000	37.36
8	IVMLVLVLV	130	3.2000	35.16
9	MRIASRSAD	340	3.0700	33.74
10	YRSDRVRSW	255	3.0000	32.97
11	MGLPPRPGS	477	2.9000	31.87
12	LVPAAVVAL	194	2.8000	30.77
13	YVIGLLPVT	372	2.8000	30.77
14	MVLSASAVR	73	2.7000	29.67
15	VVALALIVA	199	2.7000	29.67
16	VRRSVHHGA	493	2.7000	29.67
17	IFGDGLGQG	289	2.6000	28.57
18	LVLVPGIGK	135	2.5000	27.47
19	VVSAAILAV	243	2.5000	27.47
20	LIMVLSASA	71	2.4000	26.37
21	VALALIVAQ	200	2.4000	26.37
22	VVAGFSMQP	153	2.3000	25.27
23	VMLVLVLVP	131	2.2000	24.18

24	VLSASAVRS	74	2.1000	23.08
25	LLAARRMER	176	2.1000	23.08
26	ILLGLLWYA	220	2.1000	23.08
27	LIGGYVCLR	104	2.0000	21.98
28	MQPSELAKM	159	2.0000	21.98
29	VFLSSLAAV	234	2.0000	21.98
30	LRLLTATTT	351	1.9000	20.88
31	WVIFGKQVL	90	1.8000	19.78
32	MGIILLGLL	217	1.8000	19.78
33	LIGIIANAA	400	1.7100	18.79
34	LREMLIPLV	187	1.7000	18.68
35	WVLGQAFIN	361	1.7000	18.68
36	VNRLLRLPL	426	1.7000	18.68
37	LRVFLSSLA	232	1.6700	18.35
38	LIIAVAALL	58	1.6000	17.58
39	IGLLPVTGL	374	1.6000	17.58
40	FHLIIAVAA	56	1.5000	16.48
41	VSMGIILLG	215	1.5000	16.48
42	IILLGLLWY	219	1.5000	16.48
43	LRLPLPEPY	430	1.5000	16.48
44	VIFGKQVLW	91	1.3000	14.29
45	LVPGIGKEA	137	1.3000	14.29
46	LLRLPLPEP	429	1.3000	14.29
47	LAAVVVSAA	239	1.2700	13.96
48	VGLIGGYVC	102	1.2500	13.74
49	ITIVMLVLV	128	1.2000	13.19
50	LIPLVPAAV	191	1.2000	13.19
51	LGLLGLFGL	326	1.2000	13.19
52	LGRPMTSFH	49	1.1500	12.64

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	WVIFGKQVL	90	4.3000	51.19
2	LRMSVRFMR	111	2.6000	30.95
3	YRSDRVRSW	255	2.4000	28.57
4	VRFMRRIAF	115	2.3000	27.38
5	IVMLVLVLV	130	2.3000	27.38
6	VVSAAILAV	243	1.7000	20.24
7	FLRLLTATT	350	1.7000	20.24
8	FMRRIAFSG	117	1.6000	19.05
9	LVLVLVPGI	133	1.6000	19.05
10	LGLIMVLSA	69	1.5000	17.86
11	FAIWGAHLL	169	1.5000	17.86
12	LVPAAVVAL	194	1.5000	17.86
13	LRVFLSSLA	232	1.5000	17.86
14	VRRSVHHGA	493	1.5000	17.86
15	YQARQAKFA	275	1.4000	16.67
16	FGAWLGRPM	45	1.3000	15.48
17	VNRLLRLPL	426	1.3000	15.48
18	IFGKQVLWT	92	1.2000	14.29
19	WGAHLLAAR	172	1.2000	14.29
20	VVALALIVA	199	1.2000	14.29
21	LTRLLRRGT	1	1.1000	13.10
22	FHLIIAVAA	56	1.1000	13.10
23	VALALIVAQ	200	1.1000	13.10
24	IILLGLLWY	219	1.1000	13.10
25	LGLFGLFAY	329	1.1000	13.10
26	MRIASRSAD	340	1.1000	13.10
27	YAGLPLRVF	227	1.0000	11.90
28	FAITIVMLV	126	0.9000	10.71
29	VLSASAVRS	74	0.8000	9.52
30	FVVAGFSMQ	152	0.8000	9.52
31	MERASLREM	182	0.8000	9.52
32	WVLGQAFIN	361	0.8000	9.52
33	FRDRKRANP	446	0.8000	9.52
34	FGKQVLWTL	93	0.7000	8.33

35	MLIPLVPAA	190	0.7000	8.33
36	LGLLGLFGL	326	0.7000	8.33
37	YTGMRIASR	337	0.7000	8.33
38	VLTRLLRRG	0	0.6000	7.14
39	LIIAVAALL	58	0.6000	7.14
40	FSMQPSELA	157	0.6000	7.14
41	LIPLVPAAV	191	0.6000	7.14
42	YVIGLLPVT	372	0.6000	7.14
43	LIMVLSASA	71	0.5000	5.95
44	VMLVLVLVP	131	0.5000	5.95
45	VVVSAAILA	242	0.5000	5.95
46	LRLLTATTT	351	0.5000	5.95
47	MVLSASAVR	73	0.4000	4.76
48	YLPNAHNDF	303	0.4000	4.76
49	LREMLIPLV	187	0.3000	3.57
50	LLGLFGLFA	328	0.3000	3.57
51	IVAQPDLGQ	205	0.2000	2.38
52	IGLLPVTGL	374	0.2000	2.38

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	WVIFGKQVL	90	5.2600	59.77
2	VRFMRRIAF	115	4.2000	47.73
3	LRMSVRFMR	111	4.1000	46.59
4	IVMLVLVLV	130	3.3000	37.50
5	FMRRIAFSG	117	3.0000	34.09
6	YAGLPLRVF	227	2.9000	32.95
7	FGAWLGRPM	45	2.8000	31.82
8	WGAHLLAAR	172	2.7000	30.68
9	VVSAAILAV	243	2.7000	30.68
10	LVLVLVPGI	133	2.5000	28.41
11	FAIWGAHLL	169	2.4600	27.95

12	LVPAAVVAL	194	2.4600	27.95
13	IILLGLLWY	219	2.4000	27.27
14	YRSDRVRSW	255	2.4000	27.27
15	LGLFGLFAY	329	2.4000	27.27
16	FLRLLTATT	350	2.4000	27.27
17	MERASLREM	182	2.3000	26.14
18	YLPNAHNDF	303	2.3000	26.14
19	VNRLLRLPL	426	2.2600	25.68
20	YTGMRIASR	337	2.2000	25.00
21	MRIASRSAD	340	2.2000	25.00
22	VLTRLLRRG	0	2.0000	22.73
23	MVLSASAVR	73	1.9000	21.59
24	IFGKQVLWT	92	1.9000	21.59
25	FAITIVMLV	126	1.9000	21.59
26	LTRLLRRGT	1	1.8000	20.45
27	FRDRKRANP	446	1.8000	20.45
28	FGKQVLWTL	93	1.6600	18.86
29	LGLLGLFGL	326	1.6600	18.86
30	IGGYVCLRM	105	1.6000	18.18
31	LIPLVPAAV	191	1.6000	18.18
32	WVLGQAFIN	361	1.6000	18.18
33	LIIAVAALL	58	1.5600	17.73
34	LGLIMVLSA	69	1.5000	17.05
35	VMLVLVLVP	131	1.5000	17.05
36	LLAARRMER	176	1.5000	17.05
37	LRVFLSSLA	232	1.5000	17.05
38	VIGLLPVTG	373	1.5000	17.05
39	VRRSVHHGA	493	1.5000	17.05
40	MLVLVLVPG	132	1.4000	15.91
41	WFVVAGFSM	151	1.4000	15.91
42	YQARQAKFA	275	1.4000	15.91
43	LVGALGLLG	322	1.4000	15.91
44	YAGQRRTRR	505	1.4000	15.91
45	LREMLIPLV	187	1.3000	14.77

