

## MHC Class-II Binding Peptide Prediction Results

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### INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Jan 5 13:24:31 2010
Length of input sequence	89 amino acids
Number of nanomers from input sequence	81
Number of nanomers with <u>obligatory P1 anchor residue</u>	24
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	8

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	INIAVAPLC	28	1.3700	22.83
2	MSRLGGVTL	39	1.2000	20.00
3	IAHLAAGQL	2	-0.5000	0
4	LRELLSAFG	10	-0.5000	0
5	VAPLCNAMS	32	-1.2000	0
6	IATARKINI	22	-1.7000	0
7	LCNAMSRLG	35	-1.8100	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	INIAVAPLC	28	2.3700	39.50
2	MSRLGGVTL	39	2.2000	36.67
3	IAHLAAGQL	2	0.5000	8.33
4	LRELLSAFG	10	0.5000	8.33
5	VAPLCNAMS	32	-0.2000	0
6	IATARKINI	22	-0.7000	0
7	LCNAMSRLG	35	-0.8100	0

Rank	Sequence	At Position	Score	% of Highest Score
1	LAADMRAAS	77	4.4000	46.32
2	LRLQGIDVG	52	3.7000	38.95
3	INIAVAPLC	28	3.0000	31.58
4	LQGIDVGDP	54	2.9000	30.53
5	IATARKINI	22	2.3000	24.21
6	VTLKAGLR	45	2.3000	24.21
7	LRELLSAFG	10	1.3000	13.68
8	LGGVTLKA	42	0.9700	10.21

Rank	Sequence	At Position	Score	% of Highest Score
1	LAADMRAAS	77	3.0000	32.97
2	INIAVAPLC	28	2.0000	21.98
3	FGSGDIATA	17	1.9000	20.88
4	LRLQGIDVG	52	1.3000	14.29
5	LQGIDVGDP	54	0.9000	9.89

6	VIAHLAAGQ	1	0.6000	6.59
7	IATARKINI	22	0.4000	4.40

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	LAADMRAAS	77	4.0000	45.45
2	LRLQGIDVG	52	2.6000	29.55
3	VIAHLAAGQ	1	1.6000	18.18
4	INIAVAPLC	28	1.6000	18.18
5	IATARKINI	22	1.0800	12.27
6	FGSGDIATA	17	0.9000	10.23
7	IAVAPLCNA	30	0.7000	7.95
8	LGGVTLKA	42	0.7000	7.95

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	LAADMRAAS	77	4.0000	45.45
2	LRLQGIDVG	52	2.6000	29.55
3	VIAHLAAGQ	1	1.6000	18.18
4	INIAVAPLC	28	1.6000	18.18
5	IATARKINI	22	1.0800	12.27
6	FGSGDIATA	17	0.9000	10.23
7	IAVAPLCNA	30	0.7000	7.95
8	LGGVTLKA	42	0.7000	7.95

ALLELE:	Threshold for 3 % with	Highest Score achievable by		
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DRB1_0308	score: 2.08	any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LAADMRAAS	77	4.0000	45.45
2	LRLQGIDVG	52	2.6000	29.55
3	VIAHLAAGQ	1	1.6000	18.18
4	INIAVAPLC	28	1.6000	18.18
5	IATARKINI	22	1.0800	12.27
6	FGSGDIATA	17	0.9000	10.23
7	IAVAPLCNA	30	0.7000	7.95
8	LGGVTL SKA	42	0.7000	7.95

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	LAADMRAAS	77	3.4000	35.79
2	LRLQGIDVG	52	2.7000	28.42
3	INIAVAPLC	28	2.0000	21.05
4	FGSGDIATA	17	1.9000	20.00
5	LQGIDVGDP	54	1.9000	20.00
6	IATARKINI	22	1.3000	13.68
7	VTL SKAGLR	45	1.3000	13.68
8	LRELLSAFG	10	0.3000	3.16

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	LAADMRAAS	77	4.0000	45.45
2	LRLQGIDVG	52	2.6000	29.55
3	VIAHLAAGQ	1	1.6000	18.18

4	INIAVAPLC	28	1.6000	18.18
5	IATARKINI	22	1.0800	12.27
6	FGSGDIATA	17	0.9000	10.23
7	IAVAPLCNA	30	0.7000	7.95
8	LGGVTLKA	42	0.7000	7.95

