MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Mar 26 23:59:54 2010
Length of input sequence	270 amino acids
Number of nanomers from input sequence	262
Number of nanomers with obligatory P1 anchor residue	83
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	27

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	YGRLDGVLV	94	2.8000	46.67
2	FVGALIYLL	240	1.4000	23.33
3	VVLVSSVRG	151	1.3500	22.50
4	LGRVAARAL	33	0.7400	12.33
5	YLLSDASSF	246	0.7000	11.67
6	FRSAVTEWM	203	0.6800	11.33
7	WLVCRAAGR	132	0.5000	8.33
8	VRGGLGNAA	157	0.5000	8.33

9	ILITGATGS	24	0.2900	4.83
10	LVASGSNHV	101	0.2000	3.33
11	LGNAAGYSA	161	0.2000	3.33
12	VMYLDGGYT	259	0.2000	3.33
13	VNALAPTVF	195	0.1900	3.17
14	VCRAAGRVL	134	-0.0100	0
15	LTLAGGNSA	48	-0.2000	0
16	VLLEQGQGG	141	-0.3000	0
17	FYTGQVMYL	254	-0.3100	0
18	IRVNALAPT	193	-0.4600	0
19	VVTCRPDSL	72	-0.6000	0
20	LVNGAGIDD	61	-0.7000	0
21	VRGAWLVCR	128	-0.9000	0
22	VLVASGSNH	100	-1.1000	0
23	LIYLLSDAS	244	-1.1000	0
24	IYLLSDASS	245	-1.2000	0
25	MYLDGGYTA	260	-1.3000	0
26	FSVQDKSIL	17	-1.4000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLVSSVRG	151	2.3500	39.17
2	YGRLDGVLV	94	1.8000	30.00
3	LGRVAARAL	33	1.7400	29.00
4	VRGGLGNAA	157	1.5000	25.00
5	FVGALIYLL	240	1.4000	23.33
6	ILITGATGS	24	1.2900	21.50
7	LVASGSNHV	101	1.2000	20.00
8	LGNAAGYSA	161	1.2000	20.00
9	VMYLDGGYT	259	1.2000	20.00
10	VNALAPTVF	195	1.1900	19.83
11	VCRAAGRVL	134	0.9900	16.50

12	LTLAGGNSA	48	0.8000	13.33
13	VLLEQGQGG	141	0.7000	11.67
14	FRSAVTEWM	203	0.6800	11.33
15	IRVNALAPT	193	0.5400	9.00
16	VVTCRPDSL	72	0.4000	6.67
17	LVNGAGIDD	61	0.3000	5.00
18	VRGAWLVCR	128	0.1000	1.67
19	VLVASGSNH	100	-0.1000	0
20	LIYLLSDAS	244	-0.1000	0
21	IYLLSDASS	245	-0.2000	0
22	YLLSDASSF	246	-0.3000	0
23	MYLDGGYTA	260	-0.3000	0
24	FYTGQVMYL	254	-0.3100	0
25	WLVCRAAGR	132	-0.5000	0
26	LAGGNSAGL	50	-0.6000	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	LVSSVRGGL	153	4.0600	42.74
2	LLSDASSFY	247	3.7700	39.68
3	VVLVSSVRG	151	3.6000	37.89
4	MYLDGGYTA	260	3.4500	36.32
5	VRGAWLVCR	128	3.3000	34.74
6	MFTDDPKGR	211	3.2000	33.68
7	FRSAVTEWM	203	3.1000	32.63
8	LVASGSNHV	101	2.9100	30.63
9	VLVSSVRGG	152	2.9000	30.53
10	YLLSDASSF	246	2.6700	28.11
11	FYTGQVMYL	254	2.6600	28.00
12	IRVNALAPT	193	2.6000	27.37
13	ILITGATGS	24	2.5000	26.32
14	LITGATGSL	25	2.4600	25.89

15	VFRSAVTEW	202	2.3000	24.21
16	LIYLLSDAS	244	2.3000	24.21
17	LVNGAGIDD	61	2.2000	23.16
18	VRGGLGNAA	157	2.1100	22.21
19	VNALAPTVF	195	2.1000	22.11
20	VVTCRPDSL	72	1.9600	20.63
21	FVGALIYLL	240	1.9100	20.11
22	LGRYGRLDG	91	1.8000	18.95
23	MVEAALGRY	86	1.5000	15.79
24	LVCRAAGRV	133	1.5000	15.79
25	FTDDPKGRA	212	1.4000	14.74
26	LARIPLRRF	226	1.4000	14.74
27	MLARIPLRR	225	1.2000	12.63

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	FYTGQVMYL	254	2.7000	29.67
2	FRSAVTEWM	203	2.6000	28.57
3	MYLDGGYTA	260	2.4500	26.92
4	FTDDPKGRA	212	2.4000	26.37
5	LVSSVRGGL	153	2.1000	23.08
6	FVGALIYLL	240	1.9500	21.43
7	YLLSDASSF	246	1.7700	19.45
8	LLSDASSFY	247	1.4700	16.15
9	VFRSAVTEW	202	1.3000	14.29
10	VVLVSSVRG	151	1.2000	13.19
11	VRGGLGNAA	157	1.1100	12.20
12	ILITGATGS	24	1.1000	12.09
13	LVASGSNHV	101	0.9100	10.00
14	IRVNALAPT	193	0.9000	9.89
15	LIYLLSDAS	244	0.9000	9.89
16	VRGAWLVCR	128	0.8000	8.79

17	MFTDDPKGR	211	0.7000	7.69
18	FSVQDKSIL	17	0.5700	6.26
19	LITGATGSL	25	0.5000	5.49
20	WLVCRAAGR	132	0.5000	5.49
21	VLVSSVRGG	152	0.5000	5.49
22	LVNGAGIDD	61	0.1000	1.10
23	VNGAGIDDA	62	0.1000	1.10
24	VLVASGSNH	100	-0.0500	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	VRGGLGNAA	157	2.8000	31.82
2	LVASGSNHV	101	2.6000	29.55
3	VFRSAVTEW	202	2.3000	26.14
4	MFTDDPKGR	211	2.3000	26.14
5	MYLDGGYTA	260	2.3000	26.14
6	LIYLLSDAS	244	2.2000	25.00
7	LLSDASSFY	247	2.2000	25.00
8	ILITGATGS	24	2.1000	23.86
9	VVLVSSVRG	151	2.0800	23.64
10	FRSAVTEWM	203	2.0000	22.73
11	IRVNALAPT	193	1.9000	21.59
12	LVSSVRGGL	153	1.7000	19.32
13	VRGAWLVCR	128	1.6800	19.09
14	VNGAGIDDA	62	1.4000	15.91
15	FYTGQVMYL	254	1.4000	15.91
16	VVTCRPDSL	72	1.3000	14.77
17	VLVSSVRGG	152	1.2000	13.64
18	LTLAGGNSA	48	0.9000	10.23
19	LGRYGRLDG	91	0.9000	10.23
20	LVNGAGIDD	61	0.7800	8.86
21	VLVASGSNH	100	0.6800	7.73

22	LARFSVQDK	14	0.6000	6.82
23	VGALIYLLS	241	0.5000	5.68
24	YLLSDASSF	246	0.5000	5.68
25	LGLARFSVQ	12	0.4000	4.55
26	VNALAPTVF	195	0.2000	2.27
27	MLARIPLRR	225	0.2000	2.27

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	VRGGLGNAA	157	2.8000	31.82
2	LVASGSNHV	101	2.6000	29.55
3	VFRSAVTEW	202	2.3000	26.14
4	MFTDDPKGR	211	2.3000	26.14
5	MYLDGGYTA	260	2.3000	26.14
6	LIYLLSDAS	244	2.2000	25.00
7	LLSDASSFY	247	2.2000	25.00
8	ILITGATGS	24	2.1000	23.86
9	VVLVSSVRG	151	2.0800	23.64
10	FRSAVTEWM	203	2.0000	22.73
11	IRVNALAPT	193	1.9000	21.59
12	LVSSVRGGL	153	1.7000	19.32
13	VRGAWLVCR	128	1.6800	19.09
14	VNGAGIDDA	62	1.4000	15.91
15	FYTGQVMYL	254	1.4000	15.91
16	VVTCRPDSL	72	1.3000	14.77
17	VLVSSVRGG	152	1.2000	13.64
18	LTLAGGNSA	48	0.9000	10.23
19	LGRYGRLDG	91	0.9000	10.23
20	LVNGAGIDD	61	0.7800	8.86
21	VLVASGSNH	100	0.6800	7.73
22	LARFSVQDK	14	0.6000	6.82
23	VGALIYLLS	241	0.5000	5.68

