MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Feb 1 13:31:52 2010
Length of input sequence	806 amino acids
Number of nanomers from input sequence	798
Number of nanomers with obligatory P1 anchor residue	225
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	80

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	VVLLVGFEP	393	1.9000	31.67
2	LLINHPLDC	106	1.6400	27.33
3	WLPLNSAGS	777	1.3000	21.67
4	LHKMSGRLI	434	1.0900	18.17
5	YRTFEPALR	631	1.0800	18.00
6	MGIQIPRFC	40	0.9900	16.50
7	IVFLRLRKA	407	0.8900	14.83
8	VRTQLTSEI	86	0.6000	10.00
9	WSHAMAVAA	310	0.6000	10.00
10	IRVGQPEMV	8	0.5000	8.33
11	YFSGNTVQI	204	0.5000	8.33
12	VVRLSPDTA	734	0.5000	8.33
13	LRVTIGSIV	791	0.5000	8.33
14	WHIAELPAA	540	0.3700	6.17

15	VYTIAPFAT	423	0.3000	5.00
16	WRMLLDEGR	710	0.2000	3.33
17	VHRQLRVTI	787	0.2000	3.33
18	VVWLPLNSA	775	0.1000	1.67
19	IRAAELMGI	34	-0.0100	0
20	VVSLELRHS	594	-0.0100	0
21	LVIRAAELM	32	-0.0200	0
22	VVFPVAPTT	610	-0.1300	0
23	ILCARCTRF	164	-0.3100	0
24	FLRLRKAAR	409	-0.4000	0
25	VGGIEPADF	570	-0.4000	0
26	LAALDATGF	585	-0.4100	0
27	FVNWEGRYR	624	-0.4100	0
28	MGVHLGVPT	660	-0.5000	0
29	FDLVSSPSV	230	-0.5800	0
30	LRRLAGDDP	258	-0.6000	0
31	YAYAKFARI	342	-0.6000	0
32	LESAPVVLL	388	-0.6000	0
33	LLATPGAVI	464	-0.6000	0
34	YAKFARITL	344	-0.6200	0
35	FTYATQPDV	281	-0.6300	0
36	VEISVPKGT	23	-0.7000	0
37	YADLESAPV	385	-0.7000	0
38	VTIGSIVKI	793	-0.7000	0
39	VGALTGTAY	215	-0.7100	0
40	YLAGTARTP	725	-0.7100	0
41	VIIVGERLA	471	-0.7600	0
42	IVGERLATV	473	-0.8000	0
43	LRLRKAARR	410	-0.9000	0
44	FSGNTVQIC	205	-0.9600	0
45	IGAADGEAV	745	-1.1000	0
46	VRLSPDTAA	735	-1.1100	0
47	LVSSPSVCE	232	-1.2000	0
48	IGSIVKIGA	795	-1.2000	0
49	WAFTYATQP	279	-1.2100	0
50	ICPVGALTG	212	-1.2500	0
51	FVVSLELRH	593	-1.3000	0
52	LGIWDGKHA	679	-1.3000	0
53	LRHSTVTER	599	-1.3100	0
54	LVGFEPEDE	396	-1.3200	0
55	LDRERCILC	158	-1.4000	0

56	YTIAPFATG	424	-1.4000	0
57	VARAQVCAA	531	-1.4000	0
58	LMGIQIPRF	39	-1.4300	0
59	LASCTTVAT	73	-1.5000	0
60	LATPGAVII	465	-1.5000	0
61	LQDGEPYLA	719	-1.5000	0
62	LRKAARRHR	412	-1.5100	0
63	MVTLTIDGV	15	-1.6000	0
64	LAALLVGGI	565	-1.6000	0
65	VGDLLATPG	461	-1.6100	0
66	LNSAGSTVH	780	-1.6100	0
67	VFPVAPTTQ	611	-1.6600	0
68	VPGGEPAAL	445	-1.7000	0
69	FIDMQERGA	181	-1.7100	0
70	LPAAAGRDA	545	-1.7100	0
71	LPLNSAGST	778	-1.7600	0
72	VTWEDAYAY	336	-1.8000	0
73	IIVGERLAT	472	-1.8000	0
74	WVPRRAGER	501	-1.8000	0
75	WNCDKGRWA	272	-1.8100	0
76	MELLLINHP	103	-1.9000	0
77	FLAARIAGR	371	-1.9000	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	VVLLVGFEP	393	2.9000	48.33
2	LLINHPLDC	106	2.6400	44.00
3	LHKMSGRLI	434	2.0900	34.83
4	MGIQIPRFC	40	1.9900	33.17
5	IVFLRLRKA	407	1.8900	31.50
6	VRTQLTSEI	86	1.6000	26.67
7	IRVGQPEMV	8	1.5000	25.00
8	VVRLSPDTA	734	1.5000	25.00
9	LRVTIGSIV	791	1.5000	25.00
10	VYTIAPFAT	423	1.3000	21.67
11	VHRQLRVTI	787	1.2000	20.00

12	VVWLPLNSA	775	1.1000	18.33
13	INISAQVLL	150	1.0000	16.67
14	VQICPVGAL	210	1.0000	16.67
15	IRAAELMGI	34	0.9900	16.50
16	VVSLELRHS	594	0.9900	16.50
17	LVIRAAELM	32	0.9800	16.33
18	VVFPVAPTT	610	0.8700	14.50
19	ILCARCTRF	164	0.6900	11.50
20	VGGIEPADF	570	0.6000	10.00
21	LAALDATGF	585	0.5900	9.83
22	MGVHLGVPT	660	0.5000	8.33
23	LRRLAGDDP	258	0.4000	6.67
24	LESAPVVLL	388	0.4000	6.67
25	LLATPGAVI	464	0.4000	6.67
26	VEISVPKGT	23	0.3000	5.00
27	WLPLNSAGS	777	0.3000	5.00
28	VTIGSIVKI	793	0.3000	5.00
29	VGALTGTAY	215	0.2900	4.83
30	VIIVGERLA	471	0.2400	4.00
31	IVGERLATV	473	0.2000	3.33
32	LRLRKAARR	410	0.1000	1.67
33	YRTFEPALR	631	0.0800	1.33
34	IGAADGEAV	745	-0.1000	0
35	VRLSPDTAA	735	-0.1100	0
36	LVSSPSVCE	232	-0.2000	0
37	IGSIVKIGA	795	-0.2000	0
38	ICPVGALTG	212	-0.2500	0
39	LGIWDGKHA	679	-0.3000	0
40	LRHSTVTER	599	-0.3100	0
41	LVGFEPEDE	396	-0.3200	0
42	LDRERCILC	158	-0.4000	0
43	WSHAMAVAA	310	-0.4000	0
44	FLRLRKAAR	409	-0.4000	0
45	VARAQVCAA	531	-0.4000	0
46	FVNWEGRYR	624	-0.4100	0
47	LMGIQIPRF	39	-0.4300	0
48	LASCTTVAT	73	-0.5000	0
49	YFSGNTVQI	204	-0.5000	0
50	LATPGAVII	465	-0.5000	0
51	LQDGEPYLA	719	-0.5000	0
52	LRKAARRHR	412	-0.5100	0

53	FDLVSSPSV	230	-0.5800	0
54	MVTLTIDGV	15	-0.6000	0
55	LAALLVGGI	565	-0.6000	0
56	VGDLLATPG	461	-0.6100	0
57	LNSAGSTVH	780	-0.6100	0
58	FTYATQPDV	281	-0.6300	0
59	WHIAELPAA	540	-0.6300	0
60	VFPVAPTTQ	611	-0.6600	0
61	VPGGEPAAL	445	-0.7000	0
62	LPAAAGRDA	545	-0.7100	0
63	LPLNSAGST	778	-0.7600	0
64	VTWEDAYAY	336	-0.8000	0
65	IIVGERLAT	472	-0.8000	0
66	WRMLLDEGR	710	-0.8000	0
67	MELLLINHP	103	-0.9000	0
68	LRGSTLQAG	638	-0.9000	0
69	VHLGVPTVE	662	-0.9100	0
70	ILTGWRMLL	706	-0.9100	0
71	LVEVEGQRK	63	-0.9500	0
72	FSGNTVQIC	205	-0.9600	0
73	VGACRQCLV	56	-1.0000	0
74	LQNQAMSNG	125	-1.0000	0
75	LAAARGRTG	321	-1.0100	0
76	VTVSTSRGS	753	-1.0100	0
77	VIRAAELMG	33	-1.1000	0
78	IAELPAAAG	542	-1.1000	0
79	VNWEGRYRT	625	-1.1000	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	LTIDGVEIS	18	5.9000	62.11
2	IYADEPFES	195	5.3000	55.79
3	LRHSTVTER	599	4.7000	49.47
4	IRAAELMGI	34	4.1000	43.16
5	LMGIQIPRF	39	4.1000	43.16
6	VQICPVGAL	210	3.9600	41.68

7	IRVGQPEMV	8	3.8000	40.00
8	VRTQLTSEI	86	3.6700	38.63
9	LVGGRVTWE	331	3.6000	37.89
10	LRGSTLQAG	638	3.6000	37.89
11	ILTGWRMLL	706	3.5600	37.47
12	LVIRAAELM	32	3.5000	36.84
13	LLPGGRPLA	520	3.5000	36.84
14	VTIGSIVKI	793	3.5000	36.84
15	LLINHPLDC	106	3.4000	35.79
16	VHRQLRVTI	787	3.3000	34.74
17	LSPDTAAEI	737	2.9000	30.53
18	IGSIVKIGA	795	2.9000	30.53
19	INISAQVLL	150	2.8600	30.11
20	LVSSPSVCE	232	2.8000	29.47
21	LRKAARRHR	412	2.8000	29.47
22	IIVGERLAT	472	2.8000	29.47
23	LRLRKAARR	410	2.7000	28.42
24	VVSLELRHS	594	2.7000	28.42
25	VVRLSPDTA	734	2.7000	28.42
26	MVVRTQLTS	84	2.6000	27.37
27	VLLDRERCI	156	2.6000	27.37
28	IAGDPFIDM	176	2.6000	27.37
29	LIRDGGDPK	294	2.6000	27.37
30	VVLLVGFEP	393	2.6000	27.37
31	VGGIEPADF	570	2.6000	27.37
32	MVTLTIDGV	15	2.5000	26.32
33	LLLINHPLD	105	2.5000	26.32
34	FLRLRKAAR	409	2.5000	26.32
35	LLVGGIEPA	568	2.5000	26.32
36	MLLDEGRLQ	712	2.5000	26.32
37	VHLGVPTVE	662	2.4000	25.26
38	VEGQRKPLA	66	2.3000	24.21
39	VVWLPLNSA	775	2.2100	23.26
40	LAGDDPEVN	261	2.2000	23.16
41	VLVGGRVTW	330	2.2000	23.16
42	IVFLRLRKA	407	2.2000	23.16
43	WHIAELPAA	540	2.2000	23.16
44	VATDDMVVR	79	2.1000	22.11
45	YFSGNTVQI	204	2.1000	22.11
46	YRFRARPFD	223	2.1000	22.11
47	VVFPVAPTT	610	2.1000	22.11

48	VYTIAPFAT	423	1.9000	20.00
49	VARAQVCAA	531	1.9000	20.00
50	LAALLVGGI	565	1.9000	20.00
51	ILCARCTRF	164	1.8000	18.95
52	IVGERLATV	473	1.8000	18.95
53	LATGAVGDL	456	1.7600	18.53
54	LESAPVVLL	388	1.6600	17.47
55	MGIQIPRFC	40	1.6000	16.84
56	VVRTQLTSE	85	1.6000	16.84
57	LVGGIEPAD	569	1.5000	15.79
58	LQAGQSDHR	643	1.5000	15.79
59	LEAGALPTL	512	1.4600	15.37
60	MELLLINHP	103	1.4100	14.84
61	VEISVPKGT	23	1.4000	14.74
62	MSNGRTDSR	130	1.4000	14.74
63	VRLSPDTAA	735	1.4000	14.74
64	LRVTIGSIV	791	1.3700	14.42
65	LRRLAGDDP	258	1.3000	13.68
66	LGTNDIDFR	352	1.3000	13.68
67	IDFRARPHS	357	1.3000	13.68
68	LVGFEPEDE	396	1.3000	13.68
69	VFPVAPTTQ	611	1.3000	13.68
70	VTVSTSRGS	753	1.3000	13.68
71	WLPLNSAGS	777	1.3000	13.68
72	LQNQAMSNG	125	1.2700	13.37
73	LQQVGIYAD	190	1.2500	13.16
74	FLAARIAGR	371	1.2000	12.63
75	YRTFEPALR	631	1.2000	12.63
76	IDMQERGAL	182	1.1600	12.21
77	VIRAAELMG	33	1.0000	10.53
78	WVPRRAGER	501	1.0000	10.53
79	LGVPTVEAA	664	1.0000	10.53
80	VPKGTLVIR	27	0.9000	9.47

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score

1	LTIDGVEIS	18	4.5000	49.45
2	IYADEPFES	195	3.9000	42.86
3	WHIAELPAA	540	3.2000	35.16
4	LLPGGRPLA	520	2.5000	27.47
5	LLINHPLDC	106	2.4000	26.37
6	IRAAELMGI	34	2.2000	24.18
7	YFSGNTVQI	204	2.2000	24.18
8	LRHSTVTER	599	2.2000	24.18
9	MLLDEGRLQ	712	2.2000	24.18
10	FVVSLELRH	593	2.1800	23.96
11	VQICPVGAL	210	2.0000	21.98
12	YRFRARPFD	223	2.0000	21.98
13	FLRLRKAAR	409	2.0000	21.98
14	WLPLNSAGS	777	1.9000	20.88
15	IGSIVKIGA	795	1.9000	20.88
16	IRVGQPEMV	8	1.8000	19.78
17	VRTQLTSEI	86	1.7700	19.45
18	VVRLSPDTA	734	1.7000	18.68
19	ILTGWRMLL	706	1.6000	17.58
20	VTIGSIVKI	793	1.6000	17.58
21	WNCDKGRWA	272	1.5000	16.48
22	LIRDGGDPK	294	1.5000	16.48
23	LLVGGIEPA	568	1.5000	16.48
24	VHRQLRVTI	787	1.4000	15.38
25	VEGQRKPLA	66	1.3000	14.29
26	VVSLELRHS	594	1.3000	14.29
27	VVWLPLNSA	775	1.2100	13.30
28	LMGIQIPRF	39	1.2000	13.19
29	MVVRTQLTS	84	1.2000	13.19
30	FSGNTVQIC	205	1.2000	13.19
31	VLVGGRVTW	330	1.2000	13.19
32	LVGGRVTWE	331	1.2000	13.19
33	IVFLRLRKA	407	1.2000	13.19
34	LRGSTLQAG	638	1.2000	13.19
35	IIVGERLAT	472	1.1000	12.09
36	LVIRAAELM	32	1.0000	10.99
37	VFPVAPTTQ	611	1.0000	10.99
38	LSPDTAAEI	737	1.0000	10.99
39	INISAQVLL	150	0.9000	9.89
40	VARAQVCAA	531	0.9000	9.89
41	VLLDRERCI	156	0.7000	7.69

42	FLAARIAGR	371	0.7000	7.69
43	YRTFEPALR	631	0.7000	7.69
44	MGIQIPRFC	40	0.6000	6.59
45	VVLLVGFEP	393	0.6000	6.59
46	MVTLTIDGV	15	0.5000	5.49
47	FTYATQPDV	281	0.5000	5.49
48	WVPRRAGER	501	0.5000	5.49
49	LLLINHPLD	105	0.4000	4.40
50	LVSSPSVCE	232	0.4000	4.40
51	LAGDDPEVN	261	0.4000	4.40
52	VVFPVAPTT	610	0.4000	4.40
53	FPVAPTTQK	612	0.4000	4.40
54	VRLSPDTAA	735	0.4000	4.40
55	LRKAARRHR	412	0.3000	3.30
56	FEPALRGST	634	0.3000	3.30
57	LRLRKAARR	410	0.2000	2.20
58	VYTIAPFAT	423	0.2000	2.20
59	IAGDPFIDM	176	0.1000	1.10
60	WSHAMAVAA	310	0.1000	1.10
61	FARITLGTN	347	0.1000	1.10
62	LEPVGACRQ	53	-0.1000	0
63	IDFRARPHS	357	-0.1000	0
64	VFLRLRKAA	408	-0.1000	0
65	VTVSTSRGS	753	-0.1000	0
66	LNSAGSTVH	780	-0.1200	0
67	LQDGEPYLA	719	-0.1500	0
68	LATGAVGDL	456	-0.2000	0
69	IVGERLATV	473	-0.2000	0
70	VEISVPKGT	23	-0.3000	0
71	FTEAKRTFA	139	-0.3000	0
72	LESAPVVLL	388	-0.3000	0
73	VGGIEPADF	570	-0.3000	0
74	VATDDMVVR	79	-0.4000	0
75	FDLVSSPSV	230	-0.4000	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LTIDGVEIS	18	5.9000	67.05
2	LLINHPLDC	106	3.9000	44.32
3	IYADEPFES	195	3.4000	38.64
4	IRVGQPEMV	8	3.2000	36.36
5	LRHSTVTER	599	3.2000	36.36
6	VVRLSPDTA	734	3.0000	34.09
7	IRAAELMGI	34	2.9000	32.95
8	LLVGGIEPA	568	2.9000	32.95
9	MLLDEGRLQ	712	2.9000	32.95
10	VVWLPLNSA	775	2.9000	32.95
11	LIRDGGDPK	294	2.8000	31.82
12	MVVRTQLTS	84	2.7000	30.68
13	IIVGERLAT	472	2.6000	29.55
14	IGSIVKIGA	795	2.5800	29.32
15	VRTQLTSEI	86	2.5000	28.41
16	VTIGSIVKI	793	2.4800	28.18
17	LVIRAAELM	32	2.4000	27.27
18	LRGSTLQAG	638	2.3000	26.14
19	ILTGWRMLL	706	2.3000	26.14
20	VHRQLRVTI	787	2.2800	25.91
21	LVGGRVTWE	331	2.2000	25.00
22	LLPGGRPLA	520	2.1000	23.86
23	VLVGGRVTW	330	2.0800	23.64
24	VVSLELRHS	594	2.0000	22.73
25	VFPVAPTTQ	611	2.0000	22.73
26	LSPDTAAEI	737	2.0000	22.73
27	IVFLRLRKA	407	1.9000	21.59
28	VARAQVCAA	531	1.9000	21.59
29	MVTLTIDGV	15	1.8000	20.45
30	LAGDDPEVN	261	1.8000	20.45
31	INISAQVLL	150	1.7800	20.23
32	FVVSLELRH	593	1.6800	19.09
33	VQICPVGAL	210	1.6000	18.18
34	VFLRLRKAA	408	1.5000	17.05
35	VLLDRERCI	156	1.4000	15.91
36	LGVPTVEAA	664	1.4000	15.91
37	VRLSPDTAA	735	1.4000	15.91
38	VEISVPKGT	23	1.3000	14.77
39	MGIQIPRFC	40	1.3000	14.77
40	LVSSPSVCE	232	1.2800	14.55

41	LRLRKAARR	410	1.2000	13.64
42	MELLLINHP	103	1.1000	12.50
43	YFSGNTVQI	204	1.0800	12.27
44	FLRLRKAAR	409	1.0000	11.36
45	LRKAARRHR	412	1.0000	11.36
46	VHLGVPTVE	662	1.0000	11.36
47	LEPVGACRQ	53	0.9000	10.23
48	VEGQRKPLA	66	0.9000	10.23
49	VSYADLESA	383	0.9000	10.23
50	WLPLNSAGS	777	0.9000	10.23
51	LNSAGSTVH	780	0.8800	10.00
52	LMGIQIPRF	39	0.8000	9.09
53	IVGERLATV	473	0.8000	9.09
54	WHIAELPAA	540	0.8000	9.09
55	IAGDPFIDM	176	0.7800	8.86
56	VGGIEPADF	570	0.7000	7.95
57	LRRLAGDDP	258	0.6000	6.82
58	VTVSTSRGS	753	0.6000	6.82
59	LESAPVVLL	388	0.5800	6.59
60	VATDDMVVR	79	0.4800	5.45
61	IQIPRFCDH	42	0.3800	4.32
62	FSGNTVQIC	205	0.3000	3.41
63	LVGFEPEDE	396	0.3000	3.41
64	LQAGQSDHR	643	0.3000	3.41
65	VMELLLINH	102	0.2600	2.95
66	VVRTQLTSE	85	0.2000	2.27
67	LINHPLDCP	107	0.2000	2.27
68	MSNGRTDSR	130	0.2000	2.27
69	MQERGALQQ	184	0.2000	2.27
70	WNCDKGRWA	272	0.2000	2.27
71	VAAQGLAAA	316	0.2000	2.27
72	VSSPSVCEH	233	0.1800	2.05
73	VIRAAELMG	33	0.1000	1.14
74	LGTNDIDFR	352	0.1000	1.14
75	VVLLVGFEP	393	0.1000	1.14
76	VPGGLSAAA	481	0.1000	1.14
77	LRVTIGSIV	791	0.1000	1.14

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	LTIDGVEIS	18	5.9000	67.05
2	LLINHPLDC	106	3.9000	44.32
3	IYADEPFES	195	3.4000	38.64
4	IRVGQPEMV	8	3.2000	36.36
5	LRHSTVTER	599	3.2000	36.36
6	VVRLSPDTA	734	3.0000	34.09
7	IRAAELMGI	34	2.9000	32.95
8	LLVGGIEPA	568	2.9000	32.95
9	MLLDEGRLQ	712	2.9000	32.95
10	VVWLPLNSA	775	2.9000	32.95
11	LIRDGGDPK	294	2.8000	31.82
12	MVVRTQLTS	84	2.7000	30.68
13	IIVGERLAT	472	2.6000	29.55
14	IGSIVKIGA	795	2.5800	29.32
15	VRTQLTSEI	86	2.5000	28.41
16	VTIGSIVKI	793	2.4800	28.18
17	LVIRAAELM	32	2.4000	27.27
18	LRGSTLQAG	638	2.3000	26.14
19	ILTGWRMLL	706	2.3000	26.14
20	VHRQLRVTI	787	2.2800	25.91
21	LVGGRVTWE	331	2.2000	25.00
22	LLPGGRPLA	520	2.1000	23.86
23	VLVGGRVTW	330	2.0800	23.64
24	VVSLELRHS	594	2.0000	22.73
25	VFPVAPTTQ	611	2.0000	22.73
26	LSPDTAAEI	737	2.0000	22.73
27	IVFLRLRKA	407	1.9000	21.59
28	VARAQVCAA	531	1.9000	21.59
29	MVTLTIDGV	15	1.8000	20.45
30	LAGDDPEVN	261	1.8000	20.45
31	INISAQVLL	150	1.7800	20.23
32	FVVSLELRH	593	1.6800	19.09
33	VQICPVGAL	210	1.6000	18.18
34	VFLRLRKAA	408	1.5000	17.05
35	VLLDRERCI	156	1.4000	15.91
36	LGVPTVEAA	664	1.4000	15.91
37	VRLSPDTAA	735	1.4000	15.91

38	VEISVPKGT	23	1.3000	14.77
39	MGIQIPRFC	40	1.3000	14.77
40	LVSSPSVCE	232	1.2800	14.55
41	LRLRKAARR	410	1.2000	13.64
42	MELLLINHP	103	1.1000	12.50
43	YFSGNTVQI	204	1.0800	12.27
44	FLRLRKAAR	409	1.0000	11.36
45	LRKAARRHR	412	1.0000	11.36
46	VHLGVPTVE	662	1.0000	11.36
47	LEPVGACRQ	53	0.9000	10.23
48	VEGQRKPLA	66	0.9000	10.23
49	VSYADLESA	383	0.9000	10.23
50	WLPLNSAGS	777	0.9000	10.23
51	LNSAGSTVH	780	0.8800	10.00
52	LMGIQIPRF	39	0.8000	9.09
53	IVGERLATV	473	0.8000	9.09
54	WHIAELPAA	540	0.8000	9.09
55	IAGDPFIDM	176	0.7800	8.86
56	VGGIEPADF	570	0.7000	7.95
57	LRRLAGDDP	258	0.6000	6.82
58	VTVSTSRGS	753	0.6000	6.82
59	LESAPVVLL	388	0.5800	6.59
60	VATDDMVVR	79	0.4800	5.45
61	IQIPRFCDH	42	0.3800	4.32
62	FSGNTVQIC	205	0.3000	3.41
63	LVGFEPEDE	396	0.3000	3.41
64	LQAGQSDHR	643	0.3000	3.41
65	VMELLLINH	102	0.2600	2.95
66	VVRTQLTSE	85	0.2000	2.27
67	LINHPLDCP	107	0.2000	2.27
68	MSNGRTDSR	130	0.2000	2.27
69	MQERGALQQ	184	0.2000	2.27
70	WNCDKGRWA	272	0.2000	2.27
71	VAAQGLAAA	316	0.2000	2.27
72	VSSPSVCEH	233	0.1800	2.05
73	VIRAAELMG	33	0.1000	1.14
74	LGTNDIDFR	352	0.1000	1.14
75	VVLLVGFEP	393	0.1000	1.14
76	VPGGLSAAA	481	0.1000	1.14
77	LRVTIGSIV	791	0.1000	1.14

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	LTIDGVEIS	18	5.9000	67.05
2	LLINHPLDC	106	3.9000	44.32
3	IYADEPFES	195	3.4000	38.64
4	IRVGQPEMV	8	3.2000	36.36
5	LRHSTVTER	599	3.2000	36.36
6	VVRLSPDTA	734	3.0000	34.09
7	IRAAELMGI	34	2.9000	32.95
8	LLVGGIEPA	568	2.9000	32.95
9	MLLDEGRLQ	712	2.9000	32.95
10	VVWLPLNSA	775	2.9000	32.95
11	LIRDGGDPK	294	2.8000	31.82
12	MVVRTQLTS	84	2.7000	30.68
13	IIVGERLAT	472	2.6000	29.55
14	IGSIVKIGA	795	2.5800	29.32
15	VRTQLTSEI	86	2.5000	28.41
16	VTIGSIVKI	793	2.4800	28.18
17	LVIRAAELM	32	2.4000	27.27
18	LRGSTLQAG	638	2.3000	26.14
19	ILTGWRMLL	706	2.3000	26.14
20	VHRQLRVTI	787	2.2800	25.91
21	LVGGRVTWE	331	2.2000	25.00
22	LLPGGRPLA	520	2.1000	23.86
23	VLVGGRVTW	330	2.0800	23.64
24	VVSLELRHS	594	2.0000	22.73
25	VFPVAPTTQ	611	2.0000	22.73
26	LSPDTAAEI	737	2.0000	22.73
27	IVFLRLRKA	407	1.9000	21.59
28	VARAQVCAA	531	1.9000	21.59
29	MVTLTIDGV	15	1.8000	20.45
30	LAGDDPEVN	261	1.8000	20.45
31	INISAQVLL	150	1.7800	20.23
32	FVVSLELRH	593	1.6800	19.09
33	VQICPVGAL	210	1.6000	18.18
34	VFLRLRKAA	408	1.5000	17.05
35	VLLDRERCI	156	1.4000	15.91