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	VAPLCNAMS	32	2.1000	24.42
2	VIAHLAAGQ	1	1.7000	19.77
3	LRLQGIDVG	52	1.6000	18.60
4	LRELLSAFG	10	0.8000	9.30
5	INIAVAPLC	28	0.6000	6.98
6	LQGIDVGDP	54	-0.5000	0
7	FGSGDIATA	17	-1.0000	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	VIAHLAAGQ	1	2.8000	29.17
2	LCNAMSRLG	35	2.2000	22.92
3	VAPLCNAMS	32	1.7000	17.71
4	INIAVAPLC	28	1.3000	13.54
5	LSKAGLRLQ	47	0.8000	8.33
6	LRELLSAFG	10	0.4000	4.17
7	LRLQGIDVG	52	-0.4000	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	VAPLCNAMS	32	3.3000	37.50
2	LRELLSAFG	10	2.0000	22.73
3	INIAVAPLC	28	1.3000	14.77
4	LRLQGIDVG	52	0.9000	10.23
5	LQGIDVGDP	54	0.9000	10.23
6	VIAHLAAGQ	1	0.6000	6.82
7	LGGVTLSKA	42	0.6000	6.82
8	LSAFGSGDI	14	0.2000	2.27

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRELLSAFG	10	2.3000	24.47
2	VAPLCNAMS	32	2.3000	24.47
3	LRLQGIDVG	52	1.2000	12.77
4	LPQVAATPE	64	0.7000	7.45
5	VIAHLAAGQ	1	0.4000	4.26
6	INIAVAPLC	28	0.3000	3.19
7	LQGIDVGDP	54	0.3000	3.19
8	LLSAFGSGD	13	0.2000	2.13

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	VAPLCNAMS	32	2.3000	26.14
2	LRELLSAFG	10	1.0000	11.36

3	INIAVAPLC	28	0.3000	3.41
4	LRLQGIDVG	52	-0.1000	0
5	LQGIDVGDP	54	-0.1000	0
6	VIAHLAAGQ	1	-0.4000	0
7	LGGVTLSKA	42	-0.4000	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	LRELLSAFG	10	3.3000	35.11
2	VAPLCNAMS	32	3.3000	35.11
3	LRLQGIDVG	52	2.2000	23.40
4	LPQVAATPE	64	1.7000	18.09
5	VIAHLAAGQ	1	1.4000	14.89
6	INIAVAPLC	28	1.3000	13.83
7	LQGIDVGDP	54	1.3000	13.83
8	LLSAFGSGD	13	1.2000	12.77

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	LRLQGIDVG	52	3.0000	33.33
2	VAPLCNAMS	32	2.5000	27.78
3	LRELLSAFG	10	2.2000	24.44
4	VIAHLAAGQ	1	1.0000	11.11
5	INIAVAPLC	28	0.6000	6.67
6	LQGIDVGDP	54	0.5000	5.56

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	VAPLCNAMS	32	3.3000	37.50
2	LRELLSAFG	10	2.0000	22.73
3	INIAVAPLC	28	1.3000	14.77
4	LRLQGIDVG	52	0.9000	10.23
5	LQGIDVGDP	54	0.9000	10.23
6	VIAHLAAGQ	1	0.6000	6.82
7	LGGVTLKA	42	0.6000	6.82
8	LSAFGSGDI	14	0.2000	2.27

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	VAPLCNAMS	32	2.1000	24.42
2	VIAHLAAGQ	1	1.7000	19.77
3	LRLQGIDVG	52	1.6000	18.60
4	LRELLSAFG	10	0.8000	9.30
5	INIAVAPLC	28	0.6000	6.98
6	LQGIDVGDP	54	-0.5000	0
7	FGSGDIATA	17	-1.0000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	IATARKINI	22	3.7000	31.90
2	MSRLGGVTL	39	3.0000	25.86
3	LSAFGSGDI	14	2.9000	25.00



4	IAHLAAGQL	2	1.8000	15.52
5	LAAGQLREL	5	1.1000	9.48
6	INIAVAPLC	28	1.1000	9.48
7	LQGIDVGDP	54	1.0000	8.62
8	VTLSKAGLR	45	0.7000	6.03

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	IATARKINI	22	3.7000	31.90
2	MSRLGGVTL	39	3.0000	25.86
3	LSAFGSGDI	14	2.9000	25.00
4	IAHLAAGQL	2	1.8000	15.52
5	LAAGQLREL	5	1.1000	9.48
6	INIAVAPLC	28	1.1000	9.48
7	LQGIDVGDP	54	1.0000	8.62
8	VTLSKAGLR	45	0.7000	6.03