24	YLLSDASSF	246	0.5000	5.68
25	LGLARFSVQ	12	0.4000	4.55
26	VNALAPTVF	195	0.2000	2.27
27	MLARIPLRR	225	0.2000	2.27

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	VRGGLGNAA	157	2.8000	31.82
2	LVASGSNHV	101	2.6000	29.55
3	VFRSAVTEW	202	2.3000	26.14
4	MFTDDPKGR	211	2.3000	26.14
5	MYLDGGYTA	260	2.3000	26.14
6	LIYLLSDAS	244	2.2000	25.00
7	LLSDASSFY	247	2.2000	25.00
8	ILITGATGS	24	2.1000	23.86
9	VVLVSSVRG	151	2.0800	23.64
10	FRSAVTEWM	203	2.0000	22.73
11	IRVNALAPT	193	1.9000	21.59
12	LVSSVRGGL	153	1.7000	19.32
13	VRGAWLVCR	128	1.6800	19.09
14	VNGAGIDDA	62	1.4000	15.91
15	FYTGQVMYL	254	1.4000	15.91
16	VVTCRPDSL	72	1.3000	14.77
17	VLVSSVRGG	152	1.2000	13.64
18	LTLAGGNSA	48	0.9000	10.23
19	LGRYGRLDG	91	0.9000	10.23
20	LVNGAGIDD	61	0.7800	8.86
21	VLVASGSNH	100	0.6800	7.73
22	LARFSVQDK	14	0.6000	6.82
23	VGALIYLLS	241	0.5000	5.68
24	YLLSDASSF	246	0.5000	5.68
25	LGLARFSVQ	12	0.4000	4.55

26	VNALAPTVF	195	0.2000	2.27
27	MLARIPLRR	225	0.2000	2.27

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	FRSAVTEWM	203	4.1000	43.16
2	YLLSDASSF	246	3.6700	38.63
3	FYTGQVMYL	254	3.6600	38.53
4	LVSSVRGGL	153	3.0600	32.21
5	FVGALIYLL	240	2.9100	30.63
6	LLSDASSFY	247	2.7700	29.16
7	VVLVSSVRG	151	2.6000	27.37
8	MYLDGGYTA	260	2.4500	25.79
9	FTDDPKGRA	212	2.4000	25.26
10	VRGAWLVCR	128	2.3000	24.21
11	MFTDDPKGR	211	2.2000	23.16
12	WLVCRAAGR	132	2.0000	21.05
13	LVASGSNHV	101	1.9100	20.11
14	VLVSSVRGG	152	1.9000	20.00
15	IRVNALAPT	193	1.6000	16.84
16	FSVQDKSIL	17	1.5300	16.11
17	ILITGATGS	24	1.5000	15.79
18	LITGATGSL	25	1.4600	15.37
19	VFRSAVTEW	202	1.3000	13.68
20	LIYLLSDAS	244	1.3000	13.68
21	LVNGAGIDD	61	1.2000	12.63
22	VRGGLGNAA	157	1.1100	11.68
23	VNALAPTVF	195	1.1000	11.58
24	YGRLDGVLV	94	1.0000	10.53
25	VVTCRPDSL	72	0.9600	10.11
26	LGRYGRLDG	91	0.8000	8.42
27	MVEAALGRY	86	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	VRGGLGNAA	157	2.8000	31.82
2	LVASGSNHV	101	2.6000	29.55
3	VFRSAVTEW	202	2.3000	26.14
4	MFTDDPKGR	211	2.3000	26.14
5	MYLDGGYTA	260	2.3000	26.14
6	LIYLLSDAS	244	2.2000	25.00
7	LLSDASSFY	247	2.2000	25.00
8	ILITGATGS	24	2.1000	23.86
9	VVLVSSVRG	151	2.0800	23.64
10	FRSAVTEWM	203	2.0000	22.73
11	IRVNALAPT	193	1.9000	21.59
12	LVSSVRGGL	153	1.7000	19.32
13	VRGAWLVCR	128	1.6800	19.09
14	VNGAGIDDA	62	1.4000	15.91
15	FYTGQVMYL	254	1.4000	15.91
16	VVTCRPDSL	72	1.3000	14.77
17	VLVSSVRGG	152	1.2000	13.64
18	LTLAGGNSA	48	0.9000	10.23
19	LGRYGRLDG	91	0.9000	10.23
20	LVNGAGIDD	61	0.7800	8.86
21	VLVASGSNH	100	0.6800	7.73
22	LARFSVQDK	14	0.6000	6.82
23	VGALIYLLS	241	0.5000	5.68
24	YLLSDASSF	246	0.5000	5.68
25	LGLARFSVQ	12	0.4000	4.55
26	VNALAPTVF	195	0.2000	2.27
27	MLARIPLRR	225	0.2000	2.27

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	FRSAVTEWM	203	4.1000	47.67
2	LIYLLSDAS	244	3.1000	36.05
3	ILITGATGS	24	2.8000	32.56
4	LVASGSNHV	101	2.8000	32.56
5	YLLSDASSF	246	1.6000	18.60
6	LLSDASSFY	247	1.4000	16.28
7	IYLLSDASS	245	1.3000	15.12
8	VVLVSSVRG	151	1.2800	14.88
9	VFRSAVTEW	202	1.1000	12.79
10	WLVCRAAGR	132	0.5000	5.81
11	IRVNALAPT	193	0.3000	3.49
12	VGALIYLLS	241	0.2000	2.33
13	MFTDDPKGR	211	-0.1000	0
14	YGRLDGVLV	94	-0.1200	0
15	VVTCRPDSL	72	-0.2000	0
16	WMFTDDPKG	210	-0.2000	0
17	LGLARFSVQ	12	-0.3000	0
18	VNGAGIDDA	62	-0.4000	0
19	MYLDGGYTA	260	-0.4000	0
20	VNALAPTVF	195	-0.5000	0
21	LAQQVPNLG	5	-0.6000	0
22	LARFSVQDK	14	-0.6000	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	ILITGATGS	24	2.8000	29.17
2	LARFSVQDK	14	2.7000	28.13
3	VVLVSSVRG	151	2.6000	27.08

4	VMDANVRGA	123	2.4000	25.00
5	VLVSSVRGG	152	2.1000	21.88
6	LVASGSNHV	101	2.0000	20.83
7	MLARIPLRR	225	2.0000	20.83
8	FRSAVTEWM	203	1.7000	17.71
9	VASGSNHVA	102	1.3000	13.54
10	LGRVAARAL	33	1.2000	12.50
11	WGGHGIRVN	188	1.1000	11.46
12	FVGALIYLL	240	1.1000	11.46
13	LIYLLSDAS	244	0.9000	9.38
14	IYLLSDASS	245	0.9000	9.38
15	VRGGLGNAA	157	0.8000	8.33
16	LGLARFSVQ	12	0.5000	5.21
17	VRGAWLVCR	128	0.5000	5.21
18	VFRSAVTEW	202	0.5000	5.21
19	LGNAAGYSA	161	0.4000	4.17
20	LAPTVFRSA	198	0.4000	4.17
21	LARIPLRRF	226	0.3800	3.96
22	LVCRAAGRV	133	0.3000	3.12
23	LTLAGGNSA	48	0.1000	1.04
24	VGALIYLLS	241	0.1000	1.04
25	VAARALADA	36	-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	VVLVSSVRG	151	3.5000	39.77
2	LIYLLSDAS	244	3.4000	38.64
3	ILITGATGS	24	2.7000	30.68
4	IYLLSDASS	245	2.5000	28.41
5	LVASGSNHV	101	2.4000	27.27
6	FRSAVTEWM	203	2.2000	25.00
7	LARFSVQDK	14	2.1000	23.86

8	LGLARFSVQ	12	1.4000	15.91
9	VNALAPTVF	195	1.2000	13.64
10	VFRSAVTEW	202	1.1000	12.50
11	VGALIYLLS	241	1.0000	11.36
12	LLSDASSFY	247	0.6000	6.82
13	VLVASGSNH	100	0.5800	6.59
14	LTLAGGNSA	48	0.2000	2.27
15	VRGAWLVCR	128	0.2000	2.27
16	VEEMALAQQ	0	0.1000	1.14
17	VVTCRPDSL	72	-0.1000	0
18	LGRVAARAL	33	-0.2000	0
19	ITEMAVEDF	112	-0.2000	0
20	VMDANVRGA	123	-0.2000	0
21	VLVSSVRGG	152	-0.2000	0
22	YLLSDASSF	246	-0.2000	0
23	LAQQVPNLG	5	-0.3000	0
24	VNGAGIDDA	62	-0.3000	0
25	IRVNALAPT	193	-0.3000	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	FRSAVTEWM	203	4.3000	45.74
2	VVLVSSVRG	151	3.8000	40.43
3	LIYLLSDAS	244	2.4000	25.53
4	FVGALIYLL	240	2.0000	21.28
5	ILITGATGS	24	1.7000	18.09
6	LVASGSNHV	101	1.7000	18.09
7	YLLSDASSF	246	1.7000	18.09
8	IYLLSDASS	245	1.5000	15.96
9	LGLARFSVQ	12	1.2000	12.77
10	VNALAPTVF	195	1.1000	11.70
11	VFRSAVTEW	202	1.0000	10.64

