

## MHC Class-II Binding Peptide Prediction Results

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### INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Apr 26 00:24:30 2010
Length of input sequence	248 amino acids
Number of nanomers from input sequence	240
Number of nanomers with <a href="#">obligatory P1 anchor residue</a>	71
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	24

ALLELE: DRB1_0101	Threshold for 3 % with score: 0.14	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	FRRITGSAL	221	3.4000	56.67
2	LRIAVAALR	180	1.7000	28.33
3	FVVMGGTTE	152	1.2900	21.50
4	FVAENPSRS	40	1.0000	16.67
5	LANVYAQTL	98	0.1500	2.50
6	IARAKSVVA	23	-0.2000	0
7	LAYAGGVLF	32	-0.2000	0
8	YRITYDGSI	138	-0.4000	0

9	VVMGGTTEP	153	-0.4100	0
10	LRRGGIQFA	73	-0.5000	0
11	VELCVAEVA	119	-0.5000	0
12	VASLEVAVL	204	-0.5000	0
13	YFISPEQAM	4	-0.5200	0
14	VAVLDANRP	209	-0.6000	0
15	VVALAYAGG	29	-0.8000	0
16	VALAYAGGV	30	-0.8000	0
17	LVDQESPQS	233	-0.9300	0
18	YEVELCVAE	117	-1.0000	0
19	IQFADTRGY	78	-1.0100	0
20	VGFAAAGKF	59	-1.2000	0
21	VAALRAGSA	184	-1.2000	0
22	VMGGTTEPI	154	-1.5000	0
23	YAQTLGTIF	102	-1.6100	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	FRRITGSAL	221	3.4000	56.67
2	LRIAVAALR	180	2.7000	45.00
3	FVVMGGTTE	152	1.2900	21.50
4	LANVYAQTL	98	1.1500	19.17
5	FVAENPSRS	40	1.0000	16.67
6	IARAKSVVA	23	0.8000	13.33
7	LAYAGGVLF	32	0.8000	13.33
8	VVMGGTTEP	153	0.5900	9.83
9	LRRGGIQFA	73	0.5000	8.33
10	VELCVAEVA	119	0.5000	8.33
11	VASLEVAVL	204	0.5000	8.33
12	VAVLDANRP	209	0.4000	6.67
13	VVALAYAGG	29	0.2000	3.33
14	VALAYAGGV	30	0.2000	3.33

15	LVDQESPQS	233	0.0700	1.17
16	IQFADTRGY	78	-0.0100	0
17	VGFAAAGKF	59	-0.2000	0
18	VAALRAGSA	184	-0.2000	0
19	VMGGTTEPI	154	-0.5000	0
20	IFTEQAKPY	109	-0.7000	0
21	LFVAENPSR	39	-0.7300	0
22	LGTIFTEQA	106	-0.8000	0
23	LRAGSADTS	187	-0.8000	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	VVMGGTTEP	153	4.4000	46.32
2	LRIAVAALR	180	4.2000	44.21
3	LRRGGIQFA	73	4.0000	42.11
4	LRAGSADTS	187	3.2000	33.68
5	VMGGTTEPI	154	3.0000	31.58
6	ITYDGSIAD	140	2.8000	29.47
7	LVDQESPQS	233	2.5000	26.32
8	VGFAAAGKF	59	2.3000	24.21
9	LLVDQESPQ	232	2.2700	23.89
10	IQFADTRGY	78	2.2000	23.16
11	YAYDRRDVT	86	2.0000	21.05
12	LCVAEVAHY	121	2.0000	21.05
13	LFVAENPSR	39	1.9000	20.00
14	IANALKESY	162	1.9000	20.00
15	VLDANRPRR	211	1.9000	20.00
16	VYAQTLGTI	101	1.8000	18.95
17	FVAENPSRS	40	1.7700	18.63
18	FRRITGSAL	221	1.7300	18.21
19	YFISPEQAM	4	1.6000	16.84
20	LGTIFTEQA	106	1.6000	16.84

21	LQALLVDQE	229	1.5000	15.79
22	VLVFAENPS	38	1.4100	14.84
23	VALAYAGGV	30	1.4000	14.74
24	VASLEVAVL	204	1.3600	14.32

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGGIQFA	73	3.0000	32.97
2	VVMGGTTEP	153	2.4000	26.37
3	FVAENPSRS	40	2.3700	26.04
4	YAYDRRDVT	86	2.3000	25.27
5	LLVDQESPQ	232	1.9700	21.65
6	LRAGSADTS	187	1.8000	19.78
7	FRRITGSAL	221	1.7700	19.45
8	LRIAVAALR	180	1.7000	18.68
9	YAGGVLFVA	34	1.4000	15.38
10	YFISPEQAM	4	1.1000	12.09
11	VMGGTTEPI	154	1.1000	12.09
12	LVDQESPQS	233	1.1000	12.09
13	ITYDGSAD	140	0.7000	7.69
14	LGTIFTEQA	106	0.6000	6.59
15	FPYFISPEQ	2	0.4000	4.40
16	FAAAGKFNE	61	0.1000	1.10
17	YRITYDGS	138	0.1000	1.10
18	FVVMGGTTE	152	0.1000	1.10
19	VLVFAENPS	38	0.0100	0.11
20	IQFADTRGY	78	-0.1000	0
21	VYAQTLGTI	101	-0.1000	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGGIQFA	73	4.1000	46.59
2	VVMGGTTEP	153	3.4000	38.64
3	LRAGSADTS	187	3.1000	35.23
4	LRIAVAALR	180	2.7000	30.68
5	LLVDQESPQ	232	2.7000	30.68
6	VMGGTTEPI	154	2.5000	28.41
7	LGTFTEQA	106	2.0000	22.73
8	VLFAENPS	38	1.7000	19.32
9	YAYDRRDVT	86	1.6000	18.18
10	LGVASLEVA	202	1.4000	15.91
11	ITYDGSIAD	140	1.3800	15.68
12	VELCVAEVA	119	1.3000	14.77
13	FVAENPSRS	40	1.1000	12.50
14	LYRITYDGS	137	1.1000	12.50
15	IANALKESY	162	1.0000	11.36
16	LKESYAENA	166	0.8000	9.09
17	LCVAEVAHY	121	0.7000	7.95
18	LVDQESPQS	233	0.7000	7.95
19	IARAKSVVA	23	0.6800	7.73
20	IQFADTRGY	78	0.6000	6.82
21	FRRITGSAL	221	0.5000	5.68
22	LARKGIARA	18	0.4000	4.55
23	VASLEVAVL	204	0.4000	4.55
24	LQALLVDQE	229	0.4000	4.55

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGGIQFA	73	4.1000	46.59
2	VVMGGTTEP	153	3.4000	38.64
3	LRAGSADTS	187	3.1000	35.23
4	LRIAVAALR	180	2.7000	30.68

5	LLVDQESPQ	232	2.7000	30.68
6	VMGGTTEPI	154	2.5000	28.41
7	LGTIFTEQA	106	2.0000	22.73
8	VLVFAENPS	38	1.7000	19.32
9	YAYDRRDVT	86	1.6000	18.18
10	LGVASLEVA	202	1.4000	15.91
11	ITYDGSAD	140	1.3800	15.68
12	VELCVAEVA	119	1.3000	14.77
13	FVAENPSRS	40	1.1000	12.50
14	LYRITYDGS	137	1.1000	12.50
15	IANALKESY	162	1.0000	11.36
16	LKESYAENA	166	0.8000	9.09
17	LCVAEVAHY	121	0.7000	7.95
18	LVDQESPQS	233	0.7000	7.95
19	IARAKSVVA	23	0.6800	7.73
20	IQFADTRGY	78	0.6000	6.82
21	FRRITGSAL	221	0.5000	5.68
22	LARKGIARA	18	0.4000	4.55
23	VASLEVAVL	204	0.4000	4.55
24	LQALLVDQE	229	0.4000	4.55

