MHC Class-II Binding Peptide Prediction Results

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Thu Feb 11 19:55:06 2010
Length of input sequence	159 amino acids
Number of nanomers from input sequence	151
Number of nanomers with obligatory P1 anchor residue	50
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	15

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	WRRLEAQAV	110	4.3000	71.67
2	WQGVSGADM	71	1.1300	18.83
3	YRVGNAVVQ	92	1.1000	18.33
4	VVVLITQHG	83	0.7000	11.67
5	LITQHGYRV	86	0.7000	11.67
6	LRHVVVLIT	80	0.3500	5.83
7	MLRHVVVLI	79	0.3000	5.00
8	LVGLLFPSA	23	0.1700	2.83
9	VNQLPRVGL	0	0.1000	1.67

10	VGNAVVQVI	94	-0.2000	0
11	VVQVIGNRP	98	-0.2500	0
12	LSRLLNAPV	119	-0.5000	0
13	VIGNRPKIG	101	-0.8600	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	WRRLEAQAV	110	3.3000	55.00
2	VVVLITQHG	83	1.7000	28.33
3	LITQHGYRV	86	1.7000	28.33
4	LRHVVVLIT	80	1.3500	22.50
5	MLRHVVVLI	79	1.3000	21.67
6	LVGLLFPSA	23	1.1700	19.50
7	VNQLPRVGL	0	1.1000	18.33
8	VVLITQHGY	84	1.0000	16.67
9	VGNAVVQVI	94	0.8000	13.33
10	VVQVIGNRP	98	0.7500	12.50
11	LSRLLNAPV	119	0.5000	8.33
12	VIGNRPKIG	101	0.1400	2.33
13	WQGVSGADM	71	0.1300	2.17
14	VGLLFPSAD	24	0.1000	1.67
15	YRVGNAVVQ	92	0.1000	1.67

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	LLNAPVSVS	122	3.8700	40.74
2	MLRHVVVLI	79	3.7000	38.95
3	VVVLITQHG	83	3.7000	38.95
4	LRHVVVLIT	80	3.3000	34.74

5	LGTDVHPIE	8	3.1000	32.63
6	WLVGLLFPS	22	2.8000	29.47
7	VVLITQHGY	84	2.8000	29.47
8	VGNAVVQVI	94	2.7000	28.42
9	YRVGNAVVQ	92	2.2000	23.16
10	WRRLEAQAV	110	2.1000	22.11
11	VLITQHGYR	85	2.0000	21.05
12	LEAQAVLSR	113	2.0000	21.05
13	LGLTGRGEG	137	2.0000	21.05
14	VNQLPRVGL	0	1.9600	20.63
15	VHPIEPGRP	12	1.9000	20.00

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	YRVGNAVVQ	92	3.9000	42.86
2	WLVGLLFPS	22	3.4000	37.36
3	FGVDDPRWQ	64	3.4000	37.36
4	LLNAPVSVS	122	2.4700	27.14
5	WRRLEAQAV	110	2.1000	23.08
6	MLRHVVVLI	79	1.8000	19.78
7	LRHVVVLIT	80	1.6000	17.58
8	VVVLITQHG	83	1.3000	14.29
9	VGNAVVQVI	94	0.8000	8.79
10	LGTDVHPIE	8	0.7000	7.69
11	LVGLLFPSA	23	0.6000	6.59
12	VVLITQHGY	84	0.5000	5.49
13	WQGVSGADM	71	0.3000	3.30