12	VLVASGSNH	100	0.8000	8.51
13	LLSDASSFY	247	0.7000	7.45
14	WLVCRAAGR	132	0.5000	5.32
15	LRRFAEPED	231	0.5000	5.32
16	LARFSVQDK	14	0.4000	4.26
17	YGRLDGVLV	94	0.2000	2.13
18	VLVSSVRGG	152	0.1000	1.06
19	FYTGQVMYL	254	0.1000	1.06
20	VEEMALAQQ	0	-0.1000	0
21	VVTCRPDSL	72	-0.1000	0
22	YTGQVMYLD	255	-0.1000	0
23	LGRVAARAL	33	-0.2000	0
24	YSAYCPSKA	167	-0.2000	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	FRSAVTEWM	203	3.2000	36.36
2	VVLVSSVRG	151	2.5000	28.41
3	LIYLLSDAS	244	2.4000	27.27
4	ILITGATGS	24	1.7000	19.32
5	IYLLSDASS	245	1.5000	17.05
6	LVASGSNHV	101	1.4000	15.91
7	LARFSVQDK	14	1.1000	12.50
8	FVGALIYLL	240	1.0000	11.36
9	YLLSDASSF	246	0.8000	9.09
10	WLVCRAAGR	132	0.5000	5.68
11	LGLARFSVQ	12	0.4000	4.55
12	VNALAPTVF	195	0.2000	2.27
13	VFRSAVTEW	202	0.1000	1.14
14	YGRLDGVLV	94	-0.1000	0
15	YSAYCPSKA	167	-0.2000	0
16	LLSDASSFY	247	-0.4000	0

17	VLVASGSNH	100	-0.4200	0
18	LTLAGGNSA	48	-0.8000	0
19	VRGAWLVCR	128	-0.8000	0
20	VEEMALAQQ	0	-0.9000	0
21	FYTGQVMYL	254	-0.9000	0
22	VVTCRPDSL	72	-1.1000	0
23	LGRVAARAL	33	-1.2000	0
24	ITEMAVEDF	112	-1.2000	0
25	VMDANVRGA	123	-1.2000	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	VVLVSSVRG	151	4.8000	51.06
2	LIYLLSDAS	244	3.4000	36.17
3	FRSAVTEWM	203	3.3000	35.11
4	ILITGATGS	24	2.7000	28.72
5	LVASGSNHV	101	2.7000	28.72
6	IYLLSDASS	245	2.5000	26.60
7	LGLARFSVQ	12	2.2000	23.40
8	VNALAPTVF	195	2.1000	22.34
9	VFRSAVTEW	202	2.0000	21.28
10	VLVASGSNH	100	1.8000	19.15
11	LLSDASSFY	247	1.7000	18.09
12	LRRFAEPED	231	1.5000	15.96
13	LARFSVQDK	14	1.4000	14.89
14	VLVSSVRGG	152	1.1000	11.70
15	LAQQVPNLG	5	1.0000	10.64
16	FVGALIYLL	240	1.0000	10.64
17	VGALIYLLS	241	1.0000	10.64
18	VEEMALAQQ	0	0.9000	9.57
19	VVTCRPDSL	72	0.9000	9.57
20	LGRVAARAL	33	0.8000	8.51

21	ITEMAVEDF	112	0.7000	7.45
22	VEDFDAVMD	117	0.7000	7.45
23	YLLSDASSF	246	0.7000	7.45
24	LDGVLVASG	97	0.6000	6.38
25	IRVNALAPT	193	0.6000	6.38
26	LTLAGGNSA	48	0.2000	2.13
27	LAELVNGAG	58	0.2000	2.13

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	FRSAVTEWM	203	5.6000	62.22
2	LVASGSNHV	101	3.8000	42.22
3	LIYLLSDAS	244	3.5000	38.89
4	YLLSDASSF	246	3.5000	38.89
5	ILITGATGS	24	3.2000	35.56
6	LLSDASSFY	247	2.7000	30.00
7	VVLVSSVRG	151	2.6800	29.78
8	WLVCRAAGR	132	2.0000	22.22
9	IYLLSDASS	245	1.7000	18.89
10	VLLEQGQGG	141	1.4000	15.56
11	VLVSSVRGG	152	1.4000	15.56
12	VNALAPTVF	195	1.4000	15.56
13	MFTDDPKGR	211	1.4000	15.56
14	WMFTDDPKG	210	1.2000	13.33
15	VFRSAVTEW	202	1.1000	12.22
16	IRVNALAPT	193	1.0000	11.11
17	FVGALIYLL	240	0.9600	10.67
18	FYTGQVMYL	254	0.9600	10.67
19	YGRLDGVLV	94	0.8800	9.78
20	VRGAWLVCR	128	0.8800	9.78
21	LAQQVPNLG	5	0.8000	8.89
22	VVTCRPDSL	72	0.7600	8.44

23	ITEMAVEDF	112	0.7000	7.78
24	VGALIYLLS	241	0.6000	6.67
25	MAVEDFDAV	115	-0.1000	0
26	WGGHGIRVN	188	-0.1000	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	VVLVSSVRG	151	3.5000	39.77
2	LIYLLSDAS	244	3.4000	38.64
3	ILITGATGS	24	2.7000	30.68
4	IYLLSDASS	245	2.5000	28.41
5	LVASGSNHV	101	2.4000	27.27
6	FRSAVTEWM	203	2.2000	25.00
7	LARFSVQDK	14	2.1000	23.86
8	LGLARFSVQ	12	1.4000	15.91
9	VNALAPTVF	195	1.2000	13.64
10	VFRSAVTEW	202	1.1000	12.50
11	VGALIYLLS	241	1.0000	11.36
12	LLSDASSFY	247	0.6000	6.82
13	VLVASGSNH	100	0.5800	6.59
14	LTLAGGNSA	48	0.2000	2.27
15	VRGAWLVCR	128	0.2000	2.27
16	VEEMALAQQ	0	0.1000	1.14
17	VVTCRPDSL	72	-0.1000	0
18	LGRVAARAL	33	-0.2000	0
19	ITEMAVEDF	112	-0.2000	0
20	VMDANVRGA	123	-0.2000	0
21	VLVSSVRGG	152	-0.2000	0
22	YLLSDASSF	246	-0.2000	0
23	LAQQVPNLG	5	-0.3000	0
24	VNGAGIDDA	62	-0.3000	0
25	IRVNALAPT	193	-0.3000	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	FRSAVTEWM	203	4.1000	47.67
2	LIYLLSDAS	244	3.1000	36.05
3	ILITGATGS	24	2.8000	32.56
4	LVASGSNHV	101	2.8000	32.56
5	YLLSDASSF	246	1.6000	18.60
6	LLSDASSFY	247	1.4000	16.28
7	IYLLSDASS	245	1.3000	15.12
8	VVLVSSVRG	151	1.2800	14.88
9	VFRSAVTEW	202	1.1000	12.79
10	WLVCRAAGR	132	0.5000	5.81
11	IRVNALAPT	193	0.3000	3.49
12	VGALIYLLS	241	0.2000	2.33
13	MFTDDPKGR	211	-0.1000	0
14	YGRLDGVLV	94	-0.1200	0
15	VVTCRPDSL	72	-0.2000	0
16	WMFTDDPKG	210	-0.2000	0
17	LGLARFSVQ	12	-0.3000	0
18	VNGAGIDDA	62	-0.4000	0
19	MYLDGGYTA	260	-0.4000	0
20	VNALAPTVF	195	-0.5000	0
21	LAQQVPNLG	5	-0.6000	0
22	LARFSVQDK	14	-0.6000	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	FVGALIYLL	240	6.9000	59.48
2	LVASGSNHV	101	6.6000	56.90

3	YLLSDASSF	246	6.0000	51.72
4	FRSAVTEWM	203	5.2200	45.00
5	LGRVAARAL	33	5.2000	44.83
6	LVSSVRGGL	153	5.1000	43.97
7	FYTGQVMYL	254	5.1000	43.97
8	VVLVSSVRG	151	4.6000	39.66
9	VFRSAVTEW	202	3.8000	32.76
10	ILITGATGS	24	3.5000	30.17
11	YGRLDGVLV	94	3.4000	29.31
12	VCRAAGRVL	134	3.2000	27.59
13	VVTCRPDSL	72	2.7000	23.28
14	LARIPLRRF	226	2.7000	23.28
15	LITGATGSL	25	2.3200	20.00
16	VLVSSVRGG	152	2.2000	18.97
17	LAGGNSAGL	50	2.1000	18.10
18	LVCRAAGRV	133	2.0000	17.24
19	VAPITEMAV	109	1.7000	14.66
20	VNALAPTVF	195	1.5000	12.93
21	FSVQDKSIL	17	1.4000	12.07
22	VRGAWLVCR	128	1.3000	11.21
23	LAKTLAAEW	180	1.2000	10.34
24	LVNGAGIDD	61	1.1000	9.48
25	VRGGLGNAA	157	1.1000	9.48
26	LGNAAGYSA	161	1.1000	9.48
27	LTLAGGNSA	48	0.8000	6.90

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	FVGALIYLL	240	6.9000	59.48
2	LVASGSNHV	101	6.6000	56.90
3	YLLSDASSF	246	6.0000	51.72
4	FRSAVTEWM	203	5.2200	45.00

