

MHC Class-II Binding Peptide Prediction Results

[HELP](#)[HOME](#)[MHC & Prediction Algorithm](#)

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Apr 24 23:31:51 2010
Length of input sequence	93 amino acids
Number of nanomers from input sequence	85
Number of nanomers with obligatory P1 anchor residue	27
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	9

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	LMISRGLSL	77	1.4000	23.33
2	VHALGKKLL	37	-1.0000	0
3	LYWTQVLM	71	-1.2000	0
4	VLMISRGLS	76	-1.3000	0
5	FEDLFAELG	9	-1.7000	0
6	LLYWTQVLM	70	-2.0200	0
7	YWTQVLMIS	72	-2.2100	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	LMISRGLSL	77	2.4000	40.00
2	VQQSLAVKT	0	1.0000	16.67
3	LYWTQVLM	71	-0.2000	0
4	VLMISRGLS	76	-0.3000	0
5	LLYWTQVLM	70	-1.0200	0
6	VKTFEDLFA	6	-1.2200	0
7	LAEEISQLL	63	-1.5000	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	VLMISRGLS	76	5.1000	53.68
2	LSLDDVYRK	83	3.9500	41.58
3	LMISRGLSL	77	2.7600	29.05
4	LYWTQVLM	71	1.9000	20.00
5	LLYWTQVLM	70	1.8000	18.95
6	VQQSLAVKT	0	1.6000	16.84
7	YWTQVLMIS	72	1.3000	13.68
8	VHALGKKLL	37	1.1600	12.21
9	ISRGLSLDD	79	0.4000	4.21

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	VLMISRGLS	76	3.7000	40.66
2	LSLDDVYRK	83	2.8500	31.32
3	YWTQVLMIS	72	1.9000	20.88

4	LMISRGLSL	77	0.8000	8.79
5	VQQSLAVKT	0	-0.1000	0
6	WLAAEHESN	52	-0.7000	0
7	LLYWTQVLM	70	-0.7000	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	VLMISRGLS	76	3.3000	37.50
2	LSLDDVYRK	83	2.7000	30.68
3	LMISRGLSL	77	2.3000	26.14
4	LYWTQVLM	71	1.5000	17.05
5	VHALGKKLL	37	0.8000	9.09
6	VQQSLAVKT	0	0.7800	8.86
7	YWTQVLMIS	72	0.6000	6.82
8	VWLAAEHES	51	0.2000	2.27
9	LLYWTQVLM	70	0.1800	2.05

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	VLMISRGLS	76	3.3000	37.50
2	LSLDDVYRK	83	2.7000	30.68
3	LMISRGLSL	77	2.3000	26.14
4	LYWTQVLM	71	1.5000	17.05
5	VHALGKKLL	37	0.8000	9.09
6	VQQSLAVKT	0	0.7800	8.86
7	YWTQVLMIS	72	0.6000	6.82
8	VWLAAEHES	51	0.2000	2.27
9	LLYWTQVLM	70	0.1800	2.05

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	VLMISRGLS	76	3.3000	37.50
2	LSLDDVYRK	83	2.7000	30.68
3	LMISRGLSL	77	2.3000	26.14
4	LYWTQVLM	71	1.5000	17.05
5	VHALGKKLL	37	0.8000	9.09
6	VQQSLAVKT	0	0.7800	8.86
7	YWTQVLMIS	72	0.6000	6.82
8	VWLAAEHES	51	0.2000	2.27
9	LLYWTQVLM	70	0.1800	2.05

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	VLMISRGLS	76	4.1000	43.16
2	LSLDDVYRK	83	2.9500	31.05
3	YWTQVLMIS	72	2.3000	24.21
4	LMISRGLSL	77	1.7600	18.53
5	LYWTQVLM	71	0.9000	9.47
6	LLYWTQVLM	70	0.8000	8.42
7	VQQSLAVKT	0	0.6000	6.32
8	VHALGKKLL	37	0.1600	1.68
9	WLAAEHESN	52	0.1000	1.05