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	LLNAPVSVS	122	3.2000	36.36
2	LRHVVVLIT	80	3.1000	35.23
3	YRVGNAVVQ	92	2.7800	31.59
4	MLRHVVVLI	79	2.6800	30.45
5	VVVLITQHG	83	2.4000	27.27
6	VVLITQHGY	84	2.3000	26.14
7	FGVDDPRWQ	64	2.1000	23.86
8	VGNAVVQVI	94	1.9000	21.59
9	WRRLEAQAV	110	1.2000	13.64
10	LEAQAVLSR	113	1.0000	11.36
11	WLVGLLFPS	22	0.9000	10.23
12	VNQLPRVGL	0	0.8800	10.00
13	VAVHALCDA	42	0.7000	7.95
14	VVQVIGNRP	98	0.7000	7.95
15	VIGNRPKIG	101	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	LLNAPVSVS	122	3.2000	36.36
2	LRHVVVLIT	80	3.1000	35.23
3	YRVGNAVVQ	92	2.7800	31.59
4	MLRHVVVLI	79	2.6800	30.45
5	VVVLITQHG	83	2.4000	27.27
6	VVLITQHGY	84	2.3000	26.14
7	FGVDDPRWQ	64	2.1000	23.86
8	VGNAVVQVI	94	1.9000	21.59
9	WRRLEAQAV	110	1.2000	13.64
10	LEAQAVLSR	113	1.0000	11.36
11	WLVGLLFPS	22	0.9000	10.23
12	VNQLPRVGL	0	0.8800	10.00
13	VAVHALCDA	42	0.7000	7.95

14	VVQVIGNRP	98	0.7000	7.95
15	VIGNRPKIG	101	0.7000	7.95

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	LLNAPVSVS	122	3.2000	36.36
2	LRHVVVLIT	80	3.1000	35.23
3	YRVGNAVVQ	92	2.7800	31.59
4	MLRHVVVLI	79	2.6800	30.45
5	VVVLITQHG	83	2.4000	27.27
6	VVLITQHGY	84	2.3000	26.14
7	FGVDDPRWQ	64	2.1000	23.86
8	VGNAVVQVI	94	1.9000	21.59
9	WRRLEAQAV	110	1.2000	13.64
10	LEAQAVLSR	113	1.0000	11.36
11	WLVGLLFPS	22	0.9000	10.23
12	VNQLPRVGL	0	0.8800	10.00
13	VAVHALCDA	42	0.7000	7.95
14	VVQVIGNRP	98	0.7000	7.95
15	VIGNRPKIG	101	0.7000	7.95

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	WLVGLLFPS	22	3.8000	40.00
2	YRVGNAVVQ	92	3.2000	33.68
3	WRRLEAQAV	110	3.1000	32.63
4	LLNAPVSVS	122	2.8700	30.21
5	FGVDDPRWQ	64	2.7000	28.42
6	MLRHVVVLI	79	2.7000	28.42

7	VVVLITQHG	83	2.7000	28.42
8	LRHVVVLIT	80	2.3000	24.21
9	LGTDVHPIE	8	2.1000	22.11
10	WQGVSGADM	71	1.8000	18.95
11	VVLITQHGY	84	1.8000	18.95
12	VGNAVVQVI	94	1.7000	17.89
13	VLITQHGYR	85	1.0000	10.53
14	LEAQAVLSR	113	1.0000	10.53
15	LGLTGRGEG	137	1.0000	10.53

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	LLNAPVSVS	122	3.2000	36.36
2	LRHVVVLIT	80	3.1000	35.23
3	YRVGNAVVQ	92	2.7800	31.59
4	MLRHVVVLI	79	2.6800	30.45
5	VVVLITQHG	83	2.4000	27.27
6	VVLITQHGY	84	2.3000	26.14
7	FGVDDPRWQ	64	2.1000	23.86
8	VGNAVVQVI	94	1.9000	21.59
9	WRRLEAQAV	110	1.2000	13.64
10	LEAQAVLSR	113	1.0000	11.36
11	WLVGLLFPS	22	0.9000	10.23
12	VNQLPRVGL	0	0.8800	10.00
13	VAVHALCDA	42	0.7000	7.95
14	VVQVIGNRP	98	0.7000	7.95
15	VIGNRPKIG	101	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	VVVLITQHG	83	3.3000	38.37
2	WRRLEAQAV	110	3.0000	34.88
3	MLRHVVVLI	79	2.4800	28.84
4	LLNAPVSVS	122	1.9000	22.09
5	FGVDDPRWQ	64	1.7000	19.77
6	YRVGNAVVQ	92	1.6800	19.53
7	VQVIGNRPK	99	1.3000	15.12
8	LAAIATALV	146	1.0000	11.63
9	LRHVVVLIT	80	0.9000	10.47
10	LSRLLNAPV	119	0.8000	9.30
11	VGNAVVQVI	94	0.6000	6.98
12	LEAQAVLSR	113	0.5000	5.81
13	VVLITQHGY	84	0.4000	4.65
14	LVGLLFPSA	23	0.3000	3.49
15	VSVSATTTD	127	0.1000	1.16

