

MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Apr 28 23:45:38 2010
Length of input sequence	111 amino acids
Number of nanomers from input sequence	103
Number of nanomers with obligatory P1 anchor residue	29
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	11

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	LELIRSRRR	101	-0.9100	0
2	VLRGSRLGA	4	-1.5000	0
3	YRTDNGEEF	31	-1.5000	0
4	WDMLLERRS	81	-1.6100	0
5	LRGSRLGAV	5	-2.1000	0
6	WLCRNGMEG	53	-2.1100	0
7	LLKERLELI	96	-2.3000	0
8	VPFADDAEI	41	-2.7000	0

9	YETDRNHDL	15	-2.8000	0
10	LCRNGMEGT	54	-2.8600	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	LELIRSRRR	101	0.0900	1.50
2	VLRGSRLGA	4	-0.5000	0
3	LRGSRLGAV	5	-1.1000	0
4	LLKERLELI	96	-1.3000	0
5	VPFADDAEI	41	-1.7000	0
6	LCRNGMEGT	54	-1.8600	0
7	MLLERSIE	83	-2.3000	0
8	LEELLKERL	93	-2.3000	0
9	YRTDNGEEF	31	-2.5000	0
10	WDMLLERS	81	-2.6100	0

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRGSRLGAV	5	3.7000	38.95
2	YRTDNGEEF	31	3.5000	36.84
3	VLRGSRLGA	4	3.4000	35.79
4	IEGDLPEPK	64	2.7000	28.42
5	MLLERSIE	83	1.7700	18.63
6	LELIRSRRR	101	1.1000	11.58
7	LIEGDLPEP	63	1.0000	10.53
8	LLKERLELI	96	0.6000	6.32
9	LAPRQIARY	23	0.3000	3.16
10	IARYRTDNG	28	0.3000	3.16
11	LERSIEEL	85	0.2600	2.74

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	YRTDNGEEF	31	2.6000	28.57
2	VLRGSRLGA	4	2.4000	26.37
3	LRGSRLGAV	5	1.7000	18.68
4	IEGDLPEPK	64	1.6000	17.58
5	WLCRNGMEG	53	-0.6000	0
6	MLLERSIE	83	-0.6300	0
7	FEVPFADDA	39	-1.0000	0
8	FADDAEIPG	43	-1.0000	0
9	LIEGDLPEP	63	-1.0000	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	VLRGSRLGA	4	3.9000	44.32
2	IEGDLPEPK	64	3.0000	34.09
3	YRTDNGEEF	31	2.0000	22.73
4	LRGSRLGAV	5	1.3000	14.77
5	MLLERSIE	83	0.1000	1.14
6	LLKERLELI	96	0.1000	1.14
7	YETDRNHDL	15	-0.2000	0
8	LERRSIEEL	85	-0.3000	0
9	VKPPRTHWD	74	-0.5000	0
10	LEELLKERL	93	-0.6000	0

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	VLRGSRLGA	4	3.9000	44.32
2	IEGDLPEPK	64	3.0000	34.09
3	YRTDNGEEF	31	2.0000	22.73
4	LRGSRLGAV	5	1.3000	14.77
5	MLLERSIE	83	0.1000	1.14
6	LLKERLELI	96	0.1000	1.14
7	YETDRNHDL	15	-0.2000	0
8	LERRSIEEL	85	-0.3000	0
9	VKPPRTHWD	74	-0.5000	0
10	LEELLKERL	93	-0.6000	0

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	VLRGSRLGA	4	3.9000	44.32
2	IEGDLPEPK	64	3.0000	34.09
3	YRTDNGEEF	31	2.0000	22.73
4	LRGSRLGAV	5	1.3000	14.77
5	MLLERSIE	83	0.1000	1.14
6	LLKERLELI	96	0.1000	1.14
7	YETDRNHDL	15	-0.2000	0
8	LERRSIEEL	85	-0.3000	0
9	VKPPRTHWD	74	-0.5000	0
10	LEELLKERL	93	-0.6000	0