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	VLMISRGLS	76	3.3000	37.50

2	LSLDDVYRK	83	2.7000	30.68
3	LMISRGLSL	77	2.3000	26.14
4	LYWTQVLM	71	1.5000	17.05
5	VHALGKKLL	37	0.8000	9.09
6	VQQSLAVKT	0	0.7800	8.86
7	YWTQVLMIS	72	0.6000	6.82
8	VWLAAEHES	51	0.2000	2.27
9	LLYWTQVLM	70	0.1800	2.05

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	LYWTQVLM	71	1.9000	22.09
2	YWTQVLMIS	72	1.1000	12.79
3	LMISRGLSL	77	0.6000	6.98
4	LSLDDVYRK	83	0.5000	5.81
5	VQQSLAVKT	0	-0.1200	0
6	LFAELGDRA	12	-0.5000	0
7	LAEEISQLL	63	-0.7000	0
8	VLMISRGLS	76	-0.8000	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	LYWTQVLM	71	2.0000	20.83
2	LLYWTQVLM	70	1.7000	17.71
3	VKTFEDLFA	6	1.3000	13.54
4	LMISRGLSL	77	0.1000	1.04
5	LSLDDVYRK	83	-0.1000	0
6	VWLAAEHES	51	-0.3000	0
7	ISQLLYWTQ	67	-0.5000	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	VKTFEDLFA	6	1.3000	14.77
2	LYWTQVLM I	71	0.9000	10.23
3	VLMISRGLS	76	0.6000	6.82
4	LLYWTQVLM	70	-0.2500	0
5	LMISRGLSL	77	-0.3000	0
6	VQQSLAVKT	0	-0.8000	0
7	YWTQVLMIS	72	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VKTFEDLFA	6	0.3000	3.19
2	YWTQVLMIS	72	0.2000	2.13
3	LYWTQVLM I	71	0.1000	1.06
4	LLYWTQVLM	70	-0.1500	0
5	LMISRGLSL	77	-0.3000	0
6	VLMISRGLS	76	-0.4000	0
7	WLAAEHESN	52	-0.5000	0
8	FEDLFAELG	9	-0.6000	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	VKTFEDLFA	6	0.3000	3.41
2	YWTQVLMIS	72	0.2000	2.27
3	LYWTQVLM I	71	-0.1000	0

4	VLMISRGLS	76	-0.4000	0
5	LSLDDVYRK	83	-1.0000	0
6	LLYWTQVLM	70	-1.2500	0
7	LMISRGLSL	77	-1.3000	0
8	WTQVLMISR	73	-1.5200	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	VKTFEDLFA	6	1.3000	13.83
2	LYWTQVLM	71	1.1000	11.70
3	LLYWTQVLM	70	0.8500	9.04
4	LMISRGLSL	77	0.7000	7.45
5	VLMISRGLS	76	0.6000	6.38
6	ISRGLSLDD	79	0.3000	3.19
7	VQQSLAVKT	0	0.1000	1.06
8	ISQLLYWTQ	67	-0.2000	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	LYWTQVLM	71	2.8000	31.11
2	LMISRGLSL	77	1.5600	17.33
3	YWTQVLMIS	72	1.5000	16.67
4	LSLDDVYRK	83	0.6000	6.67
5	VQQSLAVKT	0	0.5800	6.44
6	LAEEISQLL	63	0.2600	2.89
7	FEDLFAELG	9	0.2000	2.22
8	VLMISRGLS	76	-0.4000	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	VKTFEDLFA	6	1.3000	14.77
2	LYWTQVLM	71	0.9000	10.23
3	VLMISRGLS	76	0.6000	6.82
4	LLYWTQVLM	70	-0.2500	0
5	LMISRGLSL	77	-0.3000	0
6	VQQSLAVKT	0	-0.8000	0
7	YWTQVLMIS	72	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LYWTQVLM	71	1.9000	22.09
2	YWTQVLMIS	72	1.1000	12.79
3	LMISRGLSL	77	0.6000	6.98
4	LSLDDVYRK	83	0.5000	5.81
5	VQQSLAVKT	0	-0.1200	0
6	LFAELGDRA	12	-0.5000	0
7	LAEEISQLL	63	-0.7000	0
8	VLMISRGLS	76	-0.8000	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	LMISRGLSL	77	8.1000	69.83
2	LYWTQVLM	71	7.0000	60.34
3	VQQSLAVKT	0	3.7000	31.90
4	LLYWTQVLM	70	2.2000	18.97
5	VHALGKKLL	37	1.8000	15.52