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	LRELLSAFG	10	0.9000	10.47
2	LQGIDVGDP	54	0.5000	5.81
3	VIAHLAAGQ	1	0.4000	4.65
4	FGSGDIATA	17	0.4000	4.65
5	INIAVAPLC	28	0.1000	1.16
6	VAPLCNAMS	32	0.1000	1.16
7	LRLQGIDVG	52	-0.2000	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	FGSGDIATA	17	0.4000	5.00
2	INIAVAPLC	28	0.1000	1.25
3	VAPLCNAMS	32	0.1000	1.25
4	LQGIDVGDP	54	0.1000	1.25
5	IAVAPLCNA	30	-0.3000	0
6	LAADMRAAS	77	-0.3000	0
7	VIAHLAAGQ	1	-0.4000	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	INIAVAPLC	28	1.1000	13.75
2	VAPLCNAMS	32	1.1000	13.75
3	LQGIDVGDP	54	1.1000	13.75
4	IAVAPLCNA	30	0.7000	8.75
5	LAADMRAAS	77	0.7000	8.75
6	VIAHLAAGQ	1	0.6000	7.50
7	LRELLSAFG	10	0.6000	7.50
8	IATARKINI	22	0.2000	2.50

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	LRELLSAFG	10	1.9000	22.09
2	LQGIDVGDP	54	1.5000	17.44
3	VIAHLAAGQ	1	1.4000	16.28

4	INIAVAPLC	28	1.1000	12.79
5	VAPLCNAMS	32	1.1000	12.79
6	LRLQGIDVG	52	0.8000	9.30
7	IAVAPLCNA	30	0.7000	8.14
8	LAADMRAAS	77	0.7000	8.14

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	LGGVTLKA	42	0.7000	8.05
2	FGSGDIATA	17	0.4000	4.60
3	INIAVAPLC	28	0.3000	3.45
4	VAPLCNAMS	32	0.1000	1.15
5	IATARKINI	22	0.0800	0.92
6	IAVAPLCNA	30	-0.3000	0
7	LRLQGIDVG	52	-0.3000	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	INIAVAPLC	28	1.2500	12.38
2	IATARKINI	22	1.0000	9.90
3	LRELLSAFG	10	0.9000	8.91
4	LQGIDVGDP	54	0.6000	5.94
5	VIAHLAGQ	1	0.4000	3.96
6	FGSGDIATA	17	0.4000	3.96
7	VAPLCNAMS	32	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	INIAVAPLC	28	1.2500	15.06
2	IATARKINI	22	0.8000	9.64
3	LQGIDVGDP	54	0.8000	9.64
4	VAPLCNAMS	32	0.5000	6.02
5	FGSGDIATA	17	-0.3000	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	VIAHLAAGQ	1	3.1000	36.90
2	LRLQGIDVG	52	2.0000	23.81
3	INIAVAPLC	28	1.8000	21.43
4	LSKAGRLRQ	47	1.6000	19.05
5	VAPLCNAMS	32	0.8000	9.52
6	IAVAPLCNA	30	0.7000	8.33
7	LCNAMSRLG	35	0.6000	7.14
8	IATARKINI	22	0.5000	5.95

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	INIAVAPLC	28	2.2500	27.11
2	IATARKINI	22	1.8000	21.69
3	LQGIDVGDP	54	1.8000	21.69
4	VAPLCNAMS	32	1.5000	18.07
5	VIAHLAAGQ	1	1.0000	12.05

6	LRELLSAFG	10	1.0000	12.05
7	IAVAPLCNA	30	0.7000	8.43

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	INIAVAPLC	28	2.2500	27.11
2	IATARKINI	22	1.8000	21.69
3	LQGIDVGDP	54	1.8000	21.69
4	VAPLCNAMS	32	1.5000	18.07
5	VIAHLAAGQ	1	1.0000	12.05
6	LRELLSAFG	10	1.0000	12.05
7	IAVAPLCNA	30	0.7000	8.43

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	LAADMRAAS	77	4.0000	43.96
2	INIAVAPLC	28	3.0000	32.97
3	LRLQGIDVG	52	2.3000	25.27
4	LQGIDVGDP	54	1.9000	20.88
5	VIAHLAAGQ	1	1.6000	17.58
6	IATARKINI	22	1.4000	15.38
7	LGGVTLKA	42	0.9700	10.66
8	FGSGDIATA	17	0.9000	9.89