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	VQVIGNRPK	99	4.4800	46.67
2	VVVLITQHG	83	4.0000	41.67
3	MLRHVVVLI	79	3.7000	38.54
4	VGNAVVQVI	94	2.7000	28.13
5	LLNAPVSVS	122	2.7000	28.13
6	LRHVVVLIT	80	2.4000	25.00
7	YRVGNAVVQ	92	1.7000	17.71
8	WRRLEAQAV	110	1.7000	17.71
9	LAAIATALV	146	1.2800	13.33
10	VVLITQHGY	84	1.1800	12.29
11	LNAPVSVSA	123	0.7000	7.29
12	VAVHALCDA	42	0.6000	6.25
13	LEAQAVLSR	113	0.6000	6.25

14	ITQHGYRVG	87	0.4000	4.17
15	VLSRLLNAP	118	0.4000	4.17

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	VVVLITQHG	83	4.3000	48.86
2	LLNAPVSVS	122	3.6000	40.91
3	LRHVVVLIT	80	2.9000	32.95
4	VQVIGNRPK	99	2.9000	32.95
5	LAAIATALV	146	2.3000	26.14
6	WRRLEAQAV	110	2.0000	22.73
7	LSRLLNAPV	119	2.0000	22.73
8	VGNAVVQVI	94	1.4000	15.91
9	VGLLFPSAD	24	1.3000	14.77
10	VVLITQHGY	84	1.3000	14.77
11	LVGLLFPSA	23	1.2000	13.64
12	MLRHVVVLI	79	1.2000	13.64
13	VVQVIGNRP	98	0.5000	5.68
14	LNAPVSVSA	123	0.4000	4.55
15	LEAQAVLSR	113	0.3000	3.41

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	VVVLITQHG	83	4.6000	48.94
2	WRRLEAQAV	110	3.3000	35.11
3	VGLLFPSAD	24	3.0000	31.91
4	LRHVVVLIT	80	2.8000	29.79
5	LLNAPVSVS	122	2.6000	27.66
6	VSVSATTTD	127	1.8000	19.15

7	LAAIATALV	146	1.6000	17.02
8	YRVGNAVVQ	92	1.5000	15.96
9	VVLITQHGY	84	1.4000	14.89
10	LSRLLNAPV	119	1.3000	13.83
11	VQVIGNRPK	99	1.2000	12.77
12	WQGVSGADM	71	1.1000	11.70
13	VGNAVVQVI	94	0.6000	6.38
14	MLRHVVVLI	79	0.4000	4.26
15	FGVDDPRWQ	64	0.3000	3.19

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	VVVLITQHG	83	3.3000	37.50
2	WRRLEAQAV	110	3.0000	34.09
3	LLNAPVSVS	122	2.6000	29.55
4	LRHVVVLIT	80	1.9000	21.59
5	VQVIGNRPK	99	1.9000	21.59
6	LAAIATALV	146	1.3000	14.77
7	LSRLLNAPV	119	1.0000	11.36
8	YRVGNAVVQ	92	0.7000	7.95
9	VGNAVVQVI	94	0.4000	4.55
10	VGLLFPSAD	24	0.3000	3.41
11	VVLITQHGY	84	0.3000	3.41
12	LVGLLFPSA	23	0.2000	2.27
13	MLRHVVVLI	79	0.2000	2.27

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	VVVLITQHG	83	5.6000	59.57

2	VGLLFPSAD	24	4.0000	42.55
3	LRHVVVLIT	80	3.8000	40.43
4	LLNAPVSVS	122	3.6000	38.30
5	VSVSATTTD	127	2.8000	29.79
6	LAAIATALV	146	2.6000	27.66
7	VVLITQHGY	84	2.4000	25.53
8	WRRLEAQAV	110	2.3000	24.47
9	LSRLLNAPV	119	2.3000	24.47
10	VQVIGNRPK	99	2.2000	23.40
11	VGNAVVQVI	94	1.6000	17.02
12	MLRHVVVLI	79	1.4000	14.89
13	LVGLLFPSA	23	1.2000	12.77
14	VLSAAGLGD	51	1.0000	10.64
15	VVQVIGNRP	98	0.9000	9.57