6	LAVKTFEDL	4	1.7000	14.66
7	WTQVLMISR	73	1.7000	14.66
8	LAEEISQLL	63	1.5000	12.93
9	VLMISRGLS	76	1.1000	9.48

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	LMISRGLSL	77	8.1000	69.83
2	LYWTQVLM	71	7.0000	60.34
3	VQQSLAVKT	0	3.7000	31.90
4	LLYWTQVLM	70	2.2000	18.97
5	VHALGKKLL	37	1.8000	15.52
6	LAVKTFEDL	4	1.7000	14.66
7	WTQVLMISR	73	1.7000	14.66
8	LAEEISQLL	63	1.5000	12.93
9	VLMISRGLS	76	1.1000	9.48

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	VLMISRGLS	76	2.9000	33.72
2	MISRGLSLD	78	2.5000	29.07
3	VHALGKKLL	37	1.0000	11.63
4	LLYWTQVLM	70	0.1000	1.16
5	VAALDGGVH	30	-0.2000	0
6	LYWTQVLM	71	-0.3000	0
7	LGKKLLEEA	40	-0.4000	0
8	LMISRGLSL	77	-0.4000	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	VLMISRGLS	76	2.9000	36.25
2	MISRGLSLD	78	-0.2000	0
3	LGKKLLEEA	40	-0.4000	0
4	LYWTQVLM	71	-0.5000	0
5	YWTQVLMIS	72	-0.5000	0
6	LLYWTQVLM	70	-1.0000	0
7	LMISRGLSL	77	-1.4000	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	VLMISRGLS	76	3.9000	48.75
2	VHALGKKLL	37	1.0000	12.50
3	MISRGLSLD	78	0.8000	10.00
4	LGKKLLEEA	40	0.6000	7.50
5	LYWTQVLM	71	0.5000	6.25
6	LMISRGLSL	77	-0.4000	0
7	VAALDGGVH	30	-0.4200	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	VLMISRGLS	76	3.9000	45.35
2	MISRGLSLD	78	3.5000	40.70
3	VHALGKKLL	37	2.0000	23.26
4	LLYWTQVLM	70	1.1000	12.79
5	VAALDGGVH	30	0.8000	9.30
6	LYWTQVLM	71	0.7000	8.14

7	LGKKLLEEA	40	0.6000	6.98
8	LMISRGLSL	77	0.6000	6.98

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7
-------------------	--------------------------------------	---

Rank	Sequence	At Position	Score	% of Highest Score
1	VLMISRGLS	76	2.2000	25.29
2	MISRGLSLD	78	1.6000	18.39
3	LGKKLLEEA	40	1.3000	14.94
4	LGDRARTRP	16	0.6000	6.90
5	YWTQVLMIS	72	0.5000	5.75
6	LYWTQVLM	71	0.1000	1.15
7	VHALGKKLL	37	-0.5000	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	VLMISRGLS	76	3.0000	29.70
2	MISRGLSLD	78	2.5000	24.75
3	VHALGKKLL	37	1.6000	15.84
4	LYWTQVLM	71	1.5000	14.85
5	LMISRGLSL	77	1.4000	13.86
6	YWTQVLMIS	72	1.1000	10.89
7	ISRGLSLDD	79	0.8000	7.92
8	LGKKLLEEA	40	0.7000	6.93
9	LLYWTQVLM	70	0.6000	5.94