36	LGVPTVEAA	664	1.4000	15.91
37	VRLSPDTAA	735	1.4000	15.91
38	VEISVPKGT	23	1.3000	14.77
39	MGIQIPRFC	40	1.3000	14.77
40	LVSSPSVCE	232	1.2800	14.55
41	LRLRKAARR	410	1.2000	13.64
42	MELLLINHP	103	1.1000	12.50
43	YFSGNTVQI	204	1.0800	12.27
44	FLRLRKAAR	409	1.0000	11.36
45	LRKAARRHR	412	1.0000	11.36
46	VHLGVPTVE	662	1.0000	11.36
47	LEPVGACRQ	53	0.9000	10.23
48	VEGQRKPLA	66	0.9000	10.23
49	VSYADLESA	383	0.9000	10.23
50	WLPLNSAGS	777	0.9000	10.23
51	LNSAGSTVH	780	0.8800	10.00
52	LMGIQIPRF	39	0.8000	9.09
53	IVGERLATV	473	0.8000	9.09
54	WHIAELPAA	540	0.8000	9.09
55	IAGDPFIDM	176	0.7800	8.86
56	VGGIEPADF	570	0.7000	7.95
57	LRRLAGDDP	258	0.6000	6.82
58	VTVSTSRGS	753	0.6000	6.82
59	LESAPVVLL	388	0.5800	6.59
60	VATDDMVVR	79	0.4800	5.45
61	IQIPRFCDH	42	0.3800	4.32
62	FSGNTVQIC	205	0.3000	3.41
63	LVGFEPEDE	396	0.3000	3.41
64	LQAGQSDHR	643	0.3000	3.41
65	VMELLLINH	102	0.2600	2.95
66	VVRTQLTSE	85	0.2000	2.27
67	LINHPLDCP	107	0.2000	2.27
68	MSNGRTDSR	130	0.2000	2.27
69	MQERGALQQ	184	0.2000	2.27
70	WNCDKGRWA	272	0.2000	2.27
71	VAAQGLAAA	316	0.2000	2.27
72	VSSPSVCEH	233	0.1800	2.05
73	VIRAAELMG	33	0.1000	1.14
74	LGTNDIDFR	352	0.1000	1.14
75	VVLLVGFEP	393	0.1000	1.14
76	VPGGLSAAA	481	0.1000	1.14

77	LRVTIGSIV	791	0.1000	1.14

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	LTIDGVEIS	18	4.9000	51.58
2	IYADEPFES	195	4.3000	45.26
3	LRHSTVTER	599	3.7000	38.95
4	FLRLRKAAR	409	3.5000	36.84
5	WHIAELPAA	540	3.2000	33.68
6	IRAAELMGI	34	3.1000	32.63
7	LMGIQIPRF	39	3.1000	32.63
8	YFSGNTVQI	204	3.1000	32.63
9	YRFRARPFD	223	3.1000	32.63
10	VQICPVGAL	210	2.9600	31.16
11	IRVGQPEMV	8	2.8000	29.47
12	VRTQLTSEI	86	2.6700	28.11
13	LVGGRVTWE	331	2.6000	27.37
14	LRGSTLQAG	638	2.6000	27.37
15	ILTGWRMLL	706	2.5600	26.95
16	LVIRAAELM	32	2.5000	26.32
17	LLPGGRPLA	520	2.5000	26.32
18	VTIGSIVKI	793	2.5000	26.32
19	LLINHPLDC	106	2.4000	25.26
20	WLPLNSAGS	777	2.3000	24.21
21	VHRQLRVTI	787	2.3000	24.21
22	FLAARIAGR	371	2.2000	23.16
23	YRTFEPALR	631	2.2000	23.16
24	WVPRRAGER	501	2.0000	21.05
25	LSPDTAAEI	737	1.9000	20.00
26	IGSIVKIGA	795	1.9000	20.00
27	INISAQVLL	150	1.8600	19.58
28	LVSSPSVCE	232	1.8000	18.95
29	LRKAARRHR	412	1.8000	18.95
30	IIVGERLAT	472	1.8000	18.95
31	LRLRKAARR	410	1.7000	17.89
32	VVSLELRHS	594	1.7000	17.89

33	VVRLSPDTA	734	1.7000	17.89
34	MVVRTQLTS	84	1.6000	16.84
35	VLLDRERCI	156	1.6000	16.84
36	IAGDPFIDM	176	1.6000	16.84
37	LIRDGGDPK	294	1.6000	16.84
38	VVLLVGFEP	393	1.6000	16.84
39	VGGIEPADF	570	1.6000	16.84
40	FVVSLELRH	593	1.6000	16.84
41	MVTLTIDGV	15	1.5000	15.79
42	LLLINHPLD	105	1.5000	15.79
43	WNCDKGRWA	272	1.5000	15.79
44	FTYATQPDV	281	1.5000	15.79
45	LLVGGIEPA	568	1.5000	15.79
46	WRMLLDEGR	710	1.5000	15.79
47	MLLDEGRLQ	712	1.5000	15.79
48	VHLGVPTVE	662	1.4000	14.74
49	VEGQRKPLA	66	1.3000	13.68
50	VVWLPLNSA	775	1.2100	12.74
51	FSGNTVQIC	205	1.2000	12.63
52	LAGDDPEVN	261	1.2000	12.63
53	VLVGGRVTW	330	1.2000	12.63
54	IVFLRLRKA	407	1.2000	12.63
55	VATDDMVVR	79	1.1000	11.58
56	VVFPVAPTT	610	1.1000	11.58
57	FATGGLHKM	429	1.0000	10.53
58	FEPALRGST	634	1.0000	10.53
59	FARITLGTN	347	0.9000	9.47
60	VYTIAPFAT	423	0.9000	9.47
61	VARAQVCAA	531	0.9000	9.47
62	LAALLVGGI	565	0.9000	9.47
63	FRARPHSAE	359	0.8700	9.16
64	ILCARCTRF	164	0.8000	8.42
65	IVGERLATV	473	0.8000	8.42
66	LATGAVGDL	456	0.7600	8.00
67	LESAPVVLL	388	0.6600	6.95
68	MGIQIPRFC	40	0.6000	6.32
69	VVRTQLTSE	85	0.6000	6.32
70	FDLVSSPSV	230	0.6000	6.32
71	YTIAPFATG	424	0.5000	5.26
72	LVGGIEPAD	569	0.5000	5.26
73	FPVAPTTQK	612	0.5000	5.26

74	FVNWEGRYR	624	0.5000	5.26
75	LQAGQSDHR	643	0.5000	5.26
76	LEAGALPTL	512	0.4600	4.84
77	MELLLINHP	103	0.4100	4.32
78	VEISVPKGT	23	0.4000	4.21
79	MSNGRTDSR	130	0.4000	4.21
80	VRLSPDTAA	735	0.4000	4.21

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	LTIDGVEIS	18	5.9000	67.05
2	LLINHPLDC	106	3.9000	44.32
3	IYADEPFES	195	3.4000	38.64
4	IRVGQPEMV	8	3.2000	36.36
5	LRHSTVTER	599	3.2000	36.36
6	VVRLSPDTA	734	3.0000	34.09
7	IRAAELMGI	34	2.9000	32.95
8	LLVGGIEPA	568	2.9000	32.95
9	MLLDEGRLQ	712	2.9000	32.95
10	VVWLPLNSA	775	2.9000	32.95
11	LIRDGGDPK	294	2.8000	31.82
12	MVVRTQLTS	84	2.7000	30.68
13	IIVGERLAT	472	2.6000	29.55
14	IGSIVKIGA	795	2.5800	29.32
15	VRTQLTSEI	86	2.5000	28.41
16	VTIGSIVKI	793	2.4800	28.18
17	LVIRAAELM	32	2.4000	27.27
18	LRGSTLQAG	638	2.3000	26.14
19	ILTGWRMLL	706	2.3000	26.14
20	VHRQLRVTI	787	2.2800	25.91
21	LVGGRVTWE	331	2.2000	25.00
22	LLPGGRPLA	520	2.1000	23.86
23	VLVGGRVTW	330	2.0800	23.64
24	VVSLELRHS	594	2.0000	22.73
25	VFPVAPTTQ	611	2.0000	22.73
26	LSPDTAAEI	737	2.0000	22.73

27	IVFLRLRKA	407	1.9000	21.59
28	VARAQVCAA	531	1.9000	21.59
29	MVTLTIDGV	15	1.8000	20.45
30	LAGDDPEVN	261	1.8000	20.45
31	INISAQVLL	150	1.7800	20.23
32	FVVSLELRH	593	1.6800	19.09
33	VQICPVGAL	210	1.6000	18.18
34	VFLRLRKAA	408	1.5000	17.05
35	VLLDRERCI	156	1.4000	15.91
36	LGVPTVEAA	664	1.4000	15.91
37	VRLSPDTAA	735	1.4000	15.91
38	VEISVPKGT	23	1.3000	14.77
39	MGIQIPRFC	40	1.3000	14.77
40	LVSSPSVCE	232	1.2800	14.55
41	LRLRKAARR	410	1.2000	13.64
42	MELLLINHP	103	1.1000	12.50
43	YFSGNTVQI	204	1.0800	12.27
44	FLRLRKAAR	409	1.0000	11.36
45	LRKAARRHR	412	1.0000	11.36
46	VHLGVPTVE	662	1.0000	11.36
47	LEPVGACRQ	53	0.9000	10.23
48	VEGQRKPLA	66	0.9000	10.23
49	VSYADLESA	383	0.9000	10.23
50	WLPLNSAGS	777	0.9000	10.23
51	LNSAGSTVH	780	0.8800	10.00
52	LMGIQIPRF	39	0.8000	9.09
53	IVGERLATV	473	0.8000	9.09
54	WHIAELPAA	540	0.8000	9.09
55	IAGDPFIDM	176	0.7800	8.86
56	VGGIEPADF	570	0.7000	7.95
57	LRRLAGDDP	258	0.6000	6.82
58	VTVSTSRGS	753	0.6000	6.82
59	LESAPVVLL	388	0.5800	6.59
60	VATDDMVVR	79	0.4800	5.45
61	IQIPRFCDH	42	0.3800	4.32
62	FSGNTVQIC	205	0.3000	3.41
63	LVGFEPEDE	396	0.3000	3.41
64	LQAGQSDHR	643	0.3000	3.41
65	VMELLLINH	102	0.2600	2.95
66	VVRTQLTSE	85	0.2000	2.27
67	LINHPLDCP	107	0.2000	2.27

68	MSNGRTDSR	130	0.2000	2.27
69	MQERGALQQ	184	0.2000	2.27
70	WNCDKGRWA	272	0.2000	2.27
71	VAAQGLAAA	316	0.2000	2.27
72	VSSPSVCEH	233	0.1800	2.05
73	VIRAAELMG	33	0.1000	1.14
74	LGTNDIDFR	352	0.1000	1.14
75	VVLLVGFEP	393	0.1000	1.14
76	VPGGLSAAA	481	0.1000	1.14
77	LRVTIGSIV	791	0.1000	1.14

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	WLPLNSAGS	777	3.8000	44.19
2	LTIDGVEIS	18	3.7000	43.02
3	VRTQLTSEI	86	3.4000	39.53
4	LLINHPLDC	106	3.1000	36.05
5	WRMLLDEGR	710	2.5000	29.07
6	VVRLSPDTA	734	2.3000	26.74
7	LRHSTVTER	599	2.0000	23.26
8	VRLSPDTAA	735	1.8000	20.93
9	FVVSLELRH	593	1.7800	20.70
10	FSGNTVQIC	205	1.7000	19.77
11	FPVAPTTQK	612	1.5000	17.44
12	LVSSPSVCE	232	1.4800	17.21
13	VVWLPLNSA	775	1.4000	16.28
14	VNEEWNCDK	268	1.1000	12.79
15	YFSGNTVQI	204	1.0800	12.56
16	IYADEPFES	195	1.0000	11.63
17	IVGERLATV	473	1.0000	11.63
18	LNSAGSTVH	780	0.9800	11.40
19	LVPTSWSHA	305	0.9000	10.47
20	MVTLTIDGV	15	0.8000	9.30
21	VTVSTSRGS	753	0.8000	9.30
22	IRAAELMGI	34	0.6000	6.98
23	MGIQIPRFC	40	0.6000	6.98

24	VARAQVCAA	531	0.6000	6.98
25	LVIRAAELM	32	0.5000	5.81
26	WHIAELPAA	540	0.5000	5.81
27	VVSLELRHS	594	0.5000	5.81
28	LTSEIADKA	90	0.4000	4.65
29	IVFLRLRKA	407	0.4000	4.65
30	VQICPVGAL	210	0.3000	3.49
31	YRTFEPALR	631	0.3000	3.49
32	MLLDEGRLQ	712	0.2000	2.33
33	MELLLINHP	103	0.1000	1.16
34	WAFTYATQP	279	0.1000	1.16
35	LIRDGGDPK	294	0.1000	1.16
36	LRGSTLQAG	638	0.1000	1.16
37	LSPDTAAEI	737	0.1000	1.16
38	LASCTTVAT	73	-0.0200	0
39	LDRERCILC	158	-0.0200	0
40	WSHAMAVAA	310	-0.0200	0
41	VEISVPKGT	23	-0.1000	0
42	VPTSWSHAM	306	-0.1000	0
43	FLAARIAGR	371	-0.1000	0
44	YADLESAPV	385	-0.2000	0
45	VGFEPEDES	397	-0.2000	0
46	FAKPINISA	146	-0.2200	0
47	INISAQVLL	150	-0.3200	0
48	IRVGQPEMV	8	-0.4000	0
49	MVVRTQLTS	84	-0.4000	0
50	VVRTQLTSE	85	-0.4000	0
51	LRRLAGDDP	258	-0.4000	0
52	VFPVAPTTQ	611	-0.4000	0
53	LPCSVTDMP	764	-0.4000	0
54	WNCDKGRWA	272	-0.5000	0
55	VGGIEPADF	570	-0.5000	0
56	LGVPTVEAA	664	-0.5000	0
57	LAGDDPEVN	261	-0.6000	0
58	YAYAKFARI	342	-0.6000	0
59	YTIAPFATG	424	-0.6000	0
60	LMGIQIPRF	39	-0.7000	0
61	LRLRKAARR	410	-0.7000	0
62	LESAPVVLL	388	-0.7200	0
63	LQNQAMSNG	125	-0.8000	0
64	IAGDPFIDM	176	-0.8200	0

65	VVLLVGFEP	393	-0.9000	0
66	FLRLRKAAR	409	-0.9000	0
67	LAALLVGGI	565	-0.9000	0
68	IQIPRFCDH	42	-0.9200	0
69	LEPVGACRQ	53	-1.0000	0
70	LINHPLDCP	107	-1.0000	0
71	LGTNDIDFR	352	-1.0000	0
72	FEPEDESPI	399	-1.0000	0
73	LLVGGIEPA	568	-1.0000	0
74	ILCARCTRF	164	-1.1000	0
75	LVGFEPEDE	396	-1.1000	0
76	LLATPGAVI	464	-1.1000	0
77	LVGGRVTWE	331	-1.2000	0
78	VMELLLINH	102	-1.2400	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	LCARCTRFS	165	5.3000	55.21
2	MVVRTQLTS	84	3.8000	39.58
3	MGIQIPRFC	40	3.3000	34.38
4	VGGRVTWED	332	3.3000	34.38
5	LRLRKAARR	410	3.2000	33.33
6	LLINHPLDC	106	3.1000	32.29
7	LVIRAAELM	32	3.0000	31.25
8	VRTQLTSEI	86	3.0000	31.25
9	VVSLELRHS	594	3.0000	31.25
10	IVFLRLRKA	407	2.9000	30.21
11	VTVSTSRGS	753	2.9000	30.21
12	MQERGALQQ	184	2.5000	26.04
13	FVNWEGRYR	624	2.4000	25.00
14	LNSAGSTVH	780	2.1800	22.71
15	LGIWDGKHA	679	2.1000	21.88
16	LELRHSTVT	597	2.0000	20.83
17	IRAAELMGI	34	1.6000	16.67
18	VARAQVCAA	531	1.6000	16.67
19	LRHSTVTER	599	1.4000	14.58

20	WLPLNSAGS	777	1.4000	14.58
21	LHKMSGRLI	434	1.3000	13.54
22	VIIVGERLA	471	1.2000	12.50
23	VRLSPDTAA	735	1.2000	12.50
24	LASCTTVAT	73	1.1000	11.46
25	YFSGNTVQI	204	1.1000	11.46
26	VFPVAPTTQ	611	1.0000	10.42
27	VVWLPLNSA	775	1.0000	10.42
28	LVGGRVTWE	331	0.9000	9.38
29	LVSSPSVCE	232	0.8000	8.33
30	IAGRHMAVS	376	0.8000	8.33
31	FPVAPTTQK	612	0.7000	7.29
32	VTIGSIVKI	793	0.6000	6.25
33	FSGNTVQIC	205	0.5000	5.21
34	VQICPVGAL	210	0.5000	5.21
35	LVPTSWSHA	305	0.5000	5.21
36	LRKAARRHR	412	0.5000	5.21
37	YRTFEPALR	631	0.5000	5.21
38	LESAPVVLL	388	0.4000	4.17
39	VFLRLRKAA	408	0.4000	4.17
40	LRGSTLQAG	638	0.4000	4.17
41	MLLDEGRLQ	712	0.4000	4.17
42	IQIPRFCDH	42	0.3800	3.96
43	VYTIAPFAT	423	0.2800	2.92
44	LEPVGACRQ	53	0.2000	2.08
45	VVLLVGFEP	393	0.2000	2.08
46	MPDRVVWLP	771	0.2000	2.08
47	IRVGQPEMV	8	0.1000	1.04
48	ILCARCTRF	164	0.1000	1.04
49	MSGRLIKTV	437	0.1000	1.04
50	LQDGEPYLA	719	0.1000	1.04
51	VVRLSPDTA	734	0.1000	1.04
52	IYADEPFES	195	-0.2000	0
53	VGGIEPADF	570	-0.2200	0
54	MELLLINHP	103	-0.3000	0
55	LVGFEPEDE	396	-0.3000	0
56	LPAAAGRDA	545	-0.3000	0
57	MGVHLGVPT	660	-0.3000	0
58	LAALGIWDG	676	-0.3000	0
59	YLAGTARTP	725	-0.3000	0
60	LTIDGVEIS	18	-0.4000	0

61	VVRTQLTSE	85	-0.4000	0
62	LQQVGIYAD	190	-0.4000	0
63	ICPVGALTG	212	-0.4000	0
64	VCEHCASGC	238	-0.4000	0
65	VPTSWSHAM	306	-0.4000	0
66	LRVTIGSIV	791	-0.4000	0
67	VSSPSVCEH	233	-0.4200	0
68	LVEVEGQRK	63	-0.5000	0
69	FAKPINISA	146	-0.5000	0
70	LLVGGIEPA	568	-0.5000	0
71	VHLGVPTVE	662	-0.5000	0
72	VWLPLNSAG	776	-0.5000	0
73	VEISVPKGT	23	-0.6000	0
74	VIRAAELMG	33	-0.6000	0
75	IAPFATGGL	426	-0.6000	0
76	VVFPVAPTT	610	-0.6000	0
77	LGVPTVEAA	664	-0.6000	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	VRTQLTSEI	86	4.3000	48.86
2	WLPLNSAGS	777	3.0000	34.09
3	VVWLPLNSA	775	2.7000	30.68
4	VVRLSPDTA	734	2.6000	29.55
5	VFPVAPTTQ	611	2.5000	28.41
6	LNSAGSTVH	780	2.4800	28.18
7	LLINHPLDC	106	2.1000	23.86
8	VVSLELRHS	594	2.0000	22.73
9	LRHSTVTER	599	2.0000	22.73
10	IVFLRLRKA	407	1.9000	21.59
11	VRLSPDTAA	735	1.8000	20.45
12	VARAQVCAA	531	1.6000	18.18
13	IRAAELMGI	34	1.5000	17.05
14	LEPVGACRQ	53	1.4000	15.91
15	MELLLINHP	103	1.4000	15.91
16	VQICPVGAL	210	1.4000	15.91

17	LTIDGVEIS	18	1.3000	14.77
18	VVLLVGFEP	393	1.2500	14.20
19	YRTFEPALR	631	1.2000	13.64
20	MVTLTIDGV	15	1.1000	12.50
21	MGIQIPRFC	40	1.1000	12.50
22	LVPTSWSHA	305	1.0000	11.36
23	IAPFATGGL	426	1.0000	11.36
24	FPVAPTTQK	612	1.0000	11.36
25	LVGFEPEDE	396	0.9000	10.23
26	LASCTTVAT	73	0.8000	9.09
27	LVSSPSVCE	232	0.8000	9.09
28	VGGIEPADF	570	0.8000	9.09
29	WRMLLDEGR	710	0.8000	9.09
30	VYTIAPFAT	423	0.7500	8.52
31	VTVSTSRGS	753	0.6000	6.82
32	IYADEPFES	195	0.4500	5.11
33	ILCARCTRF	164	0.4000	4.55
34	LAALLVGGI	565	0.4000	4.55
35	LAALDATGF	585	0.4000	4.55
36	VWLPLNSAG	776	0.4000	4.55
37	IQIPRFCDH	42	0.3800	4.32
38	LMGIQIPRF	39	0.3000	3.41
39	LVIRAAELM	32	0.1000	1.14
40	LQNQAMSNG	125	0.1000	1.14
41	ICPVGALTG	212	0.1000	1.14
42	LESAPVVLL	388	0.1000	1.14
43	LRVTIGSIV	791	0.1000	1.14
44	VMELLLINH	102	-0.0400	0
45	LRRLAGDDP	258	-0.1000	0
46	LHKMSGRLI	434	-0.1000	0
47	LGVPTVEAA	664	-0.1000	0
48	LRLRKAARR	410	-0.2000	0
49	VIIVGERLA	471	-0.2000	0
50	MVVRTQLTS	84	-0.3000	0
51	LQQVGIYAD	190	-0.3000	0
52	VGDLLATPG	461	-0.4000	0
53	VSSPSVCEH	233	-0.4200	0
54	VVRTQLTSE	85	-0.5000	0
55	VNEEWNCDK	268	-0.5000	0
56	LVGGRVTWE	331	-0.5000	0
57	IGSIVKIGA	795	-0.5200	0

58	LVEVEGQRK	63	-0.6000	0
59	VGALTGTAY	215	-0.6000	0
60	IVGERLATV	473	-0.6000	0
61	VVFPVAPTT	610	-0.6000	0
62	LRGSTLQAG	638	-0.6000	0
63	LCARCTRFS	165	-0.7000	0
64	WHIAELPAA	540	-0.8000	0
65	LAALGIWDG	676	-0.8000	0
66	LGIWDGKHA	679	-0.8500	0
67	YFSGNTVQI	204	-0.9000	0
68	FAKPINISA	146	-0.9200	0
69	VTQAADTDI	0	-1.0000	0
70	LLLINHPLD	105	-1.0000	0
71	INISAQVLL	150	-1.0000	0
72	VPTSWSHAM	306	-1.0000	0
73	YADLESAPV	385	-1.0000	0
74	VLLVGFEPE	394	-1.0000	0
75	MLLDEGRLQ	712	-1.0000	0
76	IRVGQPEMV	8	-1.1000	0
77	FSGNTVQIC	205	-1.1000	0
78	VAAQGLAAA	316	-1.1000	0
79	FLAARIAGR	371	-1.1000	0

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	WLPLNSAGS	777	4.0000	42.55
2	VRTQLTSEI	86	3.5000	37.23
3	LVGFEPEDE	396	2.9000	30.85
4	LVSSPSVCE	232	2.8000	29.79
5	LNSAGSTVH	780	2.7000	28.72
6	VFPVAPTTQ	611	2.3000	24.47
7	YRTFEPALR	631	2.2000	23.40
8	WRMLLDEGR	710	1.8000	19.15
9	VVWLPLNSA	775	1.7000	18.09
10	VVRLSPDTA	734	1.6000	17.02
11	VVRTQLTSE	85	1.5000	15.96

12	LVGGRVTWE	331	1.5000	15.96
13	LQQVGIYAD	190	1.4000	14.89
14	VQICPVGAL	210	1.4000	14.89
15	FPVAPTTQK	612	1.3000	13.83
16	LEPVGACRQ	53	1.2000	12.77
17	LLINHPLDC	106	1.1000	11.70
18	FVVSLELRH	593	1.1000	11.70
19	VLLVGFEPE	394	1.0000	10.64
20	IAPFATGGL	426	1.0000	10.64
21	VVSLELRHS	594	1.0000	10.64
22	LRHSTVTER	599	1.0000	10.64
23	IVFLRLRKA	407	0.9000	9.57
24	MELLLINHP	103	0.8000	8.51
25	VRLSPDTAA	735	0.8000	8.51
26	IRAAELMGI	34	0.7000	7.45
27	LASCTTVAT	73	0.7000	7.45
28	LLLINHPLD	105	0.7000	7.45
29	YTIAPFATG	424	0.7000	7.45
30	VGGIEPADF	570	0.7000	7.45
31	VWLPLNSAG	776	0.7000	7.45
32	VVLLVGFEP	393	0.6500	6.91
33	VYTIAPFAT	423	0.6500	6.91
34	IQIPRFCDH	42	0.6000	6.38
35	VARAQVCAA	531	0.6000	6.38
36	ITLPCSVTD	762	0.6000	6.38
37	MVTLTIDGV	15	0.4000	4.26
38	LQNQAMSNG	125	0.4000	4.26
39	ICPVGALTG	212	0.4000	4.26
40	LTIDGVEIS	18	0.3000	3.19
41	ILCARCTRF	164	0.3000	3.19
42	YFSGNTVQI	204	0.3000	3.19
43	YADLESAPV	385	0.3000	3.19
44	LAALDATGF	585	0.3000	3.19
45	VPTVEAARE	666	0.3000	3.19
46	LVIRAAELM	32	0.2000	2.13
47	LMGIQIPRF	39	0.2000	2.13
48	FRARPHSAE	359	0.2000	2.13
49	WHIAELPAA	540	0.2000	2.13
50	VMELLLINH	102	0.1800	1.91
51	MGIQIPRFC	40	0.1000	1.06
52	FARITLGTN	347	0.1000	1.06