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGGIQFA	73	4.1000	46.59
2	VVMGGTTEP	153	3.4000	38.64
3	LRAGSADTS	187	3.1000	35.23
4	LRIAVAALR	180	2.7000	30.68
5	LLVDQESPQ	232	2.7000	30.68
6	VMGGTTEPI	154	2.5000	28.41
7	LGTIFTEQA	106	2.0000	22.73
8	VLVFAENPS	38	1.7000	19.32
9	YAYDRRDVT	86	1.6000	18.18

10	LGVASLEVA	202	1.4000	15.91
11	ITYDGSIAD	140	1.3800	15.68
12	VELCVAEVA	119	1.3000	14.77
13	FVAENPSRS	40	1.1000	12.50
14	LYRITYDGS	137	1.1000	12.50
15	IANALKESY	162	1.0000	11.36
16	LKESYAENA	166	0.8000	9.09
17	LCVAEVAHY	121	0.7000	7.95
18	LVDQESPQS	233	0.7000	7.95
19	IARAKSVVA	23	0.6800	7.73
20	IQFADTRGY	78	0.6000	6.82
21	FRRITGSAL	221	0.5000	5.68
22	LARKGIARA	18	0.4000	4.55
23	VASLEVAVL	204	0.4000	4.55
24	LQALLVDQE	229	0.4000	4.55

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVMGGTTEP	153	3.4000	35.79
2	LRIAVAALR	180	3.2000	33.68
3	LRRGGIQFA	73	3.0000	31.58
4	YAYDRRDVT	86	3.0000	31.58
5	FVAENPSRS	40	2.7700	29.16
6	FRRITGSAL	221	2.7300	28.74
7	YFISPEQAM	4	2.6000	27.37
8	LRAGSADTS	187	2.2000	23.16
9	VMGGTTEPI	154	2.0000	21.05
10	ITYDGSIAD	140	1.8000	18.95
11	FAAAGKFNE	61	1.5000	15.79
12	FVVMGGTTE	152	1.5000	15.79
13	LVDQESPQS	233	1.5000	15.79
14	YAGGVLFVA	34	1.4000	14.74

15	VGFAAAGKF	59	1.3000	13.68
16	LLVDQESPQ	232	1.2700	13.37
17	IQFADTRGY	78	1.2000	12.63
18	LCVAEVAHY	121	1.0000	10.53
19	YRITYDGS	138	1.0000	10.53
20	LFVAENPSR	39	0.9000	9.47
21	FDNLRRGGI	70	0.9000	9.47
22	IANALKESY	162	0.9000	9.47
23	VLDANRPRR	211	0.9000	9.47
24	VYAQTLGTI	101	0.8000	8.42

ALLELE: DRB1_0311	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGGIQFA	73	4.1000	46.59
2	VVMGGTTEP	153	3.4000	38.64
3	LRAGSADTS	187	3.1000	35.23
4	LRIAVAALR	180	2.7000	30.68
5	LLVDQESPQ	232	2.7000	30.68
6	VMGGTTEPI	154	2.5000	28.41
7	LGTIFTEQA	106	2.0000	22.73
8	VLVFAENPS	38	1.7000	19.32
9	YAYDRRDVT	86	1.6000	18.18
10	LGVASLEVA	202	1.4000	15.91
11	ITYDGS	140	1.3800	15.68
12	VELCVAEVA	119	1.3000	14.77
13	FVAENPSRS	40	1.1000	12.50
14	LYRITYDGS	137	1.1000	12.50
15	IANALKESY	162	1.0000	11.36
16	LKESYAENA	166	0.8000	9.09
17	LCVAEVAHY	121	0.7000	7.95
18	LVDQESPQS	233	0.7000	7.95
19	IARAKSVVA	23	0.6800	7.73



20	IQFADTRGY	78	0.6000	6.82
21	FRRITGSAL	221	0.5000	5.68
22	LARKGIARA	18	0.4000	4.55
23	VASLEVAVL	204	0.4000	4.55
24	LQALLVDQE	229	0.4000	4.55

ALLELE: DRB1_0401	Threshold for 3 % with score: 1.48	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVAENPSRS	40	4.1000	47.67
2	LGTIFTEQA	106	2.4000	27.91
3	YRITYDGS	138	1.7000	19.77
4	LRIAVAALR	180	1.7000	19.77
5	LVDQESPQS	233	1.6000	18.60
6	VVMGGTTEP	153	1.4000	16.28
7	FRRITGSAL	221	1.0000	11.63
8	IARAKSVVA	23	0.7800	9.07
9	IQFADTRGY	78	0.7000	8.14
10	ITYDGS	140	0.5800	6.74
11	VMGGTTEPI	154	0.5000	5.81
12	YEVELCVAE	117	0.4800	5.58
13	YFISPEQAM	4	0.3000	3.49
14	VELCVAEVA	119	0.3000	3.49
15	LYRITYDGS	137	0.3000	3.49
16	FPYFISPEQ	2	0.2000	2.33
17	LRRGGIQFA	73	0.2000	2.33
18	FVVMGGTTE	152	0.2000	2.33
19	LFVAENPSR	39	-0.1000	0
20	LKESYAENA	166	-0.1000	0
21	VASLEVAVL	204	-0.1000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	4.6000	47.92
2	VVMGGTTEP	153	3.5000	36.46
3	LRRGGIQFA	73	3.2000	33.33
4	LRIAVAALR	180	2.7000	28.13
5	IARAKSVVA	23	1.9000	19.79
6	LGTIFTEQA	106	1.2800	13.33
7	LVDQESPQS	233	1.1000	11.46
8	VMGGTTEPI	154	1.0000	10.42
9	LARKGIARA	18	0.7000	7.29
10	LFVAENPSR	39	0.6000	6.25
11	LCVAEVAHY	121	0.4000	4.17
12	FNEFDNLRR	67	0.2000	2.08
13	FPYFISPEQ	2	0.1000	1.04
14	VAENPSRSL	41	0.1000	1.04
15	IAVAALRAG	182	0.1000	1.04
16	LRAGSADTS	187	0.1000	1.04
17	LANVYAQTL	98	-0.1000	0
18	VELCVAEVA	119	-0.1000	0
19	MRERSELAR	12	-0.4000	0
20	LYDRVGFAA	55	-0.4000	0
21	VASLEVAVL	204	-0.5000	0

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LGTIFTEQA	106	2.8000	31.82
2	LRIAVAALR	180	2.7000	30.68
3	VVMGGTTEP	153	2.1000	23.86
4	IQFADTRGY	78	2.0000	22.73

5	IARAKSVVA	23	1.6000	18.18
6	LVDQESPQS	233	1.5000	17.05
7	VLVFAENPS	38	1.3000	14.77
8	FVAENPSRS	40	1.2000	13.64
9	VASLEVAVL	204	1.1000	12.50
10	FRRITGSAL	221	1.0000	11.36
11	VAVLDANRP	209	0.9000	10.23
12	FPYFISPEQ	2	0.8000	9.09
13	LYRITYDGS	137	0.7000	7.95
14	VVALAYAGG	29	0.6000	6.82
15	LFVAENPSR	39	0.6000	6.82
16	FVVMGGTTE	152	0.6000	6.82
17	VELCVAEVA	119	0.4000	4.55
18	LCVAEVAHY	121	0.4000	4.55
19	FNEFDNLRR	67	0.2000	2.27
20	LRRGGIQFA	73	0.2000	2.27
21	LQALLVDQE	229	0.2000	2.27
22	LANVYAQTL	98	-0.2000	0
23	VMGGTTEPI	154	-0.2000	0