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	VVVLITQHG	83	4.7000	52.22
2	WRRLEAQAV	110	4.0000	44.44
3	MLRHVVVLI	79	3.3800	37.56
4	LLNAPVSVS	122	2.3000	25.56
5	LEAQAVLSR	113	2.0000	22.22
6	LAAIATALV	146	2.0000	22.22
7	LSRLLNAPV	119	1.8000	20.00
8	VVLITQHGY	84	1.7000	18.89
9	LRHVVVLIT	80	1.6000	17.78
10	VGNAVVQVI	94	1.5000	16.67
11	VQVIGNRPK	99	1.4000	15.56
12	VIGNRPKIG	101	1.3000	14.44
13	VSVSATTTD	127	1.2000	13.33
14	FGVDDPRWQ	64	1.0000	11.11
15	YRVGNAVVQ	92	0.9800	10.89

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	VVVLITQHG	83	4.3000	48.86
2	LLNAPVSVS	122	3.6000	40.91
3	LRHVVVLIT	80	2.9000	32.95
4	VQVIGNRPK	99	2.9000	32.95
5	LAAIATALV	146	2.3000	26.14
6	WRRLEAQAV	110	2.0000	22.73
7	LSRLLNAPV	119	2.0000	22.73
8	VGNAVVQVI	94	1.4000	15.91
9	VGLLFPSAD	24	1.3000	14.77
10	VVLITQHGY	84	1.3000	14.77
11	LVGLLFPSA	23	1.2000	13.64
12	MLRHVVVLI	79	1.2000	13.64
13	VVQVIGNRP	98	0.5000	5.68
14	LNAPVSVSA	123	0.4000	4.55
15	LEAQAVLSR	113	0.3000	3.41

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	VVVLITQHG	83	3.3000	38.37
2	WRRLEAQAV	110	3.0000	34.88
3	MLRHVVVLI	79	2.4800	28.84
4	LLNAPVSVS	122	1.9000	22.09
5	FGVDDPRWQ	64	1.7000	19.77
6	YRVGNAVVQ	92	1.6800	19.53
7	VQVIGNRPK	99	1.3000	15.12
8	LAAIATALV	146	1.0000	11.63
9	LRHVVVLIT	80	0.9000	10.47

10	LSRLLNAPV	119	0.8000	9.30
11	VGNAVVQVI	94	0.6000	6.98
12	LEAQAVLSR	113	0.5000	5.81
13	VVLITQHGY	84	0.4000	4.65
14	LVGLLFPSA	23	0.3000	3.49
15	VSVSATTTD	127	0.1000	1.16

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	MLRHVVVLI	79	5.9000	50.86
2	WRRLEAQAV	110	5.2000	44.83
3	LRHVVVLIT	80	5.0000	43.10
4	VGNAVVQVI	94	4.6000	39.66
5	VVLITQHGY	84	4.1000	35.34
6	IATALVVSL	149	4.1000	35.34
7	WQGVSGADM	71	3.7000	31.90
8	VNQLPRVGL	0	2.9000	25.00
9	YRVGNAVVQ	92	2.3000	19.83
10	VVQVIGNRP	98	2.2000	18.97
11	VSATTTDGL	129	2.1200	18.28
12	LAAIATALV	146	2.0200	17.41
13	LITQHGYRV	86	1.7000	14.66
14	WLVGLLFPS	22	1.3000	11.21
15	VLITQHGYR	85	1.3000	11.21

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	MLRHVVVLI	79	5.9000	50.86
2	WRRLEAQAV	110	5.2000	44.83

3	LRHVVVLIT	80	5.0000	43.10
4	VGNAVVQVI	94	4.6000	39.66
5	VVLITQHGY	84	4.1000	35.34
6	IATALVVSL	149	4.1000	35.34
7	WQGVSGADM	71	3.7000	31.90
8	VNQLPRVGL	0	2.9000	25.00
9	YRVGNAVVQ	92	2.3000	19.83
10	VVQVIGNRP	98	2.2000	18.97
11	VSATTTDGL	129	2.1200	18.28
12	LAAIATALV	146	2.0200	17.41
13	LITQHGYRV	86	1.7000	14.66
14	WLVGLLFPS	22	1.3000	11.21
15	VLITQHGYR	85	1.3000	11.21