46	YVIGLLPVT	372	1.3000	14.77
47	VLSASAVRS	74	1.2000	13.64
48	YVCLRMSVR	108	1.2000	13.64
49	MQPSELAKM	159	1.2000	13.64
50	VVALALIVA	199	1.2000	13.64
51	LRLLTATTT	351	1.2000	13.64
52	IGLLPVTGL	374	1.1600	13.18

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	LRMSVRFMR	111	3.6000	42.86
2	WVIFGKQVL	90	3.3000	39.29
3	VRFMRRIAF	115	3.3000	39.29
4	IVMLVLVLV	130	3.3000	39.29
5	VVSAAILAV	243	2.7000	32.14
6	LVLVLVPGI	133	2.6000	30.95
7	LGLIMVLSA	69	2.5000	29.76
8	LVPAAVVAL	194	2.5000	29.76
9	LRVFLSSLA	232	2.5000	29.76
10	VRRSVHHGA	493	2.5000	29.76
11	VNRLLRLPL	426	2.3000	27.38
12	IFGKQVLWT	92	2.2000	26.19
13	VVALALIVA	199	2.2000	26.19
14	LTRLLRRGT	1	2.1000	25.00
15	VALALIVAQ	200	2.1000	25.00
16	IILLGLLWY	219	2.1000	25.00
17	LGLFGLFAY	329	2.1000	25.00
18	MRIASRSAD	340	2.1000	25.00
19	VLSASAVRS	74	1.8000	21.43
20	MERASLREM	182	1.8000	21.43
21	MLIPLVPAA	190	1.7000	20.24
22	LGLLGLFGL	326	1.7000	20.24

23	VLTRLLRRG	0	1.6000	19.05
24	LIIAVAALL	58	1.6000	19.05
25	LIPLVPAAV	191	1.6000	19.05
26	LIMVLSASA	71	1.5000	17.86
27	VMLVLVLVP	131	1.5000	17.86
28	VVVSAAILA	242	1.5000	17.86
29	LRLLTATTT	351	1.5000	17.86
30	MVLSASAVR	73	1.4000	16.67
31	YRSDRVRSW	255	1.4000	16.67
32	LREMLIPLV	187	1.3000	15.48
33	LLGLFGLFA	328	1.3000	15.48
34	IVAQPDLGQ	205	1.2000	14.29
35	IGLLPVTGL	374	1.2000	14.29
36	MGLPPRPGS	477	1.2000	14.29
37	IGGYVCLRM	105	1.1000	13.10
38	ILLGLLWYA	220	1.1000	13.10
39	VIGLLPVTG	373	1.1000	13.10
40	MLVLVLVPG	132	1.0000	11.90
41	LLAARRMER	176	1.0000	11.90
42	LVGALGLLG	322	1.0000	11.90
43	LIGIIANAA	400	0.8000	9.52
44	MTSFHLIIA	53	0.7000	8.33
45	LVLVPGIGK	135	0.7000	8.33
46	MQPSELAKM	159	0.7000	8.33
47	IWGAHLLAA	171	0.7000	8.33
48	VPAAVVALA	195	0.7000	8.33
49	VFLSSLAAV	234	0.7000	8.33
50	FLRLLTATT	350	0.7000	8.33
51	IIANAARHE	403	0.7000	8.33
52	LLRRGTSDT	4	0.6000	7.14

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	VRFMRRIAF	115	5.7000	65.52
2	LVLVLVPGI	133	4.2500	48.85
3	IILLGLLWY	219	4.2000	48.28
4	WVIFGKQVL	90	4.1600	47.82
5	LGLIMVLSA	69	4.1000	47.13
6	VNRLLRLPL	426	4.0600	46.67
7	VMLVLVLVP	131	3.9000	44.83
8	VVSAAILAV	243	3.8000	43.68
9	FAITIVMLV	126	3.7000	42.53
10	IVMLVLVLV	130	3.5000	40.23
11	VVALALIVA	199	3.2000	36.78
12	FLRLLTATT	350	3.1000	35.63
13	LRMSVRFMR	111	3.0000	34.48
14	WTLVGLIGG	99	2.8000	32.18
15	LLAARRMER	176	2.8000	32.18
16	LVGALGLLG	322	2.5000	28.74
17	LVLVPGIGK	135	2.4000	27.59
18	YTGMRIASR	337	2.4000	27.59
19	LGLVGALGL	320	2.3600	27.13
20	LIPLVPAAV	191	2.3000	26.44
21	VGALGLLGL	323	2.2600	25.98
22	FHLIIAVAA	56	2.1000	24.14
23	VLVLVPGIG	134	2.1000	24.14
24	LLGLFGLFA	328	2.1000	24.14
25	YAGLPLRVF	227	2.0000	22.99
26	LVPAAVVAL	194	1.9600	22.53
27	LREMLIPLV	187	1.9500	22.41
28	FIFAIIGEE	311	1.9000	21.84
29	LIMVLSASA	71	1.8000	20.69
30	MVLSASAVR	73	1.8000	20.69
31	MRIASRSAD	340	1.8000	20.69
32	IGIIANAAR	401	1.8000	20.69
33	IFGKQVLWT	92	1.7000	19.54

34	WFVVAGFSM	151	1.7000	19.54
35	VVVSAAILA	242	1.7000	19.54
36	VIGLLPVTG	373	1.7000	19.54
37	MGIILLGLL	217	1.6600	19.08
38	LLRLPLPEP	429	1.6500	18.97
39	LVGLIGGYV	101	1.6000	18.39
40	IGGYVCLRM	105	1.6000	18.39
41	MLVLVLVPG	132	1.6000	18.39
42	LIIAVAALL	58	1.5600	17.93
43	INIGYVIGL	368	1.5600	17.93
44	YVIGLLPVT	372	1.5500	17.82
45	IIAVAALLT	59	1.5000	17.24
46	YVCLRMSVR	108	1.5000	17.24
47	WYAGLPLRV	226	1.5000	17.24
48	WNYLPNAHN	301	1.5000	17.24
49	LRLLTATTT	351	1.5000	17.24
50	LSLIGIIAN	398	1.5000	17.24
51	IGLLPVTGL	374	1.4600	16.78
52	LLPVTGLQL	376	1.4600	16.78

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	VRFMRRIAF	115	5.2000	59.09
2	LRMSVRFMR	111	5.1000	57.95
3	IVMLVLVLV	130	4.3000	48.86
4	WVIFGKQVL	90	4.2600	48.41
5	VVSAAILAV	243	3.7000	42.05
6	LVLVLVPGI	133	3.5000	39.77
7	LVPAAVVAL	194	3.4600	39.32
8	IILLGLLWY	219	3.4000	38.64
9	LGLFGLFAY	329	3.4000	38.64
10	MERASLREM	182	3.3000	37.50