ALLELE: DRB1_0405		Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4	
Rank	Sequence	At Position	Score	% of Highest Score
1	FVVMGGTTE	152	4.6000	48.94
2	FRRITGSAL	221	3.0000	31.91
3	FPYFISPEQ	2	2.6000	27.66
4	FVAENPSRS	40	2.2000	23.40
5	LQALLVDQE	229	2.2000	23.40
6	IQFADTRGY	78	2.1000	22.34
7	LGTIFTEQA	106	1.8000	19.15
8	LRIAVAALR	180	1.7000	18.09
9	VVMGGTTEP	153	1.5000	15.96
10	FNEFDNLRR	67	1.2000	12.77

11	VASLEVAVL	204	1.1000	11.70
12	VVALAYAGG	29	0.9000	9.57
13	ITYDGSIAD	140	0.7800	8.30
14	YEVELCVAE	117	0.7000	7.45
15	IARAKSVVA	23	0.6000	6.38
16	LCVAEVAHY	121	0.5000	5.32
17	LVDQESPQS	233	0.5000	5.32
18	YRITYDGSI	138	0.4000	4.26
19	YAENASLTD	170	0.4000	4.26
20	VLVFAENPS	38	0.3000	3.19
21	VAVLDANRP	209	0.3000	3.19
22	LQKISELYD	49	0.2000	2.13
23	ISPEQAMRE	6	-0.1000	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	FVAENPSRS	40	2.2000	25.00
2	FRRITGSAL	221	2.0000	22.73
3	FPYFISPEQ	2	1.8000	20.45
4	LGTIFTEQA	106	1.8000	20.45
5	LRIAVAALR	180	1.7000	19.32
6	FVVMGGTTE	152	1.6000	18.18
7	FNEFDNLRR	67	1.2000	13.64
8	VVMGGTTEP	153	1.1000	12.50
9	IQFADTRGY	78	1.0000	11.36
10	IARAKSVVA	23	0.6000	6.82
11	LVDQESPQS	233	0.5000	5.68
12	VLVFAENPS	38	0.3000	3.41
13	YRITYDGSI	138	0.2000	2.27
14	VASLEVAVL	204	0.1000	1.14
15	VAVLDANRP	209	-0.1000	0
16	LYRITYDGS	137	-0.3000	0

17	VVALAYAGG	29	-0.4000	0
18	LFVAENPSR	39	-0.4000	0
19	VELCVAEVA	119	-0.6000	0
20	LCVAEVAHY	121	-0.6000	0
21	LRRGGIQFA	73	-0.8000	0
22	LQALLVDQE	229	-0.8000	0
23	YDRVGFAAA	56	-1.2000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVVMGGTTE	152	3.6000	38.30
2	LQALLVDQE	229	3.2000	34.04
3	IQFADTRGY	78	3.1000	32.98
4	LGTIFTEQA	106	2.8000	29.79
5	LRIAVAALR	180	2.7000	28.72
6	VVMGGTTEP	153	2.5000	26.60
7	VASLEVAVL	204	2.1000	22.34
8	FRRITGSAL	221	2.0000	21.28
9	VVALAYAGG	29	1.9000	20.21
10	ITYDGSIAD	140	1.7800	18.94
11	FPYFISPEQ	2	1.6000	17.02
12	IARAKSVVA	23	1.6000	17.02
13	LCVAEVAHY	121	1.5000	15.96
14	LVDQESPQS	233	1.5000	15.96
15	VLVFAENPS	38	1.3000	13.83
16	VAVLDANRP	209	1.3000	13.83
17	FVAENPSRS	40	1.2000	12.77
18	LQKISELYD	49	1.2000	12.77
19	ISPEQAMRE	6	0.9000	9.57
20	LANVYAQTL	98	0.8000	8.51
21	LYRITYDGS	137	0.7000	7.45
22	LFVAENPSR	39	0.6000	6.38

23	VELCVAEVA	119	0.4000	4.26
24	FNEFDNLRR	67	0.2000	2.13

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVAENPSRS	40	4.5000	50.00
2	LRIAVAALR	180	3.2000	35.56
3	YRITYDGS	138	2.6000	28.89
4	LGTFTEQA	106	2.4000	26.67
5	VVMGGTTEP	153	2.4000	26.67
6	IQFADTRGY	78	2.0000	22.22
7	LVDQESPQS	233	2.0000	22.22
8	FRRITGSAL	221	1.9600	21.78
9	YEVELCVAE	117	1.8800	20.89
10	YFISPEQAM	4	1.8000	20.00
11	ITYDGS	140	1.6800	18.67
12	FVVMGGTTE	152	1.6000	17.78
13	LFVAENPSR	39	1.4000	15.56
14	VMGGTTEPI	154	1.4000	15.56
15	IFTEQAKPY	109	1.3000	14.44
16	LQALLVDQE	229	1.3000	14.44
17	FNEFDNLRR	67	1.2000	13.33
18	ISPEQAMRE	6	1.0000	11.11
19	VASLEVAVL	204	0.8600	9.56
20	VVALAYAGG	29	0.8000	8.89
21	YAENASLTD	170	0.8000	8.89
22	IARAKSVVA	23	0.7800	8.67
23	LCVAEVAHY	121	0.7000	7.78
24	LYRITYDGS	137	0.7000	7.78

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LGTFTEQA	106	2.8000	31.82
2	LRIAVAALR	180	2.7000	30.68
3	VVMGGTTEP	153	2.1000	23.86
4	IQFADTRGY	78	2.0000	22.73
5	IARAKSVVA	23	1.6000	18.18
6	LVDQESPQS	233	1.5000	17.05
7	VLVFAENPS	38	1.3000	14.77
8	FVAENPSRS	40	1.2000	13.64
9	VASLEVAVL	204	1.1000	12.50
10	FRRITGSAL	221	1.0000	11.36
11	VAVLDANRP	209	0.9000	10.23
12	FPYFISPEQ	2	0.8000	9.09
13	LYRITYDGS	137	0.7000	7.95
14	VVALAYAGG	29	0.6000	6.82
15	LFVAENPSR	39	0.6000	6.82
16	FVVMGGTTE	152	0.6000	6.82
17	VELCVAEVA	119	0.4000	4.55
18	LCVAEVAHY	121	0.4000	4.55
19	FNEFDNLRR	67	0.2000	2.27
20	LRRGGIQFA	73	0.2000	2.27
21	LQALLVDQE	229	0.2000	2.27
22	LANVYAQTL	98	-0.2000	0
23	VMGGTTEPI	154	-0.2000	0

ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVAENPSRS	40	4.1000	47.67
2	LGTFTEQA	106	2.4000	27.91

3	YRITYDGSI	138	1.7000	19.77
4	LRIAVAALR	180	1.7000	19.77
5	LVDQESPQS	233	1.6000	18.60
6	VVMGGTTEP	153	1.4000	16.28
7	FRRITGSAL	221	1.0000	11.63
8	IARAKSVVA	23	0.7800	9.07
9	IQFADTRGY	78	0.7000	8.14
10	ITYDGSIAD	140	0.5800	6.74
11	VMGGTTEPI	154	0.5000	5.81
12	YEVELCVAE	117	0.4800	5.58
13	YFISPEQAM	4	0.3000	3.49
14	VELCVAEVA	119	0.3000	3.49
15	LYRITYDGS	137	0.3000	3.49
16	FPYFISPEQ	2	0.2000	2.33
17	LRRGGIQFA	73	0.2000	2.33
18	FVVMGGTTE	152	0.2000	2.33
19	LFVAENPSR	39	-0.1000	0
20	LKESYAENA	166	-0.1000	0
21	VASLEVAVL	204	-0.1000	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	FRRITGSAL	221	7.2000	62.07
2	YRITYDGSI	138	6.0000	51.72
3	LANVYAQTL	98	4.9000	42.24
4	YFISPEQAM	4	4.4000	37.93
5	ITGSALQAL	224	4.3000	37.07
6	YAQTLGTIF	102	3.8000	32.76
7	VMGGTTEPI	154	3.4200	29.48
8	LAYAGGVLF	32	2.9000	25.00
9	YGETKRPEL	129	2.8000	24.14
10	IQFADTRGY	78	2.7200	23.45