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	YRTDNGEEF	31	4.5000	47.37
2	LRGSRLGAV	5	2.7000	28.42

3	VLRGSRLGA	4	2.4000	25.26
4	IEGDLPEPK	64	1.7000	17.89
5	YETDRNHDL	15	0.9600	10.11
6	WLCRNGMEG	53	0.8000	8.42
7	MLLERSIE	83	0.7700	8.11
8	FADDAEIPG	43	0.4000	4.21
9	LELIRSRRR	101	0.1000	1.05

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	VLRGSRLGA	4	3.9000	44.32
2	IEGDLPEPK	64	3.0000	34.09
3	YRTDNGEEF	31	2.0000	22.73
4	LRGSRLGAV	5	1.3000	14.77
5	MLLERSIE	83	0.1000	1.14
6	LLKERLELI	96	0.1000	1.14
7	YETDRNHDL	15	-0.2000	0
8	LERSIEEL	85	-0.3000	0
9	VKPPRTHWD	74	-0.5000	0
10	LEELLKERL	93	-0.6000	0

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	YETDRNHDL	15	1.8000	20.93
2	YRTDNGEEF	31	1.3000	15.12
3	IEGDLPEPK	64	0.6000	6.98
4	LLKERLELI	96	0.3000	3.49
5	LELIRSRRR	101	-0.3000	0
6	LRGSRLGAV	5	-0.9000	0

7	VKPPRTHWD	74	-1.0000	0
8	VSYETDRNH	13	-1.2200	0
9	IARYRTDNG	28	-1.3000	0
10	FEVPFADDA	39	-1.3000	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	LELIRSRRR	101	2.8800	30.00
2	MADRVLGRS	0	1.0000	10.42
3	VKPPRTHWD	74	0.8000	8.33
4	LLERSIEE	84	0.6000	6.25
5	LAPRQIARY	23	0.2000	2.08
6	VLRGSRLGA	4	-0.4000	0
7	LERSIEEL	85	-0.5000	0
8	WLCRNGMEG	53	-0.7000	0
9	IARYRTDNG	28	-0.9000	0
10	VPFADDAEI	41	-1.1000	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	LELIRSRRR	101	1.3000	14.77
2	VKPPRTHWD	74	-0.1000	0
3	VPFADDAEI	41	-1.1000	0
4	LRGSRLGAV	5	-1.3000	0
5	IEGDLPEPK	64	-1.8000	0
6	YETDRNHDL	15	-2.1000	0
7	LLKERLELI	96	-2.2000	0
8	WDMLLERS	81	-2.5000	0
9	IEELEELK	90	-2.5000	0

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	VKPPRTHWD	74	1.6000	17.02
2	IARYRTDNG	28	0.3000	3.19
3	LELIRSRRR	101	0.3000	3.19
4	YETDRNHDL	15	-0.1000	0
5	MLLERSIE	83	-0.7000	0
6	LGAVSYETD	10	-1.2000	0
7	YRTDNGEEF	31	-1.2000	0
8	LLERSIEE	84	-1.2200	0
9	MEGTLIEGD	59	-1.4000	0
10	WDMLLERS	81	-1.5000	0

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	LELIRSRRR	101	0.3000	3.41
2	IARYRTDNG	28	-1.0000	0
3	YETDRNHDL	15	-1.1000	0
4	VKPPRTHWD	74	-1.1000	0
5	WDMLLERS	81	-1.5000	0
6	FEVPFADDA	39	-1.9000	0
7	YRTDNGEEF	31	-2.1000	0
8	VPFADDAEI	41	-2.1000	0
9	LRGSRLGAV	5	-2.3000	0
10	IEGDLPEPK	64	-2.8000	0

ALLELE: DRB1_0410	Threshold for 3 % with score:	Highest Score achievable by any peptide:
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	2.6		9.4	
Rank	Sequence	At Position	Score	% of Highest Score
1	VKPPRTHWD	74	2.6000	27.66
2	IARYRTDNG	28	1.3000	13.83
3	LELIRSRRR	101	1.3000	13.83
4	MLLERSSIE	83	0.3000	3.19
5	LGAVSYETD	10	-0.2000	0
6	LLERSSIEE	84	-0.2200	0
7	MEGTLIEGD	59	-0.4000	0
8	VPFADDAEI	41	-0.9000	0
9	LRGSRLGAV	5	-1.0000	0
10	YETDRNHDL	15	-1.1000	0