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	IGNRPKIGW	102	2.7000	31.40
2	LRHVVVLIT	80	2.3000	26.74
3	VVVLITQHG	83	2.2000	25.58
4	WRRLEAQAV	110	2.0000	23.26
5	YRVGNAVVQ	92	1.9000	22.09
6	WQGVSGADM	71	1.7000	19.77
7	VGLLFPSAD	24	1.4000	16.28
8	VVLITQHGY	84	1.3000	15.12
9	FGVDDPRWQ	64	1.2000	13.95
10	LLNAPVSVS	122	1.1000	12.79
11	IGWRRLEAQ	108	0.9000	10.47
12	WLVGLLFPS	22	0.5000	5.81
13	VLSRLLNAP	118	0.5000	5.81
14	VNQLPRVGL	0	0.4000	4.65
15	VIGNRPKIG	101	0.3000	3.49

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	IGNRPKIGW	102	1.8000	22.50
2	WRRLEAQAV	110	1.7000	21.25
3	LRHVVVLIT	80	1.4000	17.50
4	YRVGNAVVQ	92	1.1000	13.75
5	LLNAPVSVS	122	1.1000	13.75
6	VVVLITQHG	83	0.9000	11.25
7	WQGVSGADM	71	0.6000	7.50
8	WLVGLLFPS	22	0.5000	6.25
9	FGVDDPRWQ	64	0.4000	5.00
10	VVLITQHGY	84	0.2000	2.50
11	IGWRRLEAQ	108	0.1000	1.25
12	VLSRLLNAP	118	0.1000	1.25
13	VGNAVVQVI	94	-0.3000	0
14	LTGRGEGLA	139	-0.4000	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	IGNRPKIGW	102	2.8000	35.00
2	LRHVVVLIT	80	2.4000	30.00
3	LLNAPVSVS	122	2.1000	26.25
4	VVVLITQHG	83	1.9000	23.75
5	VVLITQHGY	84	1.2000	15.00
6	IGWRRLEAQ	108	1.1000	13.75
7	VLSRLLNAP	118	1.1000	13.75
8	VGNAVVQVI	94	0.7000	8.75
9	WRRLEAQAV	110	0.7000	8.75
10	LTGRGEGLA	139	0.6000	7.50

11	MLRHVVVLI	79	0.5000	6.25
12	VQVIGNRPK	99	0.5000	6.25
13	VNQLPRVGL	0	0.4000	5.00
14	LVGLLFPSA	23	0.4000	5.00
15	LAAIATALV	146	0.4000	5.00

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	IGNRPKIGW	102	3.7000	43.02
2	LRHVVVLIT	80	3.3000	38.37
3	VVVLITQHG	83	3.2000	37.21
4	VGLLFPSAD	24	2.4000	27.91
5	VVLITQHGY	84	2.3000	26.74
6	LLNAPVSVS	122	2.1000	24.42
7	IGWRRLEAQ	108	1.9000	22.09
8	VLSRLLNAP	118	1.5000	17.44
9	VNQLPRVGL	0	1.4000	16.28
10	VIGNRPKIG	101	1.3000	15.12
11	LGLTGRGEG	137	1.3000	15.12
12	LPRVGLGTD	3	1.2000	13.95
13	VLSAAGLGD	51	1.2000	13.95
14	WRRLEAQAV	110	1.0000	11.63
15	YRVGNAVVQ	92	0.9000	10.47

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	LLNAPVSVS	122	2.9000	33.33
2	WRRLEAQAV	110	2.7000	31.03
3	IGNRPKIGW	102	2.6800	30.80