11	VNRLLRLPL	426	3.2600	37.05
12	MRIASRSAD	340	3.2000	36.36
13	VLTRLLRRG	0	3.0000	34.09
14	MVLSASAVR	73	2.9000	32.95
15	IFGKQVLWT	92	2.9000	32.95
16	LTRLLRRGT	1	2.8000	31.82
17	LGLLGLFGL	326	2.6600	30.23
18	IGGYVCLRM	105	2.6000	29.55
19	LIPLVPAAV	191	2.6000	29.55
20	LIIAVAALL	58	2.5600	29.09
21	LGLIMVLSA	69	2.5000	28.41
22	VMLVLVLVP	131	2.5000	28.41
23	LLAARRMER	176	2.5000	28.41
24	LRVFLSSLA	232	2.5000	28.41
25	VIGLLPVTG	373	2.5000	28.41
26	VRRSVHHGA	493	2.5000	28.41
27	MLVLVLVPG	132	2.4000	27.27
28	LVGALGLLG	322	2.4000	27.27
29	LREMLIPLV	187	2.3000	26.14
30	VLSASAVRS	74	2.2000	25.00
31	MQPSELAKM	159	2.2000	25.00
32	VVALALIVA	199	2.2000	25.00
33	LRLLTATTT	351	2.2000	25.00
34	IGLLPVTGL	374	2.1600	24.55
35	IIANAARHE	403	2.1000	23.86
36	FMRRIAFSG	117	2.0000	22.73
37	VCLRMSVRF	109	1.9000	21.59
38	YAGLPLRVF	227	1.9000	21.59
39	FGAWLGRPM	45	1.8000	20.45
40	LSASAVRSY	75	1.8000	20.45
41	VRALEGQRY	514	1.8000	20.45
42	WGAHLLAAR	172	1.7000	19.32
43	MLIPLVPAA	190	1.7000	19.32
44	VFLSSLAAV	234	1.7000	19.32

45	LGQAFINIG	363	1.7000	19.32
46	LFGLFAYTG	331	1.6000	18.18
47	MGLPPRPGS	477	1.6000	18.18
48	LIMVLSASA	71	1.5000	17.05
49	LIGGYVCLR	104	1.5000	17.05
50	VVVSAAILA	242	1.5000	17.05
51	IANAARHEP	404	1.5000	17.05
52	LLRLPLPEP	429	1.5000	17.05

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	WVIFGKQVL	90	5.2600	59.77
2	VRFMRRIAF	115	4.2000	47.73
3	LRMSVRFMR	111	4.1000	46.59
4	IVMLVLVLV	130	3.3000	37.50
5	FMRRIAFSG	117	3.0000	34.09
6	YAGLPLRVF	227	2.9000	32.95
7	FGAWLGRPM	45	2.8000	31.82
8	WGAHLLAAR	172	2.7000	30.68
9	VVSAAILAV	243	2.7000	30.68
10	LVLVLVPGI	133	2.5000	28.41
11	FAIWGAHLL	169	2.4600	27.95
12	LVPAAVVAL	194	2.4600	27.95
13	IILLGLLWY	219	2.4000	27.27
14	YRSDRVRSW	255	2.4000	27.27
15	LGLFGLFAY	329	2.4000	27.27
16	FLRLLTATT	350	2.4000	27.27
17	MERASLREM	182	2.3000	26.14
18	YLPNAHNDF	303	2.3000	26.14
19	VNRLLRLPL	426	2.2600	25.68
20	YTGMRIASR	337	2.2000	25.00
21	MRIASRSAD	340	2.2000	25.00

22	VLTRLLRRG	0	2.0000	22.73
23	MVLSASAVR	73	1.9000	21.59
24	IFGKQVLWT	92	1.9000	21.59
25	FAITIVMLV	126	1.9000	21.59
26	LTRLLRRGT	1	1.8000	20.45
27	FRDRKRANP	446	1.8000	20.45
28	FGKQVLWTL	93	1.6600	18.86
29	LGLLGLFGL	326	1.6600	18.86
30	IGGYVCLRM	105	1.6000	18.18
31	LIPLVPAAV	191	1.6000	18.18
32	WVLGQAFIN	361	1.6000	18.18
33	LIIAVAALL	58	1.5600	17.73
34	LGLIMVLSA	69	1.5000	17.05
35	VMLVLVLVP	131	1.5000	17.05
36	LLAARRMER	176	1.5000	17.05
37	LRVFLSSLA	232	1.5000	17.05
38	VIGLLPVTG	373	1.5000	17.05
39	VRRSVHHGA	493	1.5000	17.05
40	MLVLVLVPG	132	1.4000	15.91
41	WFVVAGFSM	151	1.4000	15.91
42	YQARQAKFA	275	1.4000	15.91
43	LVGALGLLG	322	1.4000	15.91
44	YAGQRRTRR	505	1.4000	15.91
45	LREMLIPLV	187	1.3000	14.77
46	YVIGLLPVT	372	1.3000	14.77
47	VLSASAVRS	74	1.2000	13.64
48	YVCLRMSVR	108	1.2000	13.64
49	MQPSELAKM	159	1.2000	13.64
50	VVALALIVA	199	1.2000	13.64
51	LRLLTATTT	351	1.2000	13.64
52	IGLLPVTGL	374	1.1600	13.18

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

	2.6	

Rank	Sequence	At Position	Score	% of Highest Score
1	MRIASRSAD	340	4.8000	53.33
2	WVIFGKQVL	90	4.3000	47.78
3	VRFMRRIAF	115	4.2000	46.67
4	IIANAARHE	403	3.7000	41.11
5	LRMSVRFMR	111	3.6000	40.00
6	IVMLVLVLV	130	3.6000	40.00
7	LVPAAVVAL	194	3.5000	38.89
8	VNRLLRLPL	426	3.3000	36.67
9	IILLGLLWY	219	3.2000	35.56
10	LGLFGLFAY	329	3.2000	35.56
11	IFGKQVLWT	92	3.1000	34.44
12	LTRLLRRGT	1	3.0000	33.33
13	VVSAAILAV	243	3.0000	33.33
14	VLTRLLRRG	0	2.9000	32.22
15	MERASLREM	182	2.9000	32.22
16	VALALIVAQ	200	2.9000	32.22
17	LVLVLVPGI	133	2.8000	31.11
18	LGLLGLFGL	326	2.7000	30.00
19	LIIAVAALL	58	2.6000	28.89
20	VRSWLNPEN	260	2.6000	28.89
21	LGLIMVLSA	69	2.5000	27.78
22	LRVFLSSLA	232	2.5000	27.78
23	VRRSVHHGA	493	2.5000	27.78
24	LRLLTATTT	351	2.4000	26.67
25	VIGLLPVTG	373	2.4000	26.67
26	MLVLVLVPG	132	2.3000	25.56
27	YRSDRVRSW	255	2.3000	25.56
28	LVGALGLLG	322	2.3000	25.56
29	IGGYVCLRM	105	2.2000	24.44
30	VVALALIVA	199	2.2000	24.44
31	IGLLPVTGL	374	2.2000	24.44
32	IVAQPDLGQ	205	2.0000	22.22

33	FMRRIAFSG	117	1.9000	21.11
34	VMLVLVLVP	131	1.9000	21.11
35	LIPLVPAAV	191	1.9000	21.11
36	VLSASAVRS	74	1.8000	20.00
37	MQPSELAKM	159	1.8000	20.00
38	WVLGQAFIN	361	1.8000	20.00
39	MLIPLVPAA	190	1.7000	18.89
40	LSASAVRSY	75	1.6000	17.78
41	LREMLIPLV	187	1.6000	17.78
42	FLRLLTATT	350	1.6000	17.78
43	LGQAFINIG	363	1.6000	17.78
44	VRALEGQRY	514	1.6000	17.78
45	LLRRGTSDT	4	1.5000	16.67
46	VEGQRTGPE	23	1.5000	16.67
47	LIMVLSASA	71	1.5000	16.67
48	FAIWGAHLL	169	1.5000	16.67
49	VVVSAAILA	242	1.5000	16.67
50	VGALGLLGL	323	1.5000	16.67
51	LFGLFAYTG	331	1.5000	16.67
52	INIGYVIGL	368	1.5000	16.67