5	LGRVAARAL	33	5.2000	44.83
6	LVSSVRGGL	153	5.1000	43.97
7	FYTGQVMYL	254	5.1000	43.97
8	VVLVSSVRG	151	4.6000	39.66
9	VFRSAVTEW	202	3.8000	32.76
10	ILITGATGS	24	3.5000	30.17
11	YGRLDGVLV	94	3.4000	29.31
12	VCRAAGRVL	134	3.2000	27.59
13	VVTCRPDSL	72	2.7000	23.28
14	LARIPLRRF	226	2.7000	23.28
15	LITGATGSL	25	2.3200	20.00
16	VLVSSVRGG	152	2.2000	18.97
17	LAGGNSAGL	50	2.1000	18.10
18	LVCRAAGRV	133	2.0000	17.24
19	VAPITEMAV	109	1.7000	14.66
20	VNALAPTVF	195	1.5000	12.93
21	FSVQDKSIL	17	1.4000	12.07
22	VRGAWLVCR	128	1.3000	11.21
23	LAKTLAAEW	180	1.2000	10.34
24	LVNGAGIDD	61	1.1000	9.48
25	VRGGLGNAA	157	1.1000	9.48
26	LGNAAGYSA	161	1.1000	9.48
27	LTLAGGNSA	48	0.8000	6.90

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	LLAKTLAAE	179	3.8000	44.19
2	LGRYGRLDG	91	3.4000	39.53
3	LVCRAAGRV	133	2.5000	29.07
4	FVGALIYLL	240	1.9000	22.09
5	IRVNALAPT	193	1.6000	18.60
6	VAARALADA	36	1.5000	17.44

7	VVLVSSVRG	151	1.5000	17.44
8	FRSAVTEWM	203	1.5000	17.44
9	MLARIPLRR	225	1.5000	17.44
10	VQDKSILIT	19	1.3000	15.12
11	YSAYCPSKA	167	1.1000	12.79
12	VEEMALAQQ	0	0.8000	9.30
13	LVSSVRGGL	153	0.8000	9.30
14	LRRFAEPED	231	0.8000	9.30
15	FYTGQVMYL	254	0.8000	9.30
16	WLVCRAAGR	132	0.5000	5.81
17	VLVSSVRGG	152	0.4000	4.65
18	WGGHGIRVN	188	0.4000	4.65
19	LVNGAGIDD	61	0.1000	1.16
20	VMYLDGGYT	259	0.1000	1.16
21	LGRVAARAL	33	-0.1000	0
22	IYLLSDASS	245	-0.1000	0
23	VPNLGLARF	9	-0.2000	0
24	VLVASGSNH	100	-0.2000	0
25	YCPSKAGTD	170	-0.2000	0
26	LIYLLSDAS	244	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVCRAAGRV	133	2.2000	27.50
2	LGRYGRLDG	91	2.1000	26.25
3	VAARALADA	36	1.5000	18.75
4	MLARIPLRR	225	1.5000	18.75
5	YSAYCPSKA	167	1.1000	13.75
6	FVGALIYLL	240	0.9000	11.25
7	LLAKTLAAE	179	0.8000	10.00
8	IRVNALAPT	193	0.7000	8.75
9	WLVCRAAGR	132	0.5000	6.25

10	VQDKSILIT	19	0.4000	5.00
11	FRSAVTEWM	203	0.4000	5.00
12	VVLVSSVRG	151	0.2000	2.50
13	LARFSVQDK	14	-0.1000	0
14	IYLLSDASS	245	-0.1000	0
15	LVSSVRGGL	153	-0.2000	0
16	LIYLLSDAS	244	-0.2000	0
17	FYTGQVMYL	254	-0.2000	0
18	VRGAWLVCR	128	-0.5000	0
19	YGRLDGVLV	94	-0.6000	0
20	VMDANVRGA	123	-0.6000	0
21	VGALIYLLS	241	-0.8000	0
22	VMYLDGGYT	259	-0.8000	0
23	VLVSSVRGG	152	-0.9000	0
24	IPLRRFAEP	229	-0.9000	0
25	VPNLGLARF	9	-1.1000	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	LVCRAAGRV	133	3.2000	40.00
2	LGRYGRLDG	91	3.1000	38.75
3	VAARALADA	36	2.5000	31.25
4	MLARIPLRR	225	2.5000	31.25
5	LLAKTLAAE	179	1.8000	22.50
6	IRVNALAPT	193	1.7000	21.25
7	VQDKSILIT	19	1.4000	17.50
8	VVLVSSVRG	151	1.2000	15.00
9	VEEMALAQQ	0	1.0000	12.50
10	LARFSVQDK	14	0.9000	11.25
11	IYLLSDASS	245	0.9000	11.25
12	LVSSVRGGL	153	0.8000	10.00
13	LIYLLSDAS	244	0.8000	10.00

14	VRGAWLVCR	128	0.5000	6.25
15	VMDANVRGA	123	0.4000	5.00
16	VGALIYLLS	241	0.2000	2.50
17	VMYLDGGYT	259	0.2000	2.50
18	VLVSSVRGG	152	0.1000	1.25
19	YSAYCPSKA	167	0.1000	1.25
20	IPLRRFAEP	229	0.1000	1.25
21	VPNLGLARF	9	-0.1000	0
22	LGRVAARAL	33	-0.1000	0
23	FVGALIYLL	240	-0.1000	0
24	ILITGATGS	24	-0.2000	0
25	MVEAALGRY	86	-0.4000	0
26	LARIPLRRF	226	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LLAKTLAAE	179	4.8000	55.81
2	LGRYGRLDG	91	4.4000	51.16
3	LVCRAAGRV	133	3.5000	40.70
4	IRVNALAPT	193	2.6000	30.23
5	VAARALADA	36	2.5000	29.07
6	VVLVSSVRG	151	2.5000	29.07
7	MLARIPLRR	225	2.5000	29.07
8	VQDKSILIT	19	2.3000	26.74
9	VEEMALAQQ	0	1.8000	20.93
10	LVSSVRGGL	153	1.8000	20.93
11	LRRFAEPED	231	1.8000	20.93
12	VLVSSVRGG	152	1.4000	16.28
13	LVNGAGIDD	61	1.1000	12.79
14	VMYLDGGYT	259	1.1000	12.79
15	LGRVAARAL	33	0.9000	10.47
16	FVGALIYLL	240	0.9000	10.47

17	IYLLSDASS	245	0.9000	10.47
18	VPNLGLARF	9	0.8000	9.30
19	VLVASGSNH	100	0.8000	9.30
20	LIYLLSDAS	244	0.8000	9.30
21	MVEAALGRY	86	0.7000	8.14
22	LDGVLVASG	97	0.7000	8.14
23	VRGAWLVCR	128	0.5000	5.81
24	FRSAVTEWM	203	0.5000	5.81
25	LARIPLRRF	226	0.5000	5.81
26	IPLRRFAEP	229	0.5000	5.81
27	LITGATGSL	25	0.4000	4.65

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	YSAYCPSKA	167	2.9000	33.33
2	LGRYGRLDG	91	2.7000	31.03
3	FRSAVTEWM	203	2.1000	24.14
4	MLARIPLRR	225	2.1000	24.14
5	FVGALIYLL	240	1.8000	20.69
6	ILITGATGS	24	1.6000	18.39
7	VAARALADA	36	1.5000	17.24
8	LVCRAAGRV	133	1.5000	17.24
9	VVLVSSVRG	151	1.2000	13.79
10	VQDKSILIT	19	1.0000	11.49
11	LIYLLSDAS	244	1.0000	11.49
12	LARFSVQDK	14	0.9000	10.34
13	LLAKTLAAE	179	0.8000	9.20
14	FYTGQVMYL	254	0.8000	9.20
15	IRVNALAPT	193	0.7000	8.05
16	VRGAWLVCR	128	0.5000	5.75
17	WLVCRAAGR	132	0.5000	5.75
18	YLLSDASSF	246	0.5000	5.75

19	YGRLDGVLV	94	0.4000	4.60
20	VRGGLGNAA	157	0.4000	4.60
21	VNALAPTVF	195	0.4000	4.60
22	VLVASGSNH	100	0.3800	4.37
23	LGLARFSVQ	12	0.1000	1.15
24	VFRSAVTEW	202	0.1000	1.15

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	LGRYGRLDG	91	5.2000	51.49
2	LLAKTLAAE	179	3.8000	37.62
3	MLARIPLRR	225	3.3000	32.67
4	VQDKSILIT	19	3.1000	30.69
5	LVCRAAGRV	133	2.6000	25.74
6	FRSAVTEWM	203	2.6000	25.74
7	FVGALIYLL	240	2.6000	25.74
8	FYTGQVMYL	254	2.4000	23.76
9	VVLVSSVRG	151	2.0000	19.80
10	LRRFAEPED	231	1.9500	19.31
11	LVNGAGIDD	61	1.7000	16.83
12	IRVNALAPT	193	1.6000	15.84
13	VAARALADA	36	1.5000	14.85
14	YSAYCPSKA	167	1.1000	10.89
15	VGALIYLLS	241	1.0000	9.90
16	LVSSVRGGL	153	0.9000	8.91
17	VEEMALAQQ	0	0.8000	7.92
18	VLVSSVRGG	152	0.6000	5.94
19	WGGHGIRVN	188	0.6000	5.94
20	WLVCRAAGR	132	0.5000	4.95
21	YGRLDGVLV	94	0.2000	1.98
22	VMYLDGGYT	259	0.2000	1.98
23	LGRVAARAL	33	0.1000	0.99