4	YRVGNAVVQ	92	2.1000	24.14
5	VLSRLLNAP	118	2.1000	24.14
6	LRHVVVLIT	80	2.0000	22.99
7	VVVLITQHG	83	1.9000	21.84
8	IGWRRLEAQ	108	1.8000	20.69
9	WLVGLLFPS	22	1.3500	15.52
10	VVLITQHGY	84	0.7000	8.05
11	VGNAVVQVI	94	0.7000	8.05
12	WQGVSGADM	71	0.6000	6.90
13	VGLLFPSAD	24	0.5000	5.75
14	MLRHVVVLI	79	0.5000	5.75
15	VNQLPRVGL	0	0.4000	4.60

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	IGNRPKIGW	102	4.3000	42.57
2	LRHVVVLIT	80	4.1000	40.59
3	YRVGNAVVQ	92	2.4000	23.76
4	VVVLITQHG	83	2.3000	22.77
5	WRRLEAQAV	110	2.1000	20.79
6	VLSAAGLGD	51	2.0000	19.80
7	VVLITQHGY	84	2.0000	19.80
8	IGWRRLEAQ	108	2.0000	19.80
9	WQGVSGADM	71	1.7000	16.83
10	VGLLFPSAD	24	1.4000	13.86
11	FGVDDPRWQ	64	1.4000	13.86
12	LLNAPVSVS	122	1.1000	10.89
13	WLVGLLFPS	22	1.0000	9.90
14	VNQLPRVGL	0	0.9000	8.91
15	VIGNRPKIG	101	0.9000	8.91

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	LRHVVVLIT	80	3.3000	39.76
2	WRRLEAQAV	110	2.2000	26.51
3	VVLITQHGY	84	1.5000	18.07
4	VVVLITQHG	83	1.4000	16.87
5	LLNAPVSVS	122	1.1000	13.25
6	LVGLLFPSA	23	0.9500	11.45
7	YRVGNAVVQ	92	0.9000	10.84
8	WQGVSGADM	71	0.7000	8.43
9	MLRHVVVLI	79	0.4000	4.82
10	IGNRPKIGW	102	0.4000	4.82
11	LEAQAVLSR	113	0.4000	4.82
12	VNQLPRVGL	0	0.3000	3.61
13	WLVGLLFPS	22	0.3000	3.61
14	VQVIGNRPK	99	0.3000	3.61

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	MLRHVVVLI	79	4.0000	47.62
2	LLNAPVSVS	122	2.5000	29.76
3	VVVLITQHG	83	2.4000	28.57
4	VAVHALCDA	42	2.2000	26.19
5	LRHVVVLIT	80	1.9000	22.62
6	VVLITQHGY	84	1.5000	17.86
7	VGNAVVQVI	94	1.5000	17.86
8	VQVIGNRPK	99	1.4000	16.67
9	LEAQAVLSR	113	1.3000	15.48
10	WRRLEAQAV	110	1.2000	14.29
11	VNQLPRVGL	0	1.1000	13.10

12	IGNRPKIGW	102	1.0000	11.90
13	VIGNRPKIG	101	0.9000	10.71
14	LVGLLFPSA	23	0.8000	9.52
15	FGVDDPRWQ	64	0.8000	9.52

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	LRHVVVLIT	80	4.3000	51.81
2	VVLITQHGY	84	2.5000	30.12
3	VVVLITQHG	83	2.4000	28.92
4	LLNAPVSVS	122	2.1000	25.30
5	LVGLLFPSA	23	1.9500	23.49
6	MLRHVVVLI	79	1.4000	16.87
7	IGNRPKIGW	102	1.4000	16.87
8	LEAQAVLSR	113	1.4000	16.87
9	VNQLPRVGL	0	1.3000	15.66
10	VQVIGNRPK	99	1.3000	15.66
11	WRRLEAQAV	110	1.2000	14.46
12	LAAIATALV	146	1.0000	12.05
13	VHPIEPGRP	12	0.8000	9.64
14	VGNAVVQVI	94	0.8000	9.64
15	VIGNRPKIG	101	0.6000	7.23

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	LRHVVVLIT	80	4.3000	51.81
2	VVLITQHGY	84	2.5000	30.12
3	VVVLITQHG	83	2.4000	28.92
4	LLNAPVSVS	122	2.1000	25.30