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	VRFMRRIAF	115	5.7000	65.52
2	LVLVLVPGI	133	4.2500	48.85
3	IILLGLLWY	219	4.2000	48.28
4	WVIFGKQVL	90	4.1600	47.82
5	LGLIMVLSA	69	4.1000	47.13
6	VNRLLRLPL	426	4.0600	46.67
7	VMLVLVLVP	131	3.9000	44.83
8	VVSAAILAV	243	3.8000	43.68
9	FAITIVMLV	126	3.7000	42.53

10	IVMLVLVLV	130	3.5000	40.23
11	VVALALIVA	199	3.2000	36.78
12	FLRLLTATT	350	3.1000	35.63
13	LRMSVRFMR	111	3.0000	34.48
14	WTLVGLIGG	99	2.8000	32.18
15	LLAARRMER	176	2.8000	32.18
16	LVGALGLLG	322	2.5000	28.74
17	LVLVPGIGK	135	2.4000	27.59
18	YTGMRIASR	337	2.4000	27.59
19	LGLVGALGL	320	2.3600	27.13
20	LIPLVPAAV	191	2.3000	26.44
21	VGALGLLGL	323	2.2600	25.98
22	FHLIIAVAA	56	2.1000	24.14
23	VLVLVPGIG	134	2.1000	24.14
24	LLGLFGLFA	328	2.1000	24.14
25	YAGLPLRVF	227	2.0000	22.99
26	LVPAAVVAL	194	1.9600	22.53
27	LREMLIPLV	187	1.9500	22.41
28	FIFAIIGEE	311	1.9000	21.84
29	LIMVLSASA	71	1.8000	20.69
30	MVLSASAVR	73	1.8000	20.69
31	MRIASRSAD	340	1.8000	20.69
32	IGIIANAAR	401	1.8000	20.69
33	IFGKQVLWT	92	1.7000	19.54
34	WFVVAGFSM	151	1.7000	19.54
35	VVVSAAILA	242	1.7000	19.54
36	VIGLLPVTG	373	1.7000	19.54
37	MGIILLGLL	217	1.6600	19.08
38	LLRLPLPEP	429	1.6500	18.97
39	LVGLIGGYV	101	1.6000	18.39
40	IGGYVCLRM	105	1.6000	18.39
41	MLVLVLVPG	132	1.6000	18.39
42	LIIAVAALL	58	1.5600	17.93
43	INIGYVIGL	368	1.5600	17.93

44	YVIGLLPVT	372	1.5500	17.82
45	IIAVAALLT	59	1.5000	17.24
46	YVCLRMSVR	108	1.5000	17.24
47	WYAGLPLRV	226	1.5000	17.24
48	WNYLPNAHN	301	1.5000	17.24
49	LRLLTATTT	351	1.5000	17.24
50	LSLIGIIAN	398	1.5000	17.24
51	IGLLPVTGL	374	1.4600	16.78
52	LLPVTGLQL	376	1.4600	16.78

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	WVIFGKQVL	90	3.1000	45.59
2	FLRLLTATT	350	2.4000	35.29
3	LGLIMVLSA	69	2.3000	33.82
4	VRFMRRIAF	115	2.2000	32.35
5	LVLVLVPGI	133	2.2000	32.35
6	IVMLVLVLV	130	2.0000	29.41
7	LIMVLSASA	71	1.8000	26.47
8	FHLIIAVAA	56	1.6000	23.53
9	VVALALIVA	199	1.6000	23.53
10	LIPLVPAAV	191	1.3000	19.12
11	VNRLLRLPL	426	1.3000	19.12
12	FAITIVMLV	126	1.1000	16.18
13	VMLVLVLVP	131	1.1000	16.18
14	IILLGLLWY	219	1.1000	16.18
15	LRMSVRFMR	111	1.0000	14.71
16	VVSAAILAV	243	1.0000	14.71
17	YTGMRIASR	337	0.9000	13.24
18	LVLVPGIGK	135	0.7000	10.29
19	LRVFLSSLA	232	0.7000	10.29
20	WNYLPNAHN	301	0.7000	10.29

21	MRIASRSAD	340	0.7000	10.29
22	LIIAVAALL	58	0.6000	8.82
23	VLVLVPGIG	134	0.6000	8.82
24	MGIILLGLL	217	0.6000	8.82
25	LVGLIGGYV	101	0.5000	7.35
26	LVPAAVVAL	194	0.5000	7.35
27	FVVAGFSMQ	152	0.4000	5.88
28	FIFAIIGEE	311	0.4000	5.88
29	MVLSASAVR	73	0.3000	4.41
30	YRSDRVRSW	255	0.3000	4.41
31	LLGLFGLFA	328	0.3000	4.41
32	IGIIANAAR	401	0.3000	4.41
33	VRRSVHHGA	493	0.2000	2.94
34	VALALIVAQ	200	0.1000	1.47
35	VVVSAAILA	242	0.1000	1.47
36	YAGLPLRVF	227	-0.1000	0
37	LGLLGLFGL	326	-0.1000	0
38	LWVLGQAFI	360	-0.1000	0
39	LIGIIANAA	400	-0.1000	0
40	FRDRKRANP	446	-0.1000	0
41	VLSASAVRS	74	-0.2000	0
42	VLWTLVGLI	97	-0.2000	0
43	WTLVGLIGG	99	-0.2000	0
44	LREMLIPLV	187	-0.2000	0
45	MLIPLVPAA	190	-0.2000	0
46	FLSSLAAVV	235	-0.2000	0
47	VIGLLPVTG	373	-0.2000	0
48	IMVLSASAV	72	-0.3000	0
49	MLVLVLVPG	132	-0.3000	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	LGLIMVLSA	69	5.1000	61.45
2	VRFMRRIAF	115	4.8000	57.83
3	LVLVLVPGI	133	4.3500	52.41
4	VVALALIVA	199	4.2000	50.60
5	VNRLLRLPL	426	4.1000	49.40
6	VMLVLVLVP	131	3.9000	46.99
7	IILLGLLWY	219	3.9000	46.99
8	VVSAAILAV	243	3.8000	45.78
9	IVMLVLVLV	130	3.5000	42.17
10	LVLVPGIGK	135	3.3000	39.76
11	LLGLFGLFA	328	3.1000	37.35
12	LIMVLSASA	71	2.8000	33.73
13	VVVSAAILA	242	2.7000	32.53
14	LRMSVRFMR	111	2.5000	30.12
15	LGLVGALGL	320	2.4000	28.92
16	LLAARRMER	176	2.3000	27.71
17	LIPLVPAAV	191	2.3000	27.71
18	VGALGLLGL	323	2.3000	27.71
19	WVIFGKQVL	90	2.2000	26.51
20	LVGALGLLG	322	2.1000	25.30
21	IFGKQVLWT	92	2.0000	24.10
22	LVPAAVVAL	194	2.0000	24.10
23	LREMLIPLV	187	1.9500	23.49
24	MLIPLVPAA	190	1.9500	23.49
25	VRRSVHHGA	493	1.9000	22.89
26	IIAVAALLT	59	1.8000	21.69
27	IWGAHLLAA	171	1.8000	21.69
28	LRLLTATTT	351	1.8000	21.69
29	FAITIVMLV	126	1.7000	20.48
30	VLVLVPGIG	134	1.7000	20.48
31	MGIILLGLL	217	1.7000	20.48
32	LRVFLSSLA	232	1.7000	20.48
33	MRIASRSAD	340	1.7000	20.48
34	LSLIGIIAN	398	1.7000	20.48