11	VGFAAAGKF	59	2.4000	20.69
12	FADTRGYAY	80	2.3000	19.83
13	FVVMGGTTE	152	2.2000	18.97
14	VALAYAGGV	30	2.0000	17.24
15	IARAKSVVA	23	1.9000	16.38
16	LRIAVAALR	180	1.9000	16.38
17	VASLEVAVL	204	1.9000	16.38
18	VVMGGTTEP	153	1.6200	13.97
19	LGTIFTEQA	106	1.4200	12.24
20	VAENPSRSL	41	1.4000	12.07
21	LRRGGIQFA	73	1.4000	12.07
22	LKESYAENA	166	1.3000	11.21
23	VELCVAEVA	119	1.0000	8.62
24	LTDALRIAV	176	1.0000	8.62

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	FRRITGSAL	221	7.2000	62.07
2	YRITYDGSI	138	6.0000	51.72
3	LANVYAQTL	98	4.9000	42.24
4	YFISPEQAM	4	4.4000	37.93
5	ITGSALQAL	224	4.3000	37.07
6	YAQTLGTIF	102	3.8000	32.76
7	VMGGTTEPI	154	3.4200	29.48
8	LAYAGGVLF	32	2.9000	25.00
9	YGETKRPEL	129	2.8000	24.14
10	IQFADTRGY	78	2.7200	23.45
11	VGFAAAGKF	59	2.4000	20.69
12	FADTRGYAY	80	2.3000	19.83
13	FVVMGGTTE	152	2.2000	18.97
14	VALAYAGGV	30	2.0000	17.24
15	IARAKSVVA	23	1.9000	16.38

16	LRIAVAALR	180	1.9000	16.38
17	VASLEVAVL	204	1.9000	16.38
18	VVMGGTTEP	153	1.6200	13.97
19	LGTIFTEQA	106	1.4200	12.24
20	VAENPSRSL	41	1.4000	12.07
21	LRRGGIQFA	73	1.4000	12.07
22	LKESYAENA	166	1.3000	11.21
23	VELCVAEVA	119	1.0000	8.62
24	LTDALRIAV	176	1.0000	8.62

Rank	Sequence	At Position	Score	% of Highest Score
ALLELE: DRB1_0801      Threshold for 3 % with score: 1.8      Highest Score achievable by any peptide: 8.6				
1	LARKGIARA	18	2.7000	31.40
2	FVVMGGTTE	152	2.2000	25.58
3	FAAAGKFNE	61	1.7000	19.77
4	LRIAVAALR	180	1.7000	19.77
5	IQFADTRGY	78	1.3000	15.12
6	VTGRQLANV	93	1.3000	15.12
7	FRRITGSAL	221	1.2000	13.95
8	VASLEVAVL	204	1.1000	12.79
9	FVAENPSRS	40	1.0000	11.63
10	LQALLVDQE	229	1.0000	11.63
11	FPYFISPEQ	2	0.8000	9.30
12	LCVAEVAHY	121	0.8000	9.30
13	VVALAYAGG	29	0.7000	8.14
14	LRRGGIQFA	73	0.4000	4.65
15	FDNLRRGGI	70	0.3000	3.49
16	LQKISELYD	49	-0.2000	0
17	YEVELCVAE	117	-0.2000	0
18	VGFAAAGKF	59	-0.3000	0
19	YRITYDGSI	138	-0.3000	0
20	MRERSELAR	12	-0.4000	0

21	YDRRDVTGR	88	-0.5000	0
22	YFISPEQAM	4	-0.6000	0
23	YAENASLTD	170	-0.6000	0

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LARKGIARA	18	2.7000	33.75
2	LRIAVAALR	180	1.7000	21.25
3	FVAENPSRS	40	1.0000	12.50
4	VTGRQLANV	93	1.0000	12.50
5	LRRGGIQFA	73	0.4000	5.00
6	IQFADTRGY	78	0.2000	2.50
7	FRRITGSAL	221	0.2000	2.50
8	FDNLRRGGI	70	0.1000	1.25
9	VASLEVAVL	204	0.1000	1.25
10	LCVAEVAHY	121	-0.3000	0
11	MRERSELAR	12	-0.4000	0
12	YDRRDVTGR	88	-0.5000	0
13	YRITYDGSI	138	-0.5000	0
14	VVALAYAGG	29	-0.6000	0
15	LYDRVGFAA	55	-0.7000	0
16	FVVMGGTTE	152	-0.8000	0
17	VAALRAGSA	184	-0.8000	0
18	VLVFAENPS	38	-0.9000	0
19	FISPEQAMR	5	-1.0000	0
20	VALAYAGGV	30	-1.2000	0
21	VGFAAAGKF	59	-1.2000	0
22	FAAAGKFNE	61	-1.3000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LARKGIARA	18	3.7000	46.25
2	LRIAVAALR	180	2.7000	33.75
3	VTGRQLANV	93	2.0000	25.00
4	LRRGGIQFA	73	1.4000	17.50
5	IQFADTRGY	78	1.2000	15.00
6	VASLEVAVL	204	1.1000	13.75
7	LCVAEVAHY	121	0.7000	8.75
8	MRERSELAR	12	0.6000	7.50
9	VVALAYAGG	29	0.4000	5.00
10	LYDRVGFAA	55	0.3000	3.75
11	VAALRAGSA	184	0.2000	2.50
12	VLVFAENPS	38	0.1000	1.25
13	VALAYAGGV	30	-0.2000	0
14	VGFAAAGKF	59	-0.2000	0
15	VVMGGTTEP	153	-0.4000	0
16	IARAKSVVA	23	-0.5000	0
17	LRAGSADTS	187	-0.5000	0
18	VYAQTLGTI	101	-0.7000	0
19	LGTIFTEQA	106	-0.8000	0
20	FRRITGSAL	221	-0.8000	0
21	LVDQESPQS	233	-0.8000	0
22	FDNLRRGGI	70	-0.9000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LARKGIARA	18	3.7000	43.02
2	LRIAVAALR	180	2.7000	31.40
3	IQFADTRGY	78	2.3000	26.74
4	VTGRQLANV	93	2.3000	26.74
5	VASLEVAVL	204	2.1000	24.42
6	LQALLVDQE	229	2.0000	23.26

7	LCVAEVAHY	121	1.8000	20.93
8	VVALAYAGG	29	1.7000	19.77
9	LRRGGIQFA	73	1.4000	16.28
10	FVVMGGTTE	152	1.2000	13.95
11	LQKISELYD	49	0.8000	9.30
12	VGFAAAGKF	59	0.7000	8.14
13	FAAAGKFNE	61	0.7000	8.14
14	MRERSELAR	12	0.6000	6.98
15	IAVAALRAG	182	0.4000	4.65
16	LYDRVGFAA	55	0.3000	3.49
17	VAALRAGSA	184	0.2000	2.33
18	FRRITGSAL	221	0.2000	2.33
19	VALAYAGGV	30	0.1000	1.16
20	VLFVAENPS	38	0.1000	1.16

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVAENPSRS	40	2.8000	32.18
2	LARKGIARA	18	2.7000	31.03
3	YDRRDVTGR	88	2.3000	26.44
4	FVVMGGTTE	152	2.0000	22.99
5	FRRITGSAL	221	2.0000	22.99
6	LRIAVAALR	180	1.7000	19.54
7	LRRGGIQFA	73	1.4000	16.09
8	VVMGGTTEP	153	1.4000	16.09
9	VLFVAENPS	38	1.1000	12.64
10	VTGRQLANV	93	1.0000	11.49
11	FPYFISPEQ	2	0.2000	2.30
12	MRERSELAR	12	0.2000	2.30
13	LYDRVGFAA	55	0.1500	1.72
14	VASLEVAVL	204	0.1000	1.15
15	IQFADTRGY	78	-0.1000	0