53	LESAPVVLL	388	0.1000	1.06
54	VHLGVPTVE	662	0.1000	1.06
55	FAKPINISA	146	0.0800	0.85
56	FSGNTVQIC	205	-0.1000	0
57	FLAARIAGR	371	-0.1000	0
58	VGDLLATPG	461	-0.1000	0
59	FDLVSSPSV	230	-0.2000	0
60	VSSPSVCEH	233	-0.2000	0
61	WSHAMAVAA	310	-0.2000	0
62	LRGSTLQAG	638	-0.3000	0
63	YAYAKFARI	342	-0.4000	0
64	LAALLVGGI	565	-0.4000	0
65	VTVSTSRGS	753	-0.4000	0
66	VGALTGTAY	215	-0.5000	0
67	VGGRVTWED	332	-0.5000	0
68	LAALGIWDG	676	-0.5000	0
69	IYADEPFES	195	-0.5500	0
70	FESYFSGNT	201	-0.6000	0
71	WAFTYATQP	279	-0.6000	0
72	LRVTIGSIV	791	-0.6000	0
73	LTGWRMLLD	707	-0.6500	0
74	LRRLAGDDP	258	-0.7000	0
75	FLRLRKAAR	409	-0.7000	0
76	LIKTVPGGE	441	-0.7000	0
77	VVFPVAPTT	610	-0.7000	0
78	VLAALDATG	584	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WLPLNSAGS	777	4.0000	45.45
2	VRTQLTSEI	86	3.3000	37.50
3	YRTFEPALR	631	2.2000	25.00
4	FPVAPTTQK	612	2.0000	22.73
5	WRMLLDEGR	710	1.8000	20.45
6	VVWLPLNSA	775	1.7000	19.32
7	VVRLSPDTA	734	1.6000	18.18

8	VFPVAPTTQ	611	1.5000	17.05
9	LNSAGSTVH	780	1.4800	16.82
10	LLINHPLDC	106	1.1000	12.50
11	VVSLELRHS	594	1.0000	11.36
12	LRHSTVTER	599	1.0000	11.36
13	IVFLRLRKA	407	0.9000	10.23
14	VRLSPDTAA	735	0.8000	9.09
15	VARAQVCAA	531	0.6000	6.82
16	IRAAELMGI	34	0.5000	5.68
17	LEPVGACRQ	53	0.4000	4.55
18	MELLLINHP	103	0.4000	4.55
19	VQICPVGAL	210	0.4000	4.55
20	LTIDGVEIS	18	0.3000	3.41
21	VVLLVGFEP	393	0.2500	2.84
22	WHIAELPAA	540	0.2000	2.27
23	MVTLTIDGV	15	0.1000	1.14
24	MGIQIPRFC	40	0.1000	1.14
25	YFSGNTVQI	204	0.1000	1.14
26	FAKPINISA	146	0.0800	0.91
27	FSGNTVQIC	205	-0.1000	0
28	FLAARIAGR	371	-0.1000	0
29	LVGFEPEDE	396	-0.1000	0
30	FVVSLELRH	593	-0.1200	0
31	LASCTTVAT	73	-0.2000	0
32	LVSSPSVCE	232	-0.2000	0
33	WSHAMAVAA	310	-0.2000	0
34	VGGIEPADF	570	-0.2000	0
35	VYTIAPFAT	423	-0.2500	0
36	VTVSTSRGS	753	-0.4000	0
37	FDLVSSPSV	230	-0.5000	0
38	IYADEPFES	195	-0.5500	0
39	ILCARCTRF	164	-0.6000	0
40	YAYAKFARI	342	-0.6000	0
41	YTIAPFATG	424	-0.6000	0
42	LAALLVGGI	565	-0.6000	0
43	LAALDATGF	585	-0.6000	0
44	VWLPLNSAG	776	-0.6000	0
45	IQIPRFCDH	42	-0.6200	0
46	LMGIQIPRF	39	-0.7000	0
47	FLRLRKAAR	409	-0.7000	0
48	FVNWEGRYR	624	-0.8500	0

49	LVIRAAELM	32	-0.9000	0
50	LQNQAMSNG	125	-0.9000	0
51	ICPVGALTG	212	-0.9000	0
52	LESAPVVLL	388	-0.9000	0
53	LRVTIGSIV	791	-0.9000	0
54	WAFTYATQP	279	-1.0000	0
55	VMELLLINH	102	-1.0400	0
56	LRRLAGDDP	258	-1.1000	0
57	LHKMSGRLI	434	-1.1000	0
58	LGVPTVEAA	664	-1.1000	0
59	LRLRKAARR	410	-1.2000	0
60	VIIVGERLA	471	-1.2000	0
61	MVVRTQLTS	84	-1.3000	0
62	LQQVGIYAD	190	-1.3000	0
63	VGDLLATPG	461	-1.4000	0
64	VSSPSVCEH	233	-1.4200	0
65	VVRTQLTSE	85	-1.5000	0
66	FESYFSGNT	201	-1.5000	0
67	VNEEWNCDK	268	-1.5000	0
68	LVGGRVTWE	331	-1.5000	0
69	IGSIVKIGA	795	-1.5200	0
70	LVEVEGQRK	63	-1.6000	0
71	VGALTGTAY	215	-1.6000	0
72	IVGERLATV	473	-1.6000	0
73	VVFPVAPTT	610	-1.6000	0
74	LRGSTLQAG	638	-1.6000	0
75	LCARCTRFS	165	-1.7000	0
76	FIDMQERGA	181	-1.7000	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	VRTQLTSEI	86	4.5000	47.87
2	LVGFEPEDE	396	3.9000	41.49
3	LVSSPSVCE	232	3.8000	40.43
4	LNSAGSTVH	780	3.7000	39.36
5	VFPVAPTTQ	611	3.3000	35.11

6	WLPLNSAGS	777	3.0000	31.91
7	VVWLPLNSA	775	2.7000	28.72
8	VVRLSPDTA	734	2.6000	27.66
9	VVRTQLTSE	85	2.5000	26.60
10	LVGGRVTWE	331	2.5000	26.60
11	LQQVGIYAD	190	2.4000	25.53
12	VQICPVGAL	210	2.4000	25.53
13	LEPVGACRQ	53	2.2000	23.40
14	LLINHPLDC	106	2.1000	22.34
15	VLLVGFEPE	394	2.0000	21.28
16	IAPFATGGL	426	2.0000	21.28
17	VVSLELRHS	594	2.0000	21.28
18	LRHSTVTER	599	2.0000	21.28
19	IVFLRLRKA	407	1.9000	20.21
20	MELLLINHP	103	1.8000	19.15
21	VRLSPDTAA	735	1.8000	19.15
22	IRAAELMGI	34	1.7000	18.09
23	LASCTTVAT	73	1.7000	18.09
24	LLLINHPLD	105	1.7000	18.09
25	VGGIEPADF	570	1.7000	18.09
26	VWLPLNSAG	776	1.7000	18.09
27	VVLLVGFEP	393	1.6500	17.55
28	VYTIAPFAT	423	1.6500	17.55
29	IQIPRFCDH	42	1.6000	17.02
30	VARAQVCAA	531	1.6000	17.02
31	ITLPCSVTD	762	1.6000	17.02
32	MVTLTIDGV	15	1.4000	14.89
33	LQNQAMSNG	125	1.4000	14.89
34	ICPVGALTG	212	1.4000	14.89
35	LTIDGVEIS	18	1.3000	13.83
36	ILCARCTRF	164	1.3000	13.83
37	LAALDATGF	585	1.3000	13.83
38	VPTVEAARE	666	1.3000	13.83
39	LVIRAAELM	32	1.2000	12.77
40	LMGIQIPRF	39	1.2000	12.77
41	YRTFEPALR	631	1.2000	12.77
42	VMELLLINH	102	1.1800	12.55
43	MGIQIPRFC	40	1.1000	11.70
44	LESAPVVLL	388	1.1000	11.70
45	VHLGVPTVE	662	1.1000	11.70
46	LVPTSWSHA	305	1.0000	10.64

47	VGDLLATPG	461	0.9000	9.57
48	VSSPSVCEH	233	0.8000	8.51
49	WRMLLDEGR	710	0.8000	8.51
50	LRGSTLQAG	638	0.7000	7.45
51	LAALLVGGI	565	0.6000	6.38
52	VTVSTSRGS	753	0.6000	6.38
53	VGALTGTAY	215	0.5000	5.32
54	VGGRVTWED	332	0.5000	5.32
55	LAALGIWDG	676	0.5000	5.32
56	IYADEPFES	195	0.4500	4.79
57	LRVTIGSIV	791	0.4000	4.26
58	LTGWRMLLD	707	0.3500	3.72
59	LRRLAGDDP	258	0.3000	3.19
60	LIKTVPGGE	441	0.3000	3.19
61	VVFPVAPTT	610	0.3000	3.19
62	FPVAPTTQK	612	0.3000	3.19
63	VLAALDATG	584	0.2000	2.13
64	VITTPLIRD	289	0.1800	1.91
65	VPTSWSHAM	306	0.1000	1.06
66	LHKMSGRLI	434	0.1000	1.06
67	IAELPAAAG	542	0.1000	1.06
68	FVVSLELRH	593	0.1000	1.06
69	VCAAWHIAE	536	-0.0200	0
70	MAVSYADLE	381	-0.1000	0
71	LGVPTVEAA	664	-0.1000	0
72	LRLRKAARR	410	-0.2000	0
73	VIIVGERLA	471	-0.2000	0
74	LELRHSTVT	597	-0.2000	0
75	MLLDEGRLQ	712	-0.2000	0
76	IPRFCDHPL	44	-0.3000	0
77	MVVRTQLTS	84	-0.3000	0

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	VRTQLTSEI	86	4.3000	47.78
2	WLPLNSAGS	777	4.2000	46.67

3	LTIDGVEIS	18	4.1000	45.56
4	WRMLLDEGR	710	4.0000	44.44
5	LRHSTVTER	599	3.5000	38.89
6	LLINHPLDC	106	3.1000	34.44
7	LVSSPSVCE	232	2.8800	32.00
8	VVRLSPDTA	734	2.3000	25.56
9	LVIRAAELM	32	2.0000	22.22
10	IVGERLATV	473	2.0000	22.22
11	YFSGNTVQI	204	1.9800	22.00
12	MVTLTIDGV	15	1.8000	20.00
13	YRTFEPALR	631	1.8000	20.00
14	VRLSPDTAA	735	1.8000	20.00
15	FSGNTVQIC	205	1.7000	18.89
16	FPVAPTTQK	612	1.6000	17.78
17	IRAAELMGI	34	1.5000	16.67
18	LRGSTLQAG	638	1.5000	16.67
19	IYADEPFES	195	1.4000	15.56
20	VPTSWSHAM	306	1.4000	15.56
21	FLAARIAGR	371	1.4000	15.56
22	VGGIEPADF	570	1.4000	15.56
23	VVWLPLNSA	775	1.4000	15.56
24	VQICPVGAL	210	1.2600	14.00
25	LMGIQIPRF	39	1.2000	13.33
26	VNEEWNCDK	268	1.2000	13.33
27	FVVSLELRH	593	1.2000	13.33
28	VTVSTSRGS	753	1.2000	13.33
29	MELLLINHP	103	1.1000	12.22
30	WAFTYATQP	279	1.1000	12.22
31	VVRTQLTSE	85	1.0000	11.11
32	LSPDTAAEI	737	1.0000	11.11
33	LRVTIGSIV	791	1.0000	11.11
34	LVPTSWSHA	305	0.9000	10.00
35	VVSLELRHS	594	0.9000	10.00
36	ILCARCTRF	164	0.8000	8.89
37	YADLESAPV	385	0.8000	8.89
38	LRLRKAARR	410	0.8000	8.89
39	YTIAPFATG	424	0.8000	8.89
40	LASCTTVAT	73	0.6800	7.56
41	IAGDPFIDM	176	0.6800	7.56
42	INISAQVLL	150	0.6400	7.11
43	IRVGQPEMV	8	0.6000	6.67

44	VEISVPKGT	23	0.6000	6.67
45	MGIQIPRFC	40	0.6000	6.67
46	LQNQAMSNG	125	0.6000	6.67
47	LRRLAGDDP	258	0.6000	6.67
48	FLRLRKAAR	409	0.6000	6.67
49	VARAQVCAA	531	0.6000	6.67
50	LAALDATGF	585	0.6000	6.67
51	LPCSVTDMP	764	0.6000	6.67
52	LGTNDIDFR	352	0.5000	5.56
53	WHIAELPAA	540	0.5000	5.56
54	LTSEIADKA	90	0.4000	4.44
55	IVFLRLRKA	407	0.4000	4.44
56	LNSAGSTVH	780	0.4000	4.44
57	YAYAKFARI	342	0.3000	3.33
58	LVGFEPEDE	396	0.3000	3.33
59	LESAPVVLL	388	0.2400	2.67
60	LAGDDPEVN	261	0.2000	2.22
61	LIRDGGDPK	294	0.2000	2.22
62	LVGGRVTWE	331	0.2000	2.22
63	VGFEPEDES	397	0.2000	2.22
64	VVLLVGFEP	393	0.1000	1.11
65	LDRERCILC	158	-0.0200	0
66	WSHAMAVAA	310	-0.0200	0
67	FEPEDESPI	399	-0.1000	0
68	VATDDMVVR	79	-0.1200	0
69	LLATPGAVI	464	-0.2000	0
70	LQAGQSDHR	643	-0.2000	0
71	VWLPLNSAG	776	-0.2000	0
72	FAKPINISA	146	-0.2200	0
73	MSNGRTDSR	130	-0.3000	0
74	MAVSYADLE	381	-0.3000	0
75	WVPRRAGER	501	-0.3000	0
76	ISAQVLLDR	152	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score

1	VRTQLTSEI	86	4.3000	48.86
2	WLPLNSAGS	777	3.0000	34.09
3	VVWLPLNSA	775	2.7000	30.68
4	VVRLSPDTA	734	2.6000	29.55
5	VFPVAPTTQ	611	2.5000	28.41
6	LNSAGSTVH	780	2.4800	28.18
7	LLINHPLDC	106	2.1000	23.86
8	VVSLELRHS	594	2.0000	22.73
9	LRHSTVTER	599	2.0000	22.73
10	IVFLRLRKA	407	1.9000	21.59
11	VRLSPDTAA	735	1.8000	20.45
12	VARAQVCAA	531	1.6000	18.18
13	IRAAELMGI	34	1.5000	17.05
14	LEPVGACRQ	53	1.4000	15.91
15	MELLLINHP	103	1.4000	15.91
16	VQICPVGAL	210	1.4000	15.91
17	LTIDGVEIS	18	1.3000	14.77
18	VVLLVGFEP	393	1.2500	14.20
19	YRTFEPALR	631	1.2000	13.64
20	MVTLTIDGV	15	1.1000	12.50
21	MGIQIPRFC	40	1.1000	12.50
22	LVPTSWSHA	305	1.0000	11.36
23	IAPFATGGL	426	1.0000	11.36
24	FPVAPTTQK	612	1.0000	11.36
25	LVGFEPEDE	396	0.9000	10.23
26	LASCTTVAT	73	0.8000	9.09
27	LVSSPSVCE	232	0.8000	9.09
28	VGGIEPADF	570	0.8000	9.09
29	WRMLLDEGR	710	0.8000	9.09
30	VYTIAPFAT	423	0.7500	8.52
31	VTVSTSRGS	753	0.6000	6.82
32	IYADEPFES	195	0.4500	5.11
33	ILCARCTRF	164	0.4000	4.55
34	LAALLVGGI	565	0.4000	4.55
35	LAALDATGF	585	0.4000	4.55
36	VWLPLNSAG	776	0.4000	4.55
37	IQIPRFCDH	42	0.3800	4.32
38	LMGIQIPRF	39	0.3000	3.41
39	LVIRAAELM	32	0.1000	1.14
40	LQNQAMSNG	125	0.1000	1.14
41	ICPVGALTG	212	0.1000	1.14

42	LESAPVVLL	388	0.1000	1.14
43	LRVTIGSIV	791	0.1000	1.14
44	VMELLLINH	102	-0.0400	0
45	LRRLAGDDP	258	-0.1000	0
46	LHKMSGRLI	434	-0.1000	0
47	LGVPTVEAA	664	-0.1000	0
48	LRLRKAARR	410	-0.2000	0
49	VIIVGERLA	471	-0.2000	0
50	MVVRTQLTS	84	-0.3000	0
51	LQQVGIYAD	190	-0.3000	0
52	VGDLLATPG	461	-0.4000	0
53	VSSPSVCEH	233	-0.4200	0
54	VVRTQLTSE	85	-0.5000	0
55	VNEEWNCDK	268	-0.5000	0
56	LVGGRVTWE	331	-0.5000	0
57	IGSIVKIGA	795	-0.5200	0
58	LVEVEGQRK	63	-0.6000	0
59	VGALTGTAY	215	-0.6000	0
60	IVGERLATV	473	-0.6000	0
61	VVFPVAPTT	610	-0.6000	0
62	LRGSTLQAG	638	-0.6000	0
63	LCARCTRFS	165	-0.7000	0
64	WHIAELPAA	540	-0.8000	0
65	LAALGIWDG	676	-0.8000	0
66	LGIWDGKHA	679	-0.8500	0
67	YFSGNTVQI	204	-0.9000	0
68	FAKPINISA	146	-0.9200	0
69	VTQAADTDI	0	-1.0000	0
70	LLLINHPLD	105	-1.0000	0
71	INISAQVLL	150	-1.0000	0
72	VPTSWSHAM	306	-1.0000	0
73	YADLESAPV	385	-1.0000	0
74	VLLVGFEPE	394	-1.0000	0
75	MLLDEGRLQ	712	-1.0000	0
76	IRVGQPEMV	8	-1.1000	0
77	FSGNTVQIC	205	-1.1000	0
78	VAAQGLAAA	316	-1.1000	0
79	FLAARIAGR	371	-1.1000	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	WLPLNSAGS	777	3.8000	44.19
2	LTIDGVEIS	18	3.7000	43.02
3	VRTQLTSEI	86	3.4000	39.53
4	LLINHPLDC	106	3.1000	36.05
5	WRMLLDEGR	710	2.5000	29.07
6	VVRLSPDTA	734	2.3000	26.74
7	LRHSTVTER	599	2.0000	23.26
8	VRLSPDTAA	735	1.8000	20.93
9	FVVSLELRH	593	1.7800	20.70
10	FSGNTVQIC	205	1.7000	19.77
11	FPVAPTTQK	612	1.5000	17.44
12	LVSSPSVCE	232	1.4800	17.21
13	VVWLPLNSA	775	1.4000	16.28
14	VNEEWNCDK	268	1.1000	12.79
15	YFSGNTVQI	204	1.0800	12.56
16	IYADEPFES	195	1.0000	11.63
17	IVGERLATV	473	1.0000	11.63
18	LNSAGSTVH	780	0.9800	11.40
19	LVPTSWSHA	305	0.9000	10.47
20	MVTLTIDGV	15	0.8000	9.30
21	VTVSTSRGS	753	0.8000	9.30
22	IRAAELMGI	34	0.6000	6.98
23	MGIQIPRFC	40	0.6000	6.98
24	VARAQVCAA	531	0.6000	6.98
25	LVIRAAELM	32	0.5000	5.81
26	WHIAELPAA	540	0.5000	5.81
27	VVSLELRHS	594	0.5000	5.81
28	LTSEIADKA	90	0.4000	4.65
29	IVFLRLRKA	407	0.4000	4.65
30	VQICPVGAL	210	0.3000	3.49
31	YRTFEPALR	631	0.3000	3.49
32	MLLDEGRLQ	712	0.2000	2.33
33	MELLLINHP	103	0.1000	1.16
34	WAFTYATQP	279	0.1000	1.16
35	LIRDGGDPK	294	0.1000	1.16
36	LRGSTLQAG	638	0.1000	1.16
37	LSPDTAAEI	737	0.1000	1.16

38	LASCTTVAT	73	-0.0200	0
39	LDRERCILC	158	-0.0200	0
40	WSHAMAVAA	310	-0.0200	0
41	VEISVPKGT	23	-0.1000	0
42	VPTSWSHAM	306	-0.1000	0
43	FLAARIAGR	371	-0.1000	0
44	YADLESAPV	385	-0.2000	0
45	VGFEPEDES	397	-0.2000	0
46	FAKPINISA	146	-0.2200	0
47	INISAQVLL	150	-0.3200	0
48	IRVGQPEMV	8	-0.4000	0
49	MVVRTQLTS	84	-0.4000	0
50	VVRTQLTSE	85	-0.4000	0
51	LRRLAGDDP	258	-0.4000	0
52	VFPVAPTTQ	611	-0.4000	0
53	LPCSVTDMP	764	-0.4000	0
54	WNCDKGRWA	272	-0.5000	0
55	VGGIEPADF	570	-0.5000	0
56	LGVPTVEAA	664	-0.5000	0
57	LAGDDPEVN	261	-0.6000	0
58	YAYAKFARI	342	-0.6000	0
59	YTIAPFATG	424	-0.6000	0
60	LMGIQIPRF	39	-0.7000	0
61	LRLRKAARR	410	-0.7000	0
62	LESAPVVLL	388	-0.7200	0
63	LQNQAMSNG	125	-0.8000	0
64	IAGDPFIDM	176	-0.8200	0
65	VVLLVGFEP	393	-0.9000	0
66	FLRLRKAAR	409	-0.9000	0
67	LAALLVGGI	565	-0.9000	0
68	IQIPRFCDH	42	-0.9200	0
69	LEPVGACRQ	53	-1.0000	0
70	LINHPLDCP	107	-1.0000	0
71	LGTNDIDFR	352	-1.0000	0
72	FEPEDESPI	399	-1.0000	0
73	LLVGGIEPA	568	-1.0000	0
74	ILCARCTRF	164	-1.1000	0
75	LVGFEPEDE	396	-1.1000	0
76	LLATPGAVI	464	-1.1000	0
77	LVGGRVTWE	331	-1.2000	0
78	VMELLLINH	102	-1.2400	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	INISAQVLL	150	6.7000	57.76
2	IRAAELMGI	34	5.5000	47.41
3	VQICPVGAL	210	5.2000	44.83
4	YAKFARITL	344	4.9000	42.24
5	LRVTIGSIV	791	4.9000	42.24
6	YFSGNTVQI	204	4.8200	41.55
7	LVSSPSVCE	232	4.7000	40.52
8	LVIRAAELM	32	4.4000	37.93
9	LESAPVVLL	388	4.4000	37.93
10	LLATPGAVI	464	4.2000	36.21
11	VTIGSIVKI	793	3.9000	33.62
12	FVVSLELRH	593	3.6000	31.03
13	VPTSWSHAM	306	3.5000	30.17
14	VRTQLTSEI	86	3.4200	29.48
15	YAYAKFARI	342	3.4000	29.31
16	LRHSTVTER	599	3.1000	26.72
17	IRVGQPEMV	8	3.0000	25.86
18	ILCARCTRF	164	3.0000	25.86
19	FDLVSSPSV	230	3.0000	25.86
20	VYTIAPFAT	423	3.0000	25.86
21	ILTGWRMLL	706	3.0000	25.86
22	VVRTQLTSE	85	2.9000	25.00
23	LHKMSGRLI	434	2.9000	25.00
24	VHRQLRVTI	787	2.9000	25.00
25	IAPFATGGL	426	2.8200	24.31
26	LMGIQIPRF	39	2.8000	24.14
27	LATPGAVII	465	2.8000	24.14
28	VGQPEMVTL	10	2.5000	21.55
29	VEISVPKGT	23	2.5000	21.55
30	WAFTYATQP	279	2.5000	21.55
31	LRGSTLQAG	638	2.5000	21.55
32	VGGIEPADF	570	2.4000	20.69
33	LAGTARTPV	726	2.4000	20.69
34	LVPTSWSHA	305	2.3000	19.83

35	VVLLVGFEP	393	2.2000	18.97
36	LLINHPLDC	106	2.1000	18.10
37	VRLSPDTAA	735	2.1000	18.10
38	IGSIVKIGA	795	2.1000	18.10
39	VTVSTSRGS	753	2.0000	17.24
40	LADTTGARL	491	1.9000	16.38
41	ICPVGALTG	212	1.8000	15.52
42	VITTPLIRD	289	1.8000	15.52
43	IGAADGEAV	745	1.8000	15.52
44	VLLVGFEPE	394	1.7000	14.66
45	LAALLVGGI	565	1.7000	14.66
46	LVGFEPEDE	396	1.6000	13.79
47	FTYATQPDV	281	1.5000	12.93
48	WSHAMAVAA	310	1.5000	12.93
49	MGVHLGVPT	660	1.5000	12.93
50	LATGAVGDL	456	1.4000	12.07
51	MVVRTQLTS	84	1.3000	11.21
52	LNSAGSTVH	780	1.3000	11.21
53	IPRFCDHPL	44	1.2000	10.34
54	IAGDPFIDM	176	1.2000	10.34
55	WHIAELPAA	540	1.2000	10.34
56	LAALDATGF	585	1.2000	10.34
57	LASCTTVAT	73	1.1200	9.66
58	LQQVGIYAD	190	1.1000	9.48
59	YRTFEPALR	631	1.1000	9.48
60	VLLDRERCI	156	1.0000	8.62
61	FRARPFDLV	225	1.0000	8.62
62	IIVGERLAT	472	1.0000	8.62
63	IVGERLATV	473	1.0000	8.62
64	LVGGRVTWE	331	0.9000	7.76
65	IVFLRLRKA	407	0.9000	7.76
66	FATGGLHKM	429	0.9000	7.76
67	LELRHSTVT	597	0.9000	7.76
68	VVFPVAPTT	610	0.9000	7.76
69	VTQAADTDI	0	0.8000	6.90
70	LAAAADETL	557	0.8000	6.90
71	FVNWEGRYR	624	0.8000	6.90
72	LSPDTAAEI	737	0.8000	6.90
73	VVWLPLNSA	775	0.8000	6.90
74	WLPLNSAGS	777	0.8000	6.90
75	VLVGGRVTW	330	0.7000	6.03

76	LIKTVPGGE	441	0.7000	6.03
77	VIIVGERLA	471	0.7000	6.03
78	FAKPINISA	146	0.6000	5.17
79	VGIYADEPF	193	0.6000	5.17
80	MVTLTIDGV	15	0.5000	4.31