35	LLRLPLPEP	429	1.6500	19.88
36	MTSFHLIIA	53	1.6000	19.28
37	LIIAVAALL	58	1.6000	19.28
38	LVGLIGGYV	101	1.6000	19.28
39	VALALIVAQ	200	1.6000	19.28
40	INIGYVIGL	368	1.6000	19.28
41	IGLLPVTGL	374	1.5000	18.07
42	LLPVTGLQL	376	1.5000	18.07
43	MGLPPRPGS	477	1.4500	17.47
44	LTTLGLIMV	66	1.4000	16.87
45	LGLLGLFGL	326	1.4000	16.87
46	FLRLLTATT	350	1.4000	16.87
47	MVLSASAVR	73	1.3000	15.66
48	VLSASAVRS	74	1.3000	15.66
49	VGLIGGYVC	102	1.3000	15.66
50	IVAQPDLGQ	205	1.3000	15.66
51	VIGLLPVTG	373	1.3000	15.66
52	IGIIANAAR	401	1.3000	15.66

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	VRFMRRIAF	115	4.7000	52.81
2	WVIFGKQVL	90	4.2000	47.19
3	LGLIMVLSA	69	4.1000	46.07
4	VNRLLRLPL	426	4.1000	46.07
5	IILLGLLWY	219	4.0000	44.94
6	LVLVLVPGI	133	3.5500	39.89
7	FIFAIIGEE	311	3.5000	39.33
8	MRIASRSAD	340	3.4000	38.20
9	VMLVLVLVP	131	3.3000	37.08
10	FLRLLTATT	350	3.3000	37.08
11	VVALALIVA	199	3.2000	35.96

12	VVSAAILAV	243	3.1000	34.83
13	FAITIVMLV	126	3.0000	33.71
14	IVMLVLVLV	130	2.8000	31.46
15	WTLVGLIGG	99	2.7000	30.34
16	WNYLPNAHN	301	2.7000	30.34
17	LSLIGIIAN	398	2.7000	30.34
18	LGLVGALGL	320	2.4000	26.97
19	LVGALGLLG	322	2.4000	26.97
20	VGALGLLGL	323	2.3000	25.84
21	FHLIIAVAA	56	2.1000	23.60
22	LLGLFGLFA	328	2.1000	23.60
23	VLVLVPGIG	134	2.0000	22.47
24	LVPAAVVAL	194	2.0000	22.47
25	IFGKQVLWT	92	1.9000	21.35
26	LIMVLSASA	71	1.8000	20.22
27	YVIGLLPVT	372	1.7500	19.66
28	IIAVAALLT	59	1.7000	19.10
29	MGIILLGLL	217	1.7000	19.10
30	VVVSAAILA	242	1.7000	19.10
31	LRLLTATTT	351	1.7000	19.10
32	LIIAVAALL	58	1.6000	17.98
33	LVLVPGIGK	135	1.6000	17.98
34	LIPLVPAAV	191	1.6000	17.98
35	WVLGQAFIN	361	1.6000	17.98
36	INIGYVIGL	368	1.6000	17.98
37	VIGLLPVTG	373	1.6000	17.98
38	LRMSVRFMR	111	1.5000	16.85
39	MLVLVLVPG	132	1.5000	16.85
40	IGLLPVTGL	374	1.5000	16.85
41	LLPVTGLQL	376	1.5000	16.85
42	VALALIVAQ	200	1.4000	15.73
43	YRSDRVRSW	255	1.4000	15.73
44	LGLLGLFGL	326	1.4000	15.73
45	WFVVAGFSM	151	1.3000	14.61

46	LLAARRMER	176	1.3000	14.61
47	LREMLIPLV	187	1.2500	14.04
48	VRSWLNPEN	260	1.2500	14.04
49	IGGYVCLRM	105	1.2000	13.48
50	FVVAGFSMQ	152	1.2000	13.48
51	FAIWGAHLL	169	1.2000	13.48
52	LTRLLRRGT	1	1.1000	12.36

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	LRMSVRFMR	111	3.6000	42.86
2	WVIFGKQVL	90	3.3000	39.29
3	VRFMRRIAF	115	3.3000	39.29
4	IVMLVLVLV	130	3.3000	39.29
5	VVSAAILAV	243	2.7000	32.14
6	LVLVLVPGI	133	2.6000	30.95
7	LGLIMVLSA	69	2.5000	29.76
8	LVPAAVVAL	194	2.5000	29.76
9	LRVFLSSLA	232	2.5000	29.76
10	VRRSVHHGA	493	2.5000	29.76
11	VNRLLRLPL	426	2.3000	27.38
12	IFGKQVLWT	92	2.2000	26.19
13	VVALALIVA	199	2.2000	26.19
14	LTRLLRRGT	1	2.1000	25.00
15	VALALIVAQ	200	2.1000	25.00
16	IILLGLLWY	219	2.1000	25.00
17	LGLFGLFAY	329	2.1000	25.00
18	MRIASRSAD	340	2.1000	25.00
19	VLSASAVRS	74	1.8000	21.43
20	MERASLREM	182	1.8000	21.43
21	MLIPLVPAA	190	1.7000	20.24
22	LGLLGLFGL	326	1.7000	20.24

23	VLTRLLRRG	0	1.6000	19.05
24	LIIAVAALL	58	1.6000	19.05
25	LIPLVPAAV	191	1.6000	19.05
26	LIMVLSASA	71	1.5000	17.86
27	VMLVLVLVP	131	1.5000	17.86
28	VVVSAAILA	242	1.5000	17.86
29	LRLLTATTT	351	1.5000	17.86
30	MVLSASAVR	73	1.4000	16.67
31	YRSDRVRSW	255	1.4000	16.67
32	LREMLIPLV	187	1.3000	15.48
33	LLGLFGLFA	328	1.3000	15.48
34	IVAQPDLGQ	205	1.2000	14.29
35	IGLLPVTGL	374	1.2000	14.29
36	MGLPPRPGS	477	1.2000	14.29
37	IGGYVCLRM	105	1.1000	13.10
38	ILLGLLWYA	220	1.1000	13.10
39	VIGLLPVTG	373	1.1000	13.10
40	MLVLVLVPG	132	1.0000	11.90
41	LLAARRMER	176	1.0000	11.90
42	LVGALGLLG	322	1.0000	11.90
43	LIGIIANAA	400	0.8000	9.52
44	MTSFHLIIA	53	0.7000	8.33
45	LVLVPGIGK	135	0.7000	8.33
46	MQPSELAKM	159	0.7000	8.33
47	IWGAHLLAA	171	0.7000	8.33
48	VPAAVVALA	195	0.7000	8.33
49	VFLSSLAAV	234	0.7000	8.33
50	FLRLLTATT	350	0.7000	8.33
51	IIANAARHE	403	0.7000	8.33
52	LLRRGTSDT	4	0.6000	7.14