16	LGTFTEQA	106	-0.1000	0
17	LCVAEVAHY	121	-0.3000	0
18	LRAGSADTS	187	-0.3000	0
19	VAVLDANRP	209	-0.4000	0
20	FAAAGKFNE	61	-0.4500	0
21	IARAKSVVA	23	-0.5000	0
22	LGVASLEVA	202	-0.5000	0
23	VVALAYAGG	29	-0.6000	0

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVVMGGTTE	152	3.3000	32.67
2	LARKGIARA	18	2.7000	26.73
3	FAAAGKFNE	61	2.2000	21.78
4	FPYFISPEQ	2	1.9500	19.31
5	LRIAVAALR	180	1.7000	16.83
6	LQKISELYD	49	1.6000	15.84
7	IQFADTRGY	78	1.5000	14.85
8	MRERSELAR	12	1.4000	13.86
9	VTGRQLANV	93	1.3000	12.87
10	YAENASLTD	170	1.2000	11.88
11	FRRITGSAL	221	1.2000	11.88
12	VASLEVAVL	204	1.1000	10.89
13	FVAENPSRS	40	1.0000	9.90
14	LCVAEVAHY	121	0.8000	7.92
15	VVALAYAGG	29	0.7000	6.93
16	LQALLVDQE	229	0.7000	6.93
17	ISPEQAMRE	6	0.6000	5.94
18	YDRRDVTGR	88	0.6000	5.94
19	LRRGGIQFA	73	0.5000	4.95
20	ITYDGSIAD	140	0.5000	4.95
21	FDNLRRGGI	70	0.4000	3.96

22	FTEQAKPYE	110	0.3500	3.47
23	YEVELCVAE	117	0.3000	2.97
24	VVMGGTTEP	153	0.1000	0.99

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	1.7000	20.48
2	FPYFISPEQ	2	1.0500	12.65
3	FRRITGSAL	221	0.8000	9.64
4	FDNLRRGGI	70	0.6000	7.23
5	VASLEVAVL	204	0.5000	6.02
6	IQFADTRGY	78	0.4000	4.82
7	FVAENPSRS	40	0.3000	3.61
8	LVDQESPQS	233	-0.0500	0
9	LARKGIARA	18	-0.1000	0
10	FNEFDNLRR	67	-0.1000	0
11	LGTIFTEQA	106	-0.1000	0
12	FVVMGGTTE	152	-0.1000	0
13	VVALAYAGG	29	-0.2000	0
14	LRRGGIQFA	73	-0.2000	0
15	LCVAEVAHY	121	-0.3000	0
16	VAALRAGSA	184	-0.3000	0
17	VLVVAENPS	38	-0.5000	0
18	LQKISELYD	49	-0.5000	0
19	FAAAGKFNE	61	-0.8000	0
20	IARAKSVVA	23	-1.0000	0
21	VYAQTLGTI	101	-1.0000	0
22	VVMGGTTEP	153	-1.0000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	3.0000	35.71
2	LRIAVAALR	180	2.7000	32.14
3	LARKGIARA	18	2.2000	26.19
4	LRRGGIQFA	73	1.7000	20.24
5	LVDQESPQS	233	1.5000	17.86
6	IAVAALRAG	182	0.9000	10.71
7	VASLEVAVL	204	0.8000	9.52
8	LCVAEVAHY	121	0.7000	8.33
9	VVMGGTTEP	153	0.6000	7.14
10	IARAKSVVA	23	0.5000	5.95
11	LDANRPRRA	212	0.5000	5.95
12	VLVFAENPS	38	0.3000	3.57
13	FVAENPSRS	40	0.3000	3.57
14	LGVASLEVA	202	0.2000	2.38
15	VVALAYAGG	29	0.1000	1.19
16	VELCVAEVA	119	0.1000	1.19
17	VTGRQLANV	93	-0.1000	0
18	VYAQTLGTI	101	-0.1000	0
19	LRAGSADTS	187	-0.1000	0
20	IANALKESY	162	-0.2000	0
21	LYDRVGFAA	55	-0.3000	0
22	LGTIFTEQA	106	-0.3000	0

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	2.7000	32.53
2	VASLEVAVL	204	1.5000	18.07
3	IQFADTRGY	78	1.4000	16.87
4	LVDQESPQS	233	0.9500	11.45
5	LARKGIARA	18	0.9000	10.84
6	LGTIFTEQA	106	0.9000	10.84



7	VVALAYAGG	29	0.8000	9.64
8	LRRGGIQFA	73	0.8000	9.64
9	LCVAEVAHY	121	0.7000	8.43
10	VAALRAGSA	184	0.7000	8.43
11	VLVFAENPS	38	0.5000	6.02
12	LQKISELYD	49	0.5000	6.02
13	FPYFISPEQ	2	0.0500	0.60
14	VALAYAGGV	30	-0.1000	0
15	VGFAAAGKF	59	-0.1000	0
16	LGVASLEVA	202	-0.1000	0
17	VELCVAEVA	119	-0.2000	0
18	LTDALRIAV	176	-0.2000	0
19	FRRITGSAL	221	-0.2000	0
20	LFVAENPSR	39	-0.3500	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	2.7000	32.53
2	VASLEVAVL	204	1.5000	18.07
3	IQFADTRGY	78	1.4000	16.87
4	LVDQESPQS	233	0.9500	11.45
5	LARKGIARA	18	0.9000	10.84
6	LGTIFTEQA	106	0.9000	10.84
7	VVALAYAGG	29	0.8000	9.64
8	LRRGGIQFA	73	0.8000	9.64
9	LCVAEVAHY	121	0.7000	8.43
10	VAALRAGSA	184	0.7000	8.43
11	VLVFAENPS	38	0.5000	6.02
12	LQKISELYD	49	0.5000	6.02
13	FPYFISPEQ	2	0.0500	0.60
14	VALAYAGGV	30	-0.1000	0
15	VGFAAAGKF	59	-0.1000	0

16	LGVASLEVA	202	-0.1000	0
17	VELCVAEVA	119	-0.2000	0
18	LTDALRIAV	176	-0.2000	0
19	FRRITGSAL	221	-0.2000	0
20	LFVAENPSR	39	-0.3500	0

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRRGGIQFA	73	4.0000	43.96
2	VVMGGTTEP	153	3.4000	37.36
3	LLVDQESPQ	232	2.9700	32.64
4	LRAGSADTS	187	2.8000	30.77
5	LRIAVAALR	180	2.7000	29.67
6	VMGGTTEPI	154	2.1000	23.08
7	LVDQESPQS	233	2.1000	23.08
8	ITYDGSIAD	140	1.7000	18.68
9	LGTIFTEQA	106	1.6000	17.58
10	FVAENPSRS	40	1.3700	15.05
11	YAYDRRDVT	86	1.3000	14.29
12	VLVFAENPS	38	1.0100	11.10
13	LGVASLEVA	202	1.0000	10.99
14	IQFADTRGY	78	0.9000	9.89
15	VYAQTLGTI	101	0.9000	9.89
16	VELCVAEVA	119	0.9000	9.89
17	IARAKSVVA	23	0.8000	8.79
18	LYRITYDGS	137	0.8000	8.79
19	FRRITGSAL	221	0.7700	8.46
20	LCVAEVAHY	121	0.7000	7.69
21	IANALKESY	162	0.6000	6.59
22	LARKGIARA	18	0.4000	4.40
23	VALAYAGGV	30	0.4000	4.40
24	YAGGVLFVA	34	0.4000	4.40

