MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Feb 2 16:46:45 2010
Length of input sequence	490 amino acids
Number of nanomers from input sequence	482
Number of nanomers with obligatory P1 anchor residue	151
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	49

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	YLALLGWSI	282	2.2200	37.00
2	IRIGVAERI	232	2.1000	35.00
3	VVLGDAWEL	373	1.8200	30.33
4	YRDVLARLL	93	1.4400	24.00
5	IRMLDVGDF	331	0.9000	15.00
6	FNWAYARHT	28	0.6900	11.50
7	VRFCPSPTG	8	0.6700	11.17
8	YRQSQRAEI	84	0.4000	6.67
9	MQRLRAARQ	476	0.2000	3.33

10	LVRGPVTFA	169	0.0900	1.50
11	LLPSTPRQL	217	-0.0100	0
12	LALLDALRW	58	-0.2000	0
13	FAHLPTVLG	243	-0.2000	0
14	LVQTRIVVL	367	-0.6000	0
15	YLAEGRQPV	146	-0.7000	0
16	VRTALFNWA	23	-0.8000	0
17	LIRIGVAER	231	-0.8000	0
18	YVIDPKAAA	390	-0.8000	0
19	FSPIRVAAT	447	-0.8000	0
20	IRVAATGTT	450	-0.8000	0
21	WSIADDHDL	288	-0.9000	0
22	VVRLRMPDD	154	-0.9300	0
23	MKITHVLRG	206	-1.0000	0
24	LRGEDLLPS	212	-1.0000	0
25	VLGEGTKKL	249	-1.1000	0
26	LLNYLALLG	279	-1.1000	0
27	LRAARQLVG	479	-1.1000	0
28	VGLVRTALF	20	-1.1500	0
29	YTLVNPCDD	195	-1.1500	0
30	LAAGEAYHA	101	-1.2000	0
31	LARLLAAGE	97	-1.3000	0
32	VRGPVTFAA	170	-1.4000	0
33	LALHQALIR	225	-1.4000	0
34	LFGLDEMVA	296	-1.4100	0
35	VRVRFCPSP	6	-1.4300	0
36	FRIEDTDAQ	42	-1.5000	0
37	FESLELLGR	464	-1.5000	0
38	FIPEGLLNY	274	-1.6000	0
39	LNYLALLGW	280	-1.6000	0
40	VFRIEDTDA	41	-1.6100	0
41	LALLGWSIA	283	-1.7000	0
42	WELLKFFND	379	-1.7000	0
43	FFNDDQYVI	384	-1.7000	0

44	VAAFDVADV	303	-1.7200	0
45	YARHTGGTF	32	-1.8000	0
46	YLALLDALR	57	-1.8000	0
47	VTFAAGSVP	174	-1.8000	0
48	LMKITHVLR	205	-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	IRIGVAERI	232	3.1000	51.67
2	VVLGDAWEL	373	2.8200	47.00
3	IRMLDVGDF	331	1.9000	31.67
4	VRFCPSPTG	8	1.6700	27.83
5	YLALLGWSI	282	1.2200	20.33
6	MQRLRAARQ	476	1.2000	20.00
7	LVRGPVTFA	169	1.0900	18.17
8	LLPSTPRQL	217	0.9900	16.50
9	LALLDALRW	58	0.8000	13.33
10	FNWAYARHT	28	0.6900	11.50
11	YRDVLARLL	93	0.4400	7.33
12	LVQTRIVVL	367	0.4000	6.67
13	VRTALFNWA	23	0.2000	3.33
14	LIRIGVAER	231	0.2000	3.33
15	IRVAATGTT	450	0.2000	3.33
16	VVRLRMPDD	154	0.0700	1.17
17	VLGEGTKKL	249	-0.1000	0
18	LLNYLALLG	279	-0.1000	0
19	LRAARQLVG	479	-0.1000	0
20	VGLVRTALF	20	-0.1500	0
21	LAAGEAYHA	101	-0.2000	0
22	FAHLPTVLG	243	-0.2000	0
23	LARLLAAGE	97	-0.3000	0
24	VRGPVTFAA	170	-0.4000	0
25	LALHQALIR	225	-0.4000	0

26	LFGLDEMVA	296	-0.4100	0
27	VRVRFCPSP	6	-0.4300	0
28	YRQSQRAEI	84	-0.6000	0
29	LNYLALLGW	280	-0.6000	0
30	VFRIEDTDA	41	-0.6100	0
31	LALLGWSIA	283	-0.7000	0
32	VAAFDVADV	303	-0.7200	0
33	VTFAAGSVP	174	-0.8000	0
34	FSPIRVAAT	447	-0.8000	0
35	LMKITHVLR	205	-0.9000	0
36	LAALTSVTD	413	-0.9000	0
37	LNAEHIRML	326	-0.9100	0
38	VRLRDHLDT	341	-1.0000	0
39	LTRASGDPL	186	-1.1000	0
40	IVVLGDAWE	372	-1.1000	0
41	LGPDGAAVL	401	-1.1000	0
42	LYTLVNPCD	194	-1.1300	0
43	VTATETVRV	0	-1.2000	0
44	VAAGRNPKL	121	-1.2300	0
45	LVRTALFNW	22	-1.3000	0
46	IALDEAAFA	354	-1.4000	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	YVIDPKAAA	390	6.2000	65.26
2	IRMLDVGDF	331	5.8000	61.05
3	LGRDRSMQR	470	5.0000	52.63
4	IRIGVAERI	232	4.6000	48.42
5	LVRGPVTFA	169	4.4000	46.32
6	IYRDVLARL	92	4.0600	42.74
7	VRFCPSPTG	8	4.0000	42.11
8	LIRIGVAER	231	4.0000	42.11
9	YRQSQRAEI	84	3.5000	36.84

10	MKITHVLRG	206	3.4000	35.79
11	IALDEAAFA	354	3.3000	34.74
12	VGLVRTALF	20	3.2000	33.68
13	IRVAATGTT	450	3.1000	32.63
14	LGPDGAAVL	401	3.0600	32.21
15	VVLGDAWEL	373	2.9600	31.16
16	LRGEDLLPS	212	2.9000	30.53
17	FFNDDQYVI	384	2.8500	30.00
18	VRGPVTFAA	170	2.7000	28.42
19	LELLGRDRS	467	2.6000	27.37
20	LRAARQLVG	479	2.5000	26.32
21	FAAGSVPDF	176	2.3000	24.21
22	LMKITHVLR	205	2.2000	23.16
23	IGVAERIPK	234	2.2000	23.16
24	VRVRFCPSP	6	2.1000	22.11
25	FGLDEMVAA	297	2.1000	22.11
26	VVRLRMPDD	154	2.0000	21.05
27	VQTRIVVLG	368	2.0000	21.05
28	LVQTRIVVL	367	1.9600	20.63
29	VLGDAWELL	374	1.8600	19.58
30	VRLRDHLDT	341	1.8000	18.95
31	FRIEDTDAQ	42	1.7000	17.89
32	LALHQALIR	225	1.7000	17.89
33	MQRLRAARQ	476	1.7000	17.89
34	LLPSTPRQL	217	1.5600	16.42
35	LVRTALFNW	22	1.5000	15.79
36	VRLRMPDDD	155	1.5000	15.79
37	LDWDEGPEV	69	1.3000	13.68
38	LGEGTKKLS	250	1.3000	13.68
39	LRWLGLDWD	64	1.2000	12.63
40	LGYDNFDRH	129	1.1000	11.58
41	LLNYLALLG	279	1.1000	11.58
42	LLGRDRSMQ	469	1.0700	11.26
43	LAWNDLVRG	164	1.0000	10.53

44	LHQALIRIG	227	1.0000	10.53
45	LNYLALLGW	280	1.0000	10.53
46	LALKPRKAF	439	1.0000	10.53
47	LGLDWDEGP	67	0.9000	9.47
48	VAATGTTVS	452	0.8000	8.42
49	IEAALKDAL	427	0.7600	8.00

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	YVIDPKAAA	390	7.2000	79.12
2	YRQSQRAEI	84	3.6000	39.56
3	FRIEDTDAQ	42	3.4000	37.36
4	LVRGPVTFA	169	3.4000	37.36
5	FGLDEMVAA	297	3.1000	34.07
6	FFNDDQYVI	384	2.9500	32.42
7	IRMLDVGDF	331	2.9000	31.87
8	IRIGVAERI	232	2.7000	29.67
9	LGRDRSMQR	470	2.5000	27.47
10	IALDEAAFA	354	2.3000	25.27
11	IYRDVLARL	92	2.1000	23.08
12	VRGPVTFAA	170	1.7000	18.68
13	VRFCPSPTG	8	1.6000	17.58
14	LRGEDLLPS	212	1.5000	16.48
15	LIRIGVAER	231	1.5000	16.48
16	FAAGSVPDF	176	1.4000	15.38
17	IRVAATGTT	450	1.4000	15.38
18	MQRLRAARQ	476	1.4000	15.38
19	LELLGRDRS	467	1.2000	13.19
20	IGVAERIPK	234	1.1000	12.09
21	LGPDGAAVL	401	1.1000	12.09
22	FDVADVNSS	306	1.0100	11.10
23	MKITHVLRG	206	1.0000	10.99
24	VVLGDAWEL	373	1.0000	10.99

25	LLGRDRSMQ	469	0.7700	8.46
26	LGYDNFDRH	129	0.6800	7.47
27	FCPSPTGTP	10	0.6000	6.59
28	LVRTALFNW	22	0.5000	5.49
29	FSPIRVAAT	447	0.5000	5.49
30	VGLVRTALF	20	0.3000	3.30
31	YLAEGRQPV	146	0.2000	2.20
32	FAHLPTVLG	243	0.2000	2.20
33	VRVRFCPSP	6	0.1000	1.10
34	FDRHLTDAQ	134	0.1000	1.10
35	VRLRDHLDT	341	0.1000	1.10
36	LRAARQLVG	479	0.1000	1.10
37	VVRLRMPDD	154	-0.1000	0
38	WNDLVRGPV	166	-0.1000	0
39	LGEGTKKLS	250	-0.1000	0
40	VLGDAWELL	374	-0.1000	0
41	YTLVNPCDD	195	-0.2000	0
42	FIPEGLLNY	274	-0.2000	0
43	VRTALFNWA	23	-0.2900	0
44	LMKITHVLR	205	-0.3000	0
45	LFGLDEMVA	296	-0.3000	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	YVIDPKAAA	390	6.2000	70.45
2	LVRGPVTFA	169	4.4000	50.00
3	IRIGVAERI	232	4.1000	46.59
4	IALDEAAFA	354	3.3000	37.50
5	LGRDRSMQR	470	3.2000	36.36
6	IYRDVLARL	92	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09
8	FRIEDTDAQ	42	2.7000	30.68
9	YRQSQRAEI	84	2.6000	29.55

10	MKITHVLRG	206	2.5000	28.41
11	LIRIGVAER	231	2.5000	28.41
12	IRMLDVGDF	331	2.5000	28.41
13	LELLGRDRS	467	2.5000	28.41
14	MQRLRAARQ	476	2.4000	27.27
15	LGPDGAAVL	401	2.1000	23.86
16	LGYDNFDRH	129	1.9800	22.50
17	FGLDEMVAA	297	1.9800	22.50
18	IGVAERIPK	234	1.7800	20.23
19	VRLRDHLDT	341	1.6000	18.18
20	LRAARQLVG	479	1.6000	18.18
21	LGEGTKKLS	250	1.5000	17.05
22	LNYLALLGW	280	1.5000	17.05
23	LLGRDRSMQ	469	1.5000	17.05
24	VRTALFNWA	23	1.4000	15.91
25	VGLVRTALF	20	1.3000	14.77
26	VLGDAWELL	374	1.3000	14.77
27	VRFCPSPTG	8	1.2000	13.64
28	VRGPVTFAA	170	1.2000	13.64
29	VVLGDAWEL	373	1.2000	13.64
30	IRVAATGTT	450	1.0000	11.36
31	LGWSIADDH	286	0.9800	11.14
32	LVQTRIVVL	367	0.8800	10.00
33	FFNDDQYVI	384	0.8000	9.09
34	LALLDALRW	58	0.7000	7.95
35	VRLRMPDDD	155	0.7000	7.95
36	LALHQALIR	225	0.7000	7.95
37	FDVADVNSS	306	0.7000	7.95
38	LMKITHVLR	205	0.5800	6.59
39	VQTRIVVLG	368	0.4800	5.45
40	LRWLGLDWD	64	0.4000	4.55
41	LFGLDEMVA	296	0.4000	4.55
42	VAATGTTVS	452	0.4000	4.55
43	LGLDWDEGP	67	0.3000	3.41

44	LLPSTPRQL	217	0.3000	3.41
45	LLNYLALLG	279	0.2000	2.27
46	IEAALKDAL	427	0.1000	1.14
47	LRMPDDDLA	157	-0.1000	0

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	YVIDPKAAA	390	6.2000	70.45
2	LVRGPVTFA	169	4.4000	50.00
3	IRIGVAERI	232	4.1000	46.59
4	IALDEAAFA	354	3.3000	37.50
5	LGRDRSMQR	470	3.2000	36.36
6	IYRDVLARL	92	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09
8	FRIEDTDAQ	42	2.7000	30.68
9	YRQSQRAEI	84	2.6000	29.55
10	MKITHVLRG	206	2.5000	28.41
11	LIRIGVAER	231	2.5000	28.41
12	IRMLDVGDF	331	2.5000	28.41
13	LELLGRDRS	467	2.5000	28.41
14	MQRLRAARQ	476	2.4000	27.27
15	LGPDGAAVL	401	2.1000	23.86
16	LGYDNFDRH	129	1.9800	22.50
17	FGLDEMVAA	297	1.9800	22.50
18	IGVAERIPK	234	1.7800	20.23
19	VRLRDHLDT	341	1.6000	18.18
20	LRAARQLVG	479	1.6000	18.18
21	LGEGTKKLS	250	1.5000	17.05
22	LNYLALLGW	280	1.5000	17.05
23	LLGRDRSMQ	469	1.5000	17.05
24	VRTALFNWA	23	1.4000	15.91
25	VGLVRTALF	20	1.3000	14.77
26	VLGDAWELL	374	1.3000	14.77

27	VRFCPSPTG	8	1.2000	13.64
28	VRGPVTFAA	170	1.2000	13.64
29	VVLGDAWEL	373	1.2000	13.64
30	IRVAATGTT	450	1.0000	11.36
31	LGWSIADDH	286	0.9800	11.14
32	LVQTRIVVL	367	0.8800	10.00
33	FFNDDQYVI	384	0.8000	9.09
34	LALLDALRW	58	0.7000	7.95
35	VRLRMPDDD	155	0.7000	7.95
36	LALHQALIR	225	0.7000	7.95
37	FDVADVNSS	306	0.7000	7.95
38	LMKITHVLR	205	0.5800	6.59
39	VQTRIVVLG	368	0.4800	5.45
40	LRWLGLDWD	64	0.4000	4.55
41	LFGLDEMVA	296	0.4000	4.55
42	VAATGTTVS	452	0.4000	4.55
43	LGLDWDEGP	67	0.3000	3.41
44	LLPSTPRQL	217	0.3000	3.41
45	LLNYLALLG	279	0.2000	2.27
46	IEAALKDAL	427	0.1000	1.14
47	LRMPDDDLA	157	-0.1000	0

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	YVIDPKAAA	390	6.2000	70.45
2	LVRGPVTFA	169	4.4000	50.00
3	IRIGVAERI	232	4.1000	46.59
4	IALDEAAFA	354	3.3000	37.50
5	LGRDRSMQR	470	3.2000	36.36
6	IYRDVLARL	92	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09
8	FRIEDTDAQ	42	2.7000	30.68
9	YRQSQRAEI	84	2.6000	29.55