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	WVIFGKQVL	90	4.3000	51.19
2	LRMSVRFMR	111	2.6000	30.95
3	YRSDRVRSW	255	2.4000	28.57
4	VRFMRRIAF	115	2.3000	27.38
5	IVMLVLVLV	130	2.3000	27.38
6	VVSAAILAV	243	1.7000	20.24
7	FLRLLTATT	350	1.7000	20.24
8	FMRRIAFSG	117	1.6000	19.05
9	LVLVLVPGI	133	1.6000	19.05
10	LGLIMVLSA	69	1.5000	17.86
11	FAIWGAHLL	169	1.5000	17.86
12	LVPAAVVAL	194	1.5000	17.86
13	LRVFLSSLA	232	1.5000	17.86
14	VRRSVHHGA	493	1.5000	17.86
15	YQARQAKFA	275	1.4000	16.67
16	FGAWLGRPM	45	1.3000	15.48
17	VNRLLRLPL	426	1.3000	15.48
18	IFGKQVLWT	92	1.2000	14.29
19	WGAHLLAAR	172	1.2000	14.29
20	VVALALIVA	199	1.2000	14.29
21	LTRLLRRGT	1	1.1000	13.10
22	FHLIIAVAA	56	1.1000	13.10
23	VALALIVAQ	200	1.1000	13.10
24	IILLGLLWY	219	1.1000	13.10
25	LGLFGLFAY	329	1.1000	13.10
26	MRIASRSAD	340	1.1000	13.10
27	YAGLPLRVF	227	1.0000	11.90
28	FAITIVMLV	126	0.9000	10.71
29	VLSASAVRS	74	0.8000	9.52
30	FVVAGFSMQ	152	0.8000	9.52
31	MERASLREM	182	0.8000	9.52
32	WVLGQAFIN	361	0.8000	9.52
33	FRDRKRANP	446	0.8000	9.52

34	FGKQVLWTL	93	0.7000	8.33
35	MLIPLVPAA	190	0.7000	8.33
36	LGLLGLFGL	326	0.7000	8.33
37	YTGMRIASR	337	0.7000	8.33
38	VLTRLLRRG	0	0.6000	7.14
39	LIIAVAALL	58	0.6000	7.14
40	FSMQPSELA	157	0.6000	7.14
41	LIPLVPAAV	191	0.6000	7.14
42	YVIGLLPVT	372	0.6000	7.14
43	LIMVLSASA	71	0.5000	5.95
44	VMLVLVLVP	131	0.5000	5.95
45	VVVSAAILA	242	0.5000	5.95
46	LRLLTATTT	351	0.5000	5.95
47	MVLSASAVR	73	0.4000	4.76
48	YLPNAHNDF	303	0.4000	4.76
49	LREMLIPLV	187	0.3000	3.57
50	LLGLFGLFA	328	0.3000	3.57
51	IVAQPDLGQ	205	0.2000	2.38
52	IGLLPVTGL	374	0.2000	2.38

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	VRFMRRIAF	115	5.2000	59.09
2	LRMSVRFMR	111	5.1000	57.95
3	IVMLVLVLV	130	4.3000	48.86
4	WVIFGKQVL	90	4.2600	48.41
5	VVSAAILAV	243	3.7000	42.05
6	LVLVLVPGI	133	3.5000	39.77
7	LVPAAVVAL	194	3.4600	39.32
8	IILLGLLWY	219	3.4000	38.64
9	LGLFGLFAY	329	3.4000	38.64
10	MERASLREM	182	3.3000	37.50

11	VNRLLRLPL	426	3.2600	37.05
12	MRIASRSAD	340	3.2000	36.36
13	VLTRLLRRG	0	3.0000	34.09
14	MVLSASAVR	73	2.9000	32.95
15	IFGKQVLWT	92	2.9000	32.95
16	LTRLLRRGT	1	2.8000	31.82
17	LGLLGLFGL	326	2.6600	30.23
18	IGGYVCLRM	105	2.6000	29.55
19	LIPLVPAAV	191	2.6000	29.55
20	LIIAVAALL	58	2.5600	29.09
21	LGLIMVLSA	69	2.5000	28.41
22	VMLVLVLVP	131	2.5000	28.41
23	LLAARRMER	176	2.5000	28.41
24	LRVFLSSLA	232	2.5000	28.41
25	VIGLLPVTG	373	2.5000	28.41
26	VRRSVHHGA	493	2.5000	28.41
27	MLVLVLVPG	132	2.4000	27.27
28	LVGALGLLG	322	2.4000	27.27
29	LREMLIPLV	187	2.3000	26.14
30	VLSASAVRS	74	2.2000	25.00
31	MQPSELAKM	159	2.2000	25.00
32	VVALALIVA	199	2.2000	25.00
33	LRLLTATTT	351	2.2000	25.00
34	IGLLPVTGL	374	2.1600	24.55
35	IIANAARHE	403	2.1000	23.86
36	FMRRIAFSG	117	2.0000	22.73
37	VCLRMSVRF	109	1.9000	21.59
38	YAGLPLRVF	227	1.9000	21.59
39	FGAWLGRPM	45	1.8000	20.45
40	LSASAVRSY	75	1.8000	20.45
41	VRALEGQRY	514	1.8000	20.45
42	WGAHLLAAR	172	1.7000	19.32
43	MLIPLVPAA	190	1.7000	19.32
44	VFLSSLAAV	234	1.7000	19.32

45	LGQAFINIG	363	1.7000	19.32
46	LFGLFAYTG	331	1.6000	18.18
47	MGLPPRPGS	477	1.6000	18.18
48	LIMVLSASA	71	1.5000	17.05
49	LIGGYVCLR	104	1.5000	17.05
50	VVVSAAILA	242	1.5000	17.05
51	IANAARHEP	404	1.5000	17.05
52	LLRLPLPEP	429	1.5000	17.05

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	VRFMRRIAF	115	5.2000	59.09
2	LRMSVRFMR	111	5.1000	57.95
3	IVMLVLVLV	130	4.3000	48.86
4	WVIFGKQVL	90	4.2600	48.41
5	VVSAAILAV	243	3.7000	42.05
6	LVLVLVPGI	133	3.5000	39.77
7	LVPAAVVAL	194	3.4600	39.32
8	IILLGLLWY	219	3.4000	38.64
9	LGLFGLFAY	329	3.4000	38.64
10	MERASLREM	182	3.3000	37.50
11	VNRLLRLPL	426	3.2600	37.05
12	MRIASRSAD	340	3.2000	36.36
13	VLTRLLRRG	0	3.0000	34.09
14	MVLSASAVR	73	2.9000	32.95
15	IFGKQVLWT	92	2.9000	32.95
16	LTRLLRRGT	1	2.8000	31.82
17	LGLLGLFGL	326	2.6600	30.23
18	IGGYVCLRM	105	2.6000	29.55
19	LIPLVPAAV	191	2.6000	29.55
20	LIIAVAALL	58	2.5600	29.09
21	LGLIMVLSA	69	2.5000	28.41

22	VMLVLVLVP	131	2.5000	28.41
23	LLAARRMER	176	2.5000	28.41
24	LRVFLSSLA	232	2.5000	28.41
25	VIGLLPVTG	373	2.5000	28.41
26	VRRSVHHGA	493	2.5000	28.41
27	MLVLVLVPG	132	2.4000	27.27
28	LVGALGLLG	322	2.4000	27.27
29	LREMLIPLV	187	2.3000	26.14
30	VLSASAVRS	74	2.2000	25.00
31	MQPSELAKM	159	2.2000	25.00
32	VVALALIVA	199	2.2000	25.00
33	LRLLTATTT	351	2.2000	25.00
34	IGLLPVTGL	374	2.1600	24.55
35	IIANAARHE	403	2.1000	23.86
36	FMRRIAFSG	117	2.0000	22.73
37	VCLRMSVRF	109	1.9000	21.59
38	YAGLPLRVF	227	1.9000	21.59
39	FGAWLGRPM	45	1.8000	20.45
40	LSASAVRSY	75	1.8000	20.45
41	VRALEGQRY	514	1.8000	20.45
42	WGAHLLAAR	172	1.7000	19.32
43	MLIPLVPAA	190	1.7000	19.32
44	VFLSSLAAV	234	1.7000	19.32
45	LGQAFINIG	363	1.7000	19.32
46	LFGLFAYTG	331	1.6000	18.18
47	MGLPPRPGS	477	1.6000	18.18
48	LIMVLSASA	71	1.5000	17.05
49	LIGGYVCLR	104	1.5000	17.05
50	VVVSAAILA	242	1.5000	17.05
51	IANAARHEP	404	1.5000	17.05
52	LLRLPLPEP	429	1.5000	17.05