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	2.0000	23.81
2	LRIAVAALR	180	1.7000	20.24
3	FVAENPSRS	40	1.3000	15.48
4	LARKGIARA	18	1.2000	14.29
5	FPYFISPEQ	2	1.0000	11.90
6	LRRGGIQFA	73	0.7000	8.33
7	LVDQESPQS	233	0.5000	5.95
8	FAAAGKFNE	61	0.2000	2.38
9	FVVMGGTTE	152	0.1000	1.19
10	IAVAALRAG	182	-0.1000	0
11	VASLEVAVL	204	-0.2000	0
12	LCVAEVAHY	121	-0.3000	0
13	FRRITGSAL	221	-0.3000	0
14	VVMGGTTEP	153	-0.4000	0
15	YFISPEQAM	4	-0.5000	0
16	IARAKSVVA	23	-0.5000	0
17	YAGGVLFVA	34	-0.5000	0
18	LDANRPRRA	212	-0.5000	0
19	VLVFAENPS	38	-0.7000	0
20	FNEFDNLRR	67	-0.8000	0
21	LGVASLEVA	202	-0.8000	0
22	VVALAYAGG	29	-0.9000	0
23	VELCVAEVA	119	-0.9000	0

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	3.3000	37.50

2	LRIAVAALR	180	3.2000	36.36
3	FVAENPSRS	40	1.7000	19.32
4	FAAAGKFNE	61	1.6000	18.18
5	FVVMGGTTE	152	1.5000	17.05
6	IAVAALRAG	182	1.3000	14.77
7	LARKGIARA	18	1.2000	13.64
8	YFISPEQAM	4	1.0000	11.36
9	LCVAEVAHY	121	1.0000	11.36
10	LVDQESPQS	233	0.9000	10.23
11	VASLEVAVL	204	0.7600	8.64
12	FNEFDNLRR	67	0.7000	7.95
13	LRRGGIQFA	73	0.7000	7.95
14	FRRITGSAL	221	0.6600	7.50
15	VVMGGTTEP	153	0.6000	6.82
16	VVALAYAGG	29	0.5000	5.68
17	YDRRDVTGR	88	0.4000	4.55
18	FPYFISPEQ	2	0.3000	3.41
19	IANALKESY	162	0.1000	1.14
20	LAYAGGVLF	32	-0.1000	0
21	VTGRQLANV	93	-0.1000	0

ALLELE: DRB1_1121	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	3.0000	35.71
2	LRIAVAALR	180	2.7000	32.14
3	LARKGIARA	18	2.2000	26.19
4	LRRGGIQFA	73	1.7000	20.24
5	LVDQESPQS	233	1.5000	17.86
6	IAVAALRAG	182	0.9000	10.71
7	VASLEVAVL	204	0.8000	9.52
8	LCVAEVAHY	121	0.7000	8.33
9	VVMGGTTEP	153	0.6000	7.14

10	IARAKSVVA	23	0.5000	5.95
11	LDANRPRRA	212	0.5000	5.95
12	VLVFAENPS	38	0.3000	3.57
13	FVAENPSRS	40	0.3000	3.57
14	LGVASLEVA	202	0.2000	2.38
15	VVALAYAGG	29	0.1000	1.19
16	VELCVAEVA	119	0.1000	1.19
17	VTGRQLANV	93	-0.1000	0
18	VYAQTLGTI	101	-0.1000	0
19	LRAGSADTS	187	-0.1000	0
20	IANALKESY	162	-0.2000	0
21	LYDRVGFAA	55	-0.3000	0
22	LGTIFTEQA	106	-0.3000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	3.2000	36.78
2	FRRITGSAL	221	1.7600	20.23
3	IQFADTRGY	78	1.7000	19.54
4	FDNLRRGGI	70	1.5000	17.24
5	VASLEVAVL	204	1.4600	16.78
6	FNEFDNLRR	67	1.4000	16.09
7	FVVMGGTTE	152	1.3000	14.94
8	VVALAYAGG	29	1.2000	13.79
9	LCVAEVAHY	121	1.0000	11.49
10	YRITYDGSI	138	0.9000	10.34
11	VGFAAAGKF	59	0.8000	9.20
12	FVAENPSRS	40	0.7000	8.05
13	LQKISELYD	49	0.6000	6.90
14	FAAAGKFNE	61	0.6000	6.90
15	FPYFISPEQ	2	0.3500	4.02
16	LVDQESPQS	233	0.3500	4.02

17	YFISPEQAM	4	0.2000	2.30
18	LFVAENPSR	39	0.1500	1.72
19	VLDANRPRR	211	0.1500	1.72
20	MRERSELAR	12	-0.1000	0
21	LARKGIARA	18	-0.1000	0
22	VALAYAGGV	30	-0.1000	0

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	4.3000	48.86
2	LRIAVAALR	180	4.2000	47.73
3	IAVAALRAG	182	2.3000	26.14
4	LARKGIARA	18	2.2000	25.00
5	LCVAEVAHY	121	2.0000	22.73
6	LVDQESPQS	233	1.9000	21.59
7	VASLEVAVL	204	1.7600	20.00
8	LRRGGIQFA	73	1.7000	19.32
9	VVMGGTTEP	153	1.6000	18.18
10	VVALAYAGG	29	1.5000	17.05
11	IANALKESY	162	1.1000	12.50
12	LQALLVDQE	229	1.0000	11.36
13	LAYAGGVLF	32	0.9000	10.23
14	VTGRQLANV	93	0.9000	10.23
15	VYAQTLGTI	101	0.8000	9.09
16	MRERSELAR	12	0.7000	7.95
17	VLVFAENPS	38	0.7000	7.95
18	LFVAENPSR	39	0.7000	7.95
19	FVAENPSRS	40	0.7000	7.95
20	VGFAAAGKF	59	0.7000	7.95
21	VAVLDANRP	209	0.7000	7.95
22	VLDANRPRR	211	0.7000	7.95
23	FAAAGKFNE	61	0.6000	6.82

24	IARAKSVVA	23	0.5000	5.68
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ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	3.3000	37.50
2	LRIAVAALR	180	3.2000	36.36
3	FVAENPSRS	40	1.7000	19.32
4	FAAAGKFNE	61	1.6000	18.18
5	FVVMGGTTE	152	1.5000	17.05
6	IAVAALRAG	182	1.3000	14.77
7	LARKGIARA	18	1.2000	13.64
8	YFISPEQAM	4	1.0000	11.36
9	LCVAEVAHY	121	1.0000	11.36
10	LVDQESPQS	233	0.9000	10.23
11	VASLEVAVL	204	0.7600	8.64
12	FNEFDNLRR	67	0.7000	7.95
13	LRRGGIQFA	73	0.7000	7.95
14	FRRITGSAL	221	0.6600	7.50
15	VVMGGTTEP	153	0.6000	6.82
16	VVALAYAGG	29	0.5000	5.68
17	YDRRDVTGR	88	0.4000	4.55
18	FPYFISPEQ	2	0.3000	3.41
19	IANALKESY	162	0.1000	1.14
20	LAYAGGVLF	32	-0.1000	0
21	VTGRQLANV	93	-0.1000	0

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	4.1000	45.56

2	LRIAVAALR	180	2.7000	30.00
3	LQALLVDQE	229	2.6000	28.89
4	LARKGIARA	18	2.2000	24.44
5	FAAAGKFNE	61	2.2000	24.44
6	IAVAALRAG	182	2.2000	24.44
7	FVVMGGTTE	152	2.1000	23.33
8	LCVAEVAHY	121	1.8000	20.00
9	VASLEVAVL	204	1.8000	20.00
10	LRRGGIQFA	73	1.7000	18.89
11	LVDQESPQS	233	1.5000	16.67
12	VVALAYAGG	29	1.4000	15.56
13	VVMGGTTEP	153	1.0000	11.11
14	IANALKESY	162	0.9000	10.00
15	FPYFISPEQ	2	0.8000	8.89
16	LQKISELYD	49	0.6000	6.67
17	IARAKSVVA	23	0.5000	5.56
18	FTEQAKPYE	110	0.5000	5.56
19	LDANRPRRA	212	0.5000	5.56
20	VLVFAENPS	38	0.3000	3.33
21	FVAENPSRS	40	0.3000	3.33
22	ISPEQAMRE	6	0.2000	2.22
23	VTGRQLANV	93	0.2000	2.22
24	LGVASLEVA	202	0.2000	2.22