10	MKITHVLRG	206	2.5000	28.41
11	LIRIGVAER	231	2.5000	28.41
12	IRMLDVGDF	331	2.5000	28.41
13	LELLGRDRS	467	2.5000	28.41
14	MQRLRAARQ	476	2.4000	27.27
15	LGPDGAAVL	401	2.1000	23.86
16	LGYDNFDRH	129	1.9800	22.50
17	FGLDEMVAA	297	1.9800	22.50
18	IGVAERIPK	234	1.7800	20.23
19	VRLRDHLDT	341	1.6000	18.18
20	LRAARQLVG	479	1.6000	18.18
21	LGEGTKKLS	250	1.5000	17.05
22	LNYLALLGW	280	1.5000	17.05
23	LLGRDRSMQ	469	1.5000	17.05
24	VRTALFNWA	23	1.4000	15.91
25	VGLVRTALF	20	1.3000	14.77
26	VLGDAWELL	374	1.3000	14.77
27	VRFCPSPTG	8	1.2000	13.64
28	VRGPVTFAA	170	1.2000	13.64
29	VVLGDAWEL	373	1.2000	13.64
30	IRVAATGTT	450	1.0000	11.36
31	LGWSIADDH	286	0.9800	11.14
32	LVQTRIVVL	367	0.8800	10.00
33	FFNDDQYVI	384	0.8000	9.09
34	LALLDALRW	58	0.7000	7.95
35	VRLRMPDDD	155	0.7000	7.95
36	LALHQALIR	225	0.7000	7.95
37	FDVADVNSS	306	0.7000	7.95
38	LMKITHVLR	205	0.5800	6.59
39	VQTRIVVLG	368	0.4800	5.45
40	LRWLGLDWD	64	0.4000	4.55
41	LFGLDEMVA	296	0.4000	4.55
42	VAATGTTVS	452	0.4000	4.55
43	LGLDWDEGP	67	0.3000	3.41

44	LLPSTPRQL	217	0.3000	3.41
45	LLNYLALLG	279	0.2000	2.27
46	IEAALKDAL	427	0.1000	1.14
47	LRMPDDDLA	157	-0.1000	0

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	YVIDPKAAA	390	7.2000	75.79
2	IRMLDVGDF	331	4.8000	50.53
3	YRQSQRAEI	84	4.5000	47.37
4	LGRDRSMQR	470	4.0000	42.11
5	FFNDDQYVI	384	3.8500	40.53
6	IRIGVAERI	232	3.6000	37.89
7	LVRGPVTFA	169	3.4000	35.79
8	FAAGSVPDF	176	3.3000	34.74
9	FGLDEMVAA	297	3.1000	32.63
10	IYRDVLARL	92	3.0600	32.21
11	VRFCPSPTG	8	3.0000	31.58
12	LIRIGVAER	231	3.0000	31.58
13	FRIEDTDAQ	42	2.7000	28.42
14	MKITHVLRG	206	2.4000	25.26
15	IALDEAAFA	354	2.3000	24.21
16	VGLVRTALF	20	2.2000	23.16
17	IRVAATGTT	450	2.1000	22.11
18	LGPDGAAVL	401	2.0600	21.68
19	VVLGDAWEL	373	1.9600	20.63
20	LRGEDLLPS	212	1.9000	20.00
21	VRGPVTFAA	170	1.7000	17.89
22	FCPSPTGTP	10	1.6000	16.84
23	FAHLPTVLG	243	1.6000	16.84
24	LELLGRDRS	467	1.6000	16.84
25	LRAARQLVG	479	1.5000	15.79
26	FDVADVNSS	306	1.4100	14.84

27	YLAEGRQPV	146	1.2000	12.63
28	LMKITHVLR	205	1.2000	12.63
29	IGVAERIPK	234	1.2000	12.63
30	FSPIRVAAT	447	1.2000	12.63
31	FESLELLGR	464	1.2000	12.63
32	VRVRFCPSP	6	1.1000	11.58
33	FIPEGLLNY	274	1.1000	11.58
34	WAYARHTGG	30	1.0000	10.53
35	YARHTGGTF	32	1.0000	10.53
36	YHAFSTPEE	107	1.0000	10.53
37	VVRLRMPDD	154	1.0000	10.53
38	VQTRIVVLG	368	1.0000	10.53
39	LVQTRIVVL	367	0.9600	10.11
40	WNDLVRGPV	166	0.9000	9.47
41	YTLVNPCDD	195	0.9000	9.47
42	FAHRDRGFI	267	0.9000	9.47
43	VLGDAWELL	374	0.8600	9.05
44	VRLRDHLDT	341	0.8000	8.42
45	LALHQALIR	225	0.7000	7.37
46	MQRLRAARQ	476	0.7000	7.37
47	LLPSTPRQL	217	0.5600	5.89
48	LVRTALFNW	22	0.5000	5.26
49	VRLRMPDDD	155	0.5000	5.26

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	YVIDPKAAA	390	6.2000	70.45
2	LVRGPVTFA	169	4.4000	50.00
3	IRIGVAERI	232	4.1000	46.59
4	IALDEAAFA	354	3.3000	37.50
5	LGRDRSMQR	470	3.2000	36.36
6	IYRDVLARL	92	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09

8	FRIEDTDAQ	42	2.7000	30.68
9	YRQSQRAEI	84	2.6000	29.55
10	MKITHVLRG	206	2.5000	28.41
11	LIRIGVAER	231	2.5000	28.41
12	IRMLDVGDF	331	2.5000	28.41
13	LELLGRDRS	467	2.5000	28.41
14	MQRLRAARQ	476	2.4000	27.27
15	LGPDGAAVL	401	2.1000	23.86
16	LGYDNFDRH	129	1.9800	22.50
17	FGLDEMVAA	297	1.9800	22.50
18	IGVAERIPK	234	1.7800	20.23
19	VRLRDHLDT	341	1.6000	18.18
20	LRAARQLVG	479	1.6000	18.18
21	LGEGTKKLS	250	1.5000	17.05
22	LNYLALLGW	280	1.5000	17.05
23	LLGRDRSMQ	469	1.5000	17.05
24	VRTALFNWA	23	1.4000	15.91
25	VGLVRTALF	20	1.3000	14.77
26	VLGDAWELL	374	1.3000	14.77
27	VRFCPSPTG	8	1.2000	13.64
28	VRGPVTFAA	170	1.2000	13.64
29	VVLGDAWEL	373	1.2000	13.64
30	IRVAATGTT	450	1.0000	11.36
31	LGWSIADDH	286	0.9800	11.14
32	LVQTRIVVL	367	0.8800	10.00
33	FFNDDQYVI	384	0.8000	9.09
34	LALLDALRW	58	0.7000	7.95
35	VRLRMPDDD	155	0.7000	7.95
36	LALHQALIR	225	0.7000	7.95
37	FDVADVNSS	306	0.7000	7.95
38	LMKITHVLR	205	0.5800	6.59
39	VQTRIVVLG	368	0.4800	5.45
40	LRWLGLDWD	64	0.4000	4.55
41	LFGLDEMVA	296	0.4000	4.55

42	VAATGTTVS	452	0.4000	4.55
43	LGLDWDEGP	67	0.3000	3.41
44	LLPSTPRQL	217	0.3000	3.41
45	LLNYLALLG	279	0.2000	2.27
46	IEAALKDAL	427	0.1000	1.14
47	LRMPDDDLA	157	-0.1000	0

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	FRIEDTDAQ	42	7.3000	84.88
2	LRGEDLLPS	212	3.2000	37.21
3	MKITHVLRG	206	2.9000	33.72
4	FDRHLTDAQ	134	2.6000	30.23
5	YVIDPKAAA	390	2.6000	30.23
6	LGRDRSMQR	470	2.4000	27.91
7	VLGEGTKKL	249	2.3000	26.74
8	VAATGTTVS	452	2.2000	25.58
9	MQRLRAARQ	476	2.2000	25.58
10	IRMLDVGDF	331	2.0000	23.26
11	FAHLPTVLG	243	1.9800	23.02
12	FGLDEMVAA	297	1.8800	21.86
13	LIRIGVAER	231	1.5000	17.44
14	FIPEGLLNY	274	1.5000	17.44
15	FDVADVNSS	306	1.4000	16.28
16	IALDEAAFA	354	1.4000	16.28
17	VRFCPSPTG	8	1.3000	15.12
18	IRVAATGTT	450	1.1000	12.79
19	LVRGPVTFA	169	1.0000	11.63
20	IRIGVAERI	232	1.0000	11.63
21	VTATETVRV	0	0.9800	11.40
22	LALHQALIR	225	0.8000	9.30
23	LVQTRIVVL	367	0.7800	9.07
24	VRTALFNWA	23	0.7000	8.14

25	VRGPVTFAA	170	0.7000	8.14
26	LLKFFNDDQ	381	0.6000	6.98
27	VGLVRTALF	20	0.5000	5.81
28	LALLDALRW	58	0.5000	5.81
29	FSPIRVAAT	447	0.5000	5.81
30	FCPSPTGTP	10	0.4000	4.65
31	LGYDNFDRH	129	0.3800	4.42
32	YRQSQRAEI	84	0.3000	3.49
33	LGPDGAAVL	401	0.2000	2.33
34	VFRIEDTDA	41	0.1000	1.16
35	LGWSIADDH	286	0.0800	0.93
36	IYRDVLARL	92	-0.1000	0
37	FALTRASGD	184	-0.2000	0
38	VLGDAWELL	374	-0.2000	0
39	YLALLDALR	57	-0.3000	0
40	WLGLDWDEG	66	-0.3000	0
41	LGLDWDEGP	67	-0.3000	0
42	FFNDDQYVI	384	-0.3000	0
43	FESLELLGR	464	-0.3000	0
44	LRMPDDDLA	157	-0.4000	0
45	LYTLVNPCD	194	-0.4000	0
46	LALLGWSIA	283	-0.4000	0
47	IVVLGDAWE	372	-0.4000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRGPVTFAA	170	3.5000	36.46
2	LVRGPVTFA	169	3.1000	32.29
3	MKITHVLRG	206	3.0000	31.25
4	VVLGDAWEL	373	2.8000	29.17
5	VRLRDHLDT	341	2.6000	27.08
6	VQTRIVVLG	368	2.3000	23.96
7	LALHQALIR	225	2.2000	22.92

8	VAATGTTVS	452	2.2000	22.92
9	VRFCPSPTG	8	2.0000	20.83
10	MQRLRAARQ	476	1.8000	18.75
11	LIRIGVAER	231	1.7800	18.54
12	VGLVRTALF	20	1.7000	17.71
13	VRTALFNWA	23	1.7000	17.71
14	LFAHRDRGF	266	1.6000	16.67
15	LKPRKAFSP	441	1.6000	16.67
16	IRIGVAERI	232	1.5000	15.62
17	LFNWAYARH	27	1.4800	15.42
18	VRVRFCPSP	6	1.4000	14.58
19	LHQALIRIG	227	1.4000	14.58
20	IRVAATGTT	450	1.3000	13.54
21	LLNYLALLG	279	1.1000	11.46
22	VGDFTVRLR	336	1.1000	11.46
23	VEARHVAAG	116	1.0000	10.42
24	LLPSTPRQL	217	1.0000	10.42
25	LLGWSIADD	285	1.0000	10.42
26	LLKFFNDDQ	381	1.0000	10.42
27	VTATETVRV	0	0.9000	9.38
28	IRMLDVGDF	331	0.8000	8.33
29	LVRTALFNW	22	0.7000	7.29
30	FRIEDTDAQ	42	0.7000	7.29
31	LRGEDLLPS	212	0.7000	7.29
32	LVQTRIVVL	367	0.7000	7.29
33	LRAARQLVG	479	0.7000	7.29
34	VFRIEDTDA	41	0.5800	6.04
35	VAAFDVADV	303	0.5000	5.21
36	LALLDALRW	58	0.4000	4.17
37	VRLRMPDDD	155	0.4000	4.17
38	LSKRDPQSN	257	0.4000	4.17
39	FDVADVNSS	306	0.4000	4.17
40	FNWAYARHT	28	0.3000	3.12
41	LAAGEAYHA	101	0.2000	2.08

42	LRDHLDTHG	343	0.1000	1.04
43	YRDVLARLL	93	-0.1000	0
44	VLARLLAAG	96	-0.1000	0
45	FDRHLTDAQ	134	-0.1000	0
46	LNYLALLGW	280	-0.1000	0
47	LLGRDRSMQ	469	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MQRLRAARQ	476	3.4000	38.64
2	IRMLDVGDF	331	3.3000	37.50
3	VRGPVTFAA	170	2.9500	33.52
4	VGLVRTALF	20	2.9000	32.95
5	FRIEDTDAQ	42	2.8000	31.82
6	LIRIGVAER	231	2.8000	31.82
7	LLKFFNDDQ	381	2.6000	29.55
8	IRVAATGTT	450	2.2000	25.00
9	VAATGTTVS	452	2.1000	23.86
10	VRFCPSPTG	8	2.0000	22.73
11	VFRIEDTDA	41	1.9000	21.59
12	MKITHVLRG	206	1.9000	21.59
13	VRTALFNWA	23	1.8000	20.45
14	LVRGPVTFA	169	1.7000	19.32
15	LALLGWSIA	283	1.5000	17.05
16	LALLDALRW	58	1.3000	14.77
17	LRGEDLLPS	212	1.2000	13.64
18	VAAFDVADV	303	1.2000	13.64
19	FAHLPTVLG	243	1.0000	11.36
20	LNYLALLGW	280	0.8000	9.09
21	IVVLGDAWE	372	0.8000	9.09
22	LGRDRSMQR	470	0.8000	9.09
23	VADVNSSPA	308	0.7000	7.95
24	LYTLVNPCD	194	0.5000	5.68

25	FDVADVNSS	306	0.5000	5.68
26	LLNYLALLG	279	0.4000	4.55
27	IRIGVAERI	232	0.3000	3.41
28	LFGLDEMVA	296	0.3000	3.41
29	VTATETVRV	0	0.2000	2.27
30	LAALTSVTD	413	0.2000	2.27
31	IALDEAAFA	354	-0.1000	0
32	LFNWAYARH	27	-0.1700	0
33	FSPIRVAAT	447	-0.2000	0
34	LVRTALFNW	22	-0.2500	0
35	LMKITHVLR	205	-0.3000	0
36	VLGEGTKKL	249	-0.3000	0
37	VNPCDDALM	198	-0.4000	0
38	LKFFNDDQY	382	-0.4000	0
39	LLGWSIADD	285	-0.6500	0
40	LALHQALIR	225	-0.7000	0
41	LRWLGLDWD	64	-0.8000	0
42	MVAAFDVAD	302	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FRIEDTDAQ	42	4.6000	48.94
2	YHAFSTPEE	107	4.0000	42.55
3	FAHLPTVLG	243	3.3000	35.11
4	IRMLDVGDF	331	3.2000	34.04
5	MQRLRAARQ	476	3.2000	34.04
6	VGLVRTALF	20	2.8000	29.79
7	IVVLGDAWE	372	2.8000	29.79
8	YTLVNPCDD	195	2.5000	26.60
9	LLKFFNDDQ	381	2.4000	25.53
10	VRFCPSPTG	8	2.3000	24.47
11	LYTLVNPCD	194	2.2000	23.40
12	MKITHVLRG	206	2.2000	23.40

13	IRVAATGTT	450	2.1000	22.34
14	LARLLAAGE	97	2.0000	21.28
15	VRGPVTFAA	170	1.9500	20.74
16	WELLKFFND	379	1.9500	20.74
17	LAALTSVTD	413	1.9000	20.21
18	LIRIGVAER	231	1.8000	19.15
19	VVRLRMPDD	154	1.7000	18.09
20	FSPIRVAAT	447	1.7000	18.09
21	FALTRASGD	184	1.6000	17.02
22	FDVADVNSS	306	1.5000	15.96
23	LALLDALRW	58	1.2000	12.77
24	VAATGTTVS	452	1.1000	11.70
25	LLGWSIADD	285	1.0500	11.17
26	VFRIEDTDA	41	0.9000	9.57
27	LRWLGLDWD	64	0.9000	9.57
28	MVAAFDVAD	302	0.9000	9.57
29	VRTALFNWA	23	0.8000	8.51
30	LVRGPVTFA	169	0.7000	7.45
31	LLNYLALLG	279	0.7000	7.45
32	LNYLALLGW	280	0.7000	7.45
33	YRDVLARLL	93	0.5000	5.32
34	LALLGWSIA	283	0.5000	5.32
35	VAAFDVADV	303	0.5000	5.32
36	FDRHLTDAQ	134	0.4000	4.26
37	WLGLDWDEG	66	0.3000	3.19
38	LRAARQLVG	479	0.3000	3.19
39	LRGEDLLPS	212	0.2000	2.13
40	WAYARHTGG	30	0.1000	1.06
41	YVIDPKAAA	390	0.1000	1.06
42	LFNWAYARH	27	0.0500	0.53
43	YLALLDALR	57	-0.1000	0
44	LGRDRSMQR	470	-0.2000	0
45	VNPCDDALM	198	-0.3000	0
46	VLGEGTKKL	249	-0.3000	0