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

	3.25	9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LLWYAGLPL	224	6.4000	65.31
2	LFAYTGMRI	334	6.2000	63.27
3	VRFMRRIAF	115	6.1000	62.24
4	LRVFLSSLA	232	6.0000	61.22
5	VNRLLRLPL	426	5.4000	55.10
6	IGGYVCLRM	105	5.1800	52.86
7	WVIFGKQVL	90	4.9000	50.00
8	IVMLVLVLV	130	4.8000	48.98
9	LRMSVRFMR	111	4.7000	47.96
10	LGLFGLFAY	329	4.6000	46.94
11	VVSAAILAV	243	4.5500	46.43
12	LLPVTGLQL	376	4.4000	44.90
13	MTSFHLIIA	53	4.3000	43.88
14	VVALALIVA	199	4.3000	43.88
15	LGLVGALGL	320	4.1000	41.84
16	LGLLGLFGL	326	4.1000	41.84
17	LLGLFGLFA	328	4.1000	41.84
18	LVLVLVPGI	133	4.0000	40.82
19	INIGYVIGL	368	4.0000	40.82
20	LVGALGLLG	322	3.9000	39.80
21	IILLGLLWY	219	3.8000	38.78
22	VVVSAAILA	242	3.8000	38.78
23	LGLIMVLSA	69	3.7000	37.76
24	LRLLTATTT	351	3.7000	37.76
25	LVGLIGGYV	101	3.6000	36.73
26	LVLVPGIGK	135	3.6000	36.73
27	VGALGLLGL	323	3.6000	36.73
28	FGLFAYTGM	332	3.5800	36.53
29	VRSYDDDGS	80	3.5000	35.71
30	LIMVLSASA	71	3.3000	33.67
31	VGLIGGYVC	102	3.3000	33.67
32	VVAGFSMQP	153	3.3000	33.67

33	MGIILLGLL	217	3.3000	33.67
34	LGQTVSMGI	211	3.2000	32.65
35	LLTTLGLIM	65	3.1800	32.45
36	LIIAVAALL	58	3.1000	31.63
37	MRRIAFSGF	118	3.1000	31.63
38	MRIASRSAD	340	3.1000	31.63
39	IIAVAALLT	59	3.0000	30.61
40	LVPAAVVAL	194	2.9000	29.59
41	LGLLWYAGL	222	2.9000	29.59
42	YVIGLLPVT	372	2.9000	29.59
43	VMLVLVLVP	131	2.8000	28.57
44	ILLGLLWYA	220	2.8000	28.57
45	IGYVIGLLP	370	2.8000	28.57
46	IMVLSASAV	72	2.7000	27.55
47	LLAARRMER	176	2.7000	27.55
48	VRRSVHHGA	493	2.7000	27.55
49	LREMLIPLV	187	2.6500	27.04
50	LVPGIGKEA	137	2.6000	26.53
51	VRSWLNPEN	260	2.6000	26.53
52	LIGIIANAA	400	2.6000	26.53

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	WVIFGKQVL	90	5.9000	60.20
2	LLWYAGLPL	224	5.4000	55.10
3	LFAYTGMRI	334	5.2000	53.06
4	VRFMRRIAF	115	5.1000	52.04
5	LRVFLSSLA	232	5.0000	51.02
6	FGLFAYTGM	332	4.5800	46.73
7	VNRLLRLPL	426	4.4000	44.90
8	IGGYVCLRM	105	4.1800	42.65
9	YVIGLLPVT	372	3.9000	39.80

10	IVMLVLVLV	130	3.8000	38.78
11	LRMSVRFMR	111	3.7000	37.76
12	LGLFGLFAY	329	3.6000	36.73
13	VVSAAILAV	243	3.5500	36.22
14	WFVVAGFSM	151	3.4800	35.51
15	LLPVTGLQL	376	3.4000	34.69
16	MTSFHLIIA	53	3.3000	33.67
17	VVALALIVA	199	3.3000	33.67
18	WVLGQAFIN	361	3.3000	33.67
19	LGLVGALGL	320	3.1000	31.63
20	LGLLGLFGL	326	3.1000	31.63
21	LLGLFGLFA	328	3.1000	31.63
22	LVLVLVPGI	133	3.0000	30.61
23	FAIWGAHLL	169	3.0000	30.61
24	INIGYVIGL	368	3.0000	30.61
25	FAITIVMLV	126	2.9000	29.59
26	WYAGLPLRV	226	2.9000	29.59
27	LVGALGLLG	322	2.9000	29.59
28	FSGFAITIV	123	2.8500	29.08
29	IILLGLLWY	219	2.8000	28.57
30	VVVSAAILA	242	2.8000	28.57
31	FHLIIAVAA	56	2.7000	27.55
32	LGLIMVLSA	69	2.7000	27.55
33	LRLLTATTT	351	2.7000	27.55
34	LVGLIGGYV	101	2.6000	26.53
35	FMRRIAFSG	117	2.6000	26.53
36	LVLVPGIGK	135	2.6000	26.53
37	VGALGLLGL	323	2.6000	26.53
38	VRSYDDDGS	80	2.5000	25.51
39	LIMVLSASA	71	2.3000	23.47
40	VGLIGGYVC	102	2.3000	23.47
41	VVAGFSMQP	153	2.3000	23.47
42	MGIILLGLL	217	2.3000	23.47
43	LGQTVSMGI	211	2.2000	22.45

44	LLTTLGLIM	65	2.1800	22.24
45	LIIAVAALL	58	2.1000	21.43
46	WTLVGLIGG	99	2.1000	21.43
47	MRRIAFSGF	118	2.1000	21.43
48	MRIASRSAD	340	2.1000	21.43
49	FINIGYVIG	367	2.1000	21.43
50	IIAVAALLT	59	2.0000	20.41
51	YVCLRMSVR	108	2.0000	20.41
52	FLRLLTATT	350	1.9600	20.00

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	LLWYAGLPL	224	6.4000	65.31
2	LFAYTGMRI	334	6.2000	63.27
3	VRFMRRIAF	115	6.1000	62.24
4	LRVFLSSLA	232	6.0000	61.22
5	VNRLLRLPL	426	5.4000	55.10
6	IGGYVCLRM	105	5.1800	52.86
7	WVIFGKQVL	90	4.9000	50.00
8	IVMLVLVLV	130	4.8000	48.98
9	LRMSVRFMR	111	4.7000	47.96
10	LGLFGLFAY	329	4.6000	46.94
11	VVSAAILAV	243	4.5500	46.43
12	LLPVTGLQL	376	4.4000	44.90
13	MTSFHLIIA	53	4.3000	43.88
14	VVALALIVA	199	4.3000	43.88
15	LGLVGALGL	320	4.1000	41.84
16	LGLLGLFGL	326	4.1000	41.84
17	LLGLFGLFA	328	4.1000	41.84
18	LVLVLVPGI	133	4.0000	40.82
19	INIGYVIGL	368	4.0000	40.82
20	LVGALGLLG	322	3.9000	39.80