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	INISAQVLL	150	6.7000	57.76
2	IRAAELMGI	34	5.5000	47.41
3	VQICPVGAL	210	5.2000	44.83
4	YAKFARITL	344	4.9000	42.24
5	LRVTIGSIV	791	4.9000	42.24
6	YFSGNTVQI	204	4.8200	41.55
7	LVSSPSVCE	232	4.7000	40.52
8	LVIRAAELM	32	4.4000	37.93
9	LESAPVVLL	388	4.4000	37.93
10	LLATPGAVI	464	4.2000	36.21
11	VTIGSIVKI	793	3.9000	33.62
12	FVVSLELRH	593	3.6000	31.03
13	VPTSWSHAM	306	3.5000	30.17
14	VRTQLTSEI	86	3.4200	29.48
15	YAYAKFARI	342	3.4000	29.31
16	LRHSTVTER	599	3.1000	26.72
17	IRVGQPEMV	8	3.0000	25.86
18	ILCARCTRF	164	3.0000	25.86
19	FDLVSSPSV	230	3.0000	25.86
20	VYTIAPFAT	423	3.0000	25.86
21	ILTGWRMLL	706	3.0000	25.86
22	VVRTQLTSE	85	2.9000	25.00
23	LHKMSGRLI	434	2.9000	25.00
24	VHRQLRVTI	787	2.9000	25.00
25	IAPFATGGL	426	2.8200	24.31
26	LMGIQIPRF	39	2.8000	24.14
27	LATPGAVII	465	2.8000	24.14
28	VGQPEMVTL	10	2.5000	21.55

29	VEISVPKGT	23	2.5000	21.55
30	WAFTYATQP	279	2.5000	21.55
31	LRGSTLQAG	638	2.5000	21.55
32	VGGIEPADF	570	2.4000	20.69
33	LAGTARTPV	726	2.4000	20.69
34	LVPTSWSHA	305	2.3000	19.83
35	VVLLVGFEP	393	2.2000	18.97
36	LLINHPLDC	106	2.1000	18.10
37	VRLSPDTAA	735	2.1000	18.10
38	IGSIVKIGA	795	2.1000	18.10
39	VTVSTSRGS	753	2.0000	17.24
40	LADTTGARL	491	1.9000	16.38
41	ICPVGALTG	212	1.8000	15.52
42	VITTPLIRD	289	1.8000	15.52
43	IGAADGEAV	745	1.8000	15.52
44	VLLVGFEPE	394	1.7000	14.66
45	LAALLVGGI	565	1.7000	14.66
46	LVGFEPEDE	396	1.6000	13.79
47	FTYATQPDV	281	1.5000	12.93
48	WSHAMAVAA	310	1.5000	12.93
49	MGVHLGVPT	660	1.5000	12.93
50	LATGAVGDL	456	1.4000	12.07
51	MVVRTQLTS	84	1.3000	11.21
52	LNSAGSTVH	780	1.3000	11.21
53	IPRFCDHPL	44	1.2000	10.34
54	IAGDPFIDM	176	1.2000	10.34
55	WHIAELPAA	540	1.2000	10.34
56	LAALDATGF	585	1.2000	10.34
57	LASCTTVAT	73	1.1200	9.66
58	LQQVGIYAD	190	1.1000	9.48
59	YRTFEPALR	631	1.1000	9.48
60	VLLDRERCI	156	1.0000	8.62
61	FRARPFDLV	225	1.0000	8.62
62	IIVGERLAT	472	1.0000	8.62
63	IVGERLATV	473	1.0000	8.62
64	LVGGRVTWE	331	0.9000	7.76
65	IVFLRLRKA	407	0.9000	7.76
66	FATGGLHKM	429	0.9000	7.76
67	LELRHSTVT	597	0.9000	7.76
68	VVFPVAPTT	610	0.9000	7.76
69	VTQAADTDI	0	0.8000	6.90

70	LAAAADETL	557	0.8000	6.90
71	FVNWEGRYR	624	0.8000	6.90
72	LSPDTAAEI	737	0.8000	6.90
73	VVWLPLNSA	775	0.8000	6.90
74	WLPLNSAGS	777	0.8000	6.90
75	VLVGGRVTW	330	0.7000	6.03
76	LIKTVPGGE	441	0.7000	6.03
77	VIIVGERLA	471	0.7000	6.03
78	FAKPINISA	146	0.6000	5.17
79	VGIYADEPF	193	0.6000	5.17
80	MVTLTIDGV	15	0.5000	4.31

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	YRFRARPFD	223	6.1000	70.93
2	FRARPHSAE	359	4.4000	51.16
3	MVVRTQLTS	84	4.0000	46.51
4	VLRRLAGDD	257	3.5000	40.70
5	LRLRKAARR	410	3.5000	40.70
6	VFLRLRKAA	408	3.3000	38.37
7	LVIRAAELM	32	3.2000	37.21
8	WVPRRAGER	501	3.2000	37.21
9	FLRLRKAAR	409	2.7000	31.40
10	VGGRVTWED	332	2.6000	30.23
11	WLPLNSAGS	777	2.6000	30.23
12	WEGRYRTFE	627	2.5000	29.07
13	VQICPVGAL	210	2.4000	27.91
14	MQERGALQQ	184	2.3000	26.74
15	VVSLELRHS	594	2.3000	26.74
16	LCARCTRFS	165	2.2000	25.58
17	IVFLRLRKA	407	2.2000	25.58
18	YRTFEPALR	631	2.2000	25.58
19	LAARIAGRH	372	2.1000	24.42
20	LLDRERCIL	157	2.0000	23.26
21	VPVYTIAPF	421	1.8000	20.93
22	LLINHPLDC	106	1.7000	19.77

23	FESYFSGNT	201	1.6000	18.60
24	FARITLGTN	347	1.3000	15.12
25	IDFRARPHS	357	1.3000	15.12
26	IAGRHMAVS	376	1.3000	15.12
27	WHIAELPAA	540	1.3000	15.12
28	LVGFEPEDE	396	1.2000	13.95
29	FVVSLELRH	593	1.2000	13.95
30	LQQVGIYAD	190	1.1000	12.79
31	IRAAELMGI	34	1.0000	11.63
32	LEPVGACRQ	53	1.0000	11.63
33	LLLINHPLD	105	1.0000	11.63
34	VARAQVCAA	531	0.9000	10.47
35	YAKFARITL	344	0.7000	8.14
36	FLAARIAGR	371	0.7000	8.14
37	MSGRLIKTV	437	0.7000	8.14
38	VVWLPLNSA	775	0.7000	8.14
39	IQIPRFCDH	42	0.6000	6.98
40	LRKAARRHR	412	0.6000	6.98
41	FEPALRGST	634	0.6000	6.98
42	VVRLSPDTA	734	0.6000	6.98
43	IGSIVKIGA	795	0.5000	5.81
44	LVSSPSVCE	232	0.4000	4.65
45	VSSPSVCEH	233	0.4000	4.65
46	LVGGRVTWE	331	0.4000	4.65
47	YTIAPFATG	424	0.4000	4.65
48	LIKTVPGGE	441	0.4000	4.65
49	LSAAARLAD	485	0.4000	4.65
50	VGGIEPADF	570	0.4000	4.65
51	VMELLLINH	102	0.3000	3.49
52	FRARPFDLV	225	0.3000	3.49
53	VVLLVGFEP	393	0.3000	3.49
54	LAALLVGGI	565	0.3000	3.49
55	FVNWEGRYR	624	0.3000	3.49
56	WDGKHAAGP	682	0.3000	3.49
57	IAPFATGGL	426	0.1000	1.16
58	IVGERLATV	473	0.1000	1.16
59	VPTVEAARE	666	0.1000	1.16
60	MGIQIPRFC	40	-0.1000	0
61	VVRTQLTSE	85	-0.1000	0
62	FSGNTVQIC	205	-0.1000	0
63	VIIVGERLA	471	-0.1000	0

64	LHKMSGRLI	434	-0.2000	0
65	VFPVAPTTQ	611	-0.2000	0
66	MVTLTIDGV	15	-0.3000	0
67	LRGSTLQAG	638	-0.3000	0
68	ILTGWRMLL	706	-0.3000	0
69	VRTQLTSEI	86	-0.4000	0
70	YFSGNTVQI	204	-0.4000	0
71	ICPVGALTG	212	-0.4000	0
72	LELRHSTVT	597	-0.4000	0
73	VITTPLIRD	289	-0.5000	0
74	VYTIAPFAT	423	-0.5000	0
75	LAALGIWDG	676	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MVVRTQLTS	84	4.0000	50.00
2	LRLRKAARR	410	3.5000	43.75
3	YRFRARPFD	223	3.4000	42.50
4	VFLRLRKAA	408	3.3000	41.25
5	WVPRRAGER	501	3.2000	40.00
6	FLRLRKAAR	409	2.7000	33.75
7	WLPLNSAGS	777	2.6000	32.50
8	VVSLELRHS	594	2.3000	28.75
9	LCARCTRFS	165	2.2000	27.50
10	IVFLRLRKA	407	2.2000	27.50
11	YRTFEPALR	631	2.2000	27.50
12	LVIRAAELM	32	2.1000	26.25
13	LLINHPLDC	106	1.7000	21.25
14	MQERGALQQ	184	1.5000	18.75
15	VQICPVGAL	210	1.4000	17.50
16	FRARPHSAE	359	1.4000	17.50
17	IDFRARPHS	357	1.3000	16.25
18	IAGRHMAVS	376	1.3000	16.25
19	WHIAELPAA	540	1.3000	16.25
20	LLDRERCIL	157	1.0000	12.50
21	VPVYTIAPF	421	0.9000	11.25

22	VARAQVCAA	531	0.9000	11.25
23	LAARIAGRH	372	0.8800	11.00
24	IRAAELMGI	34	0.8000	10.00
25	VLRRLAGDD	257	0.8000	10.00
26	FESYFSGNT	201	0.7000	8.75
27	FLAARIAGR	371	0.7000	8.75
28	VVWLPLNSA	775	0.7000	8.75
29	LRKAARRHR	412	0.6000	7.50
30	VVRLSPDTA	734	0.6000	7.50
31	IGSIVKIGA	795	0.5000	6.25
32	MSGRLIKTV	437	0.4000	5.00
33	FVNWEGRYR	624	0.3000	3.75
34	LEPVGACRQ	53	0.2000	2.50
35	LAALLVGGI	565	0.1000	1.25
36	FVVSLELRH	593	-0.0200	0
37	MGIQIPRFC	40	-0.1000	0
38	FSGNTVQIC	205	-0.1000	0
39	VGGRVTWED	332	-0.1000	0
40	VVLLVGFEP	393	-0.1000	0
41	VIIVGERLA	471	-0.1000	0
42	WDGKHAAGP	682	-0.1000	0
43	IVGERLATV	473	-0.2000	0
44	YAKFARITL	344	-0.3000	0
45	FEPALRGST	634	-0.3000	0
46	LHKMSGRLI	434	-0.4000	0
47	VGGIEPADF	570	-0.5000	0
48	WEGRYRTFE	627	-0.5000	0
49	LGIWDGKHA	679	-0.5000	0
50	MVTLTIDGV	15	-0.6000	0
51	VRTQLTSEI	86	-0.6000	0
52	YFSGNTVQI	204	-0.6000	0
53	IQIPRFCDH	42	-0.6200	0
54	FARITLGTN	347	-0.7000	0
55	FIDMQERGA	181	-0.8000	0
56	IYADEPFES	195	-0.8000	0
57	MLLDEGRLQ	712	-0.8000	0
58	VSSPSVCEH	233	-0.8200	0
59	LMGIQIPRF	39	-0.9000	0
60	YAYAKFARI	342	-0.9000	0
61	YTIAPFATG	424	-0.9000	0
62	IAPFATGGL	426	-0.9000	0

63	IIVGERLAT	472	-0.9000	0
64	LLPGGRPLA	520	-0.9000	0
65	VHRQLRVTI	787	-0.9000	0
66	VMELLLINH	102	-0.9200	0
67	LTIDGVEIS	18	-1.0000	0
68	VFPVAPTTQ	611	-1.0000	0
69	MELLLINHP	103	-1.1000	0
70	WSHAMAVAA	310	-1.2000	0
71	LATVPGGLS	478	-1.2000	0
72	VTIGSIVKI	793	-1.2000	0
73	MAVAAQGLA	314	-1.3000	0
74	LAWVPRRAG	499	-1.3000	0
75	LELRHSTVT	597	-1.3000	0
76	ILTGWRMLL	706	-1.3000	0
77	FTYATQPDV	281	-1.4000	0
78	YADLESAPV	385	-1.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MVVRTQLTS	84	5.0000	62.50
2	LRLRKAARR	410	4.5000	56.25
3	VFLRLRKAA	408	4.3000	53.75
4	VVSLELRHS	594	3.3000	41.25
5	LCARCTRFS	165	3.2000	40.00
6	IVFLRLRKA	407	3.2000	40.00
7	LVIRAAELM	32	3.1000	38.75
8	LLINHPLDC	106	2.7000	33.75
9	MQERGALQQ	184	2.5000	31.25
10	VQICPVGAL	210	2.4000	30.00
11	YRFRARPFD	223	2.4000	30.00
12	IDFRARPHS	357	2.3000	28.75
13	IAGRHMAVS	376	2.3000	28.75
14	WVPRRAGER	501	2.2000	27.50
15	LLDRERCIL	157	2.0000	25.00
16	VPVYTIAPF	421	1.9000	23.75
17	VARAQVCAA	531	1.9000	23.75

18	LAARIAGRH	372	1.8800	23.50
19	IRAAELMGI	34	1.8000	22.50
20	VLRRLAGDD	257	1.8000	22.50
21	FLRLRKAAR	409	1.7000	21.25
22	VVWLPLNSA	775	1.7000	21.25
23	LRKAARRHR	412	1.6000	20.00
24	VVRLSPDTA	734	1.6000	20.00
25	WLPLNSAGS	777	1.6000	20.00
26	IGSIVKIGA	795	1.5000	18.75
27	MSGRLIKTV	437	1.4000	17.50
28	LEPVGACRQ	53	1.2000	15.00
29	YRTFEPALR	631	1.2000	15.00
30	LAALLVGGI	565	1.1000	13.75
31	MGIQIPRFC	40	0.9000	11.25
32	VGGRVTWED	332	0.9000	11.25
33	VVLLVGFEP	393	0.9000	11.25
34	VIIVGERLA	471	0.9000	11.25
35	IVGERLATV	473	0.8000	10.00
36	LHKMSGRLI	434	0.6000	7.50
37	VGGIEPADF	570	0.5000	6.25
38	LGIWDGKHA	679	0.5000	6.25
39	MVTLTIDGV	15	0.4000	5.00
40	VRTQLTSEI	86	0.4000	5.00
41	FRARPHSAE	359	0.4000	5.00
42	IQIPRFCDH	42	0.3800	4.75
43	WHIAELPAA	540	0.3000	3.75
44	IYADEPFES	195	0.2000	2.50
45	MLLDEGRLQ	712	0.2000	2.50
46	VSSPSVCEH	233	0.1800	2.25
47	LMGIQIPRF	39	0.1000	1.25
48	IAPFATGGL	426	0.1000	1.25
49	IIVGERLAT	472	0.1000	1.25
50	LLPGGRPLA	520	0.1000	1.25
51	VHRQLRVTI	787	0.1000	1.25
52	VMELLLINH	102	0.0800	1.00
53	MELLLINHP	103	-0.1000	0
54	LATVPGGLS	478	-0.2000	0
55	VTIGSIVKI	793	-0.2000	0
56	FESYFSGNT	201	-0.3000	0
57	MAVAAQGLA	314	-0.3000	0
58	FLAARIAGR	371	-0.3000	0

59	LAWVPRRAG	499	-0.3000	0
60	LELRHSTVT	597	-0.3000	0
61	ILTGWRMLL	706	-0.3000	0
62	VYTIAPFAT	423	-0.4000	0
63	VGACRQCLV	56	-0.5000	0
64	VVFPVAPTT	610	-0.5000	0
65	VTVSTSRGS	753	-0.5000	0
66	VEGQRKPLA	66	-0.6000	0
67	LQQVGIYAD	190	-0.6000	0
68	VLVGGRVTW	330	-0.6000	0
69	LESAPVVLL	388	-0.6000	0
70	LRGSTLQAG	638	-0.6000	0
71	LLLINHPLD	105	-0.7000	0
72	ICPVGALTG	212	-0.7000	0
73	FVNWEGRYR	624	-0.7000	0
74	LRRLAGDDP	258	-0.8000	0
75	VAAQGLAAA	316	-0.8000	0
76	LVGFEPEDE	396	-0.8000	0
77	LPTLLPGGR	517	-0.8000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	YRFRARPFD	223	5.1000	59.30
2	MVVRTQLTS	84	5.0000	58.14
3	VLRRLAGDD	257	4.5000	52.33
4	LRLRKAARR	410	4.5000	52.33
5	VFLRLRKAA	408	4.3000	50.00
6	LVIRAAELM	32	4.2000	48.84
7	VGGRVTWED	332	3.6000	41.86
8	VQICPVGAL	210	3.4000	39.53
9	FRARPHSAE	359	3.4000	39.53
10	MQERGALQQ	184	3.3000	38.37
11	VVSLELRHS	594	3.3000	38.37
12	LCARCTRFS	165	3.2000	37.21
13	IVFLRLRKA	407	3.2000	37.21
14	LAARIAGRH	372	3.1000	36.05

15	LLDRERCIL	157	3.0000	34.88
16	VPVYTIAPF	421	2.8000	32.56
17	LLINHPLDC	106	2.7000	31.40
18	IDFRARPHS	357	2.3000	26.74
19	IAGRHMAVS	376	2.3000	26.74
20	LVGFEPEDE	396	2.2000	25.58
21	WVPRRAGER	501	2.2000	25.58
22	LQQVGIYAD	190	2.1000	24.42
23	IRAAELMGI	34	2.0000	23.26
24	LEPVGACRQ	53	2.0000	23.26
25	LLLINHPLD	105	2.0000	23.26
26	VARAQVCAA	531	1.9000	22.09
27	FLRLRKAAR	409	1.7000	19.77
28	MSGRLIKTV	437	1.7000	19.77
29	VVWLPLNSA	775	1.7000	19.77
30	IQIPRFCDH	42	1.6000	18.60
31	LRKAARRHR	412	1.6000	18.60
32	VVRLSPDTA	734	1.6000	18.60
33	WLPLNSAGS	777	1.6000	18.60
34	WEGRYRTFE	627	1.5000	17.44
35	IGSIVKIGA	795	1.5000	17.44
36	LVSSPSVCE	232	1.4000	16.28
37	VSSPSVCEH	233	1.4000	16.28
38	LVGGRVTWE	331	1.4000	16.28
39	LIKTVPGGE	441	1.4000	16.28
40	LSAAARLAD	485	1.4000	16.28
41	VGGIEPADF	570	1.4000	16.28
42	VMELLLINH	102	1.3000	15.12
43	VVLLVGFEP	393	1.3000	15.12
44	LAALLVGGI	565	1.3000	15.12
45	YRTFEPALR	631	1.2000	13.95
46	IAPFATGGL	426	1.1000	12.79
47	IVGERLATV	473	1.1000	12.79
48	VPTVEAARE	666	1.1000	12.79
49	LMGIQIPRF	39	1.0000	11.63
50	IIVGERLAT	472	1.0000	11.63
51	LAWVPRRAG	499	1.0000	11.63
52	MLLDEGRLQ	712	1.0000	11.63
53	MGIQIPRFC	40	0.9000	10.47
54	VVRTQLTSE	85	0.9000	10.47
55	VIIVGERLA	471	0.9000	10.47

56	LHKMSGRLI	434	0.8000	9.30
57	VFPVAPTTQ	611	0.8000	9.30
58	MVTLTIDGV	15	0.7000	8.14
59	LRGSTLQAG	638	0.7000	8.14
60	ILTGWRMLL	706	0.7000	8.14
61	VRTQLTSEI	86	0.6000	6.98
62	FESYFSGNT	201	0.6000	6.98
63	ICPVGALTG	212	0.6000	6.98
64	LELRHSTVT	597	0.6000	6.98
65	VITTPLIRD	289	0.5000	5.81
66	VYTIAPFAT	423	0.5000	5.81
67	LAALGIWDG	676	0.5000	5.81
68	LGIWDGKHA	679	0.5000	5.81
69	VIRAAELMG	33	0.4000	4.65
70	LESAPVVLL	388	0.4000	4.65
71	VCAAWHIAE	536	0.4000	4.65
72	VVFPVAPTT	610	0.4000	4.65
73	LLDEGRLQD	713	0.4000	4.65
74	MELLLINHP	103	0.3000	3.49
75	VLVGGRVTW	330	0.3000	3.49
76	FARITLGTN	347	0.3000	3.49
77	WHIAELPAA	540	0.3000	3.49
78	VHRQLRVTI	787	0.3000	3.49
79	IYADEPFES	195	0.2000	2.33
80	FVVSLELRH	593	0.2000	2.33

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	MVVRTQLTS	84	4.6000	52.87
2	LVIRAAELM	32	3.8000	43.68
3	YRFRARPFD	223	3.6000	41.38
4	LRLRKAARR	410	3.5000	40.23
5	FRARPHSAE	359	3.2000	36.78
6	VFLRLRKAA	408	2.8000	32.18
7	FLRLRKAAR	409	2.7000	31.03
8	VVWLPLNSA	775	2.7000	31.03

9	WLPLNSAGS	777	2.6000	29.89
10	WVPRRAGER	501	2.5000	28.74
11	LLINHPLDC	106	2.3000	26.44
12	WEGRYRTFE	627	2.3000	26.44
13	YRTFEPALR	631	2.2000	25.29
14	MQERGALQQ	184	2.1000	24.14
15	VVSLELRHS	594	2.0000	22.99
16	LCARCTRFS	165	1.9000	21.84
17	IVFLRLRKA	407	1.9000	21.84
18	IRAAELMGI	34	1.8000	20.69
19	VFPVAPTTQ	611	1.8000	20.69
20	VVRLSPDTA	734	1.8000	20.69
21	IDFRARPHS	357	1.5000	17.24
22	WHIAELPAA	540	1.5000	17.24
23	LELRHSTVT	597	1.5000	17.24
24	IGSIVKIGA	795	1.3800	15.86
25	IAGRHMAVS	376	1.3000	14.94
26	VRTQLTSEI	86	1.2000	13.79
27	FRARPFDLV	225	1.2000	13.79
28	LLDRERCIL	157	1.0000	11.49
29	LRHSTVTER	599	1.0000	11.49
30	MELLLINHP	103	0.9000	10.34
31	FSGNTVQIC	205	0.9000	10.34
32	VPVYTIAPF	421	0.9000	10.34
33	VARAQVCAA	531	0.9000	10.34
34	FPVAPTTQK	612	0.9000	10.34
35	VVLLVGFEP	393	0.7500	8.62
36	LTIDGVEIS	18	0.7000	8.05
37	VQICPVGAL	210	0.7000	8.05
38	FLAARIAGR	371	0.7000	8.05
39	MVTLTIDGV	15	0.6000	6.90
40	YAKFARITL	344	0.5800	6.67
41	FVVSLELRH	593	0.5800	6.67
42	YFSGNTVQI	204	0.4000	4.60
43	VGGRVTWED	332	0.4000	4.60
44	LNSAGSTVH	780	0.3800	4.37
45	LRKAARRHR	412	0.3000	3.45
46	LEPVGACRQ	53	0.2000	2.30
47	FTEAKRTFA	139	0.2000	2.30
48	LVGGRVTWE	331	0.2000	2.30
49	WRMLLDEGR	710	0.2000	2.30

50	LAARIAGRH	372	0.1800	2.07
51	VLRRLAGDD	257	0.1000	1.15
52	VHRQLRVTI	787	0.1000	1.15
53	IYADEPFES	195	0.0500	0.57
54	VMELLLINH	102	-0.0400	0
55	LVGFEPEDE	396	-0.1000	0
56	MSGRLIKTV	437	-0.1000	0
57	WDGKHAAGP	682	-0.1000	0
58	IRVGQPEMV	8	-0.2000	0
59	WSHAMAVAA	310	-0.2000	0
60	IVGERLATV	473	-0.2000	0
61	LRVTIGSIV	791	-0.2000	0
62	VTIGSIVKI	793	-0.2000	0
63	VVRTQLTSE	85	-0.3000	0
64	IIVGERLAT	472	-0.3000	0
65	VGERLATVP	474	-0.3000	0
66	ILTGWRMLL	706	-0.3000	0
67	MGIQIPRFC	40	-0.4000	0
68	VIIVGERLA	471	-0.4000	0
69	LVPTSWSHA	305	-0.5000	0
70	LLVGGIEPA	568	-0.5000	0
71	VGGIEPADF	570	-0.5000	0
72	LGVPTVEAA	664	-0.5000	0
73	VYTIAPFAT	423	-0.5500	0
74	ILCARCTRF	164	-0.6000	0
75	LRRLAGDDP	258	-0.6000	0
76	VLVGGRVTW	330	-0.6000	0
77	LESAPVVLL	388	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YRFRARPFD	223	7.2500	71.78
2	MVVRTQLTS	84	5.8000	57.43
3	FRARPHSAE	359	4.4000	43.56
4	LVIRAAELM	32	4.3000	42.57
5	MQERGALQQ	184	4.1000	40.59