47	YLALLGWSI	282	-0.3000	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	FRIEDTDAQ	42	3.8000	43.18
2	MQRLRAARQ	476	2.4000	27.27
3	IRMLDVGDF	331	2.3000	26.14
4	FAHLPTVLG	243	2.0000	22.73
5	VRGPVTFAA	170	1.9500	22.16
6	VGLVRTALF	20	1.9000	21.59
7	LIRIGVAER	231	1.8000	20.45
8	LLKFFNDDQ	381	1.6000	18.18
9	FDVADVNSS	306	1.5000	17.05
10	IRVAATGTT	450	1.2000	13.64
11	VAATGTTVS	452	1.1000	12.50
12	VRFCPSPTG	8	1.0000	11.36
13	YHAFSTPEE	107	1.0000	11.36
14	VFRIEDTDA	41	0.9000	10.23
15	MKITHVLRG	206	0.9000	10.23
16	VRTALFNWA	23	0.8000	9.09
17	FSPIRVAAT	447	0.8000	9.09
18	LVRGPVTFA	169	0.7000	7.95
19	LALLGWSIA	283	0.5000	5.68
20	LALLDALRW	58	0.3000	3.41
21	LRGEDLLPS	212	0.2000	2.27
22	VAAFDVADV	303	0.2000	2.27
23	YVIDPKAAA	390	0.1000	1.14
24	YLALLDALR	57	-0.1000	0
25	YTLVNPCDD	195	-0.2000	0
26	LNYLALLGW	280	-0.2000	0
27	IVVLGDAWE	372	-0.2000	0
28	LGRDRSMQR	470	-0.2000	0
29	VADVNSSPA	308	-0.3000	0

30	FDRHLTDAQ	134	-0.4000	0
31	YRDVLARLL	93	-0.5000	0
32	LYTLVNPCD	194	-0.5000	0
33	YLALLGWSI	282	-0.5000	0
34	FESLELLGR	464	-0.5000	0
35	LLNYLALLG	279	-0.6000	0
36	IRIGVAERI	232	-0.7000	0
37	LFGLDEMVA	296	-0.7000	0
38	WELLKFFND	379	-0.7500	0
39	VTATETVRV	0	-0.8000	0
40	FGLDEMVAA	297	-0.8000	0
41	LAALTSVTD	413	-0.8000	0
42	FCPSPTGTP	10	-1.0000	0
43	WLGLDWDEG	66	-1.0000	0
44	LARLLAAGE	97	-1.0000	0
45	VVRLRMPDD	154	-1.0000	0
46	LRMPDDDLA	157	-1.0000	0
47	LVQTRIVVL	367	-1.0000	0
48	LRAARQLVG	479	-1.0000	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	IRMLDVGDF	331	4.2000	44.68
2	MQRLRAARQ	476	4.2000	44.68
3	VGLVRTALF	20	3.8000	40.43
4	IVVLGDAWE	372	3.8000	40.43
5	FRIEDTDAQ	42	3.6000	38.30
6	LLKFFNDDQ	381	3.4000	36.17
7	VRFCPSPTG	8	3.3000	35.11
8	LYTLVNPCD	194	3.2000	34.04
9	MKITHVLRG	206	3.2000	34.04
10	IRVAATGTT	450	3.1000	32.98
11	LARLLAAGE	97	3.0000	31.91

12	YHAFSTPEE	107	3.0000	31.91
13	VRGPVTFAA	170	2.9500	31.38
14	LAALTSVTD	413	2.9000	30.85
15	LIRIGVAER	231	2.8000	29.79
16	VVRLRMPDD	154	2.7000	28.72
17	FAHLPTVLG	243	2.3000	24.47
18	LALLDALRW	58	2.2000	23.40
19	VAATGTTVS	452	2.1000	22.34
20	LLGWSIADD	285	2.0500	21.81
21	VFRIEDTDA	41	1.9000	20.21
22	LRWLGLDWD	64	1.9000	20.21
23	MVAAFDVAD	302	1.9000	20.21
24	VRTALFNWA	23	1.8000	19.15
25	LVRGPVTFA	169	1.7000	18.09
26	LLNYLALLG	279	1.7000	18.09
27	LNYLALLGW	280	1.7000	18.09
28	YTLVNPCDD	195	1.5000	15.96
29	LALLGWSIA	283	1.5000	15.96
30	VAAFDVADV	303	1.5000	15.96
31	LRAARQLVG	479	1.3000	13.83
32	LRGEDLLPS	212	1.2000	12.77
33	LFNWAYARH	27	1.0500	11.17
34	LVQTRIVVL	367	1.0000	10.64
35	WELLKFFND	379	0.9500	10.11
36	LGRDRSMQR	470	0.8000	8.51
37	VNPCDDALM	198	0.7000	7.45
38	VLGEGTKKL	249	0.7000	7.45
39	VADVNSSPA	308	0.7000	7.45
40	LKFFNDDQY	382	0.7000	7.45
41	FSPIRVAAT	447	0.7000	7.45
42	LVRTALFNW	22	0.6500	6.91
43	VRLRMPDDD	155	0.6000	6.38
44	FALTRASGD	184	0.6000	6.38
45	VTATETVRV	0	0.5000	5.32

46	IRIGVAERI	232	0.5000	5.32
47	FDVADVNSS	306	0.5000	5.32
48	VNSSPARFD	311	0.4000	4.26
49	LFGLDEMVA	296	0.3000	3.19

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	FRIEDTDAQ	42	6.6000	73.33
2	MKITHVLRG	206	4.3000	47.78
3	IRMLDVGDF	331	3.9000	43.33
4	LGRDRSMQR	470	3.9000	43.33
5	LRGEDLLPS	212	3.6000	40.00
6	FAHLPTVLG	243	3.3800	37.56
7	VLGEGTKKL	249	3.2600	36.22
8	LIRIGVAER	231	3.0000	33.33
9	FIPEGLLNY	274	2.8000	31.11
10	VRFCPSPTG	8	2.7000	30.00
11	YVIDPKAAA	390	2.6000	28.89
12	VAATGTTVS	452	2.6000	28.89
13	VGLVRTALF	20	2.4000	26.67
14	LALHQALIR	225	2.3000	25.56
15	VTATETVRV	0	1.9800	22.00
16	FDRHLTDAQ	134	1.9000	21.11
17	IRIGVAERI	232	1.9000	21.11
18	FGLDEMVAA	297	1.8800	20.89
19	FDVADVNSS	306	1.8000	20.00
20	IRVAATGTT	450	1.8000	20.00
21	LVQTRIVVL	367	1.7400	19.33
22	MQRLRAARQ	476	1.5000	16.67
23	FCPSPTGTP	10	1.4000	15.56
24	IALDEAAFA	354	1.4000	15.56
25	YLALLDALR	57	1.2000	13.33
26	YRQSQRAEI	84	1.2000	13.33

27	FSPIRVAAT	447	1.2000	13.33
28	FESLELLGR	464	1.2000	13.33
29	LGPDGAAVL	401	1.1600	12.89
30	WLGLDWDEG	66	1.1000	12.22
31	LVRGPVTFA	169	1.0000	11.11
32	IVVLGDAWE	372	1.0000	11.11
33	FALTRASGD	184	0.9000	10.00
34	IYRDVLARL	92	0.8600	9.56
35	YHAFSTPEE	107	0.8000	8.89
36	LRAARQLVG	479	0.8000	8.89
37	VLGDAWELL	374	0.7600	8.44
38	VRTALFNWA	23	0.7000	7.78
39	LGLDWDEGP	67	0.7000	7.78
40	VRGPVTFAA	170	0.7000	7.78
41	LYTLVNPCD	194	0.7000	7.78
42	FFNDDQYVI	384	0.6000	6.67
43	LALLDALRW	58	0.5000	5.56
44	YLAEGRQPV	146	0.4000	4.44
45	LAALTSVTD	413	0.2800	3.11
46	LARLLAAGE	97	0.2000	2.22
47	VVRLRMPDD	154	0.2000	2.22
48	LRDHLDTHG	343	0.2000	2.22
49	VFRIEDTDA	41	0.1000	1.11

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	MQRLRAARQ	476	3.4000	38.64
2	IRMLDVGDF	331	3.3000	37.50
3	VRGPVTFAA	170	2.9500	33.52
4	VGLVRTALF	20	2.9000	32.95
5	FRIEDTDAQ	42	2.8000	31.82
6	LIRIGVAER	231	2.8000	31.82
7	LLKFFNDDQ	381	2.6000	29.55

8	IRVAATGTT	450	2.2000	25.00
9	VAATGTTVS	452	2.1000	23.86
10	VRFCPSPTG	8	2.0000	22.73
11	VFRIEDTDA	41	1.9000	21.59
12	MKITHVLRG	206	1.9000	21.59
13	VRTALFNWA	23	1.8000	20.45
14	LVRGPVTFA	169	1.7000	19.32
15	LALLGWSIA	283	1.5000	17.05
16	LALLDALRW	58	1.3000	14.77
17	LRGEDLLPS	212	1.2000	13.64
18	VAAFDVADV	303	1.2000	13.64
19	FAHLPTVLG	243	1.0000	11.36
20	LNYLALLGW	280	0.8000	9.09
21	IVVLGDAWE	372	0.8000	9.09
22	LGRDRSMQR	470	0.8000	9.09
23	VADVNSSPA	308	0.7000	7.95
24	LYTLVNPCD	194	0.5000	5.68
25	FDVADVNSS	306	0.5000	5.68
26	LLNYLALLG	279	0.4000	4.55
27	IRIGVAERI	232	0.3000	3.41
28	LFGLDEMVA	296	0.3000	3.41
29	VTATETVRV	0	0.2000	2.27
30	LAALTSVTD	413	0.2000	2.27
31	IALDEAAFA	354	-0.1000	0
32	LFNWAYARH	27	-0.1700	0
33	FSPIRVAAT	447	-0.2000	0
34	LVRTALFNW	22	-0.2500	0
35	LMKITHVLR	205	-0.3000	0
36	VLGEGTKKL	249	-0.3000	0
37	VNPCDDALM	198	-0.4000	0
38	LKFFNDDQY	382	-0.4000	0
39	LLGWSIADD	285	-0.6500	0
40	LALHQALIR	225	-0.7000	0
41	LRWLGLDWD	64	-0.8000	0

42	MVAAFDVAD	302	-0.8000	0

ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	FRIEDTDAQ	42	7.3000	84.88
2	LRGEDLLPS	212	3.2000	37.21
3	MKITHVLRG	206	2.9000	33.72
4	FDRHLTDAQ	134	2.6000	30.23
5	YVIDPKAAA	390	2.6000	30.23
6	LGRDRSMQR	470	2.4000	27.91
7	VLGEGTKKL	249	2.3000	26.74
8	VAATGTTVS	452	2.2000	25.58
9	MQRLRAARQ	476	2.2000	25.58
10	IRMLDVGDF	331	2.0000	23.26
11	FAHLPTVLG	243	1.9800	23.02
12	FGLDEMVAA	297	1.8800	21.86
13	LIRIGVAER	231	1.5000	17.44
14	FIPEGLLNY	274	1.5000	17.44
15	FDVADVNSS	306	1.4000	16.28
16	IALDEAAFA	354	1.4000	16.28
17	VRFCPSPTG	8	1.3000	15.12
18	IRVAATGTT	450	1.1000	12.79
19	LVRGPVTFA	169	1.0000	11.63
20	IRIGVAERI	232	1.0000	11.63
21	VTATETVRV	0	0.9800	11.40
22	LALHQALIR	225	0.8000	9.30
23	LVQTRIVVL	367	0.7800	9.07
24	VRTALFNWA	23	0.7000	8.14
25	VRGPVTFAA	170	0.7000	8.14
26	LLKFFNDDQ	381	0.6000	6.98
27	VGLVRTALF	20	0.5000	5.81
28	LALLDALRW	58	0.5000	5.81
29	FSPIRVAAT	447	0.5000	5.81

30	FCPSPTGTP	10	0.4000	4.65
31	LGYDNFDRH	129	0.3800	4.42
32	YRQSQRAEI	84	0.3000	3.49
33	LGPDGAAVL	401	0.2000	2.33
34	VFRIEDTDA	41	0.1000	1.16
35	LGWSIADDH	286	0.0800	0.93
36	IYRDVLARL	92	-0.1000	0
37	FALTRASGD	184	-0.2000	0
38	VLGDAWELL	374	-0.2000	0
39	YLALLDALR	57	-0.3000	0
40	WLGLDWDEG	66	-0.3000	0
41	LGLDWDEGP	67	-0.3000	0
42	FFNDDQYVI	384	-0.3000	0
43	FESLELLGR	464	-0.3000	0
44	LRMPDDDLA	157	-0.4000	0
45	LYTLVNPCD	194	-0.4000	0
46	LALLGWSIA	283	-0.4000	0
47	IVVLGDAWE	372	-0.4000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LVQTRIVVL	367	7.0000	60.34
2	YRQSQRAEI	84	6.0000	51.72
3	YRDVLARLL	93	5.9000	50.86
4	IRIGVAERI	232	5.9000	50.86
5	VVLGDAWEL	373	5.8000	50.00
6	LLPSTPRQL	217	5.4000	46.55
7	LVRTALFNW	22	5.2000	44.83
8	MKITHVLRG	206	4.7000	40.52
9	YLALLGWSI	282	4.4000	37.93
10	IRMLDVGDF	331	4.0000	34.48
11	VTATETVRV	0	3.9200	33.79
12	FFNDDQYVI	384	3.7000	31.90

13	VGLVRTALF	20	3.4200	29.48
14	WSIADDHDL	288	3.0000	25.86
15	VRLRDHLDT	341	2.9000	25.00
16	VLGEGTKKL	249	2.6200	22.59
17	LKDALIEGL	431	2.6000	22.41
18	FIPEGLLNY	274	2.4000	20.69
19	YARHTGGTF	32	2.3000	19.83
20	VRGPVTFAA	170	2.2200	19.14
21	LALLDALRW	58	2.2000	18.97
22	IRVAATGTT	450	2.0200	17.41
23	LNAEHIRML	326	2.0000	17.24
24	VLGDAWELL	374	2.0000	17.24
25	FNWAYARHT	28	1.9000	16.38
26	LNYLALLGW	280	1.9000	16.38
27	VRFCPSPTG	8	1.8000	15.52
28	VRTALFNWA	23	1.8000	15.52
29	LVRGPVTFA	169	1.7000	14.66
30	LRAARQLVG	479	1.7000	14.66
31	LDALRWLGL	61	1.6000	13.79
32	YLAEGRQPV	146	1.6000	13.79
33	FALTRASGD	184	1.6000	13.79
34	LGPDGAAVL	401	1.6000	13.79
35	FSPIRVAAT	447	1.6000	13.79
36	IYRDVLARL	92	1.5000	12.93
37	LALHQALIR	225	1.5000	12.93
38	FAHRDRGFI	267	1.4000	12.07
39	VAAFDVADV	303	1.3000	11.21
40	VSPPLFESL	459	1.3000	11.21
41	LTRASGDPL	186	1.2000	10.34
42	LMKITHVLR	205	1.2000	10.34
43	LIRIGVAER	231	1.2000	10.34
44	LLNYLALLG	279	1.2000	10.34
45	MLDVGDFTV	333	1.2000	10.34
46	VLDAALAAL	408	1.2000	10.34

47	FCPSPTGTP	10	1.1200	9.66
48	LRGEDLLPS	212	1.0000	8.62
49	VNSSPARFD	311	1.0000	8.62

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	LVQTRIVVL	367	7.0000	60.34
2	YRQSQRAEI	84	6.0000	51.72
3	YRDVLARLL	93	5.9000	50.86
4	IRIGVAERI	232	5.9000	50.86
5	VVLGDAWEL	373	5.8000	50.00
6	LLPSTPRQL	217	5.4000	46.55
7	LVRTALFNW	22	5.2000	44.83
8	MKITHVLRG	206	4.7000	40.52
9	YLALLGWSI	282	4.4000	37.93
10	IRMLDVGDF	331	4.0000	34.48
11	VTATETVRV	0	3.9200	33.79
12	FFNDDQYVI	384	3.7000	31.90
13	VGLVRTALF	20	3.4200	29.48
14	WSIADDHDL	288	3.0000	25.86
15	VRLRDHLDT	341	2.9000	25.00
16	VLGEGTKKL	249	2.6200	22.59
17	LKDALIEGL	431	2.6000	22.41
18	FIPEGLLNY	274	2.4000	20.69
19	YARHTGGTF	32	2.3000	19.83
20	VRGPVTFAA	170	2.2200	19.14
21	LALLDALRW	58	2.2000	18.97
22	IRVAATGTT	450	2.0200	17.41
23	LNAEHIRML	326	2.0000	17.24
24	VLGDAWELL	374	2.0000	17.24
25	FNWAYARHT	28	1.9000	16.38
26	LNYLALLGW	280	1.9000	16.38
27	VRFCPSPTG	8	1.8000	15.52