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9		
Rank	Sequence	At Position	Score	% of Highest Score
1	YRTDNGEEF	31	3.2000	35.56
2	YETDRNHDL	15	2.7600	30.67
3	LLKERLELI	96	1.2000	13.33
4	LELIRSRRR	101	1.2000	13.33
5	IEGDLPEPK	64	0.7000	7.78
6	LRGSRLGAV	5	0.1000	1.11
7	IARYRTDNG	28	0.1000	1.11
8	VKPPRTHWD	74	0.1000	1.11
9	MLLERSSIE	83	-0.4000	0
10	MEGTLIEGD	59	-0.5000	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	LELIRSRRR	101	1.3000	14.77

2	VKPPRTHWD	74	-0.1000	0
3	VPFADDAEI	41	-1.1000	0
4	LRGSRLGAV	5	-1.3000	0
5	IEGDLPEPK	64	-1.8000	0
6	YETDRNHDL	15	-2.1000	0
7	LLKERLELI	96	-2.2000	0
8	WDMLLERRS	81	-2.5000	0
9	IEELEELLK	90	-2.5000	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	YETDRNHDL	15	1.8000	20.93
2	YRTDNGEEF	31	1.3000	15.12
3	IEGDLPEPK	64	0.6000	6.98
4	LLKERLELI	96	0.3000	3.49
5	LELIRSRRR	101	-0.3000	0
6	LRGSRLGAV	5	-0.9000	0
7	VKPPRTHWD	74	-1.0000	0
8	VSYETDRNH	13	-1.2200	0
9	IARYRTDNG	28	-1.3000	0
10	FEVPFADDA	39	-1.3000	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	LRGSRLGAV	5	4.0000	34.48
2	YRTDNGEEF	31	3.0000	25.86
3	LERRSIEEL	85	2.5000	21.55
4	YETDRNHDL	15	2.2000	18.97
5	LLKERLELI	96	2.0000	17.24

6	LELIRSRRR	101	1.7000	14.66
7	VLRGSRLGA	4	0.7000	6.03
8	WLCRNGMEG	53	0.5000	4.31
9	LLERSIEE	84	0.4000	3.45
10	LEELLKERL	93	0.3000	2.59
11	VPFADDAEI	41	0.2000	1.72

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	LRGSRLGAV	5	4.0000	34.48
2	YRTDNGEEF	31	3.0000	25.86
3	LERRSIEEL	85	2.5000	21.55
4	YETDRNHDL	15	2.2000	18.97
5	LLKERLELI	96	2.0000	17.24
6	LELIRSRRR	101	1.7000	14.66
7	VLRGSRLGA	4	0.7000	6.03
8	WLCRNGMEG	53	0.5000	4.31
9	LLERSIEE	84	0.4000	3.45
10	LEELLKERL	93	0.3000	2.59
11	VPFADDAEI	41	0.2000	1.72

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	WLCRNGMEG	53	2.6000	30.23
2	LAPRQIARY	23	2.4000	27.91
3	LLERSIEE	84	1.5000	17.44
4	MLLERSIE	83	1.0000	11.63
5	IARYRTDNG	28	0.6000	6.98
6	VLRGSRLGA	4	0.4000	4.65