6	VFLRLRKAA	408	3.9000	38.61
7	VLRRLAGDD	257	3.6000	35.64
8	WEGRYRTFE	627	3.6000	35.64
9	LLINHPLDC	106	3.5000	34.65
10	LRLRKAARR	410	3.5000	34.65
11	VGGRVTWED	332	3.4000	33.66
12	WVPRRAGER	501	3.3000	32.67
13	FVVSLELRH	593	3.0000	29.70
14	FLRLRKAAR	409	2.7000	26.73
15	IRAAELMGI	34	2.6000	25.74
16	WLPLNSAGS	777	2.6000	25.74
17	VQICPVGAL	210	2.5000	24.75
18	VVSLELRHS	594	2.5000	24.75
19	IDFRARPHS	357	2.4500	24.26
20	WHIAELPAA	540	2.4500	24.26
21	LCARCTRFS	165	2.4000	23.76
22	IVFLRLRKA	407	2.4000	23.76
23	YAKFARITL	344	2.3000	22.77
24	LVGFEPEDE	396	2.3000	22.77
25	LAARIAGRH	372	2.2000	21.78
26	LSAAARLAD	485	2.2000	21.78
27	YRTFEPALR	631	2.2000	21.78
28	LLLINHPLD	105	2.1500	21.29
29	IGSIVKIGA	795	2.1000	20.79
30	LLDRERCIL	157	2.0000	19.80
31	VMELLLINH	102	1.9000	18.81
32	LQQVGIYAD	190	1.8000	17.82
33	VPVYTIAPF	421	1.8000	17.82
34	IIVGERLAT	472	1.8000	17.82
35	FESYFSGNT	201	1.7000	16.83
36	LVGGRVTWE	331	1.5000	14.85
37	ICPVGALTG	212	1.4000	13.86
38	FARITLGTN	347	1.4000	13.86
39	IAGRHMAVS	376	1.3000	12.87
40	MSGRLIKTV	437	1.3000	12.87
41	ILTGWRMLL	706	1.3000	12.87
42	VIRAAELMG	33	1.2000	11.88
43	LLDEGRLQD	713	1.2000	11.88
44	LMGIQIPRF	39	1.1500	11.39
45	VITTPLIRD	289	1.1000	10.89
46	LEPVGACRQ	53	1.0000	9.90

47	VVRTQLTSE	85	1.0000	9.90
48	VCAAWHIAE	536	1.0000	9.90
49	VVWLPLNSA	775	1.0000	9.90
50	LVSSPSVCE	232	0.9000	8.91
51	VARAQVCAA	531	0.9000	8.91
52	VFPVAPTTQ	611	0.9000	8.91
53	VVLLVGFEP	393	0.8000	7.92
54	LRKAARRHR	412	0.8000	7.92
55	LTGWRMLLD	707	0.8000	7.92
56	FLAARIAGR	371	0.7000	6.93
57	LPGGRPLAD	521	0.7000	6.93
58	LELRHSTVT	597	0.7000	6.93
59	FEPALRGST	634	0.7000	6.93
60	IQIPRFCDH	42	0.6000	5.94
61	VVFPVAPTT	610	0.5500	5.45
62	LIKTVPGGE	441	0.5000	4.95
63	FVNWEGRYR	624	0.5000	4.95
64	VSSPSVCEH	233	0.4000	3.96
65	YTIAPFATG	424	0.4000	3.96
66	LAALLVGGI	565	0.4000	3.96
67	VGGIEPADF	570	0.4000	3.96
68	VHLGVPTVE	662	0.3000	2.97
69	LAALGIWDG	676	0.3000	2.97
70	WDGKHAAGP	682	0.3000	2.97
71	VVRLSPDTA	734	0.3000	2.97
72	LLPGGRPLA	520	0.2500	2.48
73	IAPFATGGL	426	0.2000	1.98
74	LAWVPRRAG	499	0.2000	1.98
75	MLLDEGRLQ	712	0.2000	1.98
76	LTIDGVEIS	18	0.1000	0.99
77	MGIQIPRFC	40	0.1000	0.99
78	YFSGNTVQI	204	0.1000	0.99
79	VIIVGERLA	471	0.1000	0.99
80	IVGERLATV	473	0.1000	0.99

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LLINHPLDC	106	3.5000	42.17
2	FLRLRKAAR	409	3.1000	37.35
3	WLPLNSAGS	777	3.0000	36.14
4	VVSLELRHS	594	2.9000	34.94
5	MVVRTQLTS	84	2.8000	33.73
6	IVFLRLRKA	407	2.8000	33.73
7	IGSIVKIGA	795	2.7000	32.53
8	WHIAELPAA	540	2.4500	29.52
9	IRAAELMGI	34	2.4000	28.92
10	YRTFEPALR	631	2.1000	25.30
11	FVVSLELRH	593	2.0800	25.06
12	YRFRARPFD	223	1.5500	18.67
13	VQICPVGAL	210	1.5000	18.07
14	VVWLPLNSA	775	1.4000	16.87
15	YAKFARITL	344	1.2000	14.46
16	VMELLLINH	102	1.0800	13.01
17	VFLRLRKAA	408	0.9000	10.84
18	VARAQVCAA	531	0.9000	10.84
19	LMGIQIPRF	39	0.8500	10.24
20	VVLLVGFEP	393	0.8000	9.64
21	LRKAARRHR	412	0.8000	9.64
22	MGIQIPRFC	40	0.7000	8.43
23	FLAARIAGR	371	0.7000	8.43
24	VVRLSPDTA	734	0.7000	8.43
25	LAALLVGGI	565	0.6000	7.23
26	LRLRKAARR	410	0.5000	6.02
27	FVNWEGRYR	624	0.4000	4.82
28	LEPVGACRQ	53	0.3000	3.61
29	MQERGALQQ	184	0.3000	3.61
30	WVPRRAGER	501	0.3000	3.61
31	LVIRAAELM	32	0.2000	2.41
32	ICPVGALTG	212	0.2000	2.41
33	VIIVGERLA	471	0.2000	2.41
34	IIVGERLAT	472	0.2000	2.41
35	VFPVAPTTQ	611	0.2000	2.41
36	VHRQLRVTI	787	0.2000	2.41
37	VEGQRKPLA	66	0.1500	1.81
38	VGGIEPADF	570	0.1000	1.20
39	LLLINHPLD	105	0.0500	0.60
40	VIRAAELMG	33	-0.1000	0

41	FEPALRGST	634	-0.2000	0
42	FTYATQPDV	281	-0.2500	0
43	VYTIAPFAT	423	-0.3000	0
44	MELLLINHP	103	-0.4000	0
45	LRHSTVTER	599	-0.4000	0
46	ILTGWRMLL	706	-0.4000	0
47	LLPGGRPLA	520	-0.4500	0
48	MVTLTIDGV	15	-0.5000	0
49	LSAAARLAD	485	-0.5000	0
50	IDFRARPHS	357	-0.5500	0
51	LTIDGVEIS	18	-0.6000	0
52	LCARCTRFS	165	-0.6000	0
53	LHKMSGRLI	434	-0.6000	0
54	LAALGIWDG	676	-0.6000	0
55	WSHAMAVAA	310	-0.7000	0
56	FDLVSSPSV	230	-0.7500	0
57	LQQVGIYAD	190	-0.8000	0
58	YFSGNTVQI	204	-0.8000	0
59	LVGFEPEDE	396	-0.8000	0
60	FPVAPTTQK	612	-0.8000	0
61	YAYAKFARI	342	-0.9000	0
62	YTIAPFATG	424	-0.9000	0
63	IAPFATGGL	426	-0.9000	0
64	IVGERLATV	473	-0.9000	0
65	VEISVPKGT	23	-1.0000	0
66	ISAQVLLDR	152	-1.0000	0
67	FIDMQERGA	181	-1.0000	0
68	IYADEPFES	195	-1.0000	0
69	YADLESAPV	385	-1.0000	0
70	LATVPGGLS	478	-1.0000	0
71	LAWVPRRAG	499	-1.0000	0
72	VTVSTSRGS	753	-1.0000	0
73	VVFPVAPTT	610	-1.0500	0
74	LESAPVVLL	388	-1.1000	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	VVSLELRHS	594	4.8000	57.14
2	IVFLRLRKA	407	4.7000	55.95
3	MGIQIPRFC	40	4.3000	51.19
4	MVVRTQLTS	84	3.6000	42.86
5	LLINHPLDC	106	3.5000	41.67
6	LRKAARRHR	412	3.4000	40.48
7	VFLRLRKAA	408	3.0000	35.71
8	LCARCTRFS	165	2.9000	34.52
9	VVWLPLNSA	775	2.8000	33.33
10	VHRQLRVTI	787	2.7000	32.14
11	LVIRAAELM	32	2.4000	28.57
12	VRTQLTSEI	86	2.4000	28.57
13	LRLRKAARR	410	2.4000	28.57
14	VVRLSPDTA	734	2.2000	26.19
15	IRAAELMGI	34	2.1000	25.00
16	VVLLVGFEP	393	2.1000	25.00
17	LGIWDGKHA	679	2.0000	23.81
18	VARAQVCAA	531	1.9000	22.62
19	LHKMSGRLI	434	1.8000	21.43
20	FVNWEGRYR	624	1.8000	21.43
21	VEGQRKPLA	66	1.7000	20.24
22	VTVSTSRGS	753	1.7000	20.24
23	MLLDEGRLQ	712	1.6000	19.05
24	VIIVGERLA	471	1.5000	17.86
25	YRTFEPALR	631	1.5000	17.86
26	VQICPVGAL	210	1.4000	16.67
27	FLRLRKAAR	409	1.4000	16.67
28	IYADEPFES	195	1.3000	15.48
29	WLPLNSAGS	777	1.3000	15.48
30	MQERGALQQ	184	1.1000	13.10
31	LRHSTVTER	599	1.1000	13.10
32	MVTLTIDGV	15	1.0000	11.90
33	LTIDGVEIS	18	1.0000	11.90
34	MELLLINHP	103	1.0000	11.90
35	YRFRARPFD	223	1.0000	11.90
36	WHIAELPAA	540	1.0000	11.90
37	IDFRARPHS	357	0.9000	10.71
38	LVGFEPEDE	396	0.9000	10.71
39	IGSIVKIGA	795	0.9000	10.71
40	VAAQGLAAA	316	0.8000	9.52

41	IVGERLATV	473	0.7000	8.33
42	LRGSTLQAG	638	0.6000	7.14
43	LINHPLDCP	107	0.5000	5.95
44	MGVHLGVPT	660	0.5000	5.95
45	LAALGIWDG	676	0.5000	5.95
46	VGGRVTWED	332	0.4000	4.76
47	LESAPVVLL	388	0.4000	4.76
48	VEISVPKGT	23	0.3000	3.57
49	INISAQVLL	150	0.3000	3.57
50	IIVGERLAT	472	0.3000	3.57
51	LAWVPRRAG	499	0.3000	3.57
52	LLPGGRPLA	520	0.3000	3.57
53	VFPVAPTTQ	611	0.3000	3.57
54	VTIGSIVKI	793	0.3000	3.57
55	IAGRHMAVS	376	0.2000	2.38
56	VYTIAPFAT	423	0.2000	2.38
57	VLLDRERCI	156	0.1000	1.19
58	VPVYTIAPF	421	0.1000	1.19
59	MSGRLIKTV	437	0.1000	1.19
60	VMELLLINH	102	0.0800	0.95
61	FVVSLELRH	593	0.0800	0.95
62	LNSAGSTVH	780	0.0800	0.95
63	LMGIQIPRF	39	-0.1000	0
64	ISAQVLLDR	152	-0.1000	0
65	LLDRERCIL	157	-0.1000	0
66	VLVGGRVTW	330	-0.1000	0
67	IQIPRFCDH	42	-0.1200	0
68	VIRAAELMG	33	-0.2000	0
69	FSGNTVQIC	205	-0.2000	0
70	LVSSPSVCE	232	-0.2000	0
71	LRRLAGDDP	258	-0.2000	0
72	LAALLVGGI	565	-0.2000	0
73	LASCTTVAT	73	-0.3000	0
74	FLAARIAGR	371	-0.3000	0
75	VSYADLESA	383	-0.3000	0
76	LLVGGIEPA	568	-0.3000	0

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LLINHPLDC	106	4.5000	54.22
2	VVSLELRHS	594	3.9000	46.99
3	MVVRTQLTS	84	3.8000	45.78
4	IVFLRLRKA	407	3.8000	45.78
5	IGSIVKIGA	795	3.7000	44.58
6	IRAAELMGI	34	3.4000	40.96
7	VQICPVGAL	210	2.5000	30.12
8	VVWLPLNSA	775	2.4000	28.92
9	FLRLRKAAR	409	2.1000	25.30
10	VMELLLINH	102	2.0800	25.06
11	WLPLNSAGS	777	2.0000	24.10
12	VFLRLRKAA	408	1.9000	22.89
13	VARAQVCAA	531	1.9000	22.89
14	LMGIQIPRF	39	1.8500	22.29
15	VVLLVGFEP	393	1.8000	21.69
16	LRKAARRHR	412	1.8000	21.69
17	MGIQIPRFC	40	1.7000	20.48
18	VVRLSPDTA	734	1.7000	20.48
19	LAALLVGGI	565	1.6000	19.28
20	LRLRKAARR	410	1.5000	18.07
21	WHIAELPAA	540	1.4500	17.47
22	LEPVGACRQ	53	1.3000	15.66
23	MQERGALQQ	184	1.3000	15.66
24	LVIRAAELM	32	1.2000	14.46
25	ICPVGALTG	212	1.2000	14.46
26	VIIVGERLA	471	1.2000	14.46
27	IIVGERLAT	472	1.2000	14.46
28	VFPVAPTTQ	611	1.2000	14.46
29	VHRQLRVTI	787	1.2000	14.46
30	VEGQRKPLA	66	1.1500	13.86
31	VGGIEPADF	570	1.1000	13.25
32	YRTFEPALR	631	1.1000	13.25
33	FVVSLELRH	593	1.0800	13.01
34	LLLINHPLD	105	1.0500	12.65
35	VRTQLTSEI	86	1.0000	12.05
36	LGIWDGKHA	679	1.0000	12.05
37	VIRAAELMG	33	0.9000	10.84
38	VYTIAPFAT	423	0.7000	8.43
39	MELLLINHP	103	0.6000	7.23

40	LRHSTVTER	599	0.6000	7.23
41	ILTGWRMLL	706	0.6000	7.23
42	YRFRARPFD	223	0.5500	6.63
43	LLPGGRPLA	520	0.5500	6.63
44	MVTLTIDGV	15	0.5000	6.02
45	LSAAARLAD	485	0.5000	6.02
46	IDFRARPHS	357	0.4500	5.42
47	LTIDGVEIS	18	0.4000	4.82
48	LCARCTRFS	165	0.4000	4.82
49	LHKMSGRLI	434	0.4000	4.82
50	LAALGIWDG	676	0.4000	4.82
51	LQQVGIYAD	190	0.2000	2.41
52	YAKFARITL	344	0.2000	2.41
53	LVGFEPEDE	396	0.2000	2.41
54	IAPFATGGL	426	0.1000	1.20
55	IVGERLATV	473	0.1000	1.20
56	VVFPVAPTT	610	-0.0500	0
57	LESAPVVLL	388	-0.1000	0
58	VITTPLIRD	289	-0.2000	0
59	MAVAAQGLA	314	-0.2000	0
60	VAAQGLAAA	316	-0.2000	0
61	LRGSTLQAG	638	-0.2000	0
62	INISAQVLL	150	-0.3000	0
63	FLAARIAGR	371	-0.3000	0
64	LPTLLPGGR	517	-0.3000	0
65	MLLDEGRLQ	712	-0.3000	0
66	IQIPRFCDH	42	-0.3200	0
67	LNSAGSTVH	780	-0.3200	0
68	VTIGSIVKI	793	-0.4000	0
69	IRVGQPEMV	8	-0.5000	0
70	VGACRQCLV	56	-0.5000	0
71	VSSPSVCEH	233	-0.5200	0
72	VVRTQLTSE	85	-0.6000	0
73	VSYADLESA	383	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LLINHPLDC	106	4.5000	54.22
2	VVSLELRHS	594	3.9000	46.99
3	MVVRTQLTS	84	3.8000	45.78
4	IVFLRLRKA	407	3.8000	45.78
5	IGSIVKIGA	795	3.7000	44.58
6	IRAAELMGI	34	3.4000	40.96
7	VQICPVGAL	210	2.5000	30.12
8	VVWLPLNSA	775	2.4000	28.92
9	FLRLRKAAR	409	2.1000	25.30
10	VMELLLINH	102	2.0800	25.06
11	WLPLNSAGS	777	2.0000	24.10
12	VFLRLRKAA	408	1.9000	22.89
13	VARAQVCAA	531	1.9000	22.89
14	LMGIQIPRF	39	1.8500	22.29
15	VVLLVGFEP	393	1.8000	21.69
16	LRKAARRHR	412	1.8000	21.69
17	MGIQIPRFC	40	1.7000	20.48
18	VVRLSPDTA	734	1.7000	20.48
19	LAALLVGGI	565	1.6000	19.28
20	LRLRKAARR	410	1.5000	18.07
21	WHIAELPAA	540	1.4500	17.47
22	LEPVGACRQ	53	1.3000	15.66
23	MQERGALQQ	184	1.3000	15.66
24	LVIRAAELM	32	1.2000	14.46
25	ICPVGALTG	212	1.2000	14.46
26	VIIVGERLA	471	1.2000	14.46
27	IIVGERLAT	472	1.2000	14.46
28	VFPVAPTTQ	611	1.2000	14.46
29	VHRQLRVTI	787	1.2000	14.46
30	VEGQRKPLA	66	1.1500	13.86
31	VGGIEPADF	570	1.1000	13.25
32	YRTFEPALR	631	1.1000	13.25
33	FVVSLELRH	593	1.0800	13.01
34	LLLINHPLD	105	1.0500	12.65
35	VRTQLTSEI	86	1.0000	12.05
36	LGIWDGKHA	679	1.0000	12.05
37	VIRAAELMG	33	0.9000	10.84
38	VYTIAPFAT	423	0.7000	8.43
39	MELLLINHP	103	0.6000	7.23
40	LRHSTVTER	599	0.6000	7.23

41	ILTGWRMLL	706	0.6000	7.23
42	YRFRARPFD	223	0.5500	6.63
43	LLPGGRPLA	520	0.5500	6.63
44	MVTLTIDGV	15	0.5000	6.02
45	LSAAARLAD	485	0.5000	6.02
46	IDFRARPHS	357	0.4500	5.42
47	LTIDGVEIS	18	0.4000	4.82
48	LCARCTRFS	165	0.4000	4.82
49	LHKMSGRLI	434	0.4000	4.82
50	LAALGIWDG	676	0.4000	4.82
51	LQQVGIYAD	190	0.2000	2.41
52	YAKFARITL	344	0.2000	2.41
53	LVGFEPEDE	396	0.2000	2.41
54	IAPFATGGL	426	0.1000	1.20
55	IVGERLATV	473	0.1000	1.20
56	VVFPVAPTT	610	-0.0500	0
57	LESAPVVLL	388	-0.1000	0
58	VITTPLIRD	289	-0.2000	0
59	MAVAAQGLA	314	-0.2000	0
60	VAAQGLAAA	316	-0.2000	0
61	LRGSTLQAG	638	-0.2000	0
62	INISAQVLL	150	-0.3000	0
63	FLAARIAGR	371	-0.3000	0
64	LPTLLPGGR	517	-0.3000	0
65	MLLDEGRLQ	712	-0.3000	0
66	IQIPRFCDH	42	-0.3200	0
67	LNSAGSTVH	780	-0.3200	0
68	VTIGSIVKI	793	-0.4000	0
69	IRVGQPEMV	8	-0.5000	0
70	VGACRQCLV	56	-0.5000	0
71	VSSPSVCEH	233	-0.5200	0
72	VVRTQLTSE	85	-0.6000	0
73	VSYADLESA	383	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score

1	LTIDGVEIS	18	5.5000	60.44
2	IYADEPFES	195	4.9000	53.85
3	LLPGGRPLA	520	3.5000	38.46
4	LLINHPLDC	106	3.4000	37.36
5	IRAAELMGI	34	3.2000	35.16
6	LRHSTVTER	599	3.2000	35.16
7	MLLDEGRLQ	712	3.2000	35.16
8	VQICPVGAL	210	3.0000	32.97
9	IGSIVKIGA	795	2.9000	31.87
10	IRVGQPEMV	8	2.8000	30.77
11	VRTQLTSEI	86	2.7700	30.44
12	VVRLSPDTA	734	2.7000	29.67
13	ILTGWRMLL	706	2.6000	28.57
14	VTIGSIVKI	793	2.6000	28.57
15	LIRDGGDPK	294	2.5000	27.47
16	LLVGGIEPA	568	2.5000	27.47
17	VHRQLRVTI	787	2.4000	26.37
18	VEGQRKPLA	66	2.3000	25.27
19	VVSLELRHS	594	2.3000	25.27
20	VVWLPLNSA	775	2.2100	24.29
21	LMGIQIPRF	39	2.2000	24.18
22	MVVRTQLTS	84	2.2000	24.18
23	VLVGGRVTW	330	2.2000	24.18
24	LVGGRVTWE	331	2.2000	24.18
25	IVFLRLRKA	407	2.2000	24.18
26	WHIAELPAA	540	2.2000	24.18
27	LRGSTLQAG	638	2.2000	24.18
28	IIVGERLAT	472	2.1000	23.08
29	LVIRAAELM	32	2.0000	21.98
30	VFPVAPTTQ	611	2.0000	21.98
31	LSPDTAAEI	737	2.0000	21.98
32	INISAQVLL	150	1.9000	20.88
33	VARAQVCAA	531	1.9000	20.88
34	VLLDRERCI	156	1.7000	18.68
35	MGIQIPRFC	40	1.6000	17.58
36	VVLLVGFEP	393	1.6000	17.58
37	MVTLTIDGV	15	1.5000	16.48
38	LLLINHPLD	105	1.4000	15.38
39	LVSSPSVCE	232	1.4000	15.38
40	LAGDDPEVN	261	1.4000	15.38
41	VVFPVAPTT	610	1.4000	15.38

42	VRLSPDTAA	735	1.4000	15.38
43	LRKAARRHR	412	1.3000	14.29
44	YFSGNTVQI	204	1.2000	13.19
45	LRLRKAARR	410	1.2000	13.19
46	VYTIAPFAT	423	1.2000	13.19
47	FVVSLELRH	593	1.1800	12.97
48	IAGDPFIDM	176	1.1000	12.09
49	YRFRARPFD	223	1.0000	10.99
50	FLRLRKAAR	409	1.0000	10.99
51	LAALLVGGI	565	1.0000	10.99
52	VHLGVPTVE	662	1.0000	10.99
53	LGVPTVEAA	664	1.0000	10.99
54	LEPVGACRQ	53	0.9000	9.89
55	IDFRARPHS	357	0.9000	9.89
56	VFLRLRKAA	408	0.9000	9.89
57	VTVSTSRGS	753	0.9000	9.89
58	WLPLNSAGS	777	0.9000	9.89
59	LNSAGSTVH	780	0.8800	9.67
60	LQDGEPYLA	719	0.8500	9.34
61	LATGAVGDL	456	0.8000	8.79
62	IVGERLATV	473	0.8000	8.79
63	VEISVPKGT	23	0.7000	7.69
64	LESAPVVLL	388	0.7000	7.69
65	VGGIEPADF	570	0.7000	7.69
66	VATDDMVVR	79	0.6000	6.59
67	VMELLLINH	102	0.5800	6.37
68	WNCDKGRWA	272	0.5000	5.49
69	VSYADLESA	383	0.5000	5.49
70	LEAGALPTL	512	0.5000	5.49
71	MELLLINHP	103	0.4100	4.51
72	LVGGIEPAD	569	0.4000	4.40
73	IQIPRFCDH	42	0.3800	4.18
74	LRVTIGSIV	791	0.3700	4.07
75	LRRLAGDDP	258	0.3000	3.30
76	MAVAAQGLA	314	0.3000	3.30
77	VIIVGERLA	471	0.3000	3.30
78	VVRTQLTSE	85	0.2000	2.20
79	IDMQERGAL	182	0.2000	2.20
80	FSGNTVQIC	205	0.2000	2.20

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	VVSLELRHS	594	3.8000	45.24
2	IVFLRLRKA	407	3.7000	44.05
3	MGIQIPRFC	40	3.3000	39.29
4	FVNWEGRYR	624	2.8000	33.33
5	MVVRTQLTS	84	2.6000	30.95
6	LLINHPLDC	106	2.5000	29.76
7	YRTFEPALR	631	2.5000	29.76
8	FLRLRKAAR	409	2.4000	28.57
9	LRKAARRHR	412	2.4000	28.57
10	WLPLNSAGS	777	2.3000	27.38
11	YRFRARPFD	223	2.0000	23.81
12	VFLRLRKAA	408	2.0000	23.81
13	WHIAELPAA	540	2.0000	23.81
14	LCARCTRFS	165	1.9000	22.62
15	VVWLPLNSA	775	1.8000	21.43
16	VHRQLRVTI	787	1.7000	20.24
17	LVIRAAELM	32	1.4000	16.67
18	VRTQLTSEI	86	1.4000	16.67
19	LRLRKAARR	410	1.4000	16.67
20	VVRLSPDTA	734	1.2000	14.29
21	IRAAELMGI	34	1.1000	13.10
22	VVLLVGFEP	393	1.1000	13.10
23	FVVSLELRH	593	1.0800	12.86
24	LGIWDGKHA	679	1.0000	11.90
25	VARAQVCAA	531	0.9000	10.71
26	FSGNTVQIC	205	0.8000	9.52
27	LHKMSGRLI	434	0.8000	9.52
28	VEGQRKPLA	66	0.7000	8.33
29	FLAARIAGR	371	0.7000	8.33
30	VTVSTSRGS	753	0.7000	8.33
31	MLLDEGRLQ	712	0.6000	7.14
32	VIIVGERLA	471	0.5000	5.95
33	FIDMQERGA	181	0.4000	4.76
34	VQICPVGAL	210	0.4000	4.76
35	IYADEPFES	195	0.3000	3.57
36	YAKFARITL	344	0.3000	3.57