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3
-------------------	--------------------------------------	---

Rank	Sequence	At Position	Score	% of Highest Score
------	----------	-------------	-------	--------------------

1	VLMISRGLS	76	3.6000	43.37
2	LYWTQVLM	71	1.7000	20.48
3	YWTQVLMIS	72	1.7000	20.48
4	VHALGKKLL	37	1.0000	12.05
5	LMISRGLSL	77	0.7000	8.43
6	VKTFEDLFA	6	-0.4000	0
7	LLYWTQVLM	70	-0.6000	0
8	WTQVLMISR	73	-0.7000	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	VLMISRGLS	76	2.0000	23.81
2	LLYWTQVLM	70	1.7000	20.24
3	VHALGKKLL	37	1.5000	17.86
4	LYWTQVLM	71	1.1000	13.10
5	LMISRGLSL	77	0.7000	8.33
6	LGKKLLEEA	40	0.5000	5.95
7	VWLAAEHES	51	0.5000	5.95
8	YWTQVLMIS	72	0.4000	4.76

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	VLMISRGLS	76	4.6000	55.42
2	LYWTQVLM	71	2.7000	32.53
3	VHALGKKLL	37	2.0000	24.10
4	LMISRGLSL	77	1.7000	20.48
5	YWTQVLMIS	72	0.7000	8.43
6	VKTFEDLFA	6	0.6000	7.23
7	LLYWTQVLM	70	0.4000	4.82

8	VAALDGGVH	30	0.0800	0.96
---	-----------	----	--------	------

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	VLMISRGLS	76	4.6000	55.42
2	LYWTQVLM	71	2.7000	32.53
3	VHALGKKLL	37	2.0000	24.10
4	LMISRGLSL	77	1.7000	20.48
5	YWTQVLMIS	72	0.7000	8.43
6	VKTFEDLFA	6	0.6000	7.23
7	LLYWTQVLM	70	0.4000	4.82
8	VAALDGGVH	30	0.0800	0.96

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	VLMISRGLS	76	4.7000	51.65
2	LSLDDVYRK	83	3.8500	42.31
3	LMISRGLSL	77	1.8000	19.78
4	LYWTQVLM	71	1.0000	10.99
5	VQQSLAVKT	0	0.9000	9.89
6	YWTQVLMIS	72	0.9000	9.89
7	LLYWTQVLM	70	0.3000	3.30
8	VHALGKKLL	37	0.2000	2.20

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	YWTQVLMIS	72	1.4000	16.67

2	VLMISRGLS	76	1.0000	11.90
3	LLYWTQVLM	70	0.7000	8.33
4	VHALGKKLL	37	0.5000	5.95
5	LYWTQVLM	71	0.1000	1.19
6	LMISRGLSL	77	-0.3000	0
7	LGKKLLEEA	40	-0.5000	0
8	VWLAAEHES	51	-0.5000	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	LLYWTQVLM	70	2.2000	25.00
2	YWTQVLMIS	72	1.8000	20.45
3	VHALGKKLL	37	1.4600	16.59
4	VLMISRGLS	76	1.4000	15.91
5	LYWTQVLM	71	1.0000	11.36
6	LMISRGLSL	77	0.6600	7.50
7	VWLAAEHES	51	-0.1000	0
8	LGKKLLEEA	40	-0.5000	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	VLMISRGLS	76	2.0000	23.81
2	LLYWTQVLM	70	1.7000	20.24
3	VHALGKKLL	37	1.5000	17.86
4	LYWTQVLM	71	1.1000	13.10
5	LMISRGLSL	77	0.7000	8.33
6	LGKKLLEEA	40	0.5000	5.95
7	VWLAAEHES	51	0.5000	5.95
8	YWTQVLMIS	72	0.4000	4.76