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	3.2000	36.78
2	FRRITGSAL	221	1.7600	20.23
3	IQFADTRGY	78	1.7000	19.54
4	FDNLRRGGI	70	1.5000	17.24
5	VASLEVAVL	204	1.4600	16.78
6	FNEFDNLRR	67	1.4000	16.09



7	FVVMGGTTE	152	1.3000	14.94
8	VVALAYAGG	29	1.2000	13.79
9	LCVAEVAHY	121	1.0000	11.49
10	YRITYDGS	138	0.9000	10.34
11	VGFAAAGKF	59	0.8000	9.20
12	FVAENPSRS	40	0.7000	8.05
13	LQKISELYD	49	0.6000	6.90
14	FAAAGKFNE	61	0.6000	6.90
15	FPYFISPEQ	2	0.3500	4.02
16	LVDQESPQS	233	0.3500	4.02
17	YFISPEQAM	4	0.2000	2.30
18	LFVAENPSR	39	0.1500	1.72
19	VLDANRPRR	211	0.1500	1.72
20	MRERSELAR	12	-0.1000	0
21	LARKGIARA	18	-0.1000	0
22	VALAYAGGV	30	-0.1000	0

ALLELE: DRB1_1307		Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8	
Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	1.7000	25.00
2	FRRITGSAL	221	0.8000	11.76
3	FDNLRRGGI	70	0.5000	7.35
4	VASLEVAVL	204	0.5000	7.35
5	FVAENPSRS	40	0.3000	4.41
6	IQFADTRGY	78	0.2000	2.94
7	FPYFISPEQ	2	-0.1000	0
8	LARKGIARA	18	-0.1000	0
9	YRITYDGS	138	-0.1000	0
10	VVALAYAGG	29	-0.2000	0
11	LRRGGIQFA	73	-0.3000	0
12	LCVAEVAHY	121	-0.3000	0
13	VAALRAGSA	184	-0.4000	0

14	VLVFAENPS	38	-0.8000	0
15	VYAQTLGTI	101	-1.1000	0
16	VALAYAGGV	30	-1.2000	0
17	VGFAAAGKF	59	-1.2000	0
18	LGTIFTEQA	106	-1.2000	0
19	FVVMGGTTE	152	-1.2000	0
20	LVDQESPQS	233	-1.2000	0
21	FAAAGKFNE	61	-1.3000	0
22	YFISPEQAM	4	-1.4000	0
23	IARAKSVVA	23	-1.5000	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	LRIAVAALR	180	2.7000	32.53
2	VASLEVAVL	204	1.5000	18.07
3	IQFADTRGY	78	1.4000	16.87
4	LVDQESPQS	233	0.9500	11.45
5	LARKGIARA	18	0.9000	10.84
6	LGTIFTEQA	106	0.9000	10.84
7	VVALAYAGG	29	0.8000	9.64
8	LRRGGIQFA	73	0.8000	9.64
9	LCVAEVAHY	121	0.7000	8.43
10	VAALRAGSA	184	0.7000	8.43
11	VLVFAENPS	38	0.5000	6.02
12	LQKISELYD	49	0.5000	6.02
13	FPYFISPEQ	2	0.0500	0.60
14	VALAYAGGV	30	-0.1000	0
15	VGFAAAGKF	59	-0.1000	0
16	LGVASLEVA	202	-0.1000	0
17	VELCVAEVA	119	-0.2000	0
18	LTDALRIAV	176	-0.2000	0
19	FRRITGSAL	221	-0.2000	0

20	LFVAENPSR	39	-0.3500	0
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ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9
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Rank	Sequence	At Position	Score	% of Highest Score
1	FVVMGGTTE	152	2.9000	32.58
2	LQKISELYD	49	2.2000	24.72
3	FAAAGKFNE	61	2.2000	24.72
4	FPYFISPEQ	2	1.8500	20.79
5	FRRITGSAL	221	1.8000	20.22
6	LRIAVAALR	180	1.7000	19.10
7	IQFADTRGY	78	1.5000	16.85
8	VASLEVAVL	204	1.5000	16.85
9	YAENASLTD	170	1.2000	13.48
10	VVALAYAGG	29	1.1000	12.36
11	LQALLVDQE	229	1.1000	12.36
12	FTEQAKPYE	110	0.9500	10.67
13	FDNLRRGGI	70	0.8000	8.99
14	LCVAEVAHY	121	0.8000	8.99
15	FVAENPSRS	40	0.3000	3.37
16	YRITYDGSI	138	0.2000	2.25
17	LVDQESPQS	233	-0.0500	0
18	ISPEQAMRE	6	-0.1000	0
19	LARKGIARA	18	-0.1000	0
20	FNEFDNLRR	67	-0.1000	0
21	LGTIFTEQA	106	-0.1000	0
22	YFISPEQAM	4	-0.2000	0
23	VGFAAAGKF	59	-0.2000	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	3.0000	35.71
2	LRIAVAALR	180	2.7000	32.14
3	LARKGIARA	18	2.2000	26.19
4	LRRGGIQFA	73	1.7000	20.24
5	LVDQESPQS	233	1.5000	17.86
6	IAVAALRAG	182	0.9000	10.71
7	VASLEVAVL	204	0.8000	9.52
8	LCVAEVAHY	121	0.7000	8.33
9	VVMGGTTEP	153	0.6000	7.14
10	IARAKSVVA	23	0.5000	5.95
11	LDANRPRRA	212	0.5000	5.95
12	VLVFAENPS	38	0.3000	3.57
13	FVAENPSRS	40	0.3000	3.57
14	LGVASLEVA	202	0.2000	2.38
15	VVALAYAGG	29	0.1000	1.19
16	VELCVAEVA	119	0.1000	1.19
17	VTGRQLANV	93	-0.1000	0
18	VYAQTLGTI	101	-0.1000	0
19	LRAGSADTS	187	-0.1000	0
20	IANALKESY	162	-0.2000	0
21	LYDRVGFAA	55	-0.3000	0
22	LGTIFTEQA	106	-0.3000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	2.0000	23.81
2	LRIAVAALR	180	1.7000	20.24
3	FVAENPSRS	40	1.3000	15.48
4	LARKGIARA	18	1.2000	14.29
5	FPYFISPEQ	2	1.0000	11.90
6	LRRGGIQFA	73	0.7000	8.33

7	LVDQESPQS	233	0.5000	5.95
8	FAAAGKFNE	61	0.2000	2.38
9	FVVMGGTTE	152	0.1000	1.19
10	IAVAALRAG	182	-0.1000	0
11	VASLEVAVL	204	-0.2000	0
12	LCVAEVAHY	121	-0.3000	0
13	FRRITGSAL	221	-0.3000	0
14	VVMGGTTEP	153	-0.4000	0
15	YFISPEQAM	4	-0.5000	0
16	IARAKSVVA	23	-0.5000	0
17	YAGGVLFVA	34	-0.5000	0
18	LDANRPRRA	212	-0.5000	0
19	VLVFAENPS	38	-0.7000	0
20	FNEFDNLRR	67	-0.8000	0
21	LGVASLEVA	202	-0.8000	0
22	VVALAYAGG	29	-0.9000	0
23	VELCVAEVA	119	-0.9000	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	IQFADTRGY	78	4.3000	48.86
2	LRIAVAALR	180	4.2000	47.73
3	IAVAALRAG	182	2.3000	26.14
4	LARKGIARA	18	2.2000	25.00
5	LCVAEVAHY	121	2.0000	22.73
6	LVDQESPQS	233	1.9000	21.59
7	VASLEVAVL	204	1.7600	20.00
8	LRRGGIQFA	73	1.7000	19.32
9	VVMGGTTEP	153	1.6000	18.18
10	VVALAYAGG	29	1.5000	17.05
11	IANALKESY	162	1.1000	12.50
12	LQALLVDQE	229	1.0000	11.36