37	MQERGALQQ	184	0.1000	1.19
38	WVPRRAGER	501	0.1000	1.19
39	LRHSTVTER	599	0.1000	1.19
40	YFSGNTVQI	204	-0.1000	0
41	WNCDKGRWA	272	-0.1000	0
42	IDFRARPHS	357	-0.1000	0
43	LVGFEPEDE	396	-0.1000	0
44	IGSIVKIGA	795	-0.1000	0
45	WSHAMAVAA	310	-0.2000	0
46	VAAQGLAAA	316	-0.2000	0
47	FRARPHSAE	359	-0.3000	0
48	IVGERLATV	473	-0.3000	0
49	FPVAPTTQK	612	-0.4000	0
50	LRGSTLQAG	638	-0.4000	0
51	WRMLLDEGR	710	-0.4000	0
52	FCDHPLLEP	47	-0.5000	0
53	LINHPLDCP	107	-0.5000	0
54	MGVHLGVPT	660	-0.5000	0
55	LAALGIWDG	676	-0.5000	0
56	VGGRVTWED	332	-0.6000	0
57	LESAPVVLL	388	-0.6000	0
58	YLAGTARTP	725	-0.6000	0
59	VEISVPKGT	23	-0.7000	0
60	INISAQVLL	150	-0.7000	0
61	FTYATQPDV	281	-0.7000	0
62	IIVGERLAT	472	-0.7000	0
63	LAWVPRRAG	499	-0.7000	0
64	LLPGGRPLA	520	-0.7000	0
65	VFPVAPTTQ	611	-0.7000	0
66	VTIGSIVKI	793	-0.7000	0
67	IAGRHMAVS	376	-0.8000	0
68	VYTIAPFAT	423	-0.8000	0
69	VLLDRERCI	156	-0.9000	0
70	YAYAKFARI	342	-0.9000	0
71	VPVYTIAPF	421	-0.9000	0
72	YTIAPFATG	424	-0.9000	0
73	MSGRLIKTV	437	-0.9000	0
74	VMELLLINH	102	-0.9200	0
75	LNSAGSTVH	780	-0.9200	0
76	IRVGQPEMV	8	-1.0000	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	FVNWEGRYR	624	4.3000	48.86
2	VVSLELRHS	594	4.2000	47.73
3	YRTFEPALR	631	4.0000	45.45
4	FLRLRKAAR	409	3.9000	44.32
5	LRKAARRHR	412	3.9000	44.32
6	IVFLRLRKA	407	3.7000	42.05
7	MGIQIPRFC	40	3.3000	37.50
8	YRFRARPFD	223	3.1000	35.23
9	MVVRTQLTS	84	3.0000	34.09
10	LVIRAAELM	32	2.9000	32.95
11	LRLRKAARR	410	2.9000	32.95
12	WLPLNSAGS	777	2.7000	30.68
13	VHRQLRVTI	787	2.6000	29.55
14	LLINHPLDC	106	2.5000	28.41
15	VRTQLTSEI	86	2.3000	26.14
16	LCARCTRFS	165	2.3000	26.14
17	FLAARIAGR	371	2.2000	25.00
18	VVLLVGFEP	393	2.1000	23.86
19	IRAAELMGI	34	2.0000	22.73
20	VFLRLRKAA	408	2.0000	22.73
21	WHIAELPAA	540	2.0000	22.73
22	VVWLPLNSA	775	1.8000	20.45
23	LHKMSGRLI	434	1.7000	19.32
24	WVPRRAGER	501	1.6000	18.18
25	LRHSTVTER	599	1.6000	18.18
26	VQICPVGAL	210	1.3600	15.45
27	LVGFEPEDE	396	1.3000	14.77
28	YAKFARITL	344	1.2600	14.32
29	VVRLSPDTA	734	1.2000	13.64
30	FRARPHSAE	359	1.1000	12.50
31	WRMLLDEGR	710	1.1000	12.50
32	VTVSTSRGS	753	1.1000	12.50
33	MVTLTIDGV	15	1.0000	11.36
34	MELLLINHP	103	1.0000	11.36
35	VPVYTIAPF	421	1.0000	11.36

36	LRGSTLQAG	638	1.0000	11.36
37	LGIWDGKHA	679	1.0000	11.36
38	VARAQVCAA	531	0.9000	10.23
39	LAALGIWDG	676	0.9000	10.23
40	LMGIQIPRF	39	0.8000	9.09
41	YFSGNTVQI	204	0.8000	9.09
42	FSGNTVQIC	205	0.8000	9.09
43	VEGQRKPLA	66	0.7000	7.95
44	IYADEPFES	195	0.7000	7.95
45	IVGERLATV	473	0.7000	7.95
46	LAWVPRRAG	499	0.7000	7.95
47	FCDHPLLEP	47	0.5000	5.68
48	LINHPLDCP	107	0.5000	5.68
49	VGGRVTWED	332	0.5000	5.68
50	YTIAPFATG	424	0.5000	5.68
51	VIIVGERLA	471	0.5000	5.68
52	VGGIEPADF	570	0.5000	5.68
53	FVVSLELRH	593	0.5000	5.68
54	LTIDGVEIS	18	0.4000	4.55
55	ISAQVLLDR	152	0.4000	4.55
56	FIDMQERGA	181	0.4000	4.55
57	YLAGTARTP	725	0.4000	4.55
58	LESAPVVLL	388	0.3600	4.09
59	FTYATQPDV	281	0.3000	3.41
60	IDFRARPHS	357	0.3000	3.41
61	WEGRYRTFE	627	0.3000	3.41
62	INISAQVLL	150	0.2600	2.95
63	VIRAAELMG	33	0.2000	2.27
64	LVSSPSVCE	232	0.2000	2.27
65	MGVHLGVPT	660	0.2000	2.27
66	VTIGSIVKI	793	0.2000	2.27
67	FATGGLHKM	429	0.1000	1.14
68	MSGRLIKTV	437	0.1000	1.14
69	LQNQAMSNG	125	-0.1000	0
70	WNCDKGRWA	272	-0.1000	0
71	LAAARGRTG	321	-0.1000	0
72	VYTIAPFAT	423	-0.1000	0
73	MLLDEGRLQ	712	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVSLELRHS	594	4.8000	57.14
2	IVFLRLRKA	407	4.7000	55.95
3	MGIQIPRFC	40	4.3000	51.19
4	MVVRTQLTS	84	3.6000	42.86
5	LLINHPLDC	106	3.5000	41.67
6	LRKAARRHR	412	3.4000	40.48
7	VFLRLRKAA	408	3.0000	35.71
8	LCARCTRFS	165	2.9000	34.52
9	VVWLPLNSA	775	2.8000	33.33
10	VHRQLRVTI	787	2.7000	32.14
11	LVIRAAELM	32	2.4000	28.57
12	VRTQLTSEI	86	2.4000	28.57
13	LRLRKAARR	410	2.4000	28.57
14	VVRLSPDTA	734	2.2000	26.19
15	IRAAELMGI	34	2.1000	25.00
16	VVLLVGFEP	393	2.1000	25.00
17	LGIWDGKHA	679	2.0000	23.81
18	VARAQVCAA	531	1.9000	22.62
19	LHKMSGRLI	434	1.8000	21.43
20	FVNWEGRYR	624	1.8000	21.43
21	VEGQRKPLA	66	1.7000	20.24
22	VTVSTSRGS	753	1.7000	20.24
23	MLLDEGRLQ	712	1.6000	19.05
24	VIIVGERLA	471	1.5000	17.86
25	YRTFEPALR	631	1.5000	17.86
26	VQICPVGAL	210	1.4000	16.67
27	FLRLRKAAR	409	1.4000	16.67
28	IYADEPFES	195	1.3000	15.48
29	WLPLNSAGS	777	1.3000	15.48
30	MQERGALQQ	184	1.1000	13.10
31	LRHSTVTER	599	1.1000	13.10
32	MVTLTIDGV	15	1.0000	11.90
33	LTIDGVEIS	18	1.0000	11.90
34	MELLLINHP	103	1.0000	11.90
35	YRFRARPFD	223	1.0000	11.90
36	WHIAELPAA	540	1.0000	11.90
37	IDFRARPHS	357	0.9000	10.71

38	LVGFEPEDE	396	0.9000	10.71
39	IGSIVKIGA	795	0.9000	10.71
40	VAAQGLAAA	316	0.8000	9.52
41	IVGERLATV	473	0.7000	8.33
42	LRGSTLQAG	638	0.6000	7.14
43	LINHPLDCP	107	0.5000	5.95
44	MGVHLGVPT	660	0.5000	5.95
45	LAALGIWDG	676	0.5000	5.95
46	VGGRVTWED	332	0.4000	4.76
47	LESAPVVLL	388	0.4000	4.76
48	VEISVPKGT	23	0.3000	3.57
49	INISAQVLL	150	0.3000	3.57
50	IIVGERLAT	472	0.3000	3.57
51	LAWVPRRAG	499	0.3000	3.57
52	LLPGGRPLA	520	0.3000	3.57
53	VFPVAPTTQ	611	0.3000	3.57
54	VTIGSIVKI	793	0.3000	3.57
55	IAGRHMAVS	376	0.2000	2.38
56	VYTIAPFAT	423	0.2000	2.38
57	VLLDRERCI	156	0.1000	1.19
58	VPVYTIAPF	421	0.1000	1.19
59	MSGRLIKTV	437	0.1000	1.19
60	VMELLLINH	102	0.0800	0.95
61	FVVSLELRH	593	0.0800	0.95
62	LNSAGSTVH	780	0.0800	0.95
63	LMGIQIPRF	39	-0.1000	0
64	ISAQVLLDR	152	-0.1000	0
65	LLDRERCIL	157	-0.1000	0
66	VLVGGRVTW	330	-0.1000	0
67	IQIPRFCDH	42	-0.1200	0
68	VIRAAELMG	33	-0.2000	0
69	FSGNTVQIC	205	-0.2000	0
70	LVSSPSVCE	232	-0.2000	0
71	LRRLAGDDP	258	-0.2000	0
72	LAALLVGGI	565	-0.2000	0
73	LASCTTVAT	73	-0.3000	0
74	FLAARIAGR	371	-0.3000	0
75	VSYADLESA	383	-0.3000	0
76	LLVGGIEPA	568	-0.3000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	FLRLRKAAR	409	4.6000	52.87
2	YRTFEPALR	631	3.6000	41.38
3	LLINHPLDC	106	3.5000	40.23
4	WLPLNSAGS	777	3.4000	39.08
5	IRAAELMGI	34	3.3000	37.93
6	VVSLELRHS	594	3.3000	37.93
7	MVVRTQLTS	84	3.2000	36.78
8	IVFLRLRKA	407	2.8000	32.18
9	LMGIQIPRF	39	2.7500	31.61
10	IGSIVKIGA	795	2.7000	31.03
11	YRFRARPFD	223	2.6500	30.46
12	VQICPVGAL	210	2.4600	28.28
13	WHIAELPAA	540	2.4500	28.16
14	LRKAARRHR	412	2.3000	26.44
15	FLAARIAGR	371	2.2000	25.29
16	YAKFARITL	344	2.1600	24.83
17	LRLRKAARR	410	2.0000	22.99
18	VGGIEPADF	570	2.0000	22.99
19	FVNWEGRYR	624	1.9000	21.84
20	VVLLVGFEP	393	1.8000	20.69
21	WVPRRAGER	501	1.8000	20.69
22	LVIRAAELM	32	1.7000	19.54
23	ICPVGALTG	212	1.6000	18.39
24	LAALLVGGI	565	1.5000	17.24
25	FVVSLELRH	593	1.5000	17.24
26	WRMLLDEGR	710	1.5000	17.24
27	VVWLPLNSA	775	1.4000	16.09
28	VIRAAELMG	33	1.3000	14.94
29	LLLINHPLD	105	1.1500	13.22
30	LRHSTVTER	599	1.1000	12.64
31	VHRQLRVTI	787	1.1000	12.64
32	VRTQLTSEI	86	0.9000	10.34
33	VFLRLRKAA	408	0.9000	10.34
34	IIVGERLAT	472	0.9000	10.34
35	VARAQVCAA	531	0.9000	10.34
36	FARITLGTN	347	0.8000	9.20

37	LAALGIWDG	676	0.8000	9.20
38	FTYATQPDV	281	0.7500	8.62
39	MGIQIPRFC	40	0.7000	8.05
40	VVRLSPDTA	734	0.7000	8.05
41	MELLLINHP	103	0.6000	6.90
42	LVGFEPEDE	396	0.6000	6.90
43	LSAAARLAD	485	0.6000	6.90
44	ILTGWRMLL	706	0.5600	6.44
45	MVTLTIDGV	15	0.5000	5.75
46	VMELLLINH	102	0.5000	5.75
47	ISAQVLLDR	152	0.5000	5.75
48	YTIAPFATG	424	0.5000	5.75
49	FEPALRGST	634	0.5000	5.75
50	VYTIAPFAT	423	0.4000	4.60
51	LAWVPRRAG	499	0.4000	4.60
52	LQQVGIYAD	190	0.3000	3.45
53	LHKMSGRLI	434	0.3000	3.45
54	FDLVSSPSV	230	0.2500	2.87
55	VIIVGERLA	471	0.2000	2.30
56	LPTLLPGGR	517	0.2000	2.30
57	LRGSTLQAG	638	0.2000	2.30
58	VEGQRKPLA	66	0.1500	1.72
59	YFSGNTVQI	204	0.1000	1.15
60	IVGERLATV	473	0.1000	1.15
61	IAPFATGGL	426	0.0600	0.69
62	VITTPLIRD	289	-0.1000	0
63	VPVYTIAPF	421	-0.1000	0
64	LESAPVVLL	388	-0.1400	0
65	IDFRARPHS	357	-0.1500	0
66	LTIDGVEIS	18	-0.2000	0
67	VVRTQLTSE	85	-0.2000	0
68	LCARCTRFS	165	-0.2000	0
69	FRARPHSAE	359	-0.2000	0
70	VEISVPKGT	23	-0.3000	0
71	LAALDATGF	585	-0.3000	0
72	INISAQVLL	150	-0.3400	0
73	VVFPVAPTT	610	-0.3500	0
74	LEPVGACRQ	53	-0.4000	0
75	ILCARCTRF	164	-0.4000	0

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVSLELRHS	594	5.2000	59.09
2	LRKAARRHR	412	4.9000	55.68
3	IVFLRLRKA	407	4.7000	53.41
4	MGIQIPRFC	40	4.3000	48.86
5	MVVRTQLTS	84	4.0000	45.45
6	LVIRAAELM	32	3.9000	44.32
7	LRLRKAARR	410	3.9000	44.32
8	VHRQLRVTI	787	3.6000	40.91
9	LLINHPLDC	106	3.5000	39.77
10	VRTQLTSEI	86	3.3000	37.50
11	LCARCTRFS	165	3.3000	37.50
12	FVNWEGRYR	624	3.3000	37.50
13	VVLLVGFEP	393	3.1000	35.23
14	IRAAELMGI	34	3.0000	34.09
15	VFLRLRKAA	408	3.0000	34.09
16	YRTFEPALR	631	3.0000	34.09
17	FLRLRKAAR	409	2.9000	32.95
18	VVWLPLNSA	775	2.8000	31.82
19	LHKMSGRLI	434	2.7000	30.68
20	LRHSTVTER	599	2.6000	29.55
21	VQICPVGAL	210	2.3600	26.82
22	LVGFEPEDE	396	2.3000	26.14
23	VVRLSPDTA	734	2.2000	25.00
24	YRFRARPFD	223	2.1000	23.86
25	VTVSTSRGS	753	2.1000	23.86
26	MVTLTIDGV	15	2.0000	22.73
27	MELLLINHP	103	2.0000	22.73
28	VPVYTIAPF	421	2.0000	22.73
29	LRGSTLQAG	638	2.0000	22.73
30	LGIWDGKHA	679	2.0000	22.73
31	VARAQVCAA	531	1.9000	21.59
32	LAALGIWDG	676	1.9000	21.59
33	LMGIQIPRF	39	1.8000	20.45
34	VEGQRKPLA	66	1.7000	19.32
35	IYADEPFES	195	1.7000	19.32
36	IVGERLATV	473	1.7000	19.32

37	LAWVPRRAG	499	1.7000	19.32
38	WLPLNSAGS	777	1.7000	19.32
39	LINHPLDCP	107	1.5000	17.05
40	VGGRVTWED	332	1.5000	17.05
41	VIIVGERLA	471	1.5000	17.05
42	VGGIEPADF	570	1.5000	17.05
43	LTIDGVEIS	18	1.4000	15.91
44	ISAQVLLDR	152	1.4000	15.91
45	LESAPVVLL	388	1.3600	15.45
46	IDFRARPHS	357	1.3000	14.77
47	INISAQVLL	150	1.2600	14.32
48	VIRAAELMG	33	1.2000	13.64
49	LVSSPSVCE	232	1.2000	13.64
50	FLAARIAGR	371	1.2000	13.64
51	MGVHLGVPT	660	1.2000	13.64
52	VTIGSIVKI	793	1.2000	13.64
53	MSGRLIKTV	437	1.1000	12.50
54	IRVGQPEMV	8	1.0000	11.36
55	VEISVPKGT	23	1.0000	11.36
56	VLLDRERCI	156	1.0000	11.36
57	ILCARCTRF	164	1.0000	11.36
58	IIVGERLAT	472	1.0000	11.36
59	WHIAELPAA	540	1.0000	11.36
60	LQNQAMSNG	125	0.9000	10.23
61	LAAARGRTG	321	0.9000	10.23
62	VYTIAPFAT	423	0.9000	10.23
63	MLLDEGRLQ	712	0.9000	10.23
64	IGSIVKIGA	795	0.9000	10.23
65	LLDRERCIL	157	0.8600	9.77
66	LRRLAGDDP	258	0.8000	9.09
67	ITTPLIRDG	290	0.8000	9.09
68	VAAQGLAAA	316	0.8000	9.09
69	LVGGRVTWE	331	0.8000	9.09
70	VVRTQLTSE	85	0.7000	7.95
71	LAALLVGGI	565	0.7000	7.95
72	IAGRHMAVS	376	0.6000	6.82
73	WVPRRAGER	501	0.6000	6.82
74	VGACRQCLV	56	0.5000	5.68
75	LSAAARLAD	485	0.5000	5.68
76	ILTGWRMLL	706	0.4600	5.23
77	LASCTTVAT	73	0.4000	4.55

78	MQERGALQQ	184	0.4000	4.55
79	LAALDATGF	585	0.4000	4.55
80	VSLELRHST	595	0.4000	4.55

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	FVNWEGRYR	624	4.3000	48.86
2	VVSLELRHS	594	4.2000	47.73
3	YRTFEPALR	631	4.0000	45.45
4	FLRLRKAAR	409	3.9000	44.32
5	LRKAARRHR	412	3.9000	44.32
6	IVFLRLRKA	407	3.7000	42.05
7	MGIQIPRFC	40	3.3000	37.50
8	YRFRARPFD	223	3.1000	35.23
9	MVVRTQLTS	84	3.0000	34.09
10	LVIRAAELM	32	2.9000	32.95
11	LRLRKAARR	410	2.9000	32.95
12	WLPLNSAGS	777	2.7000	30.68
13	VHRQLRVTI	787	2.6000	29.55
14	LLINHPLDC	106	2.5000	28.41
15	VRTQLTSEI	86	2.3000	26.14
16	LCARCTRFS	165	2.3000	26.14
17	FLAARIAGR	371	2.2000	25.00
18	VVLLVGFEP	393	2.1000	23.86
19	IRAAELMGI	34	2.0000	22.73
20	VFLRLRKAA	408	2.0000	22.73
21	WHIAELPAA	540	2.0000	22.73
22	VVWLPLNSA	775	1.8000	20.45
23	LHKMSGRLI	434	1.7000	19.32
24	WVPRRAGER	501	1.6000	18.18
25	LRHSTVTER	599	1.6000	18.18
26	VQICPVGAL	210	1.3600	15.45
27	LVGFEPEDE	396	1.3000	14.77
28	YAKFARITL	344	1.2600	14.32
29	VVRLSPDTA	734	1.2000	13.64
30	FRARPHSAE	359	1.1000	12.50

31	WRMLLDEGR	710	1.1000	12.50
32	VTVSTSRGS	753	1.1000	12.50
33	MVTLTIDGV	15	1.0000	11.36
34	MELLLINHP	103	1.0000	11.36
35	VPVYTIAPF	421	1.0000	11.36
36	LRGSTLQAG	638	1.0000	11.36
37	LGIWDGKHA	679	1.0000	11.36
38	VARAQVCAA	531	0.9000	10.23
39	LAALGIWDG	676	0.9000	10.23
40	LMGIQIPRF	39	0.8000	9.09
41	YFSGNTVQI	204	0.8000	9.09
42	FSGNTVQIC	205	0.8000	9.09
43	VEGQRKPLA	66	0.7000	7.95
44	IYADEPFES	195	0.7000	7.95
45	IVGERLATV	473	0.7000	7.95
46	LAWVPRRAG	499	0.7000	7.95
47	FCDHPLLEP	47	0.5000	5.68
48	LINHPLDCP	107	0.5000	5.68
49	VGGRVTWED	332	0.5000	5.68
50	YTIAPFATG	424	0.5000	5.68
51	VIIVGERLA	471	0.5000	5.68
52	VGGIEPADF	570	0.5000	5.68
53	FVVSLELRH	593	0.5000	5.68
54	LTIDGVEIS	18	0.4000	4.55
55	ISAQVLLDR	152	0.4000	4.55
56	FIDMQERGA	181	0.4000	4.55
57	YLAGTARTP	725	0.4000	4.55
58	LESAPVVLL	388	0.3600	4.09
59	FTYATQPDV	281	0.3000	3.41
60	IDFRARPHS	357	0.3000	3.41
61	WEGRYRTFE	627	0.3000	3.41
62	INISAQVLL	150	0.2600	2.95
63	VIRAAELMG	33	0.2000	2.27
64	LVSSPSVCE	232	0.2000	2.27
65	MGVHLGVPT	660	0.2000	2.27
66	VTIGSIVKI	793	0.2000	2.27
67	FATGGLHKM	429	0.1000	1.14
68	MSGRLIKTV	437	0.1000	1.14
69	LQNQAMSNG	125	-0.1000	0
70	WNCDKGRWA	272	-0.1000	0
71	LAAARGRTG	321	-0.1000	0

72	VYTIAPFAT	423	-0.1000	0
73	MLLDEGRLQ	712	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVSLELRHS	594	4.8000	53.33
2	IVFLRLRKA	407	4.7000	52.22
3	MGIQIPRFC	40	4.3000	47.78
4	LVGFEPEDE	396	3.9000	43.33
5	YRFRARPFD	223	3.7000	41.11
6	MVVRTQLTS	84	3.6000	40.00
7	LVIRAAELM	32	3.5000	38.89
8	LLINHPLDC	106	3.5000	38.89
9	LRKAARRHR	412	3.4000	37.78
10	VGGRVTWED	332	3.1000	34.44
11	VFLRLRKAA	408	3.0000	33.33
12	LCARCTRFS	165	2.9000	32.22
13	VHRQLRVTI	787	2.9000	32.22
14	LVSSPSVCE	232	2.8000	31.11
15	VVWLPLNSA	775	2.8000	31.11
16	VRTQLTSEI	86	2.6000	28.89
17	VVLLVGFEP	393	2.5000	27.78
18	VQICPVGAL	210	2.4000	26.67
19	LVGGRVTWE	331	2.4000	26.67
20	LRLRKAARR	410	2.4000	26.67
21	MLLDEGRLQ	712	2.4000	26.67
22	IRAAELMGI	34	2.3000	25.56
23	VVRTQLTSE	85	2.3000	25.56
24	VVRLSPDTA	734	2.2000	24.44
25	LSAAARLAD	485	2.1000	23.33
26	LHKMSGRLI	434	2.0000	22.22
27	LGIWDGKHA	679	2.0000	22.22
28	MQERGALQQ	184	1.9000	21.11
29	VARAQVCAA	531	1.9000	21.11
30	LRGSTLQAG	638	1.9000	21.11
31	LLLINHPLD	105	1.8000	20.00

32	LQQVGIYAD	190	1.8000	20.00
33	FVNWEGRYR	624	1.8000	20.00
34	LAALGIWDG	676	1.8000	20.00
35	VEGQRKPLA	66	1.7000	18.89
36	FRARPHSAE	359	1.7000	18.89
37	VTVSTSRGS	753	1.7000	18.89
38	LAWVPRRAG	499	1.6000	17.78
39	VIIVGERLA	471	1.5000	16.67
40	YRTFEPALR	631	1.5000	16.67
41	MELLLINHP	103	1.4000	15.56
42	VLRRLAGDD	257	1.4000	15.56
43	LESAPVVLL	388	1.4000	15.56
44	FLRLRKAAR	409	1.4000	15.56
45	MGVHLGVPT	660	1.4000	15.56
46	LTGWRMLLD	707	1.4000	15.56
47	MVTLTIDGV	15	1.3000	14.44
48	VMELLLINH	102	1.3000	14.44
49	INISAQVLL	150	1.3000	14.44
50	IYADEPFES	195	1.3000	14.44
51	FVVSLELRH	593	1.3000	14.44
52	WLPLNSAGS	777	1.3000	14.44
53	LNSAGSTVH	780	1.3000	14.44
54	VEISVPKGT	23	1.2000	13.33
55	IIVGERLAT	472	1.2000	13.33
56	VHLGVPTVE	662	1.2000	13.33
57	VIRAAELMG	33	1.1000	12.22
58	IQIPRFCDH	42	1.1000	12.22
59	VYTIAPFAT	423	1.1000	12.22
60	LRHSTVTER	599	1.1000	12.22
61	VFPVAPTTQ	611	1.1000	12.22
62	LTIDGVEIS	18	1.0000	11.11
63	VPVYTIAPF	421	1.0000	11.11
64	IVGERLATV	473	1.0000	11.11
65	WHIAELPAA	540	1.0000	11.11
66	LLDEGRLQD	713	1.0000	11.11
67	LINHPLDCP	107	0.9000	10.00
68	LLDRERCIL	157	0.9000	10.00
69	VSSPSVCEH	233	0.9000	10.00
70	IDFRARPHS	357	0.9000	10.00
71	WEGRYRTFE	627	0.9000	10.00
72	IGSIVKIGA	795	0.9000	10.00

73	LMGIQIPRF	39	0.8000	8.89
74	LEPVGACRQ	53	0.8000	8.89
75	LQNQAMSNG	125	0.8000	8.89
76	VAAQGLAAA	316	0.8000	8.89
77	LAAARGRTG	321	0.8000	8.89
78	VLVGGRVTW	330	0.8000	8.89
79	VITTPLIRD	289	0.7000	7.78
80	ITTPLIRDG	290	0.7000	7.78

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FLRLRKAAR	409	4.6000	52.87
2	YRTFEPALR	631	3.6000	41.38
3	LLINHPLDC	106	3.5000	40.23
4	WLPLNSAGS	777	3.4000	39.08
5	IRAAELMGI	34	3.3000	37.93
6	VVSLELRHS	594	3.3000	37.93
7	MVVRTQLTS	84	3.2000	36.78
8	IVFLRLRKA	407	2.8000	32.18
9	LMGIQIPRF	39	2.7500	31.61
10	IGSIVKIGA	795	2.7000	31.03
11	YRFRARPFD	223	2.6500	30.46
12	VQICPVGAL	210	2.4600	28.28
13	WHIAELPAA	540	2.4500	28.16
14	LRKAARRHR	412	2.3000	26.44
15	FLAARIAGR	371	2.2000	25.29
16	YAKFARITL	344	2.1600	24.83
17	LRLRKAARR	410	2.0000	22.99
18	VGGIEPADF	570	2.0000	22.99
19	FVNWEGRYR	624	1.9000	21.84
20	VVLLVGFEP	393	1.8000	20.69
21	WVPRRAGER	501	1.8000	20.69
22	LVIRAAELM	32	1.7000	19.54
23	ICPVGALTG	212	1.6000	18.39
24	LAALLVGGI	565	1.5000	17.24
25	FVVSLELRH	593	1.5000	17.24