28	VRTALFNWA	23	1.8000	15.52
29	LVRGPVTFA	169	1.7000	14.66
30	LRAARQLVG	479	1.7000	14.66
31	LDALRWLGL	61	1.6000	13.79
32	YLAEGRQPV	146	1.6000	13.79
33	FALTRASGD	184	1.6000	13.79
34	LGPDGAAVL	401	1.6000	13.79
35	FSPIRVAAT	447	1.6000	13.79
36	IYRDVLARL	92	1.5000	12.93
37	LALHQALIR	225	1.5000	12.93
38	FAHRDRGFI	267	1.4000	12.07
39	VAAFDVADV	303	1.3000	11.21
40	VSPPLFESL	459	1.3000	11.21
41	LTRASGDPL	186	1.2000	10.34
42	LMKITHVLR	205	1.2000	10.34
43	LIRIGVAER	231	1.2000	10.34
44	LLNYLALLG	279	1.2000	10.34
45	MLDVGDFTV	333	1.2000	10.34
46	VLDAALAAL	408	1.2000	10.34
47	FCPSPTGTP	10	1.1200	9.66
48	LRGEDLLPS	212	1.0000	8.62
49	VNSSPARFD	311	1.0000	8.62

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	IRMLDVGDF	331	3.9000	45.35
2	YVIDPKAAA	390	3.9000	45.35
3	VRLRDHLDT	341	3.8000	44.19
4	VRLRMPDDD	155	3.6000	41.86
5	LLGRDRSMQ	469	3.5000	40.70
6	VEARHVAAG	116	2.9000	33.72
7	FAHRDRGFI	267	2.9000	33.72
8	VQTRIVVLG	368	2.9000	33.72

9	MQRLRAARQ	476	2.9000	33.72
10	VLARLLAAG	96	2.8000	32.56
11	YTLVNPCDD	195	2.8000	32.56
12	LLNYLALLG	279	2.7000	31.40
13	FVFRIEDTD	40	2.4000	27.91
14	FRIEDTDAQ	42	2.4000	27.91
15	LALKPRKAF	439	2.4000	27.91
16	YHAFSTPEE	107	2.2000	25.58
17	YRQSQRAEI	84	2.1000	24.42
18	VRVRFCPSP	6	1.9000	22.09
19	LLGWSIADD	285	1.9000	22.09
20	MKITHVLRG	206	1.8000	20.93
21	LARLLAAGE	97	1.7000	19.77
22	IRVAATGTT	450	1.7000	19.77
23	IDPKAAAKE	392	1.6000	18.60
24	VGLVRTALF	20	1.5000	17.44
25	VVRLRMPDD	154	1.4000	16.28
26	FTVRLRDHL	339	1.4000	16.28
27	LIRIGVAER	231	1.3000	15.12
28	IVVLGDAWE	372	1.2000	13.95
29	FSPIRVAAT	447	1.2000	13.95
30	LNYLALLGW	280	1.1000	12.79
31	VRFCPSPTG	8	1.0000	11.63
32	ITHVLRGED	208	1.0000	11.63
33	LRGEDLLPS	212	1.0000	11.63
34	FAHLPTVLG	243	0.9000	10.47
35	LSKRDPQSN	257	0.9000	10.47
36	LKPRKAFSP	441	0.9000	10.47
37	LRAARQLVG	479	0.9000	10.47
38	LRWLGLDWD	64	0.7000	8.14
39	YRDVLARLL	93	0.6000	6.98
40	WELLKFFND	379	0.5000	5.81
41	YGPYRQSQR	81	0.4000	4.65
42	FIPEGLLNY	274	0.4000	4.65

43	LALLDALRW	58	0.3000	3.49
44	WNDLVRGPV	166	0.3000	3.49
45	VRGPVTFAA	170	0.3000	3.49
46	VAAFDVADV	303	0.3000	3.49
47	LFNWAYARH	27	0.2000	2.33
48	LHQALIRIG	227	0.2000	2.33
49	LELLGRDRS	467	0.1000	1.16

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVIDPKAAA	390	3.9000	48.75
2	IRMLDVGDF	331	3.0000	37.50
3	VRLRDHLDT	341	2.9000	36.25
4	FAHRDRGFI	267	2.7000	33.75
5	LLGRDRSMQ	469	2.7000	33.75
6	MQRLRAARQ	476	2.1000	26.25
7	YRQSQRAEI	84	1.9000	23.75
8	FRIEDTDAQ	42	1.6000	20.00
9	VEARHVAAG	116	1.6000	20.00
10	VQTRIVVLG	368	1.6000	20.00
11	VRVRFCPSP	6	1.5000	18.75
12	VLARLLAAG	96	1.5000	18.75
13	LALKPRKAF	439	1.5000	18.75
14	LLNYLALLG	279	1.4000	17.50
15	LIRIGVAER	231	1.3000	16.25
16	LRGEDLLPS	212	1.0000	12.50
17	VRLRMPDDD	155	0.9000	11.25
18	IRVAATGTT	450	0.8000	10.00
19	VGLVRTALF	20	0.6000	7.50
20	MKITHVLRG	206	0.5000	6.25
21	LKPRKAFSP	441	0.5000	6.25
22	YGPYRQSQR	81	0.4000	5.00
23	FTVRLRDHL	339	0.4000	5.00

24	VRGPVTFAA	170	0.3000	3.75
25	FSPIRVAAT	447	0.3000	3.75
26	LNYLALLGW	280	0.2000	2.50
27	YTLVNPCDD	195	0.1000	1.25
28	LELLGRDRS	467	0.1000	1.25
29	IGVAERIPK	234	-0.1000	0
30	FESLELLGR	464	-0.1000	0
31	VAERIPKFA	236	-0.2000	0
32	FDVADVNSS	306	-0.2000	0
33	VRFCPSPTG	8	-0.3000	0
34	FVFRIEDTD	40	-0.3000	0
35	YRDVLARLL	93	-0.4000	0
36	LVRGPVTFA	169	-0.4000	0
37	FAHLPTVLG	243	-0.4000	0
38	LRAARQLVG	479	-0.4000	0
39	YLALLGWSI	282	-0.5000	0
40	LALLDALRW	58	-0.6000	0
41	FIPEGLLNY	274	-0.7000	0
42	YHAFSTPEE	107	-0.8000	0
43	LLGWSIADD	285	-0.8000	0
44	LVRTALFNW	22	-0.9000	0
45	YLAEGRQPV	146	-0.9000	0
46	FNWAYARHT	28	-1.0000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRMLDVGDF	331	4.0000	50.00
2	VRLRDHLDT	341	3.9000	48.75
3	LLGRDRSMQ	469	3.7000	46.25
4	MQRLRAARQ	476	3.1000	38.75
5	YVIDPKAAA	390	2.9000	36.25
6	VEARHVAAG	116	2.6000	32.50
7	VQTRIVVLG	368	2.6000	32.50

8	VRVRFCPSP	6	2.5000	31.25
9	VLARLLAAG	96	2.5000	31.25
10	LALKPRKAF	439	2.5000	31.25
11	LLNYLALLG	279	2.4000	30.00
12	LIRIGVAER	231	2.3000	28.75
13	LRGEDLLPS	212	2.0000	25.00
14	VRLRMPDDD	155	1.9000	23.75
15	IRVAATGTT	450	1.8000	22.50
16	FAHRDRGFI	267	1.7000	21.25
17	VGLVRTALF	20	1.6000	20.00
18	MKITHVLRG	206	1.5000	18.75
19	LKPRKAFSP	441	1.5000	18.75
20	VRGPVTFAA	170	1.3000	16.25
21	LNYLALLGW	280	1.2000	15.00
22	LELLGRDRS	467	1.1000	13.75
23	VAAFDVADV	303	1.0000	12.50
24	YRQSQRAEI	84	0.9000	11.25
25	IGVAERIPK	234	0.9000	11.25
26	VAERIPKFA	236	0.8000	10.00
27	VRFCPSPTG	8	0.7000	8.75
28	FRIEDTDAQ	42	0.6000	7.50
29	LVRGPVTFA	169	0.6000	7.50
30	LRAARQLVG	479	0.6000	7.50
31	LALLDALRW	58	0.4000	5.00
32	LLGWSIADD	285	0.2000	2.50
33	LVRTALFNW	22	0.1000	1.25
34	LFNWAYARH	27	-0.0200	0
35	LHQALIRIG	227	-0.1000	0
36	LSKRDPQSN	257	-0.1000	0
37	VVLGDAWEL	373	-0.1000	0
38	IYRDVLARL	92	-0.2000	0
39	LARLLAAGE	97	-0.3000	0
40	VVRLRMPDD	154	-0.3000	0
41	LVQTRIVVL	367	-0.3000	0

42	LLAAGEAYH	100	-0.3200	0
43	IDPKAAAKE	392	-0.4000	0
44	VRTALFNWA	23	-0.5000	0
45	LGEGTKKLS	250	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRMLDVGDF	331	4.9000	56.98
2	VRLRDHLDT	341	4.8000	55.81
3	VRLRMPDDD	155	4.6000	53.49
4	LLGRDRSMQ	469	4.5000	52.33
5	VEARHVAAG	116	3.9000	45.35
6	VQTRIVVLG	368	3.9000	45.35
7	MQRLRAARQ	476	3.9000	45.35
8	VLARLLAAG	96	3.8000	44.19
9	LLNYLALLG	279	3.7000	43.02
10	LALKPRKAF	439	3.4000	39.53
11	VRVRFCPSP	6	2.9000	33.72
12	LLGWSIADD	285	2.9000	33.72
13	YVIDPKAAA	390	2.9000	33.72
14	MKITHVLRG	206	2.8000	32.56
15	LARLLAAGE	97	2.7000	31.40
16	IRVAATGTT	450	2.7000	31.40
17	IDPKAAAKE	392	2.6000	30.23
18	VGLVRTALF	20	2.5000	29.07
19	VVRLRMPDD	154	2.4000	27.91
20	LIRIGVAER	231	2.3000	26.74
21	IVVLGDAWE	372	2.2000	25.58
22	LNYLALLGW	280	2.1000	24.42
23	VRFCPSPTG	8	2.0000	23.26
24	ITHVLRGED	208	2.0000	23.26
25	LRGEDLLPS	212	2.0000	23.26
26	LSKRDPQSN	257	1.9000	22.09

27	FAHRDRGFI	267	1.9000	22.09
28	LKPRKAFSP	441	1.9000	22.09
29	LRAARQLVG	479	1.9000	22.09
30	YTLVNPCDD	195	1.8000	20.93
31	LRWLGLDWD	64	1.7000	19.77
32	FVFRIEDTD	40	1.4000	16.28
33	FRIEDTDAQ	42	1.4000	16.28
34	LALLDALRW	58	1.3000	15.12
35	VRGPVTFAA	170	1.3000	15.12
36	VAAFDVADV	303	1.3000	15.12
37	LFNWAYARH	27	1.2000	13.95
38	YHAFSTPEE	107	1.2000	13.95
39	LHQALIRIG	227	1.2000	13.95
40	YRQSQRAEI	84	1.1000	12.79
41	LELLGRDRS	467	1.1000	12.79
42	LVRTALFNW	22	1.0000	11.63
43	LLAAGEAYH	100	0.9000	10.47
44	VVLGDAWEL	373	0.9000	10.47
45	IYRDVLARL	92	0.8000	9.30
46	LYTLVNPCD	194	0.8000	9.30
47	VAERIPKFA	236	0.8000	9.30
48	LVQTRIVVL	367	0.7000	8.14
49	LVRGPVTFA	169	0.6000	6.98

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	LLGRDRSMQ	469	4.5000	51.72
2	YVIDPKAAA	390	3.9000	44.83
3	VRLRDHLDT	341	3.5000	40.23
4	FRIEDTDAQ	42	2.8000	32.18
5	VQTRIVVLG	368	2.6000	29.89
6	LVRGPVTFA	169	2.4000	27.59
7	IRMLDVGDF	331	2.3000	26.44

8	YGPYRQSQR	81	2.2000	25.29
9	VRLRMPDDD	155	2.1000	24.14
10	MQRLRAARQ	476	2.1000	24.14
11	FAHRDRGFI	267	2.0000	22.99
12	LLNYLALLG	279	2.0000	22.99
13	YRQSQRAEI	84	1.9000	21.84
14	FDVADVNSS	306	1.8000	20.69
15	VRVRFCPSP	6	1.7000	19.54
16	VEARHVAAG	116	1.6000	18.39
17	LRGEDLLPS	212	1.6000	18.39
18	FTVRLRDHL	339	1.6000	18.39
19	VLARLLAAG	96	1.5000	17.24
20	LKPRKAFSP	441	1.3500	15.52
21	LIRIGVAER	231	1.3000	14.94
22	LELLGRDRS	467	1.3000	14.94
23	VRGPVTFAA	170	1.1500	13.22
24	MKITHVLRG	206	1.1000	12.64
25	LALKPRKAF	439	1.0000	11.49
26	FVFRIEDTD	40	0.9000	10.34
27	LNYLALLGW	280	0.8000	9.20
28	IGVAERIPK	234	0.7800	8.97
29	IRIGVAERI	232	0.7000	8.05
30	VGLVRTALF	20	0.6000	6.90
31	FAHLPTVLG	243	0.6000	6.90
32	VRTALFNWA	23	0.5000	5.75
33	FESLELLGR	464	0.5000	5.75
34	FSPIRVAAT	447	0.3000	3.45
35	LRAARQLVG	479	0.2000	2.30
36	WAYARHTGG	30	0.1000	1.15
37	YLAEGRQPV	146	0.1000	1.15
38	YTLVNPCDD	195	0.1000	1.15
39	IRVAATGTT	450	0.1000	1.15
40	LVRTALFNW	22	-0.0500	0
41	VRFCPSPTG	8	-0.1000	0

42	LSKRDPQSN	257	-0.1000	0
43	FIPEGLLNY	274	-0.1000	0
44	VAATGTTVS	452	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLRDHLDT	341	5.6000	55.45
2	LLNYLALLG	279	4.5000	44.55
3	IRMLDVGDF	331	4.0000	39.60
4	YVIDPKAAA	390	3.9000	38.61
5	MKITHVLRG	206	3.6000	35.64
6	LLGRDRSMQ	469	3.5000	34.65
7	VQTRIVVLG	368	3.4000	33.66
8	YHAFSTPEE	107	3.3500	33.17
9	VRLRMPDDD	155	3.3000	32.67
10	VRVRFCPSP	6	3.0500	30.20
11	FAHRDRGFI	267	3.0000	29.70
12	LALKPRKAF	439	3.0000	29.70
13	VEARHVAAG	116	2.9000	28.71
14	LNYLALLGW	280	2.9000	28.71
15	MQRLRAARQ	476	2.9000	28.71
16	VLARLLAAG	96	2.8000	27.72
17	YTLVNPCDD	195	2.8000	27.72
18	LRGEDLLPS	212	2.8000	27.72
19	LRAARQLVG	479	2.7000	26.73
20	VVRLRMPDD	154	2.5500	25.25
21	FIPEGLLNY	274	2.2000	21.78
22	VRFCPSPTG	8	2.1500	21.29
23	FVFRIEDTD	40	2.1000	20.79
24	FRIEDTDAQ	42	2.1000	20.79
25	LALLDALRW	58	2.1000	20.79
26	YRQSQRAEI	84	2.1000	20.79
27	LLGWSIADD	285	1.9000	18.81