24	ILITGATGS	24	-0.1000	0

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	FVGALIYLL	240	1.6000	19.28
2	FRSAVTEWM	203	1.5000	18.07
3	VGALIYLLS	241	1.4000	16.87
4	LGRYGRLDG	91	1.0000	12.05
5	VVLVSSVRG	151	0.8000	9.64
6	IRVNALAPT	193	0.7000	8.43
7	FYTGQVMYL	254	0.7000	8.43
8	WLVCRAAGR	132	0.5000	6.02
9	ILITGATGS	24	0.3000	3.61
10	YGRLDGVLV	94	0.3000	3.61
11	MLARIPLRR	225	0.3000	3.61
12	IYLLSDASS	245	0.3000	3.61
13	LVSSVRGGL	153	0.2000	2.41
14	LARFSVQDK	14	-0.1000	0
15	LIYLLSDAS	244	-0.1000	0
16	VMYLDGGYT	259	-0.3000	0
17	VEEMALAQQ	0	-0.4000	0
18	VMDANVRGA	123	-0.4000	0
19	VLVSSVRGG	152	-0.4000	0
20	VQDKSILIT	19	-0.6000	0
21	VAPITEMAV	109	-0.6000	0
22	LARIPLRRF	226	-0.6000	0
23	VPNLGLARF	9	-0.7000	0
24	LVCRAAGRV	133	-0.7000	0
25	LGRVAARAL	33	-0.8000	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	VLVSSVRGG	152	2.3000	27.38
2	VMDANVRGA	123	2.2000	26.19
3	LARFSVQDK	14	2.0000	23.81
4	LGRYGRLDG	91	2.0000	23.81
5	IRVNALAPT	193	1.8000	21.43
6	WGGHGIRVN	188	1.7000	20.24
7	VRGAWLVCR	128	1.5000	17.86
8	LIYLLSDAS	244	1.4000	16.67
9	ILITGATGS	24	1.2000	14.29
10	MLARIPLRR	225	1.1000	13.10
11	VVLVSSVRG	151	1.0000	11.90
12	LVASGSNHV	101	0.8000	9.52
13	FRSAVTEWM	203	0.8000	9.52
14	FVGALIYLL	240	0.8000	9.52
15	VQDKSILIT	19	0.6000	7.14
16	VGALIYLLS	241	0.6000	7.14
17	IYLLSDASS	245	0.6000	7.14
18	LGRVAARAL	33	0.5000	5.95
19	LARIPLRRF	226	0.5000	5.95
20	VEEMALAQQ	0	0.4000	4.76
21	VAARALADA	36	0.4000	4.76
22	LTLAGGNSA	48	0.4000	4.76
23	VRGGLGNAA	157	0.3000	3.57
24	LLAKTLAAE	179	0.3000	3.57
25	LAQQVPNLG	5	0.2000	2.38
26	VNGAGIDDA	62	0.2000	2.38
27	VCRAAGRVL	134	0.2000	2.38

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VGALIYLLS	241	2.4000	28.92
2	LGRYGRLDG	91	2.0000	24.10
3	VVLVSSVRG	151	1.8000	21.69
4	IRVNALAPT	193	1.7000	20.48
5	ILITGATGS	24	1.3000	15.66
6	MLARIPLRR	225	1.3000	15.66
7	IYLLSDASS	245	1.3000	15.66
8	LVSSVRGGL	153	1.2000	14.46
9	VRGAWLVCR	128	1.0000	12.05
10	LARFSVQDK	14	0.9000	10.84
11	LIYLLSDAS	244	0.9000	10.84
12	VMYLDGGYT	259	0.7000	8.43
13	VEEMALAQQ	0	0.6000	7.23
14	VMDANVRGA	123	0.6000	7.23
15	VLVSSVRGG	152	0.6000	7.23
16	FVGALIYLL	240	0.6000	7.23
17	FRSAVTEWM	203	0.5000	6.02
18	VQDKSILIT	19	0.4000	4.82
19	VAPITEMAV	109	0.4000	4.82
20	LARIPLRRF	226	0.4000	4.82
21	VPNLGLARF	9	0.3000	3.61
22	LVCRAAGRV	133	0.3000	3.61
23	LGRVAARAL	33	0.2000	2.41
24	LRRFAEPED	231	0.1500	1.81
25	VNALAPTVF	195	0.1000	1.20
26	LGNAAGYSA	161	-0.1000	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	VGALIYLLS	241	2.4000	28.92
2	LGRYGRLDG	91	2.0000	24.10

3	VVLVSSVRG	151	1.8000	21.69
4	IRVNALAPT	193	1.7000	20.48
5	ILITGATGS	24	1.3000	15.66
6	MLARIPLRR	225	1.3000	15.66
7	IYLLSDASS	245	1.3000	15.66
8	LVSSVRGGL	153	1.2000	14.46
9	VRGAWLVCR	128	1.0000	12.05
10	LARFSVQDK	14	0.9000	10.84
11	LIYLLSDAS	244	0.9000	10.84
12	VMYLDGGYT	259	0.7000	8.43
13	VEEMALAQQ	0	0.6000	7.23
14	VMDANVRGA	123	0.6000	7.23
15	VLVSSVRGG	152	0.6000	7.23
16	FVGALIYLL	240	0.6000	7.23
17	FRSAVTEWM	203	0.5000	6.02
18	VQDKSILIT	19	0.4000	4.82
19	VAPITEMAV	109	0.4000	4.82
20	LARIPLRRF	226	0.4000	4.82
21	VPNLGLARF	9	0.3000	3.61
22	LVCRAAGRV	133	0.3000	3.61
23	LGRVAARAL	33	0.2000	2.41
24	LRRFAEPED	231	0.1500	1.81
25	VNALAPTVF	195	0.1000	1.20
26	LGNAAGYSA	161	-0.1000	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	MYLDGGYTA	260	3.4500	37.91
2	LVSSVRGGL	153	3.1000	34.07
3	LLSDASSFY	247	2.4700	27.14
4	VFRSAVTEW	202	2.3000	25.27
5	VVLVSSVRG	151	2.2000	24.18

6	VRGGLGNAA	157	2.1100	23.19
7	ILITGATGS	24	2.1000	23.08
8	LVASGSNHV	101	1.9100	20.99
9	IRVNALAPT	193	1.9000	20.88
10	LIYLLSDAS	244	1.9000	20.88
11	VRGAWLVCR	128	1.8000	19.78
12	MFTDDPKGR	211	1.7000	18.68
13	FYTGQVMYL	254	1.7000	18.68
14	FRSAVTEWM	203	1.6000	17.58
15	LITGATGSL	25	1.5000	16.48
16	VLVSSVRGG	152	1.5000	16.48
17	FTDDPKGRA	212	1.4000	15.38
18	LVNGAGIDD	61	1.1000	12.09
19	VNGAGIDDA	62	1.1000	12.09
20	VVTCRPDSL	72	1.0000	10.99
21	VLVASGSNH	100	0.9500	10.44
22	FVGALIYLL	240	0.9500	10.44
23	YLLSDASSF	246	0.7700	8.46
24	LGLARFSVQ	12	0.6700	7.36
25	LARFSVQDK	14	0.5000	5.49
26	LVCRAAGRV	133	0.5000	5.49
27	LGRYGRLDG	91	0.4000	4.40

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	WGGHGIRVN	188	2.7000	32.14
2	FRSAVTEWM	203	1.8000	21.43
3	FVGALIYLL	240	1.8000	21.43
4	VLVSSVRGG	152	1.3000	15.48
5	VMDANVRGA	123	1.2000	14.29
6	LARFSVQDK	14	1.0000	11.90
7	LGRYGRLDG	91	1.0000	11.90

8	IRVNALAPT	193	0.8000	9.52
9	VRGAWLVCR	128	0.5000	5.95
10	WLVCRAAGR	132	0.5000	5.95
11	LIYLLSDAS	244	0.4000	4.76
12	FSVQDKSIL	17	0.2000	2.38
13	ILITGATGS	24	0.2000	2.38
14	YGRLDGVLV	94	0.1000	1.19
15	MLARIPLRR	225	0.1000	1.19
16	LVASGSNHV	101	-0.2000	0
17	YSAYCPSKA	167	-0.3000	0
18	VQDKSILIT	19	-0.4000	0
19	VGALIYLLS	241	-0.4000	0
20	IYLLSDASS	245	-0.4000	0
21	FYTGQVMYL	254	-0.4000	0
22	LGRVAARAL	33	-0.5000	0
23	LARIPLRRF	226	-0.5000	0
24	YLLSDASSF	246	-0.5000	0
25	VEEMALAQQ	0	-0.6000	0

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	WGGHGIRVN	188	3.5000	39.77
2	FRSAVTEWM	203	3.3000	37.50
3	FVGALIYLL	240	2.7600	31.36
4	VLVSSVRGG	152	2.7000	30.68
5	LGRYGRLDG	91	2.4000	27.27
6	VRGAWLVCR	128	2.0000	22.73
7	WLVCRAAGR	132	2.0000	22.73
8	MLARIPLRR	225	1.6000	18.18
9	IRVNALAPT	193	1.5000	17.05
10	VVLVSSVRG	151	1.4000	15.91
11	LARIPLRRF	226	1.4000	15.91