7	LERRSIEEL	85	0.4000	4.65
8	MADRVLGRS	0	0.3000	3.49
9	VKPPRTHWD	74	0.3000	3.49
10	LRGSRLGAV	5	-0.3000	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	LAPRQIARY	23	1.3000	16.25
2	WLCRNGMEG	53	1.3000	16.25
3	VLRGSRLGA	4	0.4000	5.00
4	MADRVLGRS	0	0.3000	3.75
5	WDMLLERRS	81	-0.5000	0
6	LRGSRLGAV	5	-0.6000	0
7	LERRSIEEL	85	-0.6000	0
8	IARYRTDNG	28	-0.7000	0
9	LELIRSRRR	101	-1.3000	0
10	LLERRSIEE	84	-1.5000	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	LAPRQIARY	23	2.3000	28.75
2	VLRGSRLGA	4	1.4000	17.50
3	MADRVLGRS	0	1.3000	16.25
4	LRGSRLGAV	5	0.4000	5.00
5	LERRSIEEL	85	0.4000	5.00
6	IARYRTDNG	28	0.3000	3.75
7	WLCRNGMEG	53	0.3000	3.75
8	LELIRSRRR	101	-0.3000	0
9	LLERRSIEE	84	-0.5000	0

10	LKERLELIR	97	-0.5000	0
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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	LAPRQIARY	23	3.4000	39.53
2	LLERSIEE	84	2.5000	29.07
3	MLLERSIE	83	2.0000	23.26
4	IARYRTDNG	28	1.6000	18.60
5	WLCRNGMEG	53	1.6000	18.60
6	VLRGSRLGA	4	1.4000	16.28
7	LERSIEEL	85	1.4000	16.28
8	MADRVLGRS	0	1.3000	15.12
9	VKPPRTHWD	74	1.3000	15.12
10	LRGSRLGAV	5	0.7000	8.14

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	WLCRNGMEG	53	2.3000	26.44
2	LAPRQIARY	23	1.3000	14.94
3	LERSIEEL	85	1.1000	12.64
4	VLRGSRLGA	4	1.0000	11.49
5	IARYRTDNG	28	0.5000	5.75
6	MLLERSIE	83	-0.2000	0
7	LLERSIEE	84	-0.6200	0
8	WDMLLERS	81	-0.8000	0
9	LKERLELIR	97	-0.9000	0

ALLELE: DRB1_0817	Threshold for 3 % with score:	Highest Score achievable by any peptide:
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	2.8	10.1		
Rank	Sequence	At Position	Score	% of Highest Score
1	WLCRNGMEG	53	4.2000	41.58
2	LLERRSIEE	84	3.1000	30.69
3	LAPRQIARY	23	2.4000	23.76
4	VLRGSRLGA	4	2.2000	21.78
5	LERRSIEEL	85	1.5000	14.85
6	VKPPRTHWD	74	1.0000	9.90
7	MLLERRSIE	83	1.0000	9.90
8	MADRVLGRS	0	0.5000	4.95
9	IARYRTDNG	28	0.3000	2.97
10	LKERLELIR	97	0.3000	2.97

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	VLRGSRLGA	4	1.5000	18.07
2	WDMLLERRS	81	0.1000	1.20
3	WLCRNGMEG	53	-0.1000	0
4	LRGSRLGAV	5	-0.2000	0
5	LELIRSRRR	101	-0.5000	0
6	IEELEELK	90	-1.2000	0
7	LAPRQIARY	23	-1.7000	0
8	LEELKERL	93	-2.0000	0
9	VKPPRTHWD	74	-2.4000	0
10	MADRVLGRS	0	-2.5000	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	VLRGSRLGA	4	1.6000	19.05

2	MADRVLGRS	0	1.0000	11.90
3	LELIRSRRR	101	0.6000	7.14
4	LAPRQIARY	23	0.2000	2.38
5	LRGSRLGAV	5	-0.2000	0
6	LERRSIEEL	85	-0.3000	0
7	IARYRTDNG	28	-0.6000	0
8	VKPPRTHWD	74	-0.7000	0
9	MLLERSIE	83	-0.7000	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	VLRGSRLGA	4	2.5000	30.12
2	LRGSRLGAV	5	0.8000	9.64
3	LELIRSRRR	101	0.5000	6.02
4	IEELEELLK	90	-0.2000	0
5	LAPRQIARY	23	-0.7000	0
6	WDMLLERS	81	-0.9000	0
7	LEELLKERL	93	-1.0000	0
8	WLCRNGMEG	53	-1.1000	0
9	VKPPRTHWD	74	-1.4000	0
10	MADRVLGRS	0	-1.5000	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	VLRGSRLGA	4	2.5000	30.12
2	LRGSRLGAV	5	0.8000	9.64
3	LELIRSRRR	101	0.5000	6.02
4	IEELEELLK	90	-0.2000	0
5	LAPRQIARY	23	-0.7000	0