28	IRVAATGTT	450	1.8000	17.82
29	LARLLAAGE	97	1.7000	16.83
30	FESLELLGR	464	1.7000	16.83
31	IDPKAAAKE	392	1.6000	15.84
32	VGLVRTALF	20	1.5000	14.85
33	FAHLPTVLG	243	1.4000	13.86
34	FAAAAELVQ	361	1.4000	13.86
35	LKPRKAFSP	441	1.4000	13.86
36	LIRIGVAER	231	1.3000	12.87
37	IVVLGDAWE	372	1.2000	11.88
38	FSPIRVAAT	447	1.2000	11.88
39	ITHVLRGED	208	1.1000	10.89
40	FTVRLRDHL	339	1.1000	10.89
41	LSKRDPQSN	257	1.0000	9.90
42	WELLKFFND	379	1.0000	9.90
43	LYTLVNPCD	194	0.9500	9.41
44	YRDVLARLL	93	0.8000	7.92
45	VRGPVTFAA	170	0.8000	7.92
46	IGVAERIPK	234	0.8000	7.92
47	LVRGPVTFA	169	0.7000	6.93
48	VVLGDAWEL	373	0.7000	6.93
49	LFGLDEMVA	296	0.6000	5.94

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	IRMLDVGDF	331	3.5000	42.17
2	YVIDPKAAA	390	3.2000	38.55
3	MKITHVLRG	206	2.7000	32.53
4	MQRLRAARQ	476	2.5000	30.12
5	LNYLALLGW	280	2.4000	28.92
6	YRQSQRAEI	84	2.2000	26.51
7	LRGEDLLPS	212	2.1000	25.30
8	FESLELLGR	464	2.1000	25.30

9	LIRIGVAER	231	1.9000	22.89
10	VRLRDHLDT	341	1.7000	20.48
11	LALLDALRW	58	1.6000	19.28
12	IGVAERIPK	234	1.5000	18.07
13	LRAARQLVG	479	1.4000	16.87
14	LFGLDEMVA	296	1.0000	12.05
15	FSPIRVAAT	447	0.9000	10.84
16	IRVAATGTT	450	0.9000	10.84
17	VRFCPSPTG	8	0.8500	10.24
18	VGLVRTALF	20	0.7000	8.43
19	YLALLGWSI	282	0.7000	8.43
20	FRIEDTDAQ	42	0.6000	7.23
21	FAAAAELVQ	361	0.6000	7.23
22	WNDLVRGPV	166	0.5000	6.02
23	FAHLPTVLG	243	0.5000	6.02
24	FIPEGLLNY	274	0.4000	4.82
25	LLNYLALLG	279	0.3000	3.61
26	YHAFSTPEE	107	0.2500	3.01
27	VVRLRMPDD	154	0.2500	3.01
28	YTLVNPCDD	195	0.2000	2.41
29	LELLGRDRS	467	0.2000	2.41
30	VRGPVTFAA	170	0.1000	1.20
31	FDVADVNSS	306	0.1000	1.20
32	YRDVLARLL	93	-0.1000	0
33	LALHQALIR	225	-0.1000	0
34	VAAFDVADV	303	-0.1000	0
35	FAHRDRGFI	267	-0.2000	0
36	LLGRDRSMQ	469	-0.3000	0
37	VRVRFCPSP	6	-0.3500	0
38	LVQTRIVVL	367	-0.4000	0
39	IRIGVAERI	232	-0.6000	0
40	IEGLALKPR	436	-0.6000	0
41	LMKITHVLR	205	-0.7000	0
42	LALKPRKAF	439	-0.7000	0

43	FNWAYARHT	28	-0.8000	0
44	YDNFDRHLT	131	-0.8000	0
45	LARLLAAGE	97	-0.9000	0
46	LHQALIRIG	227	-0.9000	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	MQRLRAARQ	476	2.8000	33.33
2	IRMLDVGDF	331	2.7000	32.14
3	LRGEDLLPS	212	2.6000	30.95
4	VRLRDHLDT	341	2.5000	29.76
5	YVIDPKAAA	390	2.5000	29.76
6	VRGPVTFAA	170	2.3000	27.38
7	MKITHVLRG	206	2.1000	25.00
8	LLGRDRSMQ	469	2.0000	23.81
9	LALHQALIR	225	1.9000	22.62
10	LALKPRKAF	439	1.8000	21.43
11	LHQALIRIG	227	1.7000	20.24
12	LELLGRDRS	467	1.7000	20.24
13	LVRGPVTFA	169	1.6000	19.05
14	LNYLALLGW	280	1.6000	19.05
15	LVRTALFNW	22	1.5000	17.86
16	VQTRIVVLG	368	1.5000	17.86
17	VRFCPSPTG	8	1.4000	16.67
18	FRIEDTDAQ	42	1.4000	16.67
19	LLPSTPRQL	217	1.4000	16.67
20	LIRIGVAER	231	1.4000	16.67
21	VGDFTVRLR	336	1.4000	16.67
22	YRQSQRAEI	84	1.3000	15.48
23	LLNYLALLG	279	1.3000	15.48
24	VAAFDVADV	303	1.3000	15.48
25	LRAARQLVG	479	1.3000	15.48
26	IGVAERIPK	234	1.2000	14.29

27	VRVRFCPSP	6	1.1000	13.10
28	VVLGDAWEL	373	1.0000	11.90
29	VRTALFNWA	23	0.9000	10.71
30	IRIGVAERI	232	0.9000	10.71
31	LLGWSIADD	285	0.9000	10.71
32	LKPRKAFSP	441	0.9000	10.71
33	LALLDALRW	58	0.8000	9.52
34	IRVAATGTT	450	0.8000	9.52
35	VRLRMPDDD	155	0.7000	8.33
36	LFNWAYARH	27	0.6800	8.10
37	LNAEHIRML	326	0.6000	7.14
38	LVQTRIVVL	367	0.6000	7.14
39	VEARHVAAG	116	0.5000	5.95
40	VGLVRTALF	20	0.4000	4.76
41	VLARLLAAG	96	0.4000	4.76
42	LDTHGHHIA	347	0.4000	4.76
43	FDVADVNSS	306	0.2000	2.38
44	LLKFFNDDQ	381	0.2000	2.38
45	LLDALRWLG	60	0.1000	1.19
46	VVRLRMPDD	154	0.1000	1.19
47	LFAHRDRGF	266	0.1000	1.19
48	LIEAALKDA	426	0.1000	1.19

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	IRMLDVGDF	331	4.5000	54.22
2	MKITHVLRG	206	3.7000	44.58
3	MQRLRAARQ	476	3.5000	42.17
4	LNYLALLGW	280	3.4000	40.96
5	LRGEDLLPS	212	3.1000	37.35
6	LIRIGVAER	231	2.9000	34.94
7	VRLRDHLDT	341	2.7000	32.53
8	LALLDALRW	58	2.6000	31.33

9	IGVAERIPK	234	2.5000	30.12
10	LRAARQLVG	479	2.4000	28.92
11	YVIDPKAAA	390	2.2000	26.51
12	LFGLDEMVA	296	2.0000	24.10
13	IRVAATGTT	450	1.9000	22.89
14	VRFCPSPTG	8	1.8500	22.29
15	VGLVRTALF	20	1.7000	20.48
16	LLNYLALLG	279	1.3000	15.66
17	VVRLRMPDD	154	1.2500	15.06
18	YRQSQRAEI	84	1.2000	14.46
19	LELLGRDRS	467	1.2000	14.46
20	VRGPVTFAA	170	1.1000	13.25
21	FESLELLGR	464	1.1000	13.25
22	LVRTALFNW	22	1.0000	12.05
23	LVRGPVTFA	169	1.0000	12.05
24	LALHQALIR	225	0.9000	10.84
25	VAAFDVADV	303	0.9000	10.84
26	LLGRDRSMQ	469	0.7000	8.43
27	VRVRFCPSP	6	0.6500	7.83
28	LVQTRIVVL	367	0.6000	7.23
29	IRIGVAERI	232	0.4000	4.82
30	IEGLALKPR	436	0.4000	4.82
31	LMKITHVLR	205	0.3000	3.61
32	LALKPRKAF	439	0.3000	3.61
33	LARLLAAGE	97	0.1000	1.20
34	LHQALIRIG	227	0.1000	1.20
35	IPKFAHLPT	240	0.1000	1.20
36	LLGWSIADD	285	0.1000	1.20
37	VQTRIVVLG	368	0.1000	1.20
38	LIEAALKDA	426	-0.1000	0
39	FSPIRVAAT	447	-0.1000	0
40	LFNWAYARH	27	-0.1200	0
41	VRTALFNWA	23	-0.2000	0
42	LLPSTPRQL	217	-0.3000	0

43	YLALLGWSI	282	-0.3000	0
44	LGRDRSMQR	470	-0.3000	0
45	LLAAGEAYH	100	-0.3200	0
46	LYTLVNPCD	194	-0.3500	0
47	FRIEDTDAQ	42	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRMLDVGDF	331	4.5000	54.22
2	MKITHVLRG	206	3.7000	44.58
3	MQRLRAARQ	476	3.5000	42.17
4	LNYLALLGW	280	3.4000	40.96
5	LRGEDLLPS	212	3.1000	37.35
6	LIRIGVAER	231	2.9000	34.94
7	VRLRDHLDT	341	2.7000	32.53
8	LALLDALRW	58	2.6000	31.33
9	IGVAERIPK	234	2.5000	30.12
10	LRAARQLVG	479	2.4000	28.92
11	YVIDPKAAA	390	2.2000	26.51
12	LFGLDEMVA	296	2.0000	24.10
13	IRVAATGTT	450	1.9000	22.89
14	VRFCPSPTG	8	1.8500	22.29
15	VGLVRTALF	20	1.7000	20.48
16	LLNYLALLG	279	1.3000	15.66
17	VVRLRMPDD	154	1.2500	15.06
18	YRQSQRAEI	84	1.2000	14.46
19	LELLGRDRS	467	1.2000	14.46
20	VRGPVTFAA	170	1.1000	13.25
21	FESLELLGR	464	1.1000	13.25
22	LVRTALFNW	22	1.0000	12.05
23	LVRGPVTFA	169	1.0000	12.05
24	LALHQALIR	225	0.9000	10.84
25	VAAFDVADV	303	0.9000	10.84

26	LLGRDRSMQ	469	0.7000	8.43
27	VRVRFCPSP	6	0.6500	7.83
28	LVQTRIVVL	367	0.6000	7.23
29	IRIGVAERI	232	0.4000	4.82
30	IEGLALKPR	436	0.4000	4.82
31	LMKITHVLR	205	0.3000	3.61
32	LALKPRKAF	439	0.3000	3.61
33	LARLLAAGE	97	0.1000	1.20
34	LHQALIRIG	227	0.1000	1.20
35	IPKFAHLPT	240	0.1000	1.20
36	LLGWSIADD	285	0.1000	1.20
37	VQTRIVVLG	368	0.1000	1.20
38	LIEAALKDA	426	-0.1000	0
39	FSPIRVAAT	447	-0.1000	0
40	LFNWAYARH	27	-0.1200	0
41	VRTALFNWA	23	-0.2000	0
42	LLPSTPRQL	217	-0.3000	0
43	YLALLGWSI	282	-0.3000	0
44	LGRDRSMQR	470	-0.3000	0
45	LLAAGEAYH	100	-0.3200	0
46	LYTLVNPCD	194	-0.3500	0
47	FRIEDTDAQ	42	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVIDPKAAA	390	6.2000	68.13
2	LVRGPVTFA	169	4.4000	48.35
3	IRMLDVGDF	331	3.9000	42.86
4	IRIGVAERI	232	3.7000	40.66
5	LGRDRSMQR	470	3.5000	38.46
6	IALDEAAFA	354	3.3000	36.26
7	IYRDVLARL	92	3.1000	34.07
8	VRGPVTFAA	170	2.7000	29.67

9	VRFCPSPTG	8	2.6000	28.57
10	YRQSQRAEI	84	2.6000	28.57
11	LRGEDLLPS	212	2.5000	27.47
12	LIRIGVAER	231	2.5000	27.47
13	FRIEDTDAQ	42	2.4000	26.37
14	IRVAATGTT	450	2.4000	26.37
15	MQRLRAARQ	476	2.4000	26.37
16	LELLGRDRS	467	2.2000	24.18
17	IGVAERIPK	234	2.1000	23.08
18	FGLDEMVAA	297	2.1000	23.08
19	LGPDGAAVL	401	2.1000	23.08
20	MKITHVLRG	206	2.0000	21.98
21	VVLGDAWEL	373	2.0000	21.98
22	FFNDDQYVI	384	1.9500	21.43
23	LLGRDRSMQ	469	1.7700	19.45
24	LGYDNFDRH	129	1.6800	18.46
25	LVRTALFNW	22	1.5000	16.48
26	VGLVRTALF	20	1.3000	14.29
27	VRVRFCPSP	6	1.1000	12.09
28	VRLRDHLDT	341	1.1000	12.09
29	LRAARQLVG	479	1.1000	12.09
30	LNYLALLGW	280	1.0000	10.99
31	LVQTRIVVL	367	1.0000	10.99
32	VVRLRMPDD	154	0.9000	9.89
33	LGEGTKKLS	250	0.9000	9.89
34	VLGDAWELL	374	0.9000	9.89
35	VRTALFNWA	23	0.7100	7.80
36	LMKITHVLR	205	0.7000	7.69
37	LFGLDEMVA	296	0.7000	7.69
38	LGWSIADDH	286	0.6800	7.47
39	LLPSTPRQL	217	0.6000	6.59
40	VQTRIVVLG	368	0.6000	6.59
41	LAAGEAYHA	101	0.4500	4.95
42	VRLRMPDDD	155	0.4000	4.40

43	FAAGSVPDF	176	0.4000	4.40
44	VAATGTTVS	452	0.4000	4.40
45	LDWDEGPEV	69	0.3000	3.30
46	LALLDALRW	58	0.2000	2.20
47	LALHQALIR	225	0.2000	2.20
48	LRWLGLDWD	64	0.1000	1.10
49	FDVADVNSS	306	0.0100	0.11

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	YVIDPKAAA	390	3.5000	41.67
2	FRIEDTDAQ	42	2.4000	28.57
3	YRQSQRAEI	84	2.3000	27.38
4	MQRLRAARQ	476	1.8000	21.43
5	IRMLDVGDF	331	1.7000	20.24
6	LRGEDLLPS	212	1.6000	19.05
7	VRLRDHLDT	341	1.5000	17.86
8	VRGPVTFAA	170	1.3000	15.48
9	FDVADVNSS	306	1.2000	14.29
10	MKITHVLRG	206	1.1000	13.10
11	LLGRDRSMQ	469	1.0000	11.90
12	LALHQALIR	225	0.9000	10.71
13	FNWAYARHT	28	0.8000	9.52
14	YLALLGWSI	282	0.8000	9.52
15	LALKPRKAF	439	0.8000	9.52
16	FDRHLTDAQ	134	0.7000	8.33
17	LHQALIRIG	227	0.7000	8.33
18	LELLGRDRS	467	0.7000	8.33
19	LVRGPVTFA	169	0.6000	7.14
20	LNYLALLGW	280	0.6000	7.14
21	LVRTALFNW	22	0.5000	5.95
22	VQTRIVVLG	368	0.5000	5.95
23	VRFCPSPTG	8	0.4000	4.76

24	LLPSTPRQL	217	0.4000	4.76
25	LIRIGVAER	231	0.4000	4.76
26	VGDFTVRLR	336	0.4000	4.76
27	FAHLPTVLG	243	0.3000	3.57
28	LLNYLALLG	279	0.3000	3.57
29	VAAFDVADV	303	0.3000	3.57
30	FESLELLGR	464	0.3000	3.57
31	LRAARQLVG	479	0.3000	3.57
32	YRDVLARLL	93	0.2000	2.38
33	YHAFSTPEE	107	0.2000	2.38
34	IGVAERIPK	234	0.2000	2.38
35	VRVRFCPSP	6	0.1000	1.19
36	YDNFDRHLT	131	0.1000	1.19
37	VRTALFNWA	23	-0.1000	0
38	IRIGVAERI	232	-0.1000	0
39	FIPEGLLNY	274	-0.1000	0
40	LLGWSIADD	285	-0.1000	0
41	LKPRKAFSP	441	-0.1000	0
42	LALLDALRW	58	-0.2000	0
43	YLAEGRQPV	146	-0.2000	0
44	IRVAATGTT	450	-0.2000	0
45	VRLRMPDDD	155	-0.3000	0
46	LFNWAYARH	27	-0.3200	0
47	FAHRDRGFI	267	-0.4000	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	IRMLDVGDF	331	3.6000	40.91
2	YVIDPKAAA	390	3.5000	39.77
3	YRQSQRAEI	84	3.2000	36.36
4	LALKPRKAF	439	2.7000	30.68
5	MKITHVLRG	206	2.5000	28.41
6	LALHQALIR	225	2.4000	27.27