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	VLMISRGLS	76	4.0000	45.98
2	LYWTQVLM	71	2.6000	29.89
3	YWTQVLMIS	72	2.1000	24.14
4	VHALGKKLL	37	1.9600	22.53
5	LMISRGLSL	77	1.6600	19.08
6	LLYWTQVLM	70	0.9000	10.34
7	WTQVLMISR	73	0.8000	9.20
8	VKTFEDLFA	6	-0.4000	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	LLYWTQVLM	70	3.2000	36.36
2	VHALGKKLL	37	2.4600	27.95
3	VLMISRGLS	76	2.4000	27.27
4	LYWTQVLM	71	2.0000	22.73
5	LMISRGLSL	77	1.6600	18.86
6	VWLAAEHES	51	0.9000	10.23
7	YWTQVLMIS	72	0.8000	9.09
8	LGKKLLEEA	40	0.5000	5.68
9	MISRGLSLD	78	0.2000	2.27

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	LLYWTQVLM	70	2.2000	25.00

2	YWTQVLMIS	72	1.8000	20.45
3	VHALGKKLL	37	1.4600	16.59
4	VLMISRGLS	76	1.4000	15.91
5	LYWTQVLM	71	1.0000	11.36
6	LMISRGLSL	77	0.6600	7.50
7	VWLAAEHES	51	-0.1000	0
8	LGKKLLEEA	40	-0.5000	0

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	LLYWTQVLM	70	2.8000	31.11
2	VHALGKKLL	37	2.5000	27.78
3	VLMISRGLS	76	2.0000	22.22
4	MISRGLSLD	78	1.8000	20.00
5	LMISRGLSL	77	1.7000	18.89
6	LYWTQVLM	71	1.3000	14.44
7	LGKKLLEEA	40	0.5000	5.56
8	VWLAAEHES	51	0.5000	5.56
9	ISQLLYWTQ	67	0.4000	4.44

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	VLMISRGLS	76	4.0000	45.98
2	LYWTQVLM	71	2.6000	29.89
3	YWTQVLMIS	72	2.1000	24.14
4	VHALGKKLL	37	1.9600	22.53
5	LMISRGLSL	77	1.6600	19.08
6	LLYWTQVLM	70	0.9000	10.34
7	WTQVLMISR	73	0.8000	9.20

8	VKTFEDLFA	6	-0.4000	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	VLMISRGLS	76	3.5000	51.47
2	VHALGKKLL	37	0.4000	5.88
3	YWTQVLMIS	72	0.1000	1.47
4	LYWTQVLM	71	-0.1000	0
5	VAALDGGVH	30	-1.0200	0
6	LLYWTQVLM	70	-1.1000	0
7	LMISRGLSL	77	-1.1000	0
8	VWLAAEHES	51	-1.7000	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	VLMISRGLS	76	4.6000	55.42
2	LYWTQVLM	71	2.7000	32.53
3	VHALGKKLL	37	2.0000	24.10
4	LMISRGLSL	77	1.7000	20.48
5	YWTQVLMIS	72	0.7000	8.43
6	VKTFEDLFA	6	0.6000	7.23
7	LLYWTQVLM	70	0.4000	4.82
8	VAALDGGVH	30	0.0800	0.96

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	VLMISRGLS	76	3.6000	40.45

2	VHALGKKLL	37	2.0000	22.47
3	LYWTQVLM	71	1.9000	21.35
4	YWTQVLMIS	72	1.7000	19.10
5	LMISRGLSL	77	1.7000	19.10
6	LLYWTQVLM	70	0.5000	5.62
7	VAALDGGVH	30	0.3000	3.37
8	WLAAEHESN	52	0.2000	2.25
9	ISRGLSLDD	79	0.1000	1.12

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VLMISRGLS	76	2.0000	23.81
2	LLYWTQVLM	70	1.7000	20.24
3	VHALGKKLL	37	1.5000	17.86
4	LYWTQVLM	71	1.1000	13.10
5	LMISRGLSL	77	0.7000	8.33
6	LGKKLLEEA	40	0.5000	5.95
7	VWLAAEHES	51	0.5000	5.95
8	YWTQVLMIS	72	0.4000	4.76