13	LAYAGGVLF	32	0.9000	10.23
14	VTGRQLANV	93	0.9000	10.23
15	VYAQTLGTI	101	0.8000	9.09
16	MRERSELAR	12	0.7000	7.95
17	VLVFAENPS	38	0.7000	7.95
18	LFVAENPSR	39	0.7000	7.95
19	FVAENPSRS	40	0.7000	7.95
20	VGFAAAGKF	59	0.7000	7.95
21	VAVLDANRP	209	0.7000	7.95
22	VLDANRPRR	211	0.7000	7.95
23	FAAAGKFNE	61	0.6000	6.82
24	IARAKSVVA	23	0.5000	5.68

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	IQFADTRGY	78	4.3000	48.86
2	LRIAVAALR	180	4.2000	47.73
3	IAVAALRAG	182	2.3000	26.14
4	LARKGIARA	18	2.2000	25.00
5	LCVAEVAHY	121	2.0000	22.73
6	LVDQESPQS	233	1.9000	21.59
7	VASLEVAVL	204	1.7600	20.00
8	LRRGGIQFA	73	1.7000	19.32
9	VVMGGTTEP	153	1.6000	18.18
10	VVALAYAGG	29	1.5000	17.05
11	IANALKESY	162	1.1000	12.50
12	LQALLVDQE	229	1.0000	11.36
13	LAYAGGVLF	32	0.9000	10.23
14	VTGRQLANV	93	0.9000	10.23
15	VYAQTLGTI	101	0.8000	9.09
16	MRERSELAR	12	0.7000	7.95
17	VLVFAENPS	38	0.7000	7.95

18	LFVAENPSR	39	0.7000	7.95
19	FVAENPSRS	40	0.7000	7.95
20	VGFAAAGKF	59	0.7000	7.95
21	VAVLDANRP	209	0.7000	7.95
22	VLDANRPRR	211	0.7000	7.95
23	FAAAGKFNE	61	0.6000	6.82
24	IARAKSVVA	23	0.5000	5.68

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	FRRITGSAL	221	3.8000	38.78
2	YRITYDGS	138	2.7000	27.55
3	LRIAVAALR	180	2.7000	27.55
4	LRRGGIQFA	73	2.6500	27.04
5	FNEFDNLRR	67	2.6000	26.53
6	VVMGGTTEP	153	2.5600	26.12
7	VVALAYAGG	29	2.2000	22.45
8	LYDRVGFAA	55	1.7000	17.35
9	IARAKSVVA	23	1.6000	16.33
10	LYRITYDGS	137	1.6000	16.33
11	LTDALRIAV	176	1.5000	15.31
12	VLVFAENPS	38	1.4000	14.29
13	FVVMGGTTE	152	1.4000	14.29
14	VALAYAGGV	30	1.3000	13.27
15	LFVAENPSR	39	1.3000	13.27
16	VMGGTTEPI	154	1.2600	12.86
17	LAYAGGVLF	32	1.2000	12.24
18	LRAGSADTS	187	1.2000	12.24
19	MRERSELAR	12	1.1000	11.22
20	FPYFISPEQ	2	1.0000	10.20
21	VYAQTLGTI	101	1.0000	10.20
22	VGFAAAGKF	59	0.9000	9.18

23	VTGRQLANV	93	0.9000	9.18
24	LANVYAQTL	98	0.9000	9.18

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	FRRITGSAL	221	4.8000	48.98
2	YRITYDGSI	138	3.7000	37.76
3	FNEFDNLRR	67	3.6000	36.73
4	FVVMGGTTE	152	2.4000	24.49
5	FPYFISPEQ	2	2.0000	20.41
6	YAGGVLFVA	34	1.8000	18.37
7	LRIAVAALR	180	1.7000	17.35
8	LRRGGIQFA	73	1.6500	16.84
9	VVMGGTTEP	153	1.5600	15.92
10	FDNLRRGGI	70	1.4000	14.29
11	FVAENPSRS	40	1.3000	13.27
12	VVALAYAGG	29	1.2000	12.24
13	YGETKRPEL	129	0.8000	8.16
14	YFISPEQAM	4	0.7800	7.96
15	LYDRVGFAA	55	0.7000	7.14
16	IARAKSVVA	23	0.6000	6.12
17	LYRITYDGS	137	0.6000	6.12
18	YAYDRRDVT	86	0.5000	5.10
19	LTDALRIAV	176	0.5000	5.10
20	VLVAENPS	38	0.4000	4.08
21	VALAYAGGV	30	0.3000	3.06
22	LFVAENPSR	39	0.3000	3.06
23	VMGGTTEPI	154	0.2600	2.65
24	LAYAGGVLF	32	0.2000	2.04



ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	FRRITGSAL	221	3.8000	38.78
2	YRITYDGS	138	2.7000	27.55
3	LRIAVAALR	180	2.7000	27.55
4	LRRGGIQFA	73	2.6500	27.04
5	FNEFDNLRR	67	2.6000	26.53
6	VVMGGTTEP	153	2.5600	26.12
7	VVALAYAGG	29	2.2000	22.45
8	LYDRVGF	55	1.7000	17.35
9	IARAKSVVA	23	1.6000	16.33
10	LYRITYDGS	137	1.6000	16.33
11	LTDALRIAV	176	1.5000	15.31
12	VLVFAENPS	38	1.4000	14.29
13	FVVMGGTTE	152	1.4000	14.29
14	VALAYAGGV	30	1.3000	13.27
15	LVFAENPSR	39	1.3000	13.27
16	VMGGTTEPI	154	1.2600	12.86
17	LAYAGGVLF	32	1.2000	12.24
18	LRAGSADTS	187	1.2000	12.24
19	MRERSELAR	12	1.1000	11.22
20	FPYFISPEQ	2	1.0000	10.20
21	VYAQTLGTI	101	1.0000	10.20
22	VGFAAAGKF	59	0.9000	9.18
23	VTGRQLANV	93	0.9000	9.18
24	LANVYAQTL	98	0.9000	9.18

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	5.2000	53.06

2	FRRITGSAL	221	5.0000	51.02
3	YRITYDGS	138	3.8000	38.78
4	FVVMGGTTE	152	3.7000	37.76
5	IQFADTRGY	78	2.8000	28.57
6	LANVYAQTL	98	2.6000	26.53
7	VGFAAAGKF	59	2.1000	21.43
8	FVAENPSRS	40	1.5000	15.31
9	YAQTLGTIF	102	1.5000	15.31
10	FADTRGYAY	80	1.2000	12.24
11	VVALAYAGG	29	1.1000	11.22
12	VLVFAENPS	38	1.1000	11.22
13	YFISPEQAM	4	1.0000	10.20
14	FISPEQAMR	5	0.9000	9.18
15	LFVAENPSR	39	0.9000	9.18
16	FNEFDNLRR	67	0.8000	8.16
17	IFTEQAKPY	109	0.7000	7.14
18	VALAYAGGV	30	0.4000	4.08
19	LAYAGGVLF	32	0.4000	4.08
20	FDNLRRGGI	70	0.3000	3.06
21	IAVAALRAG	182	0.2000	2.04
22	VAALRAGSA	184	0.2000	2.04
23	LYRITYDGS	137	0.1000	1.02

ALLELE: DRB5_0105	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRIAVAALR	180	5.2000	53.06
2	FRRITGSAL	221	5.0000	51.02
3	YRITYDGS	138	3.8000	38.78
4	FVVMGGTTE	152	3.7000	37.76
5	IQFADTRGY	78	2.8000	28.57
6	LANVYAQTL	98	2.6000	26.53
7	VGFAAAGKF	59	2.1000	21.43

8	FVAENPSRS	40	1.5000	15.31
9	YAQTLGTIF	102	1.5000	15.31
10	FADTRGYAY	80	1.2000	12.24
11	VVALAYAGG	29	1.1000	11.22
12	VLVFAENPS	38	1.1000	11.22
13	YFISPEQAM	4	1.0000	10.20
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