7	VRLRDHLDT	341	2.2000	25.00
8	LHQALIRIG	227	2.1000	23.86
9	LRGEDLLPS	212	2.0000	22.73
10	LIRIGVAER	231	1.9000	21.59
11	VGDFTVRLR	336	1.9000	21.59
12	VQTRIVVLG	368	1.9000	21.59
13	VRFCPSPTG	8	1.8000	20.45
14	FESLELLGR	464	1.8000	20.45
15	FRIEDTDAQ	42	1.7000	19.32
16	FAHLPTVLG	243	1.7000	19.32
17	LLNYLALLG	279	1.7000	19.32
18	YLALLGWSI	282	1.7000	19.32
19	LRAARQLVG	479	1.7000	19.32
20	YHAFSTPEE	107	1.6000	18.18
21	FDVADVNSS	306	1.6000	18.18
22	FNWAYARHT	28	1.5000	17.05
23	LLPSTPRQL	217	1.3600	15.45
24	VGLVRTALF	20	1.3000	14.77
25	VRGPVTFAA	170	1.3000	14.77
26	VAAFDVADV	303	1.3000	14.77
27	FIPEGLLNY	274	1.2000	13.64
28	YRDVLARLL	93	1.1600	13.18
29	VRVRFCPSP	6	1.1000	12.50
30	LELLGRDRS	467	1.1000	12.50
31	MQRLRAARQ	476	1.1000	12.50
32	LFAHRDRGF	266	1.0000	11.36
33	LLGWSIADD	285	1.0000	11.36
34	VVLGDAWEL	373	0.9600	10.91
35	YARHTGGTF	32	0.9000	10.23
36	VEARHVAAG	116	0.9000	10.23
37	LKPRKAFSP	441	0.9000	10.23
38	VLARLLAAG	96	0.8000	9.09
39	YDNFDRHLT	131	0.8000	9.09
40	YLAEGRQPV	146	0.8000	9.09

41	VRLRMPDDD	155	0.8000	9.09
42	IRIGVAERI	232	0.8000	9.09
43	LVRGPVTFA	169	0.6000	6.82
44	LNYLALLGW	280	0.6000	6.82
45	LNAEHIRML	326	0.5600	6.36
46	LVQTRIVVL	367	0.5600	6.36
47	LVRTALFNW	22	0.5000	5.68
48	LLDALRWLG	60	0.5000	5.68
49	YGPYRQSQR	81	0.5000	5.68

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	MQRLRAARQ	476	2.8000	33.33
2	IRMLDVGDF	331	2.7000	32.14
3	LRGEDLLPS	212	2.6000	30.95
4	VRLRDHLDT	341	2.5000	29.76
5	YVIDPKAAA	390	2.5000	29.76
6	VRGPVTFAA	170	2.3000	27.38
7	MKITHVLRG	206	2.1000	25.00
8	LLGRDRSMQ	469	2.0000	23.81
9	LALHQALIR	225	1.9000	22.62
10	LALKPRKAF	439	1.8000	21.43
11	LHQALIRIG	227	1.7000	20.24
12	LELLGRDRS	467	1.7000	20.24
13	LVRGPVTFA	169	1.6000	19.05
14	LNYLALLGW	280	1.6000	19.05
15	LVRTALFNW	22	1.5000	17.86
16	VQTRIVVLG	368	1.5000	17.86
17	VRFCPSPTG	8	1.4000	16.67
18	FRIEDTDAQ	42	1.4000	16.67
19	LLPSTPRQL	217	1.4000	16.67
20	LIRIGVAER	231	1.4000	16.67
21	VGDFTVRLR	336	1.4000	16.67

22	YRQSQRAEI	84	1.3000	15.48
23	LLNYLALLG	279	1.3000	15.48
24	VAAFDVADV	303	1.3000	15.48
25	LRAARQLVG	479	1.3000	15.48
26	IGVAERIPK	234	1.2000	14.29
27	VRVRFCPSP	6	1.1000	13.10
28	VVLGDAWEL	373	1.0000	11.90
29	VRTALFNWA	23	0.9000	10.71
30	IRIGVAERI	232	0.9000	10.71
31	LLGWSIADD	285	0.9000	10.71
32	LKPRKAFSP	441	0.9000	10.71
33	LALLDALRW	58	0.8000	9.52
34	IRVAATGTT	450	0.8000	9.52
35	VRLRMPDDD	155	0.7000	8.33
36	LFNWAYARH	27	0.6800	8.10
37	LNAEHIRML	326	0.6000	7.14
38	LVQTRIVVL	367	0.6000	7.14
39	VEARHVAAG	116	0.5000	5.95
40	VGLVRTALF	20	0.4000	4.76
41	VLARLLAAG	96	0.4000	4.76
42	LDTHGHHIA	347	0.4000	4.76
43	FDVADVNSS	306	0.2000	2.38
44	LLKFFNDDQ	381	0.2000	2.38
45	LLDALRWLG	60	0.1000	1.19
46	VVRLRMPDD	154	0.1000	1.19
47	LFAHRDRGF	266	0.1000	1.19
48	LIEAALKDA	426	0.1000	1.19

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	IRMLDVGDF	331	5.4000	62.07
2	MKITHVLRG	206	4.1000	47.13
3	FESLELLGR	464	3.6000	41.38

4	LIRIGVAER	231	3.4000	39.08
5	YVIDPKAAA	390	3.2000	36.78
6	YRQSQRAEI	84	3.1000	35.63
7	LRAARQLVG	479	2.8000	32.18
8	VGLVRTALF	20	2.6000	29.89
9	LRGEDLLPS	212	2.5000	28.74
10	LNYLALLGW	280	2.4000	27.59
11	VRLRDHLDT	341	2.4000	27.59
12	VRFCPSPTG	8	2.2500	25.86
13	FAHLPTVLG	243	1.9000	21.84
14	MQRLRAARQ	476	1.8000	20.69
15	FIPEGLLNY	274	1.7000	19.54
16	LLNYLALLG	279	1.7000	19.54
17	YHAFSTPEE	107	1.6500	18.97
18	LALLDALRW	58	1.6000	18.39
19	IGVAERIPK	234	1.6000	18.39
20	YLALLGWSI	282	1.6000	18.39
21	FSPIRVAAT	447	1.6000	18.39
22	IRVAATGTT	450	1.6000	18.39
23	WNDLVRGPV	166	1.5000	17.24
24	LALHQALIR	225	1.4000	16.09
25	VVRLRMPDD	154	1.3500	15.52
26	YTLVNPCDD	195	1.3000	14.94
27	LALKPRKAF	439	1.2000	13.79
28	LFGLDEMVA	296	1.0000	11.49
29	VAAFDVADV	303	0.9000	10.34
30	IEGLALKPR	436	0.9000	10.34
31	YRDVLARLL	93	0.8600	9.89
32	LMKITHVLR	205	0.8000	9.20
33	FAHRDRGFI	267	0.7000	8.05
34	VRVRFCPSP	6	0.6500	7.47
35	LELLGRDRS	467	0.6000	6.90
36	LVQTRIVVL	367	0.5600	6.44
37	LARLLAAGE	97	0.5000	5.75

38	LHQALIRIG	227	0.5000	5.75
39	FDVADVNSS	306	0.5000	5.75
40	VQTRIVVLG	368	0.5000	5.75
41	FAAGSVPDF	176	0.3500	4.02
42	IRIGVAERI	232	0.3000	3.45
43	YLALLDALR	57	0.2000	2.30
44	LLGWSIADD	285	0.2000	2.30
45	LGRDRSMQR	470	0.2000	2.30
46	VRGPVTFAA	170	0.1000	1.15

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	IRMLDVGDF	331	4.6000	52.27
2	LALKPRKAF	439	3.7000	42.05
3	MKITHVLRG	206	3.5000	39.77
4	LALHQALIR	225	3.4000	38.64
5	VRLRDHLDT	341	3.2000	36.36
6	LHQALIRIG	227	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09
8	LIRIGVAER	231	2.9000	32.95
9	VGDFTVRLR	336	2.9000	32.95
10	VQTRIVVLG	368	2.9000	32.95
11	VRFCPSPTG	8	2.8000	31.82
12	LLNYLALLG	279	2.7000	30.68
13	LRAARQLVG	479	2.7000	30.68
14	YVIDPKAAA	390	2.5000	28.41
15	LLPSTPRQL	217	2.3600	26.82
16	VGLVRTALF	20	2.3000	26.14
17	VRGPVTFAA	170	2.3000	26.14
18	VAAFDVADV	303	2.3000	26.14
19	YRQSQRAEI	84	2.2000	25.00
20	VRVRFCPSP	6	2.1000	23.86
21	LELLGRDRS	467	2.1000	23.86

22	MQRLRAARQ	476	2.1000	23.86
23	LFAHRDRGF	266	2.0000	22.73
24	LLGWSIADD	285	2.0000	22.73
25	VVLGDAWEL	373	1.9600	22.27
26	VEARHVAAG	116	1.9000	21.59
27	LKPRKAFSP	441	1.9000	21.59
28	VLARLLAAG	96	1.8000	20.45
29	VRLRMPDDD	155	1.8000	20.45
30	IRIGVAERI	232	1.8000	20.45
31	LVRGPVTFA	169	1.6000	18.18
32	LNYLALLGW	280	1.6000	18.18
33	LNAEHIRML	326	1.5600	17.73
34	LVQTRIVVL	367	1.5600	17.73
35	LVRTALFNW	22	1.5000	17.05
36	LLDALRWLG	60	1.5000	17.05
37	IRVAATGTT	450	1.5000	17.05
38	IEGLALKPR	436	1.4000	15.91
39	IGVAERIPK	234	1.3000	14.77
40	LLGRDRSMQ	469	1.3000	14.77
41	VVRLRMPDD	154	1.2000	13.64
42	VNSSPARFD	311	1.0000	11.36
43	VRTALFNWA	23	0.9000	10.23
44	VLGEGTKKL	249	0.8600	9.77
45	LALLDALRW	58	0.8000	9.09
46	LARLLAAGE	97	0.8000	9.09
47	LMKITHVLR	205	0.8000	9.09
48	FESLELLGR	464	0.8000	9.09
49	FRIEDTDAQ	42	0.7000	7.95

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	IRMLDVGDF	331	3.6000	40.91
2	YVIDPKAAA	390	3.5000	39.77

3	YRQSQRAEI	84	3.2000	36.36
4	LALKPRKAF	439	2.7000	30.68
5	MKITHVLRG	206	2.5000	28.41
6	LALHQALIR	225	2.4000	27.27
7	VRLRDHLDT	341	2.2000	25.00
8	LHQALIRIG	227	2.1000	23.86
9	LRGEDLLPS	212	2.0000	22.73
10	LIRIGVAER	231	1.9000	21.59
11	VGDFTVRLR	336	1.9000	21.59
12	VQTRIVVLG	368	1.9000	21.59
13	VRFCPSPTG	8	1.8000	20.45
14	FESLELLGR	464	1.8000	20.45
15	FRIEDTDAQ	42	1.7000	19.32
16	FAHLPTVLG	243	1.7000	19.32
17	LLNYLALLG	279	1.7000	19.32
18	YLALLGWSI	282	1.7000	19.32
19	LRAARQLVG	479	1.7000	19.32
20	YHAFSTPEE	107	1.6000	18.18
21	FDVADVNSS	306	1.6000	18.18
22	FNWAYARHT	28	1.5000	17.05
23	LLPSTPRQL	217	1.3600	15.45
24	VGLVRTALF	20	1.3000	14.77
25	VRGPVTFAA	170	1.3000	14.77
26	VAAFDVADV	303	1.3000	14.77
27	FIPEGLLNY	274	1.2000	13.64
28	YRDVLARLL	93	1.1600	13.18
29	VRVRFCPSP	6	1.1000	12.50
30	LELLGRDRS	467	1.1000	12.50
31	MQRLRAARQ	476	1.1000	12.50
32	LFAHRDRGF	266	1.0000	11.36
33	LLGWSIADD	285	1.0000	11.36
34	VVLGDAWEL	373	0.9600	10.91
35	YARHTGGTF	32	0.9000	10.23
36	VEARHVAAG	116	0.9000	10.23

37	LKPRKAFSP	441	0.9000	10.23
38	VLARLLAAG	96	0.8000	9.09
39	YDNFDRHLT	131	0.8000	9.09
40	YLAEGRQPV	146	0.8000	9.09
41	VRLRMPDDD	155	0.8000	9.09
42	IRIGVAERI	232	0.8000	9.09
43	LVRGPVTFA	169	0.6000	6.82
44	LNYLALLGW	280	0.6000	6.82
45	LNAEHIRML	326	0.5600	6.36
46	LVQTRIVVL	367	0.5600	6.36
47	LVRTALFNW	22	0.5000	5.68
48	LLDALRWLG	60	0.5000	5.68
49	YGPYRQSQR	81	0.5000	5.68

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	LLGWSIADD	285	3.6000	40.00
2	IRMLDVGDF	331	3.6000	40.00
3	MQRLRAARQ	476	3.6000	40.00
4	VRLRMPDDD	155	3.4000	37.78
5	MKITHVLRG	206	3.4000	37.78
6	VRLRDHLDT	341	3.4000	37.78
7	LHQALIRIG	227	3.0000	33.33
8	VVRLRMPDD	154	2.8000	31.11
9	VQTRIVVLG	368	2.8000	31.11
10	LLGRDRSMQ	469	2.8000	31.11
11	VRFCPSPTG	8	2.7000	30.00
12	LALKPRKAF	439	2.7000	30.00
13	LRGEDLLPS	212	2.6000	28.89
14	LLNYLALLG	279	2.6000	28.89
15	VNSSPARFD	311	2.6000	28.89
16	LRAARQLVG	479	2.6000	28.89
17	LNYLALLGW	280	2.5000	27.78

18	YVIDPKAAA	390	2.5000	27.78
19	LVRTALFNW	22	2.4000	26.67
20	LARLLAAGE	97	2.4000	26.67
21	LLPSTPRQL	217	2.4000	26.67
22	LRWLGLDWD	64	2.3000	25.56
23	VRGPVTFAA	170	2.3000	25.56
24	FRIEDTDAQ	42	2.2000	24.44
25	YHAFSTPEE	107	2.2000	24.44
26	VVLGDAWEL	373	2.0000	22.22
27	LFNWAYARH	27	1.9000	21.11
28	LALHQALIR	225	1.9000	21.11
29	IVVLGDAWE	372	1.9000	21.11
30	VEARHVAAG	116	1.8000	20.00
31	LALLDALRW	58	1.7000	18.89
32	VLARLLAAG	96	1.7000	18.89
33	IRVAATGTT	450	1.7000	18.89
34	LELLGRDRS	467	1.7000	18.89
35	LVRGPVTFA	169	1.6000	17.78
36	VAAFDVADV	303	1.6000	17.78
37	LNAEHIRML	326	1.6000	17.78
38	LVQTRIVVL	367	1.6000	17.78
39	VRVRFCPSP	6	1.5000	16.67
40	YRQSQRAEI	84	1.5000	16.67
41	LLDALRWLG	60	1.4000	15.56
42	LIRIGVAER	231	1.4000	15.56
43	VGDFTVRLR	336	1.4000	15.56
44	VGLVRTALF	20	1.3000	14.44
45	LKPRKAFSP	441	1.3000	14.44
46	LYTLVNPCD	194	1.2000	13.33
47	LAALTSVTD	413	1.2000	13.33
48	IRIGVAERI	232	1.1000	12.22
49	IDPKAAAKE	392	1.1000	12.22