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	YWTQVLMIS	72	1.4000	16.67
2	VLMISRGLS	76	1.0000	11.90
3	LLYWTQVLM	70	0.7000	8.33
4	VHALGKKLL	37	0.5000	5.95
5	LYWTQVLM	71	0.1000	1.19
6	LMISRGLSL	77	-0.3000	0
7	LGKKLLEEA	40	-0.5000	0

8	VWLAAEHES	51	-0.5000	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	LLYWTQVLM	70	3.2000	36.36
2	VHALGKKLL	37	2.4600	27.95
3	VLMISRGLS	76	2.4000	27.27
4	LYWTQVLM	71	2.0000	22.73
5	LMISRGLSL	77	1.6600	18.86
6	VWLAAEHES	51	0.9000	10.23
7	YWTQVLMIS	72	0.8000	9.09
8	LGKKLLEEA	40	0.5000	5.68
9	MISRGLSLD	78	0.2000	2.27

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	LLYWTQVLM	70	3.2000	36.36
2	VHALGKKLL	37	2.4600	27.95
3	VLMISRGLS	76	2.4000	27.27
4	LYWTQVLM	71	2.0000	22.73
5	LMISRGLSL	77	1.6600	18.86
6	VWLAAEHES	51	0.9000	10.23
7	YWTQVLMIS	72	0.8000	9.09
8	LGKKLLEEA	40	0.5000	5.68
9	MISRGLSLD	78	0.2000	2.27

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	LMISRGLSL	77	5.2000	53.06
2	VKTFEDLFA	6	5.0000	51.02
3	VLMISRGLS	76	3.7000	37.76
4	LYWTQVLM	71	2.9000	29.59
5	LLYWTQVLM	70	1.7800	18.16
6	VHALGKKLL	37	1.2000	12.24
7	VQQSLAVKT	0	1.0000	10.20
8	ISRGLSLDD	79	1.0000	10.20
9	VWLAAEHES	51	0.2000	2.04

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	LMISRGLSL	77	4.2000	42.86
2	VKTFEDLFA	6	4.0000	40.82
3	VLMISRGLS	76	2.7000	27.55
4	LYWTQVLM	71	1.9000	19.39
5	WTQVLMISR	73	0.8000	8.16
6	LLYWTQVLM	70	0.7800	7.96
7	YWTQVLMIS	72	0.7000	7.14
8	VHALGKKLL	37	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	LMISRGLSL	77	5.2000	53.06
2	VKTFEDLFA	6	5.0000	51.02
3	VLMISRGLS	76	3.7000	37.76
4	LYWTQVLM	71	2.9000	29.59
5	LLYWTQVLM	70	1.7800	18.16

6	VHALGKKLL	37	1.2000	12.24
7	VQQSLAVKT	0	1.0000	10.20
8	ISRGLSLDD	79	1.0000	10.20
9	VWLAAEHES	51	0.2000	2.04

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	WTQVLMISR	73	3.3000	33.67
2	VLMISRGLS	76	2.7000	27.55
3	LMISRGLSL	77	2.7000	27.55
4	FAELGDRAR	13	1.2000	12.24
5	VHALGKKLL	37	1.1000	11.22
6	VAALDGGVH	30	0.9000	9.18
7	LYWTQVLM	71	0.7000	7.14
8	LSLDDVYRK	83	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	WTQVLMISR	73	3.3000	33.67
2	VLMISRGLS	76	2.7000	27.55
3	LMISRGLSL	77	2.7000	27.55
4	FAELGDRAR	13	1.2000	12.24
5	VHALGKKLL	37	1.1000	11.22
6	VAALDGGVH	30	0.9000	9.18
7	LYWTQVLM	71	0.7000	7.14
8	LSLDDVYRK	83	0.4000	4.08