21	IILLGLLWY	219	3.8000	38.78
22	VVVSAAILA	242	3.8000	38.78
23	LGLIMVLSA	69	3.7000	37.76
24	LRLLTATTT	351	3.7000	37.76
25	LVGLIGGYV	101	3.6000	36.73
26	LVLVPGIGK	135	3.6000	36.73
27	VGALGLLGL	323	3.6000	36.73
28	FGLFAYTGM	332	3.5800	36.53
29	VRSYDDDGS	80	3.5000	35.71
30	LIMVLSASA	71	3.3000	33.67
31	VGLIGGYVC	102	3.3000	33.67
32	VVAGFSMQP	153	3.3000	33.67
33	MGIILLGLL	217	3.3000	33.67
34	LGQTVSMGI	211	3.2000	32.65
35	LLTTLGLIM	65	3.1800	32.45
36	LIIAVAALL	58	3.1000	31.63
37	MRRIAFSGF	118	3.1000	31.63
38	MRIASRSAD	340	3.1000	31.63
39	IIAVAALLT	59	3.0000	30.61
40	LVPAAVVAL	194	2.9000	29.59
41	LGLLWYAGL	222	2.9000	29.59
42	YVIGLLPVT	372	2.9000	29.59
43	VMLVLVLVP	131	2.8000	28.57
44	ILLGLLWYA	220	2.8000	28.57
45	IGYVIGLLP	370	2.8000	28.57
46	IMVLSASAV	72	2.7000	27.55
47	LLAARRMER	176	2.7000	27.55
48	VRRSVHHGA	493	2.7000	27.55
49	LREMLIPLV	187	2.6500	27.04
50	LVPGIGKEA	137	2.6000	26.53
51	VRSWLNPEN	260	2.6000	26.53
52	LIGIIANAA	400	2.6000	26.53

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	LVLVPGIGK	135	6.8000	69.39
2	LRMSVRFMR	111	4.8000	48.98
3	VRFMRRIAF	115	4.8000	48.98
4	ILAVSAGYR	248	4.2000	42.86
5	WFVVAGFSM	151	4.1000	41.84
6	MVLSASAVR	73	3.6000	36.73
7	WVIFGKQVL	90	3.5000	35.71
8	YVCLRMSVR	108	3.5000	35.71
9	LGLVGALGL	320	3.5000	35.71
10	IGIIANAAR	401	3.5000	35.71
11	VRALEGQRY	514	3.5000	35.71
12	MGIILLGLL	217	3.2000	32.65
13	YTGMRIASR	337	3.0000	30.61
14	WVLGQAFIN	361	3.0000	30.61
15	LLPVTGLQL	376	3.0000	30.61
16	LIIAVAALL	58	2.9000	29.59
17	LGLLGLFGL	326	2.9000	29.59
18	LRLLTATTT	351	2.9000	29.59
19	FHLIIAVAA	56	2.8000	28.57
20	WTLVGLIGG	99	2.7000	27.55
21	VGLIGGYVC	102	2.7000	27.55
22	FAIWGAHLL	169	2.6000	26.53
23	IILLGLLWY	219	2.6000	26.53
24	MRRIAFSGF	118	2.5000	25.51
25	LVLVLVPGI	133	2.5000	25.51
26	FALAQGGIF	282	2.5000	25.51
27	VLVLVPGIG	134	2.3000	23.47
28	YAGLPLRVF	227	2.3000	23.47
29	VVVSAAILA	242	2.3000	23.47
30	LFGLFAYTG	331	2.2000	22.45
31	LIMVLSASA	71	2.1000	21.43

32	LIGIIANAA	400	2.1000	21.43
33	LVGLIGGYV	101	2.0000	20.41
34	FMRRIAFSG	117	2.0000	20.41
35	LVGALGLLG	322	2.0000	20.41
36	FINIGYVIG	367	2.0000	20.41
37	VVALALIVA	199	1.9000	19.39
38	LGLFGLFAY	329	1.7000	17.35
39	VNRLLRLPL	426	1.7000	17.35
40	IIAVAALLT	59	1.6000	16.33
41	IVMLVLVLV	130	1.6000	16.33
42	LLAARRMER	176	1.6000	16.33
43	FVVAGFSMQ	152	1.4000	14.29
44	LGLLWYAGL	222	1.4000	14.29
45	IGLLPVTGL	374	1.4000	14.29
46	VRRSVHHGA	493	1.4000	14.29
47	FLRLLTATT	350	1.3000	13.27
48	LRLPLPEPY	430	1.3000	13.27
49	IFAIIGEEL	312	1.2000	12.24
50	VIGLLPVTG	373	1.2000	12.24
51	LPLISAGGT	384	1.2000	12.24
52	LLTTLGLIM	65	1.1000	11.22

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	LVLVPGIGK	135	6.8000	69.39
2	LRMSVRFMR	111	4.8000	48.98
3	VRFMRRIAF	115	4.8000	48.98
4	ILAVSAGYR	248	4.2000	42.86
5	WFVVAGFSM	151	4.1000	41.84
6	MVLSASAVR	73	3.6000	36.73
7	WVIFGKQVL	90	3.5000	35.71
8	YVCLRMSVR	108	3.5000	35.71

9	LGLVGALGL	320	3.5000	35.71
10	IGIIANAAR	401	3.5000	35.71
11	VRALEGQRY	514	3.5000	35.71
12	MGIILLGLL	217	3.2000	32.65
13	YTGMRIASR	337	3.0000	30.61
14	WVLGQAFIN	361	3.0000	30.61
15	LLPVTGLQL	376	3.0000	30.61
16	LIIAVAALL	58	2.9000	29.59
17	LGLLGLFGL	326	2.9000	29.59
18	LRLLTATTT	351	2.9000	29.59
19	FHLIIAVAA	56	2.8000	28.57
20	WTLVGLIGG	99	2.7000	27.55
21	VGLIGGYVC	102	2.7000	27.55
22	FAIWGAHLL	169	2.6000	26.53
23	IILLGLLWY	219	2.6000	26.53
24	MRRIAFSGF	118	2.5000	25.51
25	LVLVLVPGI	133	2.5000	25.51
26	FALAQGGIF	282	2.5000	25.51
27	VLVLVPGIG	134	2.3000	23.47
28	YAGLPLRVF	227	2.3000	23.47
29	VVVSAAILA	242	2.3000	23.47
30	LFGLFAYTG	331	2.2000	22.45
31	LIMVLSASA	71	2.1000	21.43
32	LIGIIANAA	400	2.1000	21.43
33	LVGLIGGYV	101	2.0000	20.41
34	FMRRIAFSG	117	2.0000	20.41
35	LVGALGLLG	322	2.0000	20.41
36	FINIGYVIG	367	2.0000	20.41
37	VVALALIVA	199	1.9000	19.39
38	LGLFGLFAY	329	1.7000	17.35
39	VNRLLRLPL	426	1.7000	17.35
40	IIAVAALLT	59	1.6000	16.33
41	IVMLVLVLV	130	1.6000	16.33
42	LLAARRMER	176	1.6000	16.33

43	FVVAGFSMQ	152	1.4000	14.29
44	LGLLWYAGL	222	1.4000	14.29
45	IGLLPVTGL	374	1.4000	14.29
46	VRRSVHHGA	493	1.4000	14.29
47	FLRLLTATT	350	1.3000	13.27
48	LRLPLPEPY	430	1.3000	13.27
49	IFAIIGEEL	312	1.2000	12.24
50	VIGLLPVTG	373	1.2000	12.24
51	LPLISAGGT	384	1.2000	12.24
52	LLTTLGLIM	65	1.1000	11.22