12	YLLSDASSF	246	1.4000	15.91
13	VMDANVRGA	123	1.2000	13.64
14	FSVQDKSIL	17	1.1600	13.18
15	LARFSVQDK	14	1.1000	12.50
16	YGRLDGVLV	94	1.1000	12.50
17	LVASGSNHV	101	0.8000	9.09
18	LIYLLSDAS	244	0.8000	9.09
19	LLAKTLAAE	179	0.7000	7.95
20	VNALAPTVF	195	0.7000	7.95
21	LAQQVPNLG	5	0.6000	6.82
22	ILITGATGS	24	0.6000	6.82
23	FYTGQVMYL	254	0.5600	6.36
24	VPNLGLARF	9	0.5000	5.68
25	LGRVAARAL	33	0.4600	5.23
26	VQDKSILIT	19	0.3000	3.41
27	LRRFAEPED	231	0.2000	2.27

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	VLVSSVRGG	152	2.3000	27.38
2	VMDANVRGA	123	2.2000	26.19
3	LARFSVQDK	14	2.0000	23.81
4	LGRYGRLDG	91	2.0000	23.81
5	IRVNALAPT	193	1.8000	21.43
6	WGGHGIRVN	188	1.7000	20.24
7	VRGAWLVCR	128	1.5000	17.86
8	LIYLLSDAS	244	1.4000	16.67
9	ILITGATGS	24	1.2000	14.29
10	MLARIPLRR	225	1.1000	13.10
11	VVLVSSVRG	151	1.0000	11.90
12	LVASGSNHV	101	0.8000	9.52
13	FRSAVTEWM	203	0.8000	9.52

14	FVGALIYLL	240	0.8000	9.52
15	VQDKSILIT	19	0.6000	7.14
16	VGALIYLLS	241	0.6000	7.14
17	IYLLSDASS	245	0.6000	7.14
18	LGRVAARAL	33	0.5000	5.95
19	LARIPLRRF	226	0.5000	5.95
20	VEEMALAQQ	0	0.4000	4.76
21	VAARALADA	36	0.4000	4.76
22	LTLAGGNSA	48	0.4000	4.76
23	VRGGLGNAA	157	0.3000	3.57
24	LLAKTLAAE	179	0.3000	3.57
25	LAQQVPNLG	5	0.2000	2.38
26	VNGAGIDDA	62	0.2000	2.38
27	VCRAAGRVL	134	0.2000	2.38

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FRSAVTEWM	203	3.0000	34.48
2	FVGALIYLL	240	2.5600	29.43
3	LGRYGRLDG	91	2.4000	27.59
4	VVLVSSVRG	151	2.2000	25.29
5	WLVCRAAGR	132	2.0000	22.99
6	MLARIPLRR	225	1.8000	20.69
7	VGALIYLLS	241	1.8000	20.69
8	FYTGQVMYL	254	1.6600	19.08
9	VRGAWLVCR	128	1.5000	17.24
10	IRVNALAPT	193	1.4000	16.09
11	YGRLDGVLV	94	1.3000	14.94
12	LARIPLRRF	226	1.3000	14.94
13	VPNLGLARF	9	1.2000	13.79
14	LVSSVRGGL	153	1.1600	13.33
15	VLVSSVRGG	152	1.0000	11.49

16	VNALAPTVF	195	1.0000	11.49
17	YLLSDASSF	246	0.9000	10.34
18	ILITGATGS	24	0.7000	8.05
19	IYLLSDASS	245	0.7000	8.05
20	VAPITEMAV	109	0.4000	4.60
21	VMYLDGGYT	259	0.4000	4.60
22	LVCRAAGRV	133	0.3000	3.45
23	LIYLLSDAS	244	0.3000	3.45
24	LRRFAEPED	231	0.2500	2.87
25	LGRVAARAL	33	0.1600	1.84
26	VQDKSILIT	19	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	VLVSSVRGG	152	3.7000	42.05
2	LGRYGRLDG	91	3.4000	38.64
3	VRGAWLVCR	128	3.0000	34.09
4	MLARIPLRR	225	2.6000	29.55
5	WGGHGIRVN	188	2.5000	28.41
6	IRVNALAPT	193	2.5000	28.41
7	VVLVSSVRG	151	2.4000	27.27
8	LARIPLRRF	226	2.4000	27.27
9	FRSAVTEWM	203	2.3000	26.14
10	VMDANVRGA	123	2.2000	25.00
11	LARFSVQDK	14	2.1000	23.86
12	LVASGSNHV	101	1.8000	20.45
13	LIYLLSDAS	244	1.8000	20.45
14	FVGALIYLL	240	1.7600	20.00
15	LLAKTLAAE	179	1.7000	19.32
16	VNALAPTVF	195	1.7000	19.32
17	LAQQVPNLG	5	1.6000	18.18
18	ILITGATGS	24	1.6000	18.18

19	VPNLGLARF	9	1.5000	17.05
20	LGRVAARAL	33	1.4600	16.59
21	VQDKSILIT	19	1.3000	14.77
22	LRRFAEPED	231	1.2000	13.64
23	VCRAAGRVL	134	1.1600	13.18
24	LVSSVRGGL	153	1.1600	13.18
25	LVCRAAGRV	133	1.1000	12.50
26	VVTCRPDSL	72	1.0600	12.05
27	VEAALGRYG	87	1.0000	11.36

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	WGGHGIRVN	188	3.5000	39.77
2	FRSAVTEWM	203	3.3000	37.50
3	FVGALIYLL	240	2.7600	31.36
4	VLVSSVRGG	152	2.7000	30.68
5	LGRYGRLDG	91	2.4000	27.27
6	VRGAWLVCR	128	2.0000	22.73
7	WLVCRAAGR	132	2.0000	22.73
8	MLARIPLRR	225	1.6000	18.18
9	IRVNALAPT	193	1.5000	17.05
10	VVLVSSVRG	151	1.4000	15.91
11	LARIPLRRF	226	1.4000	15.91
12	YLLSDASSF	246	1.4000	15.91
13	VMDANVRGA	123	1.2000	13.64
14	FSVQDKSIL	17	1.1600	13.18
15	LARFSVQDK	14	1.1000	12.50
16	YGRLDGVLV	94	1.1000	12.50
17	LVASGSNHV	101	0.8000	9.09
18	LIYLLSDAS	244	0.8000	9.09
19	LLAKTLAAE	179	0.7000	7.95
20	VNALAPTVF	195	0.7000	7.95

21	LAQQVPNLG	5	0.6000	6.82
22	ILITGATGS	24	0.6000	6.82
23	FYTGQVMYL	254	0.5600	6.36
24	VPNLGLARF	9	0.5000	5.68
25	LGRVAARAL	33	0.4600	5.23
26	VQDKSILIT	19	0.3000	3.41
27	LRRFAEPED	231	0.2000	2.27

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	WGGHGIRVN	188	3.7000	41.11
2	VLVSSVRGG	152	3.6000	40.00
3	LGRYGRLDG	91	3.3000	36.67
4	LLAKTLAAE	179	3.3000	36.67
5	LRRFAEPED	231	2.8000	31.11
6	IRVNALAPT	193	2.7000	30.00
7	VVLVSSVRG	151	2.3000	25.56
8	VMDANVRGA	123	2.2000	24.44
9	FRSAVTEWM	203	1.9000	21.11
10	FVGALIYLL	240	1.8000	20.00
11	LAQQVPNLG	5	1.5000	16.67
12	VQDKSILIT	19	1.5000	16.67
13	LGRVAARAL	33	1.5000	16.67
14	VRGAWLVCR	128	1.5000	16.67
15	LARIPLRRF	226	1.4000	15.56
16	LIYLLSDAS	244	1.4000	15.56
17	LARFSVQDK	14	1.3000	14.44
18	VEEMALAQQ	0	1.2000	13.33
19	MALAQQVPN	3	1.2000	13.33
20	ILITGATGS	24	1.2000	13.33
21	VLVASGSNH	100	1.2000	13.33
22	VCRAAGRVL	134	1.2000	13.33

23	LVSSVRGGL	153	1.2000	13.33
24	VVTCRPDSL	72	1.1000	12.22
25	LVASGSNHV	101	1.1000	12.22
26	VFRSAVTEW	202	1.1000	12.22
27	MLARIPLRR	225	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	FRSAVTEWM	203	3.0000	34.48
2	FVGALIYLL	240	2.5600	29.43
3	LGRYGRLDG	91	2.4000	27.59
4	VVLVSSVRG	151	2.2000	25.29
5	WLVCRAAGR	132	2.0000	22.99
6	MLARIPLRR	225	1.8000	20.69
7	VGALIYLLS	241	1.8000	20.69
8	FYTGQVMYL	254	1.6600	19.08
9	VRGAWLVCR	128	1.5000	17.24
10	IRVNALAPT	193	1.4000	16.09
11	YGRLDGVLV	94	1.3000	14.94
12	LARIPLRRF	226	1.3000	14.94
13	VPNLGLARF	9	1.2000	13.79
14	LVSSVRGGL	153	1.1600	13.33
15	VLVSSVRGG	152	1.0000	11.49
16	VNALAPTVF	195	1.0000	11.49
17	YLLSDASSF	246	0.9000	10.34
18	ILITGATGS	24	0.7000	8.05
19	IYLLSDASS	245	0.7000	8.05
20	VAPITEMAV	109	0.4000	4.60
21	VMYLDGGYT	259	0.4000	4.60
22	LVCRAAGRV	133	0.3000	3.45
23	LIYLLSDAS	244	0.3000	3.45
24	LRRFAEPED	231	0.2500	2.87