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	IRMLDVGDF	331	5.4000	62.07
2	MKITHVLRG	206	4.1000	47.13
3	FESLELLGR	464	3.6000	41.38
4	LIRIGVAER	231	3.4000	39.08
5	YVIDPKAAA	390	3.2000	36.78
6	YRQSQRAEI	84	3.1000	35.63
7	LRAARQLVG	479	2.8000	32.18
8	VGLVRTALF	20	2.6000	29.89
9	LRGEDLLPS	212	2.5000	28.74
10	LNYLALLGW	280	2.4000	27.59
11	VRLRDHLDT	341	2.4000	27.59
12	VRFCPSPTG	8	2.2500	25.86
13	FAHLPTVLG	243	1.9000	21.84
14	MQRLRAARQ	476	1.8000	20.69
15	FIPEGLLNY	274	1.7000	19.54
16	LLNYLALLG	279	1.7000	19.54
17	YHAFSTPEE	107	1.6500	18.97
18	LALLDALRW	58	1.6000	18.39
19	IGVAERIPK	234	1.6000	18.39
20	YLALLGWSI	282	1.6000	18.39
21	FSPIRVAAT	447	1.6000	18.39
22	IRVAATGTT	450	1.6000	18.39
23	WNDLVRGPV	166	1.5000	17.24
24	LALHQALIR	225	1.4000	16.09
25	VVRLRMPDD	154	1.3500	15.52
26	YTLVNPCDD	195	1.3000	14.94
27	LALKPRKAF	439	1.2000	13.79
28	LFGLDEMVA	296	1.0000	11.49
29	VAAFDVADV	303	0.9000	10.34
30	IEGLALKPR	436	0.9000	10.34
31	YRDVLARLL	93	0.8600	9.89
32	LMKITHVLR	205	0.8000	9.20

33	FAHRDRGFI	267	0.7000	8.05
34	VRVRFCPSP	6	0.6500	7.47
35	LELLGRDRS	467	0.6000	6.90
36	LVQTRIVVL	367	0.5600	6.44
37	LARLLAAGE	97	0.5000	5.75
38	LHQALIRIG	227	0.5000	5.75
39	FDVADVNSS	306	0.5000	5.75
40	VQTRIVVLG	368	0.5000	5.75
41	FAAGSVPDF	176	0.3500	4.02
42	IRIGVAERI	232	0.3000	3.45
43	YLALLDALR	57	0.2000	2.30
44	LLGWSIADD	285	0.2000	2.30
45	LGRDRSMQR	470	0.2000	2.30
46	VRGPVTFAA	170	0.1000	1.15

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	IRMLDVGDF	331	3.4000	50.00
2	YVIDPKAAA	390	3.2000	47.06
3	MQRLRAARQ	476	2.5000	36.76
4	YRQSQRAEI	84	2.2000	32.35
5	LIRIGVAER	231	1.9000	27.94
6	FRIEDTDAQ	42	0.9000	13.24
7	MKITHVLRG	206	0.9000	13.24
8	FSPIRVAAT	447	0.9000	13.24
9	IRVAATGTT	450	0.8000	11.76
10	VGLVRTALF	20	0.7000	10.29
11	LNYLALLGW	280	0.6000	8.82
12	LELLGRDRS	467	0.5000	7.35
13	WNDLVRGPV	166	0.4000	5.88
14	LRGEDLLPS	212	0.3000	4.41
15	FESLELLGR	464	0.3000	4.41
16	YTLVNPCDD	195	0.2000	2.94

17	IGVAERIPK	234	-0.1000	0
18	YLALLGWSI	282	-0.1000	0
19	VAAFDVADV	303	-0.1000	0
20	VRLRDHLDT	341	-0.1000	0
21	LALLDALRW	58	-0.2000	0
22	FDVADVNSS	306	-0.2000	0
23	VRFCPSPTG	8	-0.3000	0
24	YRDVLARLL	93	-0.3000	0
25	FAHRDRGFI	267	-0.3000	0
26	LLGRDRSMQ	469	-0.3000	0
27	VRGPVTFAA	170	-0.4000	0
28	LRAARQLVG	479	-0.4000	0
29	LVRTALFNW	22	-0.5000	0
30	LFGLDEMVA	296	-0.6000	0
31	LARLLAAGE	97	-0.9000	0
32	YHAFSTPEE	107	-0.9000	0
33	VVRLRMPDD	154	-0.9000	0
34	LLGWSIADD	285	-0.9000	0
35	LVQTRIVVL	367	-0.9000	0
36	FNWAYARHT	28	-1.0000	0
37	LVRGPVTFA	169	-1.1000	0
38	LHQALIRIG	227	-1.1000	0
39	LFNWAYARH	27	-1.1200	0
40	LMKITHVLR	205	-1.2000	0
41	FAAAAELVQ	361	-1.2000	0
42	IEGLALKPR	436	-1.2000	0
43	YLALLDALR	57	-1.3000	0
44	LALKPRKAF	439	-1.3000	0
45	LLAAGEAYH	100	-1.3200	0
46	FCPSPTGTP	10	-1.4000	0
47	VEARHVAAG	116	-1.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRMLDVGDF	331	4.5000	54.22
2	MKITHVLRG	206	3.7000	44.58
3	MQRLRAARQ	476	3.5000	42.17
4	LNYLALLGW	280	3.4000	40.96
5	LRGEDLLPS	212	3.1000	37.35
6	LIRIGVAER	231	2.9000	34.94
7	VRLRDHLDT	341	2.7000	32.53
8	LALLDALRW	58	2.6000	31.33
9	IGVAERIPK	234	2.5000	30.12
10	LRAARQLVG	479	2.4000	28.92
11	YVIDPKAAA	390	2.2000	26.51
12	LFGLDEMVA	296	2.0000	24.10
13	IRVAATGTT	450	1.9000	22.89
14	VRFCPSPTG	8	1.8500	22.29
15	VGLVRTALF	20	1.7000	20.48
16	LLNYLALLG	279	1.3000	15.66
17	VVRLRMPDD	154	1.2500	15.06
18	YRQSQRAEI	84	1.2000	14.46
19	LELLGRDRS	467	1.2000	14.46
20	VRGPVTFAA	170	1.1000	13.25
21	FESLELLGR	464	1.1000	13.25
22	LVRTALFNW	22	1.0000	12.05
23	LVRGPVTFA	169	1.0000	12.05
24	LALHQALIR	225	0.9000	10.84
25	VAAFDVADV	303	0.9000	10.84
26	LLGRDRSMQ	469	0.7000	8.43
27	VRVRFCPSP	6	0.6500	7.83
28	LVQTRIVVL	367	0.6000	7.23
29	IRIGVAERI	232	0.4000	4.82
30	IEGLALKPR	436	0.4000	4.82
31	LMKITHVLR	205	0.3000	3.61
32	LALKPRKAF	439	0.3000	3.61
33	LARLLAAGE	97	0.1000	1.20

34	LHQALIRIG	227	0.1000	1.20
35	IPKFAHLPT	240	0.1000	1.20
36	LLGWSIADD	285	0.1000	1.20
37	VQTRIVVLG	368	0.1000	1.20
38	LIEAALKDA	426	-0.1000	0
39	FSPIRVAAT	447	-0.1000	0
40	LFNWAYARH	27	-0.1200	0
41	VRTALFNWA	23	-0.2000	0
42	LLPSTPRQL	217	-0.3000	0
43	YLALLGWSI	282	-0.3000	0
44	LGRDRSMQR	470	-0.3000	0
45	LLAAGEAYH	100	-0.3200	0
46	LYTLVNPCD	194	-0.3500	0
47	FRIEDTDAQ	42	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRMLDVGDF	331	4.4000	49.44
2	MKITHVLRG	206	4.0000	44.94
3	LNYLALLGW	280	3.3000	37.08
4	MQRLRAARQ	476	3.3000	37.08
5	YHAFSTPEE	107	3.2500	36.52
6	YVIDPKAAA	390	3.2000	35.96
7	VVRLRMPDD	154	2.9500	33.15
8	YTLVNPCDD	195	2.9000	32.58
9	LRAARQLVG	479	2.7000	30.34
10	VRLRDHLDT	341	2.6000	29.21
11	LALLDALRW	58	2.5000	28.09
12	YRQSQRAEI	84	2.4000	26.97
13	VRFCPSPTG	8	2.1500	24.16
14	LARLLAAGE	97	2.1000	23.60
15	LRGEDLLPS	212	2.1000	23.60
16	FESLELLGR	464	2.1000	23.60

17	LIRIGVAER	231	1.9000	21.35
18	FAHLPTVLG	243	1.8000	20.22
19	LLGWSIADD	285	1.8000	20.22
20	FSPIRVAAT	447	1.8000	20.22
21	IRVAATGTT	450	1.8000	20.22
22	VGLVRTALF	20	1.6000	17.98
23	LLNYLALLG	279	1.6000	17.98
24	IVVLGDAWE	372	1.6000	17.98
25	FIPEGLLNY	274	1.5000	16.85
26	FRIEDTDAQ	42	1.4000	15.73
27	FAAAAELVQ	361	1.4000	15.73
28	WELLKFFND	379	1.4000	15.73
29	LYTLVNPCD	194	1.3500	15.17
30	ITHVLRGED	208	1.2000	13.48
31	LFGLDEMVA	296	1.0000	11.24
32	LVRTALFNW	22	0.9000	10.11
33	YRDVLARLL	93	0.9000	10.11
34	YLALLGWSI	282	0.9000	10.11
35	LRWLGLDWD	64	0.8000	8.99
36	WNDLVRGPV	166	0.8000	8.99
37	IGVAERIPK	234	0.8000	8.99
38	LVQTRIVVL	367	0.6000	6.74
39	LLGRDRSMQ	469	0.5000	5.62
40	LHQALIRIG	227	0.4000	4.49
41	VQTRIVVLG	368	0.4000	4.49
42	LAALTSVTD	413	0.4000	4.49
43	VRLRMPDDD	155	0.3000	3.37
44	VAAFDVADV	303	0.2000	2.25
45	LALKPRKAF	439	0.2000	2.25
46	LELLGRDRS	467	0.2000	2.25
47	LFNWAYARH	27	0.1000	1.12
48	FNWAYARHT	28	0.1000	1.12
49	YDNFDRHLT	131	0.1000	1.12

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	MQRLRAARQ	476	2.8000	33.33
2	IRMLDVGDF	331	2.7000	32.14
3	LRGEDLLPS	212	2.6000	30.95
4	VRLRDHLDT	341	2.5000	29.76
5	YVIDPKAAA	390	2.5000	29.76
6	VRGPVTFAA	170	2.3000	27.38
7	MKITHVLRG	206	2.1000	25.00
8	LLGRDRSMQ	469	2.0000	23.81
9	LALHQALIR	225	1.9000	22.62
10	LALKPRKAF	439	1.8000	21.43
11	LHQALIRIG	227	1.7000	20.24
12	LELLGRDRS	467	1.7000	20.24
13	LVRGPVTFA	169	1.6000	19.05
14	LNYLALLGW	280	1.6000	19.05
15	LVRTALFNW	22	1.5000	17.86
16	VQTRIVVLG	368	1.5000	17.86
17	VRFCPSPTG	8	1.4000	16.67
18	FRIEDTDAQ	42	1.4000	16.67
19	LLPSTPRQL	217	1.4000	16.67
20	LIRIGVAER	231	1.4000	16.67
21	VGDFTVRLR	336	1.4000	16.67
22	YRQSQRAEI	84	1.3000	15.48
23	LLNYLALLG	279	1.3000	15.48
24	VAAFDVADV	303	1.3000	15.48
25	LRAARQLVG	479	1.3000	15.48
26	IGVAERIPK	234	1.2000	14.29
27	VRVRFCPSP	6	1.1000	13.10
28	VVLGDAWEL	373	1.0000	11.90
29	VRTALFNWA	23	0.9000	10.71
30	IRIGVAERI	232	0.9000	10.71
31	LLGWSIADD	285	0.9000	10.71

32	LKPRKAFSP	441	0.9000	10.71
33	LALLDALRW	58	0.8000	9.52
34	IRVAATGTT	450	0.8000	9.52
35	VRLRMPDDD	155	0.7000	8.33
36	LFNWAYARH	27	0.6800	8.10
37	LNAEHIRML	326	0.6000	7.14
38	LVQTRIVVL	367	0.6000	7.14
39	VEARHVAAG	116	0.5000	5.95
40	VGLVRTALF	20	0.4000	4.76
41	VLARLLAAG	96	0.4000	4.76
42	LDTHGHHIA	347	0.4000	4.76
43	FDVADVNSS	306	0.2000	2.38
44	LLKFFNDDQ	381	0.2000	2.38
45	LLDALRWLG	60	0.1000	1.19
46	VVRLRMPDD	154	0.1000	1.19
47	LFAHRDRGF	266	0.1000	1.19
48	LIEAALKDA	426	0.1000	1.19

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	YVIDPKAAA	390	3.5000	41.67
2	FRIEDTDAQ	42	2.4000	28.57
3	YRQSQRAEI	84	2.3000	27.38
4	MQRLRAARQ	476	1.8000	21.43
5	IRMLDVGDF	331	1.7000	20.24
6	LRGEDLLPS	212	1.6000	19.05
7	VRLRDHLDT	341	1.5000	17.86
8	VRGPVTFAA	170	1.3000	15.48
9	FDVADVNSS	306	1.2000	14.29
10	MKITHVLRG	206	1.1000	13.10
11	LLGRDRSMQ	469	1.0000	11.90
12	LALHQALIR	225	0.9000	10.71
13	FNWAYARHT	28	0.8000	9.52

14	YLALLGWSI	282	0.8000	9.52
15	LALKPRKAF	439	0.8000	9.52
16	FDRHLTDAQ	134	0.7000	8.33
17	LHQALIRIG	227	0.7000	8.33
18	LELLGRDRS	467	0.7000	8.33
19	LVRGPVTFA	169	0.6000	7.14
20	LNYLALLGW	280	0.6000	7.14
21	LVRTALFNW	22	0.5000	5.95
22	VQTRIVVLG	368	0.5000	5.95
23	VRFCPSPTG	8	0.4000	4.76
24	LLPSTPRQL	217	0.4000	4.76
25	LIRIGVAER	231	0.4000	4.76
26	VGDFTVRLR	336	0.4000	4.76
27	FAHLPTVLG	243	0.3000	3.57
28	LLNYLALLG	279	0.3000	3.57
29	VAAFDVADV	303	0.3000	3.57
30	FESLELLGR	464	0.3000	3.57
31	LRAARQLVG	479	0.3000	3.57
32	YRDVLARLL	93	0.2000	2.38
33	YHAFSTPEE	107	0.2000	2.38
34	IGVAERIPK	234	0.2000	2.38
35	VRVRFCPSP	6	0.1000	1.19
36	YDNFDRHLT	131	0.1000	1.19
37	VRTALFNWA	23	-0.1000	0
38	IRIGVAERI	232	-0.1000	0
39	FIPEGLLNY	274	-0.1000	0
40	LLGWSIADD	285	-0.1000	0
41	LKPRKAFSP	441	-0.1000	0
42	LALLDALRW	58	-0.2000	0
43	YLAEGRQPV	146	-0.2000	0
44	IRVAATGTT	450	-0.2000	0
45	VRLRMPDDD	155	-0.3000	0
46	LFNWAYARH	27	-0.3200	0
47	FAHRDRGFI	267	-0.4000	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	IRMLDVGDF	331	4.6000	52.27
2	LALKPRKAF	439	3.7000	42.05
3	MKITHVLRG	206	3.5000	39.77
4	LALHQALIR	225	3.4000	38.64
5	VRLRDHLDT	341	3.2000	36.36
6	LHQALIRIG	227	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09
8	LIRIGVAER	231	2.9000	32.95
9	VGDFTVRLR	336	2.9000	32.95
10	VQTRIVVLG	368	2.9000	32.95
11	VRFCPSPTG	8	2.8000	31.82
12	LLNYLALLG	279	2.7000	30.68
13	LRAARQLVG	479	2.7000	30.68
14	YVIDPKAAA	390	2.5000	28.41
15	LLPSTPRQL	217	2.3600	26.82
16	VGLVRTALF	20	2.3000	26.14
17	VRGPVTFAA	170	2.3000	26.14
18	VAAFDVADV	303	2.3000	26.14
19	YRQSQRAEI	84	2.2000	25.00
20	VRVRFCPSP	6	2.1000	23.86
21	LELLGRDRS	467	2.1000	23.86
22	MQRLRAARQ	476	2.1000	23.86
23	LFAHRDRGF	266	2.0000	22.73
24	LLGWSIADD	285	2.0000	22.73
25	VVLGDAWEL	373	1.9600	22.27
26	VEARHVAAG	116	1.9000	21.59
27	LKPRKAFSP	441	1.9000	21.59
28	VLARLLAAG	96	1.8000	20.45
29	VRLRMPDDD	155	1.8000	20.45
30	IRIGVAERI	232	1.8000	20.45