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	VIAHLAAGQ	1	2.1000	25.00
2	LRLQGIDVG	52	1.0000	11.90
3	INIAVAPLC	28	0.8000	9.52
4	LSKAGLRLQ	47	0.6000	7.14
5	FGSGDIATA	17	-0.1000	0
6	VAPLCNAMS	32	-0.2000	0
7	IAVAPLCNA	30	-0.3000	0

Rank	Sequence	At Position	Score	% of Highest Score
1	LRLQGIDVG	52	2.4000	27.27
2	VIAHLAAGQ	1	1.4000	15.91
3	LCNAMSRLG	35	1.0000	11.36
4	INIAVAPLC	28	0.8000	9.09
5	LRELLSAFG	10	0.7000	7.95
6	IATARKINI	22	0.4000	4.55
7	VAPLCNAMS	32	0.2000	2.27

Rank	Sequence	At Position	Score	% of Highest Score
1	VIAHLAAGQ	1	3.1000	36.90
2	LRLQGIDVG	52	2.0000	23.81
3	INIAVAPLC	28	1.8000	21.43
4	LSKAGLRLQ	47	1.6000	19.05
5	VAPLCNAMS	32	0.8000	9.52
6	IAVAPLCNA	30	0.7000	8.33

7	LCNAMSRLG	35	0.6000	7.14
8	IATARKINI	22	0.5000	5.95

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	LQGIDVGD	54	1.8000	20.69
2	IATARKINI	22	1.7000	19.54
3	LRELLSAFG	10	1.4000	16.09
4	INIAVAPLC	28	1.2500	14.37
5	VAPLCNAMS	32	0.9000	10.34
6	LRLQGIDVG	52	0.2000	2.30
7	IAHLAAGQL	2	-0.1400	0

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8		
Rank	Sequence	At Position	Score	% of Highest Score
1	LRLQGIDVG	52	3.4000	38.64
2	VIAHLAAGQ	1	2.4000	27.27
3	LCNAMSRLG	35	2.0000	22.73
4	INIAVAPLC	28	1.8000	20.45
5	LRELLSAFG	10	1.7000	19.32
6	IATARKINI	22	1.4000	15.91
7	VAPLCNAMS	32	1.2000	13.64
8	LSKAGLRLQ	47	0.9000	10.23

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	LRLQGIDVG	52	2.4000	27.27
2	VIAHLAAGQ	1	1.4000	15.91
3	LCNAMSR LG	35	1.0000	11.36
4	INIAVAPLC	28	0.8000	9.09
5	LRELLSAFG	10	0.7000	7.95
6	IATARKINI	22	0.4000	4.55
7	VAPLCNAMS	32	0.2000	2.27

Rank	Sequence	At Position	Score	% of Highest Score
1	VIAHLAAGQ	1	3.9000	43.33
2	LRLQGIDVG	52	3.3000	36.67
3	LSKAGLRLQ	47	2.4000	26.67
4	LCNAMSR LG	35	1.9000	21.11
5	INIAVAPLC	28	1.8000	20.00
6	LRELLSAFG	10	1.6000	17.78
7	VAPLCNAMS	32	0.8000	8.89
8	IATARKINI	22	0.7000	7.78

Rank	Sequence	At Position	Score	% of Highest Score
1	LQGIDVGDP	54	1.8000	20.69
2	IATARKINI	22	1.7000	19.54
3	LRELLSAFG	10	1.4000	16.09
4	INIAVAPLC	28	1.2500	14.37
5	VAPLCNAMS	32	0.9000	10.34



6	LRLQGIDVG	52	0.2000	2.30
7	IAHLAAGQL	2	-0.1400	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	LQGIDVGDP	54	0.7000	10.29
2	VAPLCNAMS	32	0.5000	7.35
3	INIAVAPLC	28	0.1000	1.47
4	FGSGDIATA	17	-0.3000	0
5	IAVAPLCNA	30	-0.3000	0

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3		
Rank	Sequence	At Position	Score	% of Highest Score
1	INIAVAPLC	28	2.2500	27.11
2	IATARKINI	22	1.8000	21.69
3	LQGIDVGDP	54	1.8000	21.69
4	VAPLCNAMS	32	1.5000	18.07
5	VIAHLAAGQ	1	1.0000	12.05
6	LRELLSAFG	10	1.0000	12.05
7	IAVAPLCNA	30	0.7000	8.43