25	LGRVAARAL	33	0.1600	1.84
26	VQDKSILIT	19	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	FVGALIYLL	240	0.9000	13.24
2	IRVNALAPT	193	0.7000	10.29
3	WLVCRAAGR	132	0.5000	7.35
4	FRSAVTEWM	203	0.4000	5.88
5	VVLVSSVRG	151	0.3000	4.41
6	IYLLSDASS	245	0.3000	4.41
7	LIYLLSDAS	244	0.2000	2.94
8	LVSSVRGGL	153	0.1000	1.47
9	LARFSVQDK	14	-0.2000	0
10	YGRLDGVLV	94	-0.2000	0
11	VEEMALAQQ	0	-0.4000	0
12	VGALIYLLS	241	-0.4000	0
13	VMYLDGGYT	259	-0.4000	0
14	VRGAWLVCR	128	-0.5000	0
15	VMDANVRGA	123	-0.6000	0
16	VLVSSVRGG	152	-0.6000	0
17	VPNLGLARF	9	-0.7000	0
18	ILITGATGS	24	-0.8000	0
19	LGRYGRLDG	91	-0.8000	0
20	LVCRAAGRV	133	-0.8000	0
21	LARIPLRRF	226	-0.8000	0
22	FYTGQVMYL	254	-0.9000	0
23	LGRVAARAL	33	-1.0000	0
24	YLLSDASSF	246	-1.0000	0
25	FSVQDKSIL	17	-1.2000	0
26	WGGHGIRVN	188	-1.2000	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	VGALIYLLS	241	2.4000	28.92
2	LGRYGRLDG	91	2.0000	24.10
3	VVLVSSVRG	151	1.8000	21.69
4	IRVNALAPT	193	1.7000	20.48
5	ILITGATGS	24	1.3000	15.66
6	MLARIPLRR	225	1.3000	15.66
7	IYLLSDASS	245	1.3000	15.66
8	LVSSVRGGL	153	1.2000	14.46
9	VRGAWLVCR	128	1.0000	12.05
10	LARFSVQDK	14	0.9000	10.84
11	LIYLLSDAS	244	0.9000	10.84
12	VMYLDGGYT	259	0.7000	8.43
13	VEEMALAQQ	0	0.6000	7.23
14	VMDANVRGA	123	0.6000	7.23
15	VLVSSVRGG	152	0.6000	7.23
16	FVGALIYLL	240	0.6000	7.23
17	FRSAVTEWM	203	0.5000	6.02
18	VQDKSILIT	19	0.4000	4.82
19	VAPITEMAV	109	0.4000	4.82
20	LARIPLRRF	226	0.4000	4.82
21	VPNLGLARF	9	0.3000	3.61
22	LVCRAAGRV	133	0.3000	3.61
23	LGRVAARAL	33	0.2000	2.41
24	LRRFAEPED	231	0.1500	1.81
25	VNALAPTVF	195	0.1000	1.20
26	LGNAAGYSA	161	-0.1000	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	FRSAVTEWM	203	2.6000	29.21
2	FVGALIYLL	240	2.6000	29.21
3	LGRYGRLDG	91	2.3000	25.84
4	VVLVSSVRG	151	2.1000	23.60
5	LRRFAEPED	231	1.8500	20.79
6	FYTGQVMYL	254	1.7000	19.10
7	IRVNALAPT	193	1.6000	17.98
8	VGALIYLLS	241	1.4000	15.73
9	LVSSVRGGL	153	1.2000	13.48
10	LVNGAGIDD	61	1.0000	11.24
11	LLAKTLAAE	179	1.0000	11.24
12	WGGHGIRVN	188	1.0000	11.24
13	VLVSSVRGG	152	0.9000	10.11
14	YGRLDGVLV	94	0.6000	6.74
15	VMYLDGGYT	259	0.6000	6.74
16	WLVCRAAGR	132	0.5000	5.62
17	VEEMALAQQ	0	0.4000	4.49
18	VQDKSILIT	19	0.3000	3.37
19	ILITGATGS	24	0.3000	3.37
20	MLARIPLRR	225	0.3000	3.37
21	LARIPLRRF	226	0.3000	3.37
22	IYLLSDASS	245	0.3000	3.37
23	VPNLGLARF	9	0.2000	2.25
24	LGRVAARAL	33	0.2000	2.25
25	YCPSKAGTD	170	0.2000	2.25

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VLVSSVRGG	152	2.3000	27.38
2	VMDANVRGA	123	2.2000	26.19
3	LARFSVQDK	14	2.0000	23.81

4	LGRYGRLDG	91	2.0000	23.81
5	IRVNALAPT	193	1.8000	21.43
6	WGGHGIRVN	188	1.7000	20.24
7	VRGAWLVCR	128	1.5000	17.86
8	LIYLLSDAS	244	1.4000	16.67
9	ILITGATGS	24	1.2000	14.29
10	MLARIPLRR	225	1.1000	13.10
11	VVLVSSVRG	151	1.0000	11.90
12	LVASGSNHV	101	0.8000	9.52
13	FRSAVTEWM	203	0.8000	9.52
14	FVGALIYLL	240	0.8000	9.52
15	VQDKSILIT	19	0.6000	7.14
16	VGALIYLLS	241	0.6000	7.14
17	IYLLSDASS	245	0.6000	7.14
18	LGRVAARAL	33	0.5000	5.95
19	LARIPLRRF	226	0.5000	5.95
20	VEEMALAQQ	0	0.4000	4.76
21	VAARALADA	36	0.4000	4.76
22	LTLAGGNSA	48	0.4000	4.76
23	VRGGLGNAA	157	0.3000	3.57
24	LLAKTLAAE	179	0.3000	3.57
25	LAQQVPNLG	5	0.2000	2.38
26	VNGAGIDDA	62	0.2000	2.38
27	VCRAAGRVL	134	0.2000	2.38

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WGGHGIRVN	188	2.7000	32.14
2	FRSAVTEWM	203	1.8000	21.43
3	FVGALIYLL	240	1.8000	21.43
4	VLVSSVRGG	152	1.3000	15.48
5	VMDANVRGA	123	1.2000	14.29

6	LARFSVQDK	14	1.0000	11.90
7	LGRYGRLDG	91	1.0000	11.90
8	IRVNALAPT	193	0.8000	9.52
9	VRGAWLVCR	128	0.5000	5.95
10	WLVCRAAGR	132	0.5000	5.95
11	LIYLLSDAS	244	0.4000	4.76
12	FSVQDKSIL	17	0.2000	2.38
13	ILITGATGS	24	0.2000	2.38
14	YGRLDGVLV	94	0.1000	1.19
15	MLARIPLRR	225	0.1000	1.19
16	LVASGSNHV	101	-0.2000	0
17	YSAYCPSKA	167	-0.3000	0
18	VQDKSILIT	19	-0.4000	0
19	VGALIYLLS	241	-0.4000	0
20	IYLLSDASS	245	-0.4000	0
21	FYTGQVMYL	254	-0.4000	0
22	LGRVAARAL	33	-0.5000	0
23	LARIPLRRF	226	-0.5000	0
24	YLLSDASSF	246	-0.5000	0
25	VEEMALAQQ	0	-0.6000	0

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VLVSSVRGG	152	3.7000	42.05
2	LGRYGRLDG	91	3.4000	38.64
3	VRGAWLVCR	128	3.0000	34.09
4	MLARIPLRR	225	2.6000	29.55
5	WGGHGIRVN	188	2.5000	28.41
6	IRVNALAPT	193	2.5000	28.41
7	VVLVSSVRG	151	2.4000	27.27
8	LARIPLRRF	226	2.4000	27.27
9	FRSAVTEWM	203	2.3000	26.14

10	VMDANVRGA	123	2.2000	25.00
11	LARFSVQDK	14	2.1000	23.86
12	LVASGSNHV	101	1.8000	20.45
13	LIYLLSDAS	244	1.8000	20.45
14	FVGALIYLL	240	1.7600	20.00
15	LLAKTLAAE	179	1.7000	19.32
16	VNALAPTVF	195	1.7000	19.32
17	LAQQVPNLG	5	1.6000	18.18
18	ILITGATGS	24	1.6000	18.18
19	VPNLGLARF	9	1.5000	17.05
20	LGRVAARAL	33	1.4600	16.59
21	VQDKSILIT	19	1.3000	14.77
22	LRRFAEPED	231	1.2000	13.64
23	VCRAAGRVL	134	1.1600	13.18
24	LVSSVRGGL	153	1.1600	13.18
25	LVCRAAGRV	133	1.1000	12.50
26	VVTCRPDSL	72	1.0600	12.05
27	VEAALGRYG	87	1.0000	11.36