26	WRMLLDEGR	710	1.5000	17.24
27	VVWLPLNSA	775	1.4000	16.09
28	VIRAAELMG	33	1.3000	14.94
29	LLLINHPLD	105	1.1500	13.22
30	LRHSTVTER	599	1.1000	12.64
31	VHRQLRVTI	787	1.1000	12.64
32	VRTQLTSEI	86	0.9000	10.34
33	VFLRLRKAA	408	0.9000	10.34
34	IIVGERLAT	472	0.9000	10.34
35	VARAQVCAA	531	0.9000	10.34
36	FARITLGTN	347	0.8000	9.20
37	LAALGIWDG	676	0.8000	9.20
38	FTYATQPDV	281	0.7500	8.62
39	MGIQIPRFC	40	0.7000	8.05
40	VVRLSPDTA	734	0.7000	8.05
41	MELLLINHP	103	0.6000	6.90
42	LVGFEPEDE	396	0.6000	6.90
43	LSAAARLAD	485	0.6000	6.90
44	ILTGWRMLL	706	0.5600	6.44
45	MVTLTIDGV	15	0.5000	5.75
46	VMELLLINH	102	0.5000	5.75
47	ISAQVLLDR	152	0.5000	5.75
48	YTIAPFATG	424	0.5000	5.75
49	FEPALRGST	634	0.5000	5.75
50	VYTIAPFAT	423	0.4000	4.60
51	LAWVPRRAG	499	0.4000	4.60
52	LQQVGIYAD	190	0.3000	3.45
53	LHKMSGRLI	434	0.3000	3.45
54	FDLVSSPSV	230	0.2500	2.87
55	VIIVGERLA	471	0.2000	2.30
56	LPTLLPGGR	517	0.2000	2.30
57	LRGSTLQAG	638	0.2000	2.30
58	VEGQRKPLA	66	0.1500	1.72
59	YFSGNTVQI	204	0.1000	1.15
60	IVGERLATV	473	0.1000	1.15
61	IAPFATGGL	426	0.0600	0.69
62	VITTPLIRD	289	-0.1000	0
63	VPVYTIAPF	421	-0.1000	0
64	LESAPVVLL	388	-0.1400	0
65	IDFRARPHS	357	-0.1500	0
66	LTIDGVEIS	18	-0.2000	0

67	VVRTQLTSE	85	-0.2000	0
68	LCARCTRFS	165	-0.2000	0
69	FRARPHSAE	359	-0.2000	0
70	VEISVPKGT	23	-0.3000	0
71	LAALDATGF	585	-0.3000	0
72	INISAQVLL	150	-0.3400	0
73	VVFPVAPTT	610	-0.3500	0
74	LEPVGACRQ	53	-0.4000	0
75	ILCARCTRF	164	-0.4000	0

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FLRLRKAAR	409	3.1000	45.59
2	WLPLNSAGS	777	3.0000	44.12
3	VVSLELRHS	594	2.7000	39.71
4	IVFLRLRKA	407	2.6000	38.24
5	YRTFEPALR	631	2.1000	30.88
6	LLINHPLDC	106	1.7000	25.00
7	VQICPVGAL	210	1.4000	20.59
8	WHIAELPAA	540	1.3000	19.12
9	VVWLPLNSA	775	1.1000	16.18
10	IGSIVKIGA	795	1.1000	16.18
11	MVVRTQLTS	84	1.0000	14.71
12	VVRLSPDTA	734	1.0000	14.71
13	VARAQVCAA	531	0.9000	13.24
14	IRAAELMGI	34	0.8000	11.76
15	FLAARIAGR	371	0.7000	10.29
16	LRKAARRHR	412	0.6000	8.82
17	MGIQIPRFC	40	0.5000	7.35
18	LRLRKAARR	410	0.5000	7.35
19	LAALLVGGI	565	0.5000	7.35
20	YRFRARPFD	223	0.4000	5.88
21	LEPVGACRQ	53	0.3000	4.41
22	VVLLVGFEP	393	0.3000	4.41
23	VFLRLRKAA	408	0.3000	4.41
24	FVVSLELRH	593	0.2800	4.12

25	WVPRRAGER	501	0.2000	2.94
26	FVNWEGRYR	624	0.2000	2.94
27	VGGIEPADF	570	0.1000	1.47
28	FSGNTVQIC	205	-0.1000	0
29	FARITLGTN	347	-0.1000	0
30	MVTLTIDGV	15	-0.2000	0
31	LMGIQIPRF	39	-0.3000	0
32	FEPALRGST	634	-0.3000	0
33	VHRQLRVTI	787	-0.3000	0
34	YAKFARITL	344	-0.4000	0
35	VMELLLINH	102	-0.5200	0
36	LGIWDGKHA	679	-0.6000	0
37	MELLLINHP	103	-0.7000	0
38	LCARCTRFS	165	-0.8000	0
39	VYTIAPFAT	423	-0.8000	0
40	LHKMSGRLI	434	-0.8000	0
41	LVIRAAELM	32	-0.9000	0
42	YAYAKFARI	342	-0.9000	0
43	YTIAPFATG	424	-0.9000	0
44	IVGERLATV	473	-0.9000	0
45	VFPVAPTTQ	611	-0.9000	0
46	VEGQRKPLA	66	-1.0000	0
47	YADLESAPV	385	-1.0000	0
48	IAPFATGGL	426	-1.0000	0
49	LLLINHPLD	105	-1.1000	0
50	LATVPGGLS	478	-1.1000	0
51	WRMLLDEGR	710	-1.1000	0
52	FIDMQERGA	181	-1.2000	0
53	WSHAMAVAA	310	-1.2000	0
54	VAAQGLAAA	316	-1.2000	0
55	LAWVPRRAG	499	-1.2000	0
56	VTVSTSRGS	753	-1.2000	0
57	YFSGNTVQI	204	-1.3000	0
58	MAVAAQGLA	314	-1.3000	0
59	LRGSTLQAG	638	-1.3000	0
60	IQIPRFCDH	42	-1.3200	0
61	LRRLAGDDP	258	-1.4000	0
62	FTYATQPDV	281	-1.4000	0
63	LPTLLPGGR	517	-1.4000	0
64	LAALGIWDG	676	-1.4000	0
65	VGACRQCLV	56	-1.5000	0

66	MQERGALQQ	184	-1.5000	0
67	LQQVGIYAD	190	-1.5000	0
68	IYADEPFES	195	-1.5000	0
69	LRHSTVTER	599	-1.5000	0
70	MLLDEGRLQ	712	-1.5000	0
71	VSSPSVCEH	233	-1.5200	0
72	VEISVPKGT	23	-1.6000	0
73	ICPVGALTG	212	-1.6000	0
74	FRARPHSAE	359	-1.6000	0
75	LESAPVVLL	388	-1.6000	0
76	LLATPGAVI	464	-1.6000	0
77	IIVGERLAT	472	-1.6000	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	LLINHPLDC	106	4.5000	54.22
2	VVSLELRHS	594	3.9000	46.99
3	MVVRTQLTS	84	3.8000	45.78
4	IVFLRLRKA	407	3.8000	45.78
5	IGSIVKIGA	795	3.7000	44.58
6	IRAAELMGI	34	3.4000	40.96
7	VQICPVGAL	210	2.5000	30.12
8	VVWLPLNSA	775	2.4000	28.92
9	FLRLRKAAR	409	2.1000	25.30
10	VMELLLINH	102	2.0800	25.06
11	WLPLNSAGS	777	2.0000	24.10
12	VFLRLRKAA	408	1.9000	22.89
13	VARAQVCAA	531	1.9000	22.89
14	LMGIQIPRF	39	1.8500	22.29
15	VVLLVGFEP	393	1.8000	21.69
16	LRKAARRHR	412	1.8000	21.69
17	MGIQIPRFC	40	1.7000	20.48
18	VVRLSPDTA	734	1.7000	20.48
19	LAALLVGGI	565	1.6000	19.28
20	LRLRKAARR	410	1.5000	18.07
21	WHIAELPAA	540	1.4500	17.47

22	LEPVGACRQ	53	1.3000	15.66
23	MQERGALQQ	184	1.3000	15.66
24	LVIRAAELM	32	1.2000	14.46
25	ICPVGALTG	212	1.2000	14.46
26	VIIVGERLA	471	1.2000	14.46
27	IIVGERLAT	472	1.2000	14.46
28	VFPVAPTTQ	611	1.2000	14.46
29	VHRQLRVTI	787	1.2000	14.46
30	VEGQRKPLA	66	1.1500	13.86
31	VGGIEPADF	570	1.1000	13.25
32	YRTFEPALR	631	1.1000	13.25
33	FVVSLELRH	593	1.0800	13.01
34	LLLINHPLD	105	1.0500	12.65
35	VRTQLTSEI	86	1.0000	12.05
36	LGIWDGKHA	679	1.0000	12.05
37	VIRAAELMG	33	0.9000	10.84
38	VYTIAPFAT	423	0.7000	8.43
39	MELLLINHP	103	0.6000	7.23
40	LRHSTVTER	599	0.6000	7.23
41	ILTGWRMLL	706	0.6000	7.23
42	YRFRARPFD	223	0.5500	6.63
43	LLPGGRPLA	520	0.5500	6.63
44	MVTLTIDGV	15	0.5000	6.02
45	LSAAARLAD	485	0.5000	6.02
46	IDFRARPHS	357	0.4500	5.42
47	LTIDGVEIS	18	0.4000	4.82
48	LCARCTRFS	165	0.4000	4.82
49	LHKMSGRLI	434	0.4000	4.82
50	LAALGIWDG	676	0.4000	4.82
51	LQQVGIYAD	190	0.2000	2.41
52	YAKFARITL	344	0.2000	2.41
53	LVGFEPEDE	396	0.2000	2.41
54	IAPFATGGL	426	0.1000	1.20
55	IVGERLATV	473	0.1000	1.20
56	VVFPVAPTT	610	-0.0500	0
57	LESAPVVLL	388	-0.1000	0
58	VITTPLIRD	289	-0.2000	0
59	MAVAAQGLA	314	-0.2000	0
60	VAAQGLAAA	316	-0.2000	0
61	LRGSTLQAG	638	-0.2000	0
62	INISAQVLL	150	-0.3000	0

63	FLAARIAGR	371	-0.3000	0
64	LPTLLPGGR	517	-0.3000	0
65	MLLDEGRLQ	712	-0.3000	0
66	IQIPRFCDH	42	-0.3200	0
67	LNSAGSTVH	780	-0.3200	0
68	VTIGSIVKI	793	-0.4000	0
69	IRVGQPEMV	8	-0.5000	0
70	VGACRQCLV	56	-0.5000	0
71	VSSPSVCEH	233	-0.5200	0
72	VVRTQLTSE	85	-0.6000	0
73	VSYADLESA	383	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YRFRARPFD	223	4.2500	47.75
2	LLINHPLDC	106	3.5000	39.33
3	FVVSLELRH	593	3.3000	37.08
4	FLRLRKAAR	409	3.1000	34.83
5	WLPLNSAGS	777	3.0000	33.71
6	VVSLELRHS	594	2.9000	32.58
7	MVVRTQLTS	84	2.8000	31.46
8	IVFLRLRKA	407	2.8000	31.46
9	LLLINHPLD	105	2.7500	30.90
10	IGSIVKIGA	795	2.7000	30.34
11	IRAAELMGI	34	2.6000	29.21
12	VQICPVGAL	210	2.5000	28.09
13	WHIAELPAA	540	2.4500	27.53
14	VMELLLINH	102	2.3000	25.84
15	YAKFARITL	344	2.2000	24.72
16	LVGFEPEDE	396	2.2000	24.72
17	LSAAARLAD	485	2.2000	24.72
18	YRTFEPALR	631	2.1000	23.60
19	FARITLGTN	347	2.0000	22.47
20	LQQVGIYAD	190	1.9000	21.35
21	LMGIQIPRF	39	1.7500	19.66
22	ICPVGALTG	212	1.5000	16.85

23	VITTPLIRD	289	1.5000	16.85
24	VVRTQLTSE	85	1.4000	15.73
25	FRARPHSAE	359	1.4000	15.73
26	VVWLPLNSA	775	1.4000	15.73
27	LVIRAAELM	32	1.3000	14.61
28	VIRAAELMG	33	1.2000	13.48
29	LVSSPSVCE	232	1.2000	13.48
30	VVLLVGFEP	393	1.2000	13.48
31	LEPVGACRQ	53	1.1000	12.36
32	MQERGALQQ	184	1.1000	12.36
33	IIVGERLAT	472	1.1000	12.36
34	VCAAWHIAE	536	1.0000	11.24
35	VGGIEPADF	570	1.0000	11.24
36	VFPVAPTTQ	611	1.0000	11.24
37	VFLRLRKAA	408	0.9000	10.11
38	LIKTVPGGE	441	0.9000	10.11
39	VARAQVCAA	531	0.9000	10.11
40	LVGGRVTWE	331	0.8000	8.99
41	LRKAARRHR	412	0.8000	8.99
42	LAALLVGGI	565	0.8000	8.99
43	MGIQIPRFC	40	0.7000	7.87
44	FLAARIAGR	371	0.7000	7.87
45	FEPALRGST	634	0.7000	7.87
46	LAALGIWDG	676	0.7000	7.87
47	LTGWRMLLD	707	0.7000	7.87
48	VVRLSPDTA	734	0.7000	7.87
49	VLRRLAGDD	257	0.6000	6.74
50	VYTIAPFAT	423	0.6000	6.74
51	WEGRYRTFE	627	0.6000	6.74
52	ILTGWRMLL	706	0.6000	6.74
53	LRLRKAARR	410	0.5000	5.62
54	LLDEGRLQD	713	0.5000	5.62
55	VGGRVTWED	332	0.4000	4.49
56	YTIAPFATG	424	0.4000	4.49
57	FVNWEGRYR	624	0.4000	4.49
58	VHRQLRVTI	787	0.4000	4.49
59	LAWVPRRAG	499	0.3000	3.37
60	WVPRRAGER	501	0.3000	3.37
61	VRTQLTSEI	86	0.2000	2.25
62	VIIVGERLA	471	0.2000	2.25
63	VPTVEAARE	666	0.2000	2.25

64	VEGQRKPLA	66	0.1500	1.69
65	IAPFATGGL	426	0.1000	1.12
66	LRGSTLQAG	638	0.1000	1.12
67	FTYATQPDV	281	0.0500	0.56
68	VEISVPKGT	23	-0.1000	0
69	IQIPRFCDH	42	-0.1000	0
70	LESAPVVLL	388	-0.1000	0
71	LNSAGSTVH	780	-0.1000	0
72	VVFPVAPTT	610	-0.1500	0
73	MVTLTIDGV	15	-0.2000	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VVSLELRHS	594	4.8000	57.14
2	IVFLRLRKA	407	4.7000	55.95
3	MGIQIPRFC	40	4.3000	51.19
4	MVVRTQLTS	84	3.6000	42.86
5	LLINHPLDC	106	3.5000	41.67
6	LRKAARRHR	412	3.4000	40.48
7	VFLRLRKAA	408	3.0000	35.71
8	LCARCTRFS	165	2.9000	34.52
9	VVWLPLNSA	775	2.8000	33.33
10	VHRQLRVTI	787	2.7000	32.14
11	LVIRAAELM	32	2.4000	28.57
12	VRTQLTSEI	86	2.4000	28.57
13	LRLRKAARR	410	2.4000	28.57
14	VVRLSPDTA	734	2.2000	26.19
15	IRAAELMGI	34	2.1000	25.00
16	VVLLVGFEP	393	2.1000	25.00
17	LGIWDGKHA	679	2.0000	23.81
18	VARAQVCAA	531	1.9000	22.62
19	LHKMSGRLI	434	1.8000	21.43
20	FVNWEGRYR	624	1.8000	21.43
21	VEGQRKPLA	66	1.7000	20.24
22	VTVSTSRGS	753	1.7000	20.24
23	MLLDEGRLQ	712	1.6000	19.05

24	VIIVGERLA	471	1.5000	17.86
25	YRTFEPALR	631	1.5000	17.86
26	VQICPVGAL	210	1.4000	16.67
27	FLRLRKAAR	409	1.4000	16.67
28	IYADEPFES	195	1.3000	15.48
29	WLPLNSAGS	777	1.3000	15.48
30	MQERGALQQ	184	1.1000	13.10
31	LRHSTVTER	599	1.1000	13.10
32	MVTLTIDGV	15	1.0000	11.90
33	LTIDGVEIS	18	1.0000	11.90
34	MELLLINHP	103	1.0000	11.90
35	YRFRARPFD	223	1.0000	11.90
36	WHIAELPAA	540	1.0000	11.90
37	IDFRARPHS	357	0.9000	10.71
38	LVGFEPEDE	396	0.9000	10.71
39	IGSIVKIGA	795	0.9000	10.71
40	VAAQGLAAA	316	0.8000	9.52
41	IVGERLATV	473	0.7000	8.33
42	LRGSTLQAG	638	0.6000	7.14
43	LINHPLDCP	107	0.5000	5.95
44	MGVHLGVPT	660	0.5000	5.95
45	LAALGIWDG	676	0.5000	5.95
46	VGGRVTWED	332	0.4000	4.76
47	LESAPVVLL	388	0.4000	4.76
48	VEISVPKGT	23	0.3000	3.57
49	INISAQVLL	150	0.3000	3.57
50	IIVGERLAT	472	0.3000	3.57
51	LAWVPRRAG	499	0.3000	3.57
52	LLPGGRPLA	520	0.3000	3.57
53	VFPVAPTTQ	611	0.3000	3.57
54	VTIGSIVKI	793	0.3000	3.57
55	IAGRHMAVS	376	0.2000	2.38
56	VYTIAPFAT	423	0.2000	2.38
57	VLLDRERCI	156	0.1000	1.19
58	VPVYTIAPF	421	0.1000	1.19
59	MSGRLIKTV	437	0.1000	1.19
60	VMELLLINH	102	0.0800	0.95
61	FVVSLELRH	593	0.0800	0.95
62	LNSAGSTVH	780	0.0800	0.95
63	LMGIQIPRF	39	-0.1000	0
64	ISAQVLLDR	152	-0.1000	0

65	LLDRERCIL	157	-0.1000	0
66	VLVGGRVTW	330	-0.1000	0
67	IQIPRFCDH	42	-0.1200	0
68	VIRAAELMG	33	-0.2000	0
69	FSGNTVQIC	205	-0.2000	0
70	LVSSPSVCE	232	-0.2000	0
71	LRRLAGDDP	258	-0.2000	0
72	LAALLVGGI	565	-0.2000	0
73	LASCTTVAT	73	-0.3000	0
74	FLAARIAGR	371	-0.3000	0
75	VSYADLESA	383	-0.3000	0
76	LLVGGIEPA	568	-0.3000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VVSLELRHS	594	3.8000	45.24
2	IVFLRLRKA	407	3.7000	44.05
3	MGIQIPRFC	40	3.3000	39.29
4	FVNWEGRYR	624	2.8000	33.33
5	MVVRTQLTS	84	2.6000	30.95
6	LLINHPLDC	106	2.5000	29.76
7	YRTFEPALR	631	2.5000	29.76
8	FLRLRKAAR	409	2.4000	28.57
9	LRKAARRHR	412	2.4000	28.57
10	WLPLNSAGS	777	2.3000	27.38
11	YRFRARPFD	223	2.0000	23.81
12	VFLRLRKAA	408	2.0000	23.81
13	WHIAELPAA	540	2.0000	23.81
14	LCARCTRFS	165	1.9000	22.62
15	VVWLPLNSA	775	1.8000	21.43
16	VHRQLRVTI	787	1.7000	20.24
17	LVIRAAELM	32	1.4000	16.67
18	VRTQLTSEI	86	1.4000	16.67
19	LRLRKAARR	410	1.4000	16.67
20	VVRLSPDTA	734	1.2000	14.29
21	IRAAELMGI	34	1.1000	13.10

22	VVLLVGFEP	393	1.1000	13.10
23	FVVSLELRH	593	1.0800	12.86
24	LGIWDGKHA	679	1.0000	11.90
25	VARAQVCAA	531	0.9000	10.71
26	FSGNTVQIC	205	0.8000	9.52
27	LHKMSGRLI	434	0.8000	9.52
28	VEGQRKPLA	66	0.7000	8.33
29	FLAARIAGR	371	0.7000	8.33
30	VTVSTSRGS	753	0.7000	8.33
31	MLLDEGRLQ	712	0.6000	7.14
32	VIIVGERLA	471	0.5000	5.95
33	FIDMQERGA	181	0.4000	4.76
34	VQICPVGAL	210	0.4000	4.76
35	IYADEPFES	195	0.3000	3.57
36	YAKFARITL	344	0.3000	3.57
37	MQERGALQQ	184	0.1000	1.19
38	WVPRRAGER	501	0.1000	1.19
39	LRHSTVTER	599	0.1000	1.19
40	YFSGNTVQI	204	-0.1000	0
41	WNCDKGRWA	272	-0.1000	0
42	IDFRARPHS	357	-0.1000	0
43	LVGFEPEDE	396	-0.1000	0
44	IGSIVKIGA	795	-0.1000	0
45	WSHAMAVAA	310	-0.2000	0
46	VAAQGLAAA	316	-0.2000	0
47	FRARPHSAE	359	-0.3000	0
48	IVGERLATV	473	-0.3000	0
49	FPVAPTTQK	612	-0.4000	0
50	LRGSTLQAG	638	-0.4000	0
51	WRMLLDEGR	710	-0.4000	0
52	FCDHPLLEP	47	-0.5000	0
53	LINHPLDCP	107	-0.5000	0
54	MGVHLGVPT	660	-0.5000	0
55	LAALGIWDG	676	-0.5000	0
56	VGGRVTWED	332	-0.6000	0
57	LESAPVVLL	388	-0.6000	0
58	YLAGTARTP	725	-0.6000	0
59	VEISVPKGT	23	-0.7000	0
60	INISAQVLL	150	-0.7000	0
61	FTYATQPDV	281	-0.7000	0
62	IIVGERLAT	472	-0.7000	0

63	LAWVPRRAG	499	-0.7000	0
64	LLPGGRPLA	520	-0.7000	0
65	VFPVAPTTQ	611	-0.7000	0
66	VTIGSIVKI	793	-0.7000	0
67	IAGRHMAVS	376	-0.8000	0
68	VYTIAPFAT	423	-0.8000	0
69	VLLDRERCI	156	-0.9000	0
70	YAYAKFARI	342	-0.9000	0
71	VPVYTIAPF	421	-0.9000	0
72	YTIAPFATG	424	-0.9000	0
73	MSGRLIKTV	437	-0.9000	0
74	VMELLLINH	102	-0.9200	0
75	LNSAGSTVH	780	-0.9200	0
76	IRVGQPEMV	8	-1.0000	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	VVSLELRHS	594	5.2000	59.09
2	LRKAARRHR	412	4.9000	55.68
3	IVFLRLRKA	407	4.7000	53.41
4	MGIQIPRFC	40	4.3000	48.86
5	MVVRTQLTS	84	4.0000	45.45
6	LVIRAAELM	32	3.9000	44.32
7	LRLRKAARR	410	3.9000	44.32
8	VHRQLRVTI	787	3.6000	40.91
9	LLINHPLDC	106	3.5000	39.77
10	VRTQLTSEI	86	3.3000	37.50
11	LCARCTRFS	165	3.3000	37.50
12	FVNWEGRYR	624	3.3000	37.50
13	VVLLVGFEP	393	3.1000	35.23
14	IRAAELMGI	34	3.0000	34.09
15	VFLRLRKAA	408	3.0000	34.09
16	YRTFEPALR	631	3.0000	34.09
17	FLRLRKAAR	409	2.9000	32.95
18	VVWLPLNSA	775	2.8000	31.82
19	LHKMSGRLI	434	2.7000	30.68

20	LRHSTVTER	599	2.6000	29.55
21	VQICPVGAL	210	2.3600	26.82
22	LVGFEPEDE	396	2.3000	26.14
23	VVRLSPDTA	734	2.2000	25.00
24	YRFRARPFD	223	2.1000	23.86
25	VTVSTSRGS	753	2.1000	23.86
26	MVTLTIDGV	15	2.0000	22.73
27	MELLLINHP	103	2.0000	22.73
28	VPVYTIAPF	421	2.0000	22.73
29	LRGSTLQAG	638	2.0000	22.73
30	LGIWDGKHA	679	2.0000	22.73
31	VARAQVCAA	531	1.9000	21.59
32	LAALGIWDG	676	1.9000	21.59
33	LMGIQIPRF	39	1.8000	20.45
34	VEGQRKPLA	66	1.7000	19.32
35	IYADEPFES	195	1.7000	19.32
36	IVGERLATV	473	1.7000	19.32
37	LAWVPRRAG	499	1.7000	19.32
38	WLPLNSAGS	777	1.7000	19.32
39	LINHPLDCP	107	1.5000	17.05
40	VGGRVTWED	332	1.5000	17.05
41	VIIVGERLA	471	1.5000	17.05
42	VGGIEPADF	570	1.5000	17.05
43	LTIDGVEIS	18	1.4000	15.91
44	ISAQVLLDR	152	1.4000	15.91
45	LESAPVVLL	388	1.3600	15.45
46	IDFRARPHS	357	1.3000	14.77
47	INISAQVLL	150	1.2600	14.32
48	VIRAAELMG	33	1.2000	13.64
49	LVSSPSVCE	232	1.2000	13.64
50	FLAARIAGR	371	1.2000	13.64
51	MGVHLGVPT	660	1.2000	13.64
52	VTIGSIVKI	793	1.2000	13.64
53	MSGRLIKTV	437	1.1000	12.50
54	IRVGQPEMV	8	1.0000	11.36
55	VEISVPKGT	23	1.0000	11.36
56	VLLDRERCI	156	1.0000	11.36
57	ILCARCTRF	164	1.0000	11.36
58	IIVGERLAT	472	1.0000	11.36
59	WHIAELPAA	540	1.0000	11.36
60	LQNQAMSNG	125	0.9000	10.23