31	LVRGPVTFA	169	1.6000	18.18
32	LNYLALLGW	280	1.6000	18.18
33	LNAEHIRML	326	1.5600	17.73
34	LVQTRIVVL	367	1.5600	17.73
35	LVRTALFNW	22	1.5000	17.05
36	LLDALRWLG	60	1.5000	17.05
37	IRVAATGTT	450	1.5000	17.05
38	IEGLALKPR	436	1.4000	15.91
39	IGVAERIPK	234	1.3000	14.77
40	LLGRDRSMQ	469	1.3000	14.77
41	VVRLRMPDD	154	1.2000	13.64
42	VNSSPARFD	311	1.0000	11.36
43	VRTALFNWA	23	0.9000	10.23
44	VLGEGTKKL	249	0.8600	9.77
45	LALLDALRW	58	0.8000	9.09
46	LARLLAAGE	97	0.8000	9.09
47	LMKITHVLR	205	0.8000	9.09
48	FESLELLGR	464	0.8000	9.09
49	FRIEDTDAQ	42	0.7000	7.95

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	IRMLDVGDF	331	4.6000	52.27
2	LALKPRKAF	439	3.7000	42.05
3	MKITHVLRG	206	3.5000	39.77
4	LALHQALIR	225	3.4000	38.64
5	VRLRDHLDT	341	3.2000	36.36
6	LHQALIRIG	227	3.1000	35.23
7	LRGEDLLPS	212	3.0000	34.09
8	LIRIGVAER	231	2.9000	32.95
9	VGDFTVRLR	336	2.9000	32.95
10	VQTRIVVLG	368	2.9000	32.95
11	VRFCPSPTG	8	2.8000	31.82

12	LLNYLALLG	279	2.7000	30.68
13	LRAARQLVG	479	2.7000	30.68
14	YVIDPKAAA	390	2.5000	28.41
15	LLPSTPRQL	217	2.3600	26.82
16	VGLVRTALF	20	2.3000	26.14
17	VRGPVTFAA	170	2.3000	26.14
18	VAAFDVADV	303	2.3000	26.14
19	YRQSQRAEI	84	2.2000	25.00
20	VRVRFCPSP	6	2.1000	23.86
21	LELLGRDRS	467	2.1000	23.86
22	MQRLRAARQ	476	2.1000	23.86
23	LFAHRDRGF	266	2.0000	22.73
24	LLGWSIADD	285	2.0000	22.73
25	VVLGDAWEL	373	1.9600	22.27
26	VEARHVAAG	116	1.9000	21.59
27	LKPRKAFSP	441	1.9000	21.59
28	VLARLLAAG	96	1.8000	20.45
29	VRLRMPDDD	155	1.8000	20.45
30	IRIGVAERI	232	1.8000	20.45
31	LVRGPVTFA	169	1.6000	18.18
32	LNYLALLGW	280	1.6000	18.18
33	LNAEHIRML	326	1.5600	17.73
34	LVQTRIVVL	367	1.5600	17.73
35	LVRTALFNW	22	1.5000	17.05
36	LLDALRWLG	60	1.5000	17.05
37	IRVAATGTT	450	1.5000	17.05
38	IEGLALKPR	436	1.4000	15.91
39	IGVAERIPK	234	1.3000	14.77
40	LLGRDRSMQ	469	1.3000	14.77
41	VVRLRMPDD	154	1.2000	13.64
42	VNSSPARFD	311	1.0000	11.36
43	VRTALFNWA	23	0.9000	10.23
44	VLGEGTKKL	249	0.8600	9.77
45	LALLDALRW	58	0.8000	9.09

46	LARLLAAGE	97	0.8000	9.09
47	LMKITHVLR	205	0.8000	9.09
48	FESLELLGR	464	0.8000	9.09
49	FRIEDTDAQ	42	0.7000	7.95

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	LLNYLALLG	279	5.1000	52.04
2	VRLRDHLDT	341	4.6000	46.94
3	VVLGDAWEL	373	4.2000	42.86
4	IRIGVAERI	232	3.7000	37.76
5	LRGEDLLPS	212	3.6000	36.73
6	VRGPVTFAA	170	3.4600	35.31
7	IRMLDVGDF	331	3.4000	34.69
8	VRFCPSPTG	8	3.1000	31.63
9	MKITHVLRG	206	3.1000	31.63
10	IPKFAHLPT	240	3.1000	31.63
11	LALHQALIR	225	3.0000	30.61
12	LNYLALLGW	280	2.8000	28.57
13	LVRTALFNW	22	2.7000	27.55
14	LVRGPVTFA	169	2.7000	27.55
15	LVQTRIVVL	367	2.6500	27.04
16	VRTALFNWA	23	2.6000	26.53
17	YRQSQRAEI	84	2.6000	26.53
18	LRAARQLVG	479	2.5000	25.51
19	IRVAATGTT	450	2.4600	25.10
20	VAAFDVADV	303	2.4000	24.49
21	YLALLGWSI	282	2.3000	23.47
22	LKFFNDDQY	382	2.3000	23.47
23	LRMPDDDLA	157	2.2000	22.45
24	LFGLDEMVA	296	2.2000	22.45
25	VRVRFCPSP	6	2.1000	21.43
26	VLRGEDLLP	211	2.1000	21.43

27	LGRDRSMQR	470	2.1000	21.43
28	LALLDALRW	58	2.0000	20.41
29	YDNFDRHLT	131	2.0000	20.41
30	VFRIEDTDA	41	1.9000	19.39
31	IYRDVLARL	92	1.9000	19.39
32	YVIDPKAAA	390	1.9000	19.39
33	LKPRKAFSP	441	1.9000	19.39
34	VVRLRMPDD	154	1.8000	18.37
35	IGVAERIPK	234	1.8000	18.37
36	LLKFFNDDQ	381	1.8000	18.37
37	LVNPCDDAL	197	1.7000	17.35
38	LELLGRDRS	467	1.6000	16.33
39	VAAGRNPKL	121	1.5000	15.31
40	LALLGWSIA	283	1.4000	14.29
41	VGLVRTALF	20	1.2600	12.86
42	LDALRWLGL	61	1.2000	12.24
43	MLDVGDFTV	333	1.2000	12.24
44	LIRIGVAER	231	1.1000	11.22
45	FAHRDRGFI	267	1.1000	11.22
46	LLGRDRSMQ	469	1.1000	11.22
47	LFNWAYARH	27	1.0000	10.20
48	VPDFALTRA	181	1.0000	10.20
49	LTRASGDPL	186	1.0000	10.20

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	LLNYLALLG	279	4.1000	41.84
2	YRQSQRAEI	84	3.6000	36.73
3	VRLRDHLDT	341	3.6000	36.73
4	YLALLGWSI	282	3.3000	33.67
5	VVLGDAWEL	373	3.2000	32.65
6	YDNFDRHLT	131	3.0000	30.61
7	YVIDPKAAA	390	2.9000	29.59

8	IRIGVAERI	232	2.7000	27.55
9	LRGEDLLPS	212	2.6000	26.53
10	VRGPVTFAA	170	2.4600	25.10
11	IRMLDVGDF	331	2.4000	24.49
12	VRFCPSPTG	8	2.1000	21.43
13	MKITHVLRG	206	2.1000	21.43
14	IPKFAHLPT	240	2.1000	21.43
15	FAHRDRGFI	267	2.1000	21.43
16	LALHQALIR	225	2.0000	20.41
17	FIPEGLLNY	274	2.0000	20.41
18	YARHTGGTF	32	1.9000	19.39
19	WSIADDHDL	288	1.9000	19.39
20	FESLELLGR	464	1.9000	19.39
21	YGPYRQSQR	81	1.8000	18.37
22	LNYLALLGW	280	1.8000	18.37
23	LVRTALFNW	22	1.7000	17.35
24	LVRGPVTFA	169	1.7000	17.35
25	LVQTRIVVL	367	1.6500	16.84
26	VRTALFNWA	23	1.6000	16.33
27	YHAFSTPEE	107	1.5600	15.92
28	FGLDEMVAA	297	1.5000	15.31
29	FTVRLRDHL	339	1.5000	15.31
30	FFNDDQYVI	384	1.5000	15.31
31	LRAARQLVG	479	1.5000	15.31
32	IRVAATGTT	450	1.4600	14.90
33	YLAEGRQPV	146	1.4000	14.29
34	VAAFDVADV	303	1.4000	14.29
35	WNDLVRGPV	166	1.3000	13.27
36	LKFFNDDQY	382	1.3000	13.27
37	LRMPDDDLA	157	1.2000	12.24
38	LFGLDEMVA	296	1.2000	12.24
39	VRVRFCPSP	6	1.1000	11.22
40	YRDVLARLL	93	1.1000	11.22
41	VLRGEDLLP	211	1.1000	11.22

42	LGRDRSMQR	470	1.1000	11.22
43	LALLDALRW	58	1.0000	10.20
44	VFRIEDTDA	41	0.9000	9.18
45	IYRDVLARL	92	0.9000	9.18
46	LKPRKAFSP	441	0.9000	9.18
47	VVRLRMPDD	154	0.8000	8.16
48	IGVAERIPK	234	0.8000	8.16
49	WELLKFFND	379	0.8000	8.16

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LLNYLALLG	279	5.1000	52.04
2	VRLRDHLDT	341	4.6000	46.94
3	VVLGDAWEL	373	4.2000	42.86
4	IRIGVAERI	232	3.7000	37.76
5	LRGEDLLPS	212	3.6000	36.73
6	VRGPVTFAA	170	3.4600	35.31
7	IRMLDVGDF	331	3.4000	34.69
8	VRFCPSPTG	8	3.1000	31.63
9	MKITHVLRG	206	3.1000	31.63
10	IPKFAHLPT	240	3.1000	31.63
11	LALHQALIR	225	3.0000	30.61
12	LNYLALLGW	280	2.8000	28.57
13	LVRTALFNW	22	2.7000	27.55
14	LVRGPVTFA	169	2.7000	27.55
15	LVQTRIVVL	367	2.6500	27.04
16	VRTALFNWA	23	2.6000	26.53
17	YRQSQRAEI	84	2.6000	26.53
18	LRAARQLVG	479	2.5000	25.51
19	IRVAATGTT	450	2.4600	25.10
20	VAAFDVADV	303	2.4000	24.49
21	YLALLGWSI	282	2.3000	23.47
22	LKFFNDDQY	382	2.3000	23.47

23	LRMPDDDLA	157	2.2000	22.45
24	LFGLDEMVA	296	2.2000	22.45
25	VRVRFCPSP	6	2.1000	21.43
26	VLRGEDLLP	211	2.1000	21.43
27	LGRDRSMQR	470	2.1000	21.43
28	LALLDALRW	58	2.0000	20.41
29	YDNFDRHLT	131	2.0000	20.41
30	VFRIEDTDA	41	1.9000	19.39
31	IYRDVLARL	92	1.9000	19.39
32	YVIDPKAAA	390	1.9000	19.39
33	LKPRKAFSP	441	1.9000	19.39
34	VVRLRMPDD	154	1.8000	18.37
35	IGVAERIPK	234	1.8000	18.37
36	LLKFFNDDQ	381	1.8000	18.37
37	LVNPCDDAL	197	1.7000	17.35
38	LELLGRDRS	467	1.6000	16.33
39	VAAGRNPKL	121	1.5000	15.31
40	LALLGWSIA	283	1.4000	14.29
41	VGLVRTALF	20	1.2600	12.86
42	LDALRWLGL	61	1.2000	12.24
43	MLDVGDFTV	333	1.2000	12.24
44	LIRIGVAER	231	1.1000	11.22
45	FAHRDRGFI	267	1.1000	11.22
46	LLGRDRSMQ	469	1.1000	11.22
47	LFNWAYARH	27	1.0000	10.20
48	VPDFALTRA	181	1.0000	10.20
49	LTRASGDPL	186	1.0000	10.20

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	YRDVLARLL	93	4.6000	46.94
2	IRMLDVGDF	331	3.7000	37.76
3	LIRIGVAER	231	3.3000	33.67

4	FESLELLGR	464	3.0000	30.61
5	YLALLGWSI	282	2.9000	29.59
6	LLPSTPRQL	217	2.6000	26.53
7	IGVAERIPK	234	2.6000	26.53
8	LMKITHVLR	205	2.4000	24.49
9	IEGLALKPR	436	2.3000	23.47
10	VVLGDAWEL	373	2.2000	22.45
11	MQRLRAARQ	476	2.2000	22.45
12	YLALLDALR	57	2.1000	21.43
13	VGLVRTALF	20	2.0000	20.41
14	LVRTALFNW	22	1.9000	19.39
15	FNWAYARHT	28	1.9000	19.39
16	LALHQALIR	225	1.7000	17.35
17	WSIADDHDL	288	1.7000	17.35
18	YRQSQRAEI	84	1.6000	16.33
19	MKITHVLRG	206	1.6000	16.33
20	IRIGVAERI	232	1.4000	14.29
21	VRFCPSPTG	8	1.3000	13.27
22	IRVAATGTT	450	1.3000	13.27
23	YGPYRQSQR	81	1.1000	11.22
24	FIPEGLLNY	274	1.0000	10.20
25	LVQTRIVVL	367	1.0000	10.20
26	LLNYLALLG	279	0.9000	9.18
27	YARHTGGTF	32	0.8000	8.16
28	FRIEDTDAQ	42	0.8000	8.16
29	YTLVNPCDD	195	0.8000	8.16
30	LRAARQLVG	479	0.8000	8.16
31	LGRDRSMQR	470	0.7000	7.14
32	VRGPVTFAA	170	0.6000	6.12
33	LALLDALRW	58	0.5000	5.10
34	LRGEDLLPS	212	0.4000	4.08
35	FFNDDQYVI	384	0.4000	4.08
36	WAYARHTGG	30	0.3000	3.06
37	VLGEGTKKL	249	0.3000	3.06

38	YVIDPKAAA	390	0.2000	2.04
39	VFRIEDTDA	41	0.1000	1.02
40	LHQALIRIG	227	0.1000	1.02
41	FAHLPTVLG	243	0.1000	1.02
42	LNYLALLGW	280	0.1000	1.02
43	VGDFTVRLR	336	0.1000	1.02
44	VGGPYGPYR	77	-0.2000	0
45	FSPIRVAAT	447	-0.2000	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	YRDVLARLL	93	4.6000	46.94
2	IRMLDVGDF	331	3.7000	37.76
3	LIRIGVAER	231	3.3000	33.67
4	FESLELLGR	464	3.0000	30.61
5	YLALLGWSI	282	2.9000	29.59
6	LLPSTPRQL	217	2.6000	26.53
7	IGVAERIPK	234	2.6000	26.53
8	LMKITHVLR	205	2.4000	24.49
9	IEGLALKPR	436	2.3000	23.47
10	VVLGDAWEL	373	2.2000	22.45
11	MQRLRAARQ	476	2.2000	22.45
12	YLALLDALR	57	2.1000	21.43
13	VGLVRTALF	20	2.0000	20.41
14	LVRTALFNW	22	1.9000	19.39
15	FNWAYARHT	28	1.9000	19.39
16	LALHQALIR	225	1.7000	17.35
17	WSIADDHDL	288	1.7000	17.35
18	YRQSQRAEI	84	1.6000	16.33
19	MKITHVLRG	206	1.6000	16.33
20	IRIGVAERI	232	1.4000	14.29
21	VRFCPSPTG	8	1.3000	13.27
22	IRVAATGTT	450	1.3000	13.27

23	YGPYRQSQR	81	1.1000	11.22
24	FIPEGLLNY	274	1.0000	10.20
25	LVQTRIVVL	367	1.0000	10.20
26	LLNYLALLG	279	0.9000	9.18
27	YARHTGGTF	32	0.8000	8.16
28	FRIEDTDAQ	42	0.8000	8.16
29	YTLVNPCDD	195	0.8000	8.16
30	LRAARQLVG	479	0.8000	8.16
31	LGRDRSMQR	470	0.7000	7.14
32	VRGPVTFAA	170	0.6000	6.12
33	LALLDALRW	58	0.5000	5.10
34	LRGEDLLPS	212	0.4000	4.08
35	FFNDDQYVI	384	0.4000	4.08
36	WAYARHTGG	30	0.3000	3.06
37	VLGEGTKKL	249	0.3000	3.06
38	YVIDPKAAA	390	0.2000	2.04
39	VFRIEDTDA	41	0.1000	1.02
40	LHQALIRIG	227	0.1000	1.02
41	FAHLPTVLG	243	0.1000	1.02
42	LNYLALLGW	280	0.1000	1.02
43	VGDFTVRLR	336	0.1000	1.02
44	VGGPYGPYR	77	-0.2000	0
45	FSPIRVAAT	447	-0.2000	0