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	VLVSSVRGG	152	3.7000	42.05
2	LGRYGRLDG	91	3.4000	38.64
3	VRGAWLVCR	128	3.0000	34.09
4	MLARIPLRR	225	2.6000	29.55
5	WGGHGIRVN	188	2.5000	28.41
6	IRVNALAPT	193	2.5000	28.41
7	VVLVSSVRG	151	2.4000	27.27
8	LARIPLRRF	226	2.4000	27.27
9	FRSAVTEWM	203	2.3000	26.14
10	VMDANVRGA	123	2.2000	25.00
11	LARFSVQDK	14	2.1000	23.86

12	LVASGSNHV	101	1.8000	20.45
13	LIYLLSDAS	244	1.8000	20.45
14	FVGALIYLL	240	1.7600	20.00
15	LLAKTLAAE	179	1.7000	19.32
16	VNALAPTVF	195	1.7000	19.32
17	LAQQVPNLG	5	1.6000	18.18
18	ILITGATGS	24	1.6000	18.18
19	VPNLGLARF	9	1.5000	17.05
20	LGRVAARAL	33	1.4600	16.59
21	VQDKSILIT	19	1.3000	14.77
22	LRRFAEPED	231	1.2000	13.64
23	VCRAAGRVL	134	1.1600	13.18
24	LVSSVRGGL	153	1.1600	13.18
25	LVCRAAGRV	133	1.1000	12.50
26	VVTCRPDSL	72	1.0600	12.05
27	VEAALGRYG	87	1.0000	11.36

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	LGRYGRLDG	91	5.8000	59.18
2	VRGGLGNAA	157	3.6000	36.73
3	LVSSVRGGL	153	3.5000	35.71
4	LVASGSNHV	101	3.4000	34.69
5	VVLVSSVRG	151	3.4000	34.69
6	VGALIYLLS	241	3.0000	30.61
7	LVNGAGIDD	61	2.7000	27.55
8	LRRFAEPED	231	2.7000	27.55
9	VMYLDGGYT	259	2.7000	27.55
10	MYLDGGYTA	260	2.7000	27.55
11	LVCRAAGRV	133	2.6000	26.53
12	FVGALIYLL	240	2.5500	26.02
13	IRVNALAPT	193	2.5000	25.51

14	LTLAGGNSA	48	2.2000	22.45
15	LGNAAGYSA	161	2.2000	22.45
16	ILITGATGS	24	2.1000	21.43
17	LIYLLSDAS	244	2.0000	20.41
18	VAPITEMAV	109	1.9000	19.39
19	VRGAWLVCR	128	1.9000	19.39
20	MLARIPLRR	225	1.9000	19.39
21	YGRLDGVLV	94	1.8000	18.37
22	FYTGQVMYL	254	1.8000	18.37
23	VVTCRPDSL	72	1.7000	17.35
24	IYLLSDASS	245	1.7000	17.35
25	LITGATGSL	25	1.5600	15.92
26	VASGSNHVA	102	1.5000	15.31
27	LGRVAARAL	33	1.4000	14.29

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	LGRYGRLDG	91	4.8000	48.98
2	FVGALIYLL	240	3.5500	36.22
3	YGRLDGVLV	94	2.8000	28.57
4	FYTGQVMYL	254	2.8000	28.57
5	VRGGLGNAA	157	2.6000	26.53
6	LVSSVRGGL	153	2.5000	25.51
7	LVASGSNHV	101	2.4000	24.49
8	VVLVSSVRG	151	2.4000	24.49
9	YSAYCPSKA	167	2.3000	23.47
10	VGALIYLLS	241	2.0000	20.41
11	FRSAVTEWM	203	1.7400	17.76
12	LVNGAGIDD	61	1.7000	17.35
13	LRRFAEPED	231	1.7000	17.35
14	VMYLDGGYT	259	1.7000	17.35
15	MYLDGGYTA	260	1.7000	17.35

16	LVCRAAGRV	133	1.6000	16.33
17	YLLSDASSF	246	1.6000	16.33
18	IRVNALAPT	193	1.5000	15.31
19	LTLAGGNSA	48	1.2000	12.24
20	LGNAAGYSA	161	1.2000	12.24
21	ILITGATGS	24	1.1000	11.22
22	LIYLLSDAS	244	1.0000	10.20
23	VAPITEMAV	109	0.9000	9.18
24	VRGAWLVCR	128	0.9000	9.18
25	MLARIPLRR	225	0.9000	9.18
26	VVTCRPDSL	72	0.7000	7.14
27	WMFTDDPKG	210	0.7000	7.14

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	LGRYGRLDG	91	5.8000	59.18
2	VRGGLGNAA	157	3.6000	36.73
3	LVSSVRGGL	153	3.5000	35.71
4	LVASGSNHV	101	3.4000	34.69
5	VVLVSSVRG	151	3.4000	34.69
6	VGALIYLLS	241	3.0000	30.61
7	LVNGAGIDD	61	2.7000	27.55
8	LRRFAEPED	231	2.7000	27.55
9	VMYLDGGYT	259	2.7000	27.55
10	MYLDGGYTA	260	2.7000	27.55
11	LVCRAAGRV	133	2.6000	26.53
12	FVGALIYLL	240	2.5500	26.02
13	IRVNALAPT	193	2.5000	25.51
14	LTLAGGNSA	48	2.2000	22.45
15	LGNAAGYSA	161	2.2000	22.45
16	ILITGATGS	24	2.1000	21.43
17	LIYLLSDAS	244	2.0000	20.41

18	VAPITEMAV	109	1.9000	19.39
19	VRGAWLVCR	128	1.9000	19.39
20	MLARIPLRR	225	1.9000	19.39
21	YGRLDGVLV	94	1.8000	18.37
22	FYTGQVMYL	254	1.8000	18.37
23	VVTCRPDSL	72	1.7000	17.35
24	IYLLSDASS	245	1.7000	17.35
25	LITGATGSL	25	1.5600	15.92
26	VASGSNHVA	102	1.5000	15.31
27	LGRVAARAL	33	1.4000	14.29

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	WLVCRAAGR	132	4.0000	40.82
2	LGRVAARAL	33	3.9000	39.80
3	FVGALIYLL	240	3.4000	34.69
4	ILITGATGS	24	2.8000	28.57
5	VVLVSSVRG	151	2.8000	28.57
6	VRGAWLVCR	128	2.6000	26.53
7	LARIPLRRF	226	2.5000	25.51
8	YLLSDASSF	246	2.5000	25.51
9	VNALAPTVF	195	2.1000	21.43
10	VCRAAGRVL	134	2.0000	20.41
11	MLARIPLRR	225	1.6000	16.33
12	VMYLDGGYT	259	1.6000	16.33
13	MFTDDPKGR	211	1.5000	15.31
14	LVSSVRGGL	153	1.4000	14.29
15	LARFSVQDK	14	1.2000	12.24
16	FRSAVTEWM	203	1.2000	12.24
17	VVTCRPDSL	72	1.1000	11.22
18	YGRLDGVLV	94	1.0000	10.20
19	VLVASGSNH	100	1.0000	10.20

20	LGNAAGYSA	161	0.9000	9.18
21	MVEAALGRY	86	0.8000	8.16
22	VSSVRGGLG	154	0.7000	7.14
23	VEAALGRYG	87	0.5000	5.10
24	VLLEQGQGG	141	0.5000	5.10
25	LVASGSNHV	101	0.4000	4.08
26	VLVSSVRGG	152	0.4000	4.08
27	VGALIYLLS	241	0.4000	4.08

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WLVCRAAGR	132	4.0000	40.82
2	LGRVAARAL	33	3.9000	39.80
3	FVGALIYLL	240	3.4000	34.69
4	ILITGATGS	24	2.8000	28.57
5	VVLVSSVRG	151	2.8000	28.57
6	VRGAWLVCR	128	2.6000	26.53
7	LARIPLRRF	226	2.5000	25.51
8	YLLSDASSF	246	2.5000	25.51
9	VNALAPTVF	195	2.1000	21.43
10	VCRAAGRVL	134	2.0000	20.41
11	MLARIPLRR	225	1.6000	16.33
12	VMYLDGGYT	259	1.6000	16.33
13	MFTDDPKGR	211	1.5000	15.31
14	LVSSVRGGL	153	1.4000	14.29
15	LARFSVQDK	14	1.2000	12.24
16	FRSAVTEWM	203	1.2000	12.24
17	VVTCRPDSL	72	1.1000	11.22
18	YGRLDGVLV	94	1.0000	10.20
19	VLVASGSNH	100	1.0000	10.20
20	LGNAAGYSA	161	0.9000	9.18
21	MVEAALGRY	86	0.8000	8.16

22	VSSVRGGLG	154	0.7000	7.14
23	VEAALGRYG	87	0.5000	5.10
24	VLLEQGQGG	141	0.5000	5.10
25	LVASGSNHV	101	0.4000	4.08
26	VLVSSVRGG	152	0.4000	4.08
27	VGALIYLLS	241	0.4000	4.08