6	WDMLLERRS	81	-0.9000	0
7	LEELLKERL	93	-1.0000	0
8	WLCRNGMEG	53	-1.1000	0
9	VKPPRTHWD	74	-1.4000	0
10	MADRVLGRS	0	-1.5000	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	VLRGSRLGA	4	3.4000	37.36
2	LRGSRLGAV	5	2.7000	29.67
3	IEGDLPEPK	64	2.6000	28.57
4	YRTDNGEEF	31	1.6000	17.58
5	MLLERRSIE	83	0.3700	4.07
6	LLKERLELI	96	-0.3000	0
7	LELIRSRRR	101	-0.4000	0
8	LERRSIEEL	85	-0.7000	0
9	YETDRNHDL	15	-1.0000	0

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	WDMLLERRS	81	1.0000	11.90
2	VLRGSRLGA	4	0.6000	7.14
3	LELIRSRRR	101	-0.4000	0
4	WLCRNGMEG	53	-0.5000	0
5	LAPRQIARY	23	-0.8000	0
6	LRGSRLGAV	5	-1.2000	0
7	LERRSIEEL	85	-1.3000	0
8	IARYRTDNG	28	-1.6000	0
9	VKPPRTHWD	74	-1.7000	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	WDMLLERRS	81	1.4000	15.91
2	LELIRSRRR	101	1.1000	12.50
3	WLCRNGMEG	53	0.9000	10.23
4	VLRGSRLGA	4	0.6000	6.82
5	LAPRQIARY	23	0.5000	5.68
6	MADRVLGRS	0	0.4000	4.55
7	LRGSRLGAV	5	-0.2000	0
8	IARYRTDNG	28	-0.2000	0
9	MLLERRSIE	83	-0.3000	0

ALLELE: DRB1_1121		Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4	
Rank	Sequence	At Position	Score	% of Highest Score
1	VLRGSRLGA	4	1.6000	19.05
2	MADRVLGRS	0	1.0000	11.90
3	LELIRSRRR	101	0.6000	7.14
4	LAPRQIARY	23	0.2000	2.38
5	LRGSRLGAV	5	-0.2000	0
6	LERRSIEEL	85	-0.3000	0
7	IARYRTDNG	28	-0.6000	0
8	VKPPRTHWD	74	-0.7000	0
9	MLLERRSIE	83	-0.7000	0

ALLELE: DRB1_1128		Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7	
Rank	Sequence	At Position	Score	% of Highest Score

1	VLRGSRLGA	4	1.5000	17.24
2	WLCRNGMEG	53	1.3000	14.94
3	LELIRSRRR	101	1.0000	11.49
4	LRGSRLGAV	5	0.8000	9.20
5	WDMLLERRS	81	0.5000	5.75
6	LAPRQIARY	23	-0.4000	0
7	YRTDNGEEF	31	-0.6000	0
8	LEELLKERL	93	-1.0400	0
9	IEELEELLK	90	-1.1000	0
10	LKERLELIR	97	-1.2000	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	LELIRSRRR	101	2.1000	23.86
2	VLRGSRLGA	4	1.6000	18.18
3	LAPRQIARY	23	1.5000	17.05
4	MADRVLGRS	0	1.4000	15.91
5	LRGSRLGAV	5	0.8000	9.09
6	IARYRTDNG	28	0.8000	9.09
7	MLLERRSIE	83	0.7000	7.95
8	LERRSIEEL	85	0.6600	7.50
9	VKPPRTHWD	74	0.4000	4.55
10	WDMLLERRS	81	0.4000	4.55

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	WDMLLERRS	81	1.4000	15.91
2	LELIRSRRR	101	1.1000	12.50
3	WLCRNGMEG	53	0.9000	10.23