61	LAAARGRTG	321	0.9000	10.23
62	VYTIAPFAT	423	0.9000	10.23
63	MLLDEGRLQ	712	0.9000	10.23
64	IGSIVKIGA	795	0.9000	10.23
65	LLDRERCIL	157	0.8600	9.77
66	LRRLAGDDP	258	0.8000	9.09
67	ITTPLIRDG	290	0.8000	9.09
68	VAAQGLAAA	316	0.8000	9.09
69	LVGGRVTWE	331	0.8000	9.09
70	VVRTQLTSE	85	0.7000	7.95
71	LAALLVGGI	565	0.7000	7.95
72	IAGRHMAVS	376	0.6000	6.82
73	WVPRRAGER	501	0.6000	6.82
74	VGACRQCLV	56	0.5000	5.68
75	LSAAARLAD	485	0.5000	5.68
76	ILTGWRMLL	706	0.4600	5.23
77	LASCTTVAT	73	0.4000	4.55
78	MQERGALQQ	184	0.4000	4.55
79	LAALDATGF	585	0.4000	4.55
80	VSLELRHST	595	0.4000	4.55

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	VVSLELRHS	594	5.2000	59.09
2	LRKAARRHR	412	4.9000	55.68
3	IVFLRLRKA	407	4.7000	53.41
4	MGIQIPRFC	40	4.3000	48.86
5	MVVRTQLTS	84	4.0000	45.45
6	LVIRAAELM	32	3.9000	44.32
7	LRLRKAARR	410	3.9000	44.32
8	VHRQLRVTI	787	3.6000	40.91
9	LLINHPLDC	106	3.5000	39.77
10	VRTQLTSEI	86	3.3000	37.50
11	LCARCTRFS	165	3.3000	37.50
12	FVNWEGRYR	624	3.3000	37.50
13	VVLLVGFEP	393	3.1000	35.23

14	IRAAELMGI	34	3.0000	34.09
15	VFLRLRKAA	408	3.0000	34.09
16	YRTFEPALR	631	3.0000	34.09
17	FLRLRKAAR	409	2.9000	32.95
18	VVWLPLNSA	775	2.8000	31.82
19	LHKMSGRLI	434	2.7000	30.68
20	LRHSTVTER	599	2.6000	29.55
21	VQICPVGAL	210	2.3600	26.82
22	LVGFEPEDE	396	2.3000	26.14
23	VVRLSPDTA	734	2.2000	25.00
24	YRFRARPFD	223	2.1000	23.86
25	VTVSTSRGS	753	2.1000	23.86
26	MVTLTIDGV	15	2.0000	22.73
27	MELLLINHP	103	2.0000	22.73
28	VPVYTIAPF	421	2.0000	22.73
29	LRGSTLQAG	638	2.0000	22.73
30	LGIWDGKHA	679	2.0000	22.73
31	VARAQVCAA	531	1.9000	21.59
32	LAALGIWDG	676	1.9000	21.59
33	LMGIQIPRF	39	1.8000	20.45
34	VEGQRKPLA	66	1.7000	19.32
35	IYADEPFES	195	1.7000	19.32
36	IVGERLATV	473	1.7000	19.32
37	LAWVPRRAG	499	1.7000	19.32
38	WLPLNSAGS	777	1.7000	19.32
39	LINHPLDCP	107	1.5000	17.05
40	VGGRVTWED	332	1.5000	17.05
41	VIIVGERLA	471	1.5000	17.05
42	VGGIEPADF	570	1.5000	17.05
43	LTIDGVEIS	18	1.4000	15.91
44	ISAQVLLDR	152	1.4000	15.91
45	LESAPVVLL	388	1.3600	15.45
46	IDFRARPHS	357	1.3000	14.77
47	INISAQVLL	150	1.2600	14.32
48	VIRAAELMG	33	1.2000	13.64
49	LVSSPSVCE	232	1.2000	13.64
50	FLAARIAGR	371	1.2000	13.64
51	MGVHLGVPT	660	1.2000	13.64
52	VTIGSIVKI	793	1.2000	13.64
53	MSGRLIKTV	437	1.1000	12.50
54	IRVGQPEMV	8	1.0000	11.36

55	VEISVPKGT	23	1.0000	11.36
56	VLLDRERCI	156	1.0000	11.36
57	ILCARCTRF	164	1.0000	11.36
58	IIVGERLAT	472	1.0000	11.36
59	WHIAELPAA	540	1.0000	11.36
60	LQNQAMSNG	125	0.9000	10.23
61	LAAARGRTG	321	0.9000	10.23
62	VYTIAPFAT	423	0.9000	10.23
63	MLLDEGRLQ	712	0.9000	10.23
64	IGSIVKIGA	795	0.9000	10.23
65	LLDRERCIL	157	0.8600	9.77
66	LRRLAGDDP	258	0.8000	9.09
67	ITTPLIRDG	290	0.8000	9.09
68	VAAQGLAAA	316	0.8000	9.09
69	LVGGRVTWE	331	0.8000	9.09
70	VVRTQLTSE	85	0.7000	7.95
71	LAALLVGGI	565	0.7000	7.95
72	IAGRHMAVS	376	0.6000	6.82
73	WVPRRAGER	501	0.6000	6.82
74	VGACRQCLV	56	0.5000	5.68
75	LSAAARLAD	485	0.5000	5.68
76	ILTGWRMLL	706	0.4600	5.23
77	LASCTTVAT	73	0.4000	4.55
78	MQERGALQQ	184	0.4000	4.55
79	LAALDATGF	585	0.4000	4.55
80	VSLELRHST	595	0.4000	4.55

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	IRAAELMGI	34	4.8000	48.98
2	YAKFARITL	344	4.4000	44.90
3	VVLLVGFEP	393	4.4000	44.90
4	IIVGERLAT	472	4.3000	43.88
5	ILTGWRMLL	706	4.2000	42.86
6	LLINHPLDC	106	4.0000	40.82
7	MVVRTQLTS	84	3.6000	36.73

8	VVWLPLNSA	775	3.5000	35.71
9	LRVTIGSIV	791	3.5000	35.71
10	IPRFCDHPL	44	3.3000	33.67
11	LVIRAAELM	32	3.1800	32.45
12	IAPFATGGL	426	3.1600	32.24
13	IVFLRLRKA	407	3.1000	31.63
14	VGIYADEPF	193	3.0000	30.61
15	VQICPVGAL	210	2.9000	29.59
16	VFLRLRKAA	408	2.7000	27.55
17	VVFPVAPTT	610	2.7000	27.55
18	MGVHLGVPT	660	2.7000	27.55
19	VRLSPDTAA	735	2.7000	27.55
20	VHRQLRVTI	787	2.7000	27.55
21	LLPGGRPLA	520	2.6000	26.53
22	LGIWDGKHA	679	2.6000	26.53
23	VTIGSIVKI	793	2.5500	26.02
24	VYTIAPFAT	423	2.5000	25.51
25	LHKMSGRLI	434	2.5000	25.51
26	IGSIVKIGA	795	2.5000	25.51
27	LRLRKAARR	410	2.4000	24.49
28	YRTFEPALR	631	2.4000	24.49
29	VVRLSPDTA	734	2.4000	24.49
30	VRTQLTSEI	86	2.3600	24.08
31	MVTLTIDGV	15	2.2500	22.96
32	FESYFSGNT	201	2.2000	22.45
33	IVGERLATV	473	2.2000	22.45
34	VVSLELRHS	594	2.2000	22.45
35	VPVYTIAPF	421	2.1500	21.94
36	IRVGQPEMV	8	2.1000	21.43
37	LRRLAGDDP	258	2.1000	21.43
38	INISAQVLL	150	2.0000	20.41
39	LVPTSWSHA	305	2.0000	20.41
40	VIRAAELMG	33	1.9000	19.39
41	LVGFEPEDE	396	1.9000	19.39
42	LLATPGAVI	464	1.9000	19.39
43	LELRHSTVT	597	1.9000	19.39
44	LMGIQIPRF	39	1.8500	18.88
45	WHIAELPAA	540	1.8000	18.37
46	LRKAARRHR	412	1.7000	17.35
47	VNWEGRYRT	625	1.7000	17.35
48	ICPVGALTG	212	1.6000	16.33

49	YRFRARPFD	223	1.6000	16.33
50	VSLELRHST	595	1.5000	15.31
51	LLDRERCIL	157	1.4000	14.29
52	IYADEPFES	195	1.4000	14.29
53	VLVGGRVTW	330	1.4000	14.29
54	LAGTARTPV	726	1.4000	14.29
55	VIIVGERLA	471	1.3000	13.27
56	MELLLINHP	103	1.2500	12.76
57	LRGSTLQAG	638	1.2000	12.24
58	VGQPEMVTL	10	1.1000	11.22
59	LINHPLDCP	107	1.1000	11.22
60	LEAGALPTL	512	1.1000	11.22
61	FVVSLELRH	593	1.1000	11.22
62	WLPLNSAGS	777	1.1000	11.22
63	IAGDPFIDM	176	1.0800	11.02
64	IQIPRFCDH	42	1.0000	10.20
65	VVRTQLTSE	85	1.0000	10.20
66	VMELLLINH	102	1.0000	10.20
67	LVSSPSVCE	232	1.0000	10.20
68	LRHSTVTER	599	1.0000	10.20
69	FVNWEGRYR	624	1.0000	10.20
70	WRMLLDEGR	710	1.0000	10.20
71	YFSGNTVQI	204	0.9600	9.80
72	ISVPKGTLV	25	0.9000	9.18
73	FAKPINISA	146	0.9000	9.18
74	LAALLVGGI	565	0.9000	9.18
75	LLVGGIEPA	568	0.8500	8.67
76	VLLDRERCI	156	0.8000	8.16
77	ILCARCTRF	164	0.8000	8.16
78	IDMQERGAL	182	0.8000	8.16
79	VGALTGTAY	215	0.8000	8.16
80	LESAPVVLL	388	0.8000	8.16

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	YAKFARITL	344	5.4000	55.10

2	IRAAELMGI	34	3.8000	38.78
3	VVLLVGFEP	393	3.4000	34.69
4	YRTFEPALR	631	3.4000	34.69
5	IIVGERLAT	472	3.3000	33.67
6	FESYFSGNT	201	3.2000	32.65
7	ILTGWRMLL	706	3.2000	32.65
8	LLINHPLDC	106	3.0000	30.61
9	WHIAELPAA	540	2.8000	28.57
10	MVVRTQLTS	84	2.6000	26.53
11	YRFRARPFD	223	2.6000	26.53
12	VVWLPLNSA	775	2.5000	25.51
13	LRVTIGSIV	791	2.5000	25.51
14	IPRFCDHPL	44	2.3000	23.47
15	LVIRAAELM	32	2.1800	22.24
16	IAPFATGGL	426	2.1600	22.04
17	IVFLRLRKA	407	2.1000	21.43
18	FVVSLELRH	593	2.1000	21.43
19	WLPLNSAGS	777	2.1000	21.43
20	VGIYADEPF	193	2.0000	20.41
21	FVNWEGRYR	624	2.0000	20.41
22	WRMLLDEGR	710	2.0000	20.41
23	YFSGNTVQI	204	1.9600	20.00
24	FAKPINISA	146	1.9000	19.39
25	VQICPVGAL	210	1.9000	19.39
26	FRARPFDLV	225	1.7000	17.35
27	VFLRLRKAA	408	1.7000	17.35
28	VVFPVAPTT	610	1.7000	17.35
29	MGVHLGVPT	660	1.7000	17.35
30	VRLSPDTAA	735	1.7000	17.35
31	VHRQLRVTI	787	1.7000	17.35
32	WVPRRAGER	501	1.6000	16.33
33	LLPGGRPLA	520	1.6000	16.33
34	LGIWDGKHA	679	1.6000	16.33
35	VTIGSIVKI	793	1.5500	15.82
36	VYTIAPFAT	423	1.5000	15.31
37	LHKMSGRLI	434	1.5000	15.31
38	IGSIVKIGA	795	1.5000	15.31
39	LRLRKAARR	410	1.4000	14.29
40	VVRLSPDTA	734	1.4000	14.29
41	VRTQLTSEI	86	1.3600	13.88
42	MVTLTIDGV	15	1.2500	12.76

43	YAYAKFARI	342	1.2000	12.24
44	IVGERLATV	473	1.2000	12.24
45	VVSLELRHS	594	1.2000	12.24
46	FEPALRGST	634	1.2000	12.24
47	VPVYTIAPF	421	1.1500	11.73
48	IRVGQPEMV	8	1.1000	11.22
49	FDLVSSPSV	230	1.1000	11.22
50	LRRLAGDDP	258	1.1000	11.22
51	INISAQVLL	150	1.0000	10.20
52	LVPTSWSHA	305	1.0000	10.20
53	VIRAAELMG	33	0.9000	9.18
54	LVGFEPEDE	396	0.9000	9.18
55	FLRLRKAAR	409	0.9000	9.18
56	LLATPGAVI	464	0.9000	9.18
57	LELRHSTVT	597	0.9000	9.18
58	FATGGLHKM	429	0.8800	8.98
59	LMGIQIPRF	39	0.8500	8.67
60	FCDHPLLEP	47	0.8000	8.16
61	LRKAARRHR	412	0.7000	7.14
62	VNWEGRYRT	625	0.7000	7.14
63	ICPVGALTG	212	0.6000	6.12
64	FTYATQPDV	281	0.6000	6.12
65	VSLELRHST	595	0.5000	5.10
66	LLDRERCIL	157	0.4000	4.08
67	IYADEPFES	195	0.4000	4.08
68	WNCDKGRWA	272	0.4000	4.08
69	VLVGGRVTW	330	0.4000	4.08
70	YTIAPFATG	424	0.4000	4.08
71	LAGTARTPV	726	0.4000	4.08
72	FARITLGTN	347	0.3000	3.06
73	FRARPHSAE	359	0.3000	3.06
74	VIIVGERLA	471	0.3000	3.06
75	MELLLINHP	103	0.2500	2.55
76	WSHAMAVAA	310	0.2000	2.04
77	LRGSTLQAG	638	0.2000	2.04
78	VGQPEMVTL	10	0.1000	1.02
79	LINHPLDCP	107	0.1000	1.02
80	YADLESAPV	385	0.1000	1.02

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	IRAAELMGI	34	4.8000	48.98
2	YAKFARITL	344	4.4000	44.90
3	VVLLVGFEP	393	4.4000	44.90
4	IIVGERLAT	472	4.3000	43.88
5	ILTGWRMLL	706	4.2000	42.86
6	LLINHPLDC	106	4.0000	40.82
7	MVVRTQLTS	84	3.6000	36.73
8	VVWLPLNSA	775	3.5000	35.71
9	LRVTIGSIV	791	3.5000	35.71
10	IPRFCDHPL	44	3.3000	33.67
11	LVIRAAELM	32	3.1800	32.45
12	IAPFATGGL	426	3.1600	32.24
13	IVFLRLRKA	407	3.1000	31.63
14	VGIYADEPF	193	3.0000	30.61
15	VQICPVGAL	210	2.9000	29.59
16	VFLRLRKAA	408	2.7000	27.55
17	VVFPVAPTT	610	2.7000	27.55
18	MGVHLGVPT	660	2.7000	27.55
19	VRLSPDTAA	735	2.7000	27.55
20	VHRQLRVTI	787	2.7000	27.55
21	LLPGGRPLA	520	2.6000	26.53
22	LGIWDGKHA	679	2.6000	26.53
23	VTIGSIVKI	793	2.5500	26.02
24	VYTIAPFAT	423	2.5000	25.51
25	LHKMSGRLI	434	2.5000	25.51
26	IGSIVKIGA	795	2.5000	25.51
27	LRLRKAARR	410	2.4000	24.49
28	YRTFEPALR	631	2.4000	24.49
29	VVRLSPDTA	734	2.4000	24.49
30	VRTQLTSEI	86	2.3600	24.08
31	MVTLTIDGV	15	2.2500	22.96
32	FESYFSGNT	201	2.2000	22.45
33	IVGERLATV	473	2.2000	22.45
34	VVSLELRHS	594	2.2000	22.45
35	VPVYTIAPF	421	2.1500	21.94
36	IRVGQPEMV	8	2.1000	21.43
37	LRRLAGDDP	258	2.1000	21.43

38	INISAQVLL	150	2.0000	20.41
39	LVPTSWSHA	305	2.0000	20.41
40	VIRAAELMG	33	1.9000	19.39
41	LVGFEPEDE	396	1.9000	19.39
42	LLATPGAVI	464	1.9000	19.39
43	LELRHSTVT	597	1.9000	19.39
44	LMGIQIPRF	39	1.8500	18.88
45	WHIAELPAA	540	1.8000	18.37
46	LRKAARRHR	412	1.7000	17.35
47	VNWEGRYRT	625	1.7000	17.35
48	ICPVGALTG	212	1.6000	16.33
49	YRFRARPFD	223	1.6000	16.33
50	VSLELRHST	595	1.5000	15.31
51	LLDRERCIL	157	1.4000	14.29
52	IYADEPFES	195	1.4000	14.29
53	VLVGGRVTW	330	1.4000	14.29
54	LAGTARTPV	726	1.4000	14.29
55	VIIVGERLA	471	1.3000	13.27
56	MELLLINHP	103	1.2500	12.76
57	LRGSTLQAG	638	1.2000	12.24
58	VGQPEMVTL	10	1.1000	11.22
59	LINHPLDCP	107	1.1000	11.22
60	LEAGALPTL	512	1.1000	11.22
61	FVVSLELRH	593	1.1000	11.22
62	WLPLNSAGS	777	1.1000	11.22
63	IAGDPFIDM	176	1.0800	11.02
64	IQIPRFCDH	42	1.0000	10.20
65	VVRTQLTSE	85	1.0000	10.20
66	VMELLLINH	102	1.0000	10.20
67	LVSSPSVCE	232	1.0000	10.20
68	LRHSTVTER	599	1.0000	10.20
69	FVNWEGRYR	624	1.0000	10.20
70	WRMLLDEGR	710	1.0000	10.20
71	YFSGNTVQI	204	0.9600	9.80
72	ISVPKGTLV	25	0.9000	9.18
73	FAKPINISA	146	0.9000	9.18
74	LAALLVGGI	565	0.9000	9.18
75	LLVGGIEPA	568	0.8500	8.67
76	VLLDRERCI	156	0.8000	8.16
77	ILCARCTRF	164	0.8000	8.16
78	IDMQERGAL	182	0.8000	8.16

79	VGALTGTAY	215	0.8000	8.16
80	LESAPVVLL	388	0.8000	8.16

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	FVNWEGRYR	624	4.7000	47.96
2	YRTFEPALR	631	4.3000	43.88
3	LVEVEGQRK	63	4.1000	41.84
4	WVPRRAGER	501	3.8000	38.78
5	WRMLLDEGR	710	3.8000	38.78
6	LRKAARRHR	412	3.7000	37.76
7	LHKMSGRLI	434	3.7000	37.76
8	FLRLRKAAR	409	3.3000	33.67
9	VVLLVGFEP	393	3.1000	31.63
10	LRLRKAARR	410	3.0000	30.61
11	VVSLELRHS	594	2.9000	29.59
12	IVFLRLRKA	407	2.8000	28.57
13	WEDAYAYAK	338	2.7000	27.55
14	VYTIAPFAT	423	2.7000	27.55
15	LPTLLPGGR	517	2.4000	24.49
16	VGGIEPADF	570	2.4000	24.49
17	LRHSTVTER	599	2.4000	24.49
18	VFPVAPTTQ	611	2.4000	24.49
19	VQICPVGAL	210	2.3000	23.47
20	LTGTAYRFR	218	2.3000	23.47
21	FPVAPTTQK	612	2.2000	22.45
22	FLAARIAGR	371	2.1000	21.43
23	WLPLNSAGS	777	2.1000	21.43
24	VIIVGERLA	471	2.0000	20.41
25	IRAAELMGI	34	1.8000	18.37
26	MGIQIPRFC	40	1.8000	18.37
27	FVVSLELRH	593	1.7000	17.35
28	FARITLGTN	347	1.6000	16.33
29	ILCARCTRF	164	1.5000	15.31
30	ICPVGALTG	212	1.4000	14.29
31	VGALTGTAY	215	1.4000	14.29

32	LRVTIGSIV	791	1.3000	13.27
33	LEPVGACRQ	53	1.2000	12.24
34	LLATPGAVI	464	1.2000	12.24
35	VVWLPLNSA	775	1.2000	12.24
36	LATVPGGLS	478	1.1000	11.22
37	LAALDATGF	585	1.1000	11.22
38	VVRLSPDTA	734	1.1000	11.22
39	VEISVPKGT	23	1.0000	10.20
40	LRGSTLQAG	638	1.0000	10.20
41	LMGIQIPRF	39	0.8000	8.16
42	VVRTQLTSE	85	0.8000	8.16
43	FIDMQERGA	181	0.8000	8.16
44	MLLDEGRLQ	712	0.8000	8.16
45	LNSAGSTVH	780	0.8000	8.16
46	VRTQLTSEI	86	0.7000	7.14
47	VMELLLINH	102	0.7000	7.14
48	IKTVPGGEP	442	0.7000	7.14
49	WHIAELPAA	540	0.7000	7.14
50	IGSIVKIGA	795	0.7000	7.14
51	LLINHPLDC	106	0.6000	6.12
52	WAFTYATQP	279	0.6000	6.12
53	YAKFARITL	344	0.6000	6.12
54	LIKTVPGGE	441	0.6000	6.12
55	LVIRAAELM	32	0.5000	5.10
56	LAWVPRRAG	499	0.5000	5.10
57	VTVSTSRGS	753	0.5000	5.10
58	INISAQVLL	150	0.4000	4.08
59	IYADEPFES	195	0.4000	4.08
60	LAAARGRTG	321	0.4000	4.08
61	YAYAKFARI	342	0.3000	3.06
62	VTWEDAYAY	336	0.2000	2.04
63	YTIAPFATG	424	0.2000	2.04
64	LGIWDGKHA	679	0.2000	2.04
65	ISAQVLLDR	152	0.1000	1.02
66	LAALLVGGI	565	0.1000	1.02
67	LRRLAGDDP	258	-0.1000	0
68	WNCDKGRWA	272	-0.1000	0
69	YLAGTARTP	725	-0.1000	0
70	VIRAAELMG	33	-0.2000	0
71	MVVRTQLTS	84	-0.2000	0
72	LIRDGGDPK	294	-0.2000	0

73	LVPTSWSHA	305	-0.2000	0
74	IAPFATGGL	426	-0.2000	0
75	VLLDRERCI	156	-0.4000	0
76	LQQVGIYAD	190	-0.4000	0
77	FESYFSGNT	201	-0.4000	0
78	WSHAMAVAA	310	-0.4000	0

ALLELE: DRB5_0105	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FVNWEGRYR	624	4.7000	47.96
2	YRTFEPALR	631	4.3000	43.88
3	LVEVEGQRK	63	4.1000	41.84
4	WVPRRAGER	501	3.8000	38.78
5	WRMLLDEGR	710	3.8000	38.78
6	LRKAARRHR	412	3.7000	37.76
7	LHKMSGRLI	434	3.7000	37.76
8	FLRLRKAAR	409	3.3000	33.67
9	VVLLVGFEP	393	3.1000	31.63
10	LRLRKAARR	410	3.0000	30.61
11	VVSLELRHS	594	2.9000	29.59
12	IVFLRLRKA	407	2.8000	28.57
13	WEDAYAYAK	338	2.7000	27.55
14	VYTIAPFAT	423	2.7000	27.55
15	LPTLLPGGR	517	2.4000	24.49
16	VGGIEPADF	570	2.4000	24.49
17	LRHSTVTER	599	2.4000	24.49
18	VFPVAPTTQ	611	2.4000	24.49
19	VQICPVGAL	210	2.3000	23.47
20	LTGTAYRFR	218	2.3000	23.47
21	FPVAPTTQK	612	2.2000	22.45
22	FLAARIAGR	371	2.1000	21.43
23	WLPLNSAGS	777	2.1000	21.43
24	VIIVGERLA	471	2.0000	20.41
25	IRAAELMGI	34	1.8000	18.37
26	MGIQIPRFC	40	1.8000	18.37
27	FVVSLELRH	593	1.7000	17.35

28	FARITLGTN	347	1.6000	16.33
29	ILCARCTRF	164	1.5000	15.31
30	ICPVGALTG	212	1.4000	14.29
31	VGALTGTAY	215	1.4000	14.29
32	LRVTIGSIV	791	1.3000	13.27
33	LEPVGACRQ	53	1.2000	12.24
34	LLATPGAVI	464	1.2000	12.24
35	VVWLPLNSA	775	1.2000	12.24
36	LATVPGGLS	478	1.1000	11.22
37	LAALDATGF	585	1.1000	11.22
38	VVRLSPDTA	734	1.1000	11.22
39	VEISVPKGT	23	1.0000	10.20
40	LRGSTLQAG	638	1.0000	10.20
41	LMGIQIPRF	39	0.8000	8.16
42	VVRTQLTSE	85	0.8000	8.16
43	FIDMQERGA	181	0.8000	8.16
44	MLLDEGRLQ	712	0.8000	8.16
45	LNSAGSTVH	780	0.8000	8.16
46	VRTQLTSEI	86	0.7000	7.14
47	VMELLLINH	102	0.7000	7.14
48	IKTVPGGEP	442	0.7000	7.14
49	WHIAELPAA	540	0.7000	7.14
50	IGSIVKIGA	795	0.7000	7.14
51	LLINHPLDC	106	0.6000	6.12
52	WAFTYATQP	279	0.6000	6.12
53	YAKFARITL	344	0.6000	6.12
54	LIKTVPGGE	441	0.6000	6.12
55	LVIRAAELM	32	0.5000	5.10
56	LAWVPRRAG	499	0.5000	5.10
57	VTVSTSRGS	753	0.5000	5.10
58	INISAQVLL	150	0.4000	4.08
59	IYADEPFES	195	0.4000	4.08
60	LAAARGRTG	321	0.4000	4.08
61	YAYAKFARI	342	0.3000	3.06
62	VTWEDAYAY	336	0.2000	2.04
63	YTIAPFATG	424	0.2000	2.04
64	LGIWDGKHA	679	0.2000	2.04
65	ISAQVLLDR	152	0.1000	1.02
66	LAALLVGGI	565	0.1000	1.02
67	LRRLAGDDP	258	-0.1000	0
68	WNCDKGRWA	272	-0.1000	0

69	YLAGTARTP	725	-0.1000	0
70	VIRAAELMG	33	-0.2000	0
71	MVVRTQLTS	84	-0.2000	0
72	LIRDGGDPK	294	-0.2000	0
73	LVPTSWSHA	305	-0.2000	0
74	IAPFATGGL	426	-0.2000	0
75	VLLDRERCI	156	-0.4000	0
76	LQQVGIYAD	190	-0.4000	0
77	FESYFSGNT	201	-0.4000	0
78	WSHAMAVAA	310	-0.4000	0