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	LRELLSAFG	10	1.3000	14.61
2	INIAVAPLC	28	1.2500	14.04

3	LQGIDVGD	54	1.2000	13.48
4	IATARKINI	22	1.0000	11.24
5	VIAHLAAGQ	1	0.8000	8.99
6	VAPLCNAMS	32	0.5000	5.62
7	LRLQGIDVG	52	0.1000	1.12

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	VIAHLAAGQ	1	3.1000	36.90
2	LRLQGIDVG	52	2.0000	23.81
3	INIAVAPLC	28	1.8000	21.43
4	LSKAGLRLQ	47	1.6000	19.05
5	VAPLCNAMS	32	0.8000	9.52
6	IAVAPLCNA	30	0.7000	8.33
7	LCNAMSRG	35	0.6000	7.14
8	IATARKINI	22	0.5000	5.95

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	VIAHLAAGQ	1	2.1000	25.00
2	LRLQGIDVG	52	1.0000	11.90
3	INIAVAPLC	28	0.8000	9.52
4	LSKAGLRLQ	47	0.6000	7.14
5	FGSGDIATA	17	-0.1000	0
6	VAPLCNAMS	32	-0.2000	0
7	IAVAPLCNA	30	-0.3000	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	LRLQGIDVG	52	3.4000	38.64	
2	VIAHLAAGQ	1	2.4000	27.27	
3	LCNAMSR LG	35	2.0000	22.73	
4	INIAVAPLC	28	1.8000	20.45	
5	LRELLSAFG	10	1.7000	19.32	
6	IATARKINI	22	1.4000	15.91	
7	VAPLCNAMS	32	1.2000	13.64	
8	LSKAGLRLQ	47	0.9000	10.23	

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	LRLQGIDVG	52	3.4000	38.64	
2	VIAHLAAGQ	1	2.4000	27.27	
3	LCNAMSR LG	35	2.0000	22.73	
4	INIAVAPLC	28	1.8000	20.45	
5	LRELLSAFG	10	1.7000	19.32	
6	IATARKINI	22	1.4000	15.91	
7	VAPLCNAMS	32	1.2000	13.64	
8	LSKAGLRLQ	47	0.9000	10.23	

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	LSAFGSGDI	14	3.4000	34.69	
2	INIAVAPLC	28	2.6000	26.53	

3	MSRLGGVTL	39	2.2000	22.45
4	IATARKINI	22	1.9000	19.39
5	LGGVTLKA	42	1.4000	14.29
6	LRELLSAFG	10	1.3000	13.27
7	IAHLAAGQL	2	1.2000	12.24
8	VAPLCNAMS	32	1.2000	12.24

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	LSAFGSGDI	14	2.4000	24.49	
2	INIAVAPLC	28	1.6000	16.33	
3	MSRLGGVTL	39	1.2000	12.24	
4	IATARKINI	22	0.9000	9.18	
5	FGSGDIATA	17	0.7500	7.65	
6	LGGVTLKA	42	0.4000	4.08	
7	LRELLSAFG	10	0.3000	3.06	
8	IAHLAAGQL	2	0.2000	2.04	

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	LSAFGSGDI	14	3.4000	34.69	
2	INIAVAPLC	28	2.6000	26.53	
3	MSRLGGVTL	39	2.2000	22.45	
4	IATARKINI	22	1.9000	19.39	
5	LGGVTLKA	42	1.4000	14.29	
6	LRELLSAFG	10	1.3000	13.27	
7	IAHLAAGQL	2	1.2000	12.24	

8	VAPLCNAMS	32	1.2000	12.24
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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	VTLKAGLR	45	2.6000	26.53
2	IAHLAAGQL	2	1.7000	17.35
3	INIAVAPLC	28	0.7000	7.14
4	LCNAMSRLG	35	0.7000	7.14
5	MSRLGGVTL	39	0.7000	7.14
6	LRELLSAFG	10	0.5000	5.10
7	LQGIDVGDP	54	0.2000	2.04

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	VTLKAGLR	45	2.6000	26.53
2	IAHLAAGQL	2	1.7000	17.35
3	INIAVAPLC	28	0.7000	7.14
4	LCNAMSRLG	35	0.7000	7.14
5	MSRLGGVTL	39	0.7000	7.14
6	LRELLSAFG	10	0.5000	5.10
7	LQGIDVGDP	54	0.2000	2.04