4	VLRGSRLGA	4	0.6000	6.82
5	LAPRQIARY	23	0.5000	5.68
6	MADRVLGRS	0	0.4000	4.55
7	LRGSRLGAV	5	-0.2000	0
8	IARYRTDNG	28	-0.2000	0
9	MLLERSIE	83	-0.3000	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	MLLERSIE	83	2.3000	25.56
2	VKPPRTHWD	74	2.0000	22.22
3	VLRGSRLGA	4	1.6000	17.78
4	LAPRQIARY	23	1.3000	14.44
5	MADRVLGRS	0	1.0000	11.11
6	IARYRTDNG	28	0.7000	7.78
7	LLERSIEE	84	0.7000	7.78
8	LERSIEEL	85	0.7000	7.78
9	LELIRSRRR	101	0.6000	6.67
10	LRGSRLGAV	5	0.1000	1.11

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	VLRGSRLGA	4	1.5000	17.24
2	WLCRNGMEG	53	1.3000	14.94
3	LELIRSRRR	101	1.0000	11.49
4	LRGSRLGAV	5	0.8000	9.20
5	WDMLLERS	81	0.5000	5.75
6	LAPRQIARY	23	-0.4000	0
7	YRTDNGEEF	31	-0.6000	0

8	LEELLKERL	93	-1.0400	0
9	IEELEELLK	90	-1.1000	0
10	LKERLELIR	97	-1.2000	0

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	WDMLLERRS	81	-0.1000	0
2	VLRGSRLGA	4	-0.3000	0
3	LRGSRLGAV	5	-0.3000	0
4	LELIRSRRR	101	-0.7000	0
5	LAPRQIARY	23	-1.7000	0
6	WLCRNGMEG	53	-1.7000	0
7	MADRVLGRS	0	-2.7000	0
8	MLLERRSIE	83	-2.7000	0
9	IEELEELLK	90	-3.0000	0
10	IPGTWLCRN	49	-3.1000	0

ALLELE: DRB1_1311	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	VLRGSRLGA	4	2.5000	30.12
2	LRGSRLGAV	5	0.8000	9.64
3	LELIRSRRR	101	0.5000	6.02
4	IEELEELLK	90	-0.2000	0
5	LAPRQIARY	23	-0.7000	0
6	WDMLLERRS	81	-0.9000	0
7	LEELLKERL	93	-1.0000	0
8	WLCRNGMEG	53	-1.1000	0
9	VKPPRTHWD	74	-1.4000	0
10	MADRVLGRS	0	-1.5000	0

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	VLRGSRLGA	4	1.5000	16.85
2	WLCRNGMEG	53	1.2000	13.48
3	VKPPRTHWD	74	0.3000	3.37
4	MLLERSIE	83	0.3000	3.37
5	LRGSRLGAV	5	0.1000	1.12
6	WDMLLERS	81	0.1000	1.12
7	LLERSIEE	84	0.1000	1.12
8	LELIRSRRR	101	-0.5000	0
9	LAPRQIARY	23	-0.6000	0
10	MEGTLIEGD	59	-0.9000	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	VLRGSRLGA	4	1.6000	19.05
2	MADRVLGRS	0	1.0000	11.90
3	LELIRSRRR	101	0.6000	7.14
4	LAPRQIARY	23	0.2000	2.38
5	LRGSRLGAV	5	-0.2000	0
6	LERSIEEL	85	-0.3000	0
7	IARYRTDNG	28	-0.6000	0
8	VKPPRTHWD	74	-0.7000	0
9	MLLERSIE	83	-0.7000	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	WDMLLERRS	81	1.0000	11.90
2	VLRGSRLGA	4	0.6000	7.14
3	LELIRSRRR	101	-0.4000	0
4	WLCRNGMEG	53	-0.5000	0
5	LAPRQIARY	23	-0.8000	0
6	LRGSRLGAV	5	-1.2000	0
7	LERRSIEEL	85	-1.3000	0
8	IARYRTDNG	28	-1.6000	0
9	VKPPRTHWD	74	-1.7000	0

ALLELE: DRB1_1327	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	LELIRSRRR	101	2.1000	23.86
2	VLRGSRLGA	4	1.6000	18.18
3	LAPRQIARY	23	1.5000	17.05
4	MADRVLGRS	0	1.4000	15.91
5	LRGSRLGAV	5	0.8000	9.09
6	IARYRTDNG	28	0.8000	9.09
7	MLLERRSIE	83	0.7000	7.95
8	LERRSIEEL	85	0.6600	7.50
9	VKPPRTHWD	74	0.4000	4.55
10	WDMLLERRS	81	0.4000	4.55

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	LELIRSRRR	101	2.1000	23.86
2	VLRGSRLGA	4	1.6000	18.18
3	LAPRQIARY	23	1.5000	17.05

4	MADRVLGRS	0	1.4000	15.91
5	LRGSRLGAV	5	0.8000	9.09
6	IARYRTDNG	28	0.8000	9.09
7	MLLERSIE	83	0.7000	7.95
8	LERSIEEL	85	0.6600	7.50
9	VKPPRTHWD	74	0.4000	4.55
10	WDMLLERS	81	0.4000	4.55

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	VLRGSRLGA	4	4.6000	46.94
2	LRGSRLGAV	5	2.6000	26.53
3	IARYRTDNG	28	1.6600	16.94
4	WLCRNGMEG	53	1.6000	16.33
5	LERSIEEL	85	0.8500	8.67
6	MLLERSIE	83	0.8000	8.16
7	LELIRSRRR	101	0.8000	8.16
8	VPFADDAEI	41	0.6000	6.12
9	LLKERLELI	96	0.6000	6.12
10	YETDRNHDL	15	0.5000	5.10
11	YRTDNGEEF	31	0.2000	2.04

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	VLRGSRLGA	4	3.6000	36.73
2	WLCRNGMEG	53	2.6000	26.53
3	LRGSRLGAV	5	1.6000	16.33
4	YETDRNHDL	15	1.5000	15.31
5	YRTDNGEEF	31	1.2000	12.24

6	IARYRTDNG	28	0.6600	6.73
7	LERRSIEEL	85	-0.1500	0
8	MLLERRSIE	83	-0.2000	0
9	LELIRSRRR	101	-0.2000	0
10	FEVPFADDA	39	-0.4000	0

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	VLRGSRLGA	4	4.6000	46.94
2	LRGSRLGAV	5	2.6000	26.53
3	IARYRTDNG	28	1.6600	16.94
4	WLCRNGMEG	53	1.6000	16.33
5	LERRSIEEL	85	0.8500	8.67
6	MLLERRSIE	83	0.8000	8.16
7	LELIRSRRR	101	0.8000	8.16
8	VPFADDAEI	41	0.6000	6.12
9	LLKERLELI	96	0.6000	6.12
10	YETDRNHDL	15	0.5000	5.10
11	YRTDNGEEF	31	0.2000	2.04

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	LELIRSRRR	101	4.7000	47.96
2	WDMLLERRS	81	0.7000	7.14
3	LRGSRLGAV	5	0.3000	3.06
4	YRTDNGEEF	31	0.3000	3.06
5	WLCRNGMEG	53	-0.2000	0
6	IEELEELLK	90	-0.2000	0
7	YETDRNHDL	15	-0.6000	0

8	IEGDLPEPK	64	-0.6000	0
9	VSYETDRNH	13	-1.5000	0
10	VPFADDAEI	41	-1.5000	0

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	LELIRSRRR	101	4.7000	47.96
2	WDMLLERRS	81	0.7000	7.14
3	LRGSRLGAV	5	0.3000	3.06
4	YRTDNGEEF	31	0.3000	3.06
5	WLCRNGMEG	53	-0.2000	0
6	IEELEELLK	90	-0.2000	0
7	YETDRNHDL	15	-0.6000	0
8	IEGDLPEPK	64	-0.6000	0
9	VSYETDRNH	13	-1.5000	0
10	VPFADDAEI	41	-1.5000	0