5	LVGLLFPSA	23	1.9500	23.49
6	MLRHVVVLI	79	1.4000	16.87
7	IGNRPKIGW	102	1.4000	16.87
8	LEAQAVLSR	113	1.4000	16.87
9	VNQLPRVGL	0	1.3000	15.66
10	VQVIGNRPK	99	1.3000	15.66
11	WRRLEAQAV	110	1.2000	14.46
12	LAAIATALV	146	1.0000	12.05
13	VHPIEPGRP	12	0.8000	9.64
14	VGNAVVQVI	94	0.8000	9.64
15	VIGNRPKIG	101	0.6000	7.23

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	LLNAPVSVS	122	3.4700	38.13
2	YRVGNAVVQ	92	2.9000	31.87
3	MLRHVVVLI	79	2.8000	30.77
4	LRHVVVLIT	80	2.6000	28.57
5	WLVGLLFPS	22	2.4000	26.37
6	FGVDDPRWQ	64	2.4000	26.37
7	VVVLITQHG	83	2.3000	25.27
8	VGNAVVQVI	94	1.8000	19.78
9	LGTDVHPIE	8	1.7000	18.68
10	LVGLLFPSA	23	1.6000	17.58
11	VVLITQHGY	84	1.5000	16.48
12	WRRLEAQAV	110	1.1000	12.09
13	VNQLPRVGL	0	1.0000	10.99
14	VHPIEPGRP	12	0.9000	9.89
15	VAVHALCDA	42	0.7000	7.69

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	MLRHVVVLI	79	3.0000	35.71
2	WRRLEAQAV	110	2.2000	26.19
3	FGVDDPRWQ	64	1.8000	21.43
4	YRVGNAVVQ	92	1.6000	19.05
5	WLVGLLFPS	22	1.5000	17.86
6	LLNAPVSVS	122	1.5000	17.86
7	VVVLITQHG	83	1.4000	16.67
8	VAVHALCDA	42	1.2000	14.29
9	LRHVVVLIT	80	0.9000	10.71
10	VVLITQHGY	84	0.5000	5.95
11	VGNAVVQVI	94	0.5000	5.95
12	VQVIGNRPK	99	0.4000	4.76
13	LEAQAVLSR	113	0.3000	3.57
14	VNQLPRVGL	0	0.1000	1.19

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	MLRHVVVLI	79	3.9000	44.32
2	WRRLEAQAV	110	3.2000	36.36
3	VVVLITQHG	83	2.8000	31.82
4	WLVGLLFPS	22	1.9000	21.59
5	LLNAPVSVS	122	1.9000	21.59
6	VVLITQHGY	84	1.8000	20.45
7	LEAQAVLSR	113	1.8000	20.45
8	LRHVVVLIT	80	1.6000	18.18
9	VGNAVVQVI	94	1.4000	15.91
10	VIGNRPKIG	101	1.3000	14.77
11	VAVHALCDA	42	1.2000	13.64

12	FGVDDPRWQ	64	1.1000	12.50
13	VNQLPRVGL	0	1.0600	12.05
14	WQGVSGADM	71	0.9000	10.23
15	YRVGNAVVQ	92	0.9000	10.23

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	MLRHVVVLI	79	4.0000	47.62
2	LLNAPVSVS	122	2.5000	29.76
3	VVVLITQHG	83	2.4000	28.57
4	VAVHALCDA	42	2.2000	26.19
5	LRHVVVLIT	80	1.9000	22.62
6	VVLITQHGY	84	1.5000	17.86
7	VGNAVVQVI	94	1.5000	17.86
8	VQVIGNRPK	99	1.4000	16.67
9	LEAQAVLSR	113	1.3000	15.48
10	WRRLEAQAV	110	1.2000	14.29
11	VNQLPRVGL	0	1.1000	13.10
12	IGNRPKIGW	102	1.0000	11.90
13	VIGNRPKIG	101	0.9000	10.71
14	LVGLLFPSA	23	0.8000	9.52
15	FGVDDPRWQ	64	0.8000	9.52

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	LRHVVVLIT	80	4.0000	45.98
2	WRRLEAQAV	110	3.2000	36.78
3	VVVLITQHG	83	2.8000	32.18
4	VVLITQHGY	84	2.8000	32.18

5	WQGVSGADM	71	2.2000	25.29
6	LEAQAVLSR	113	1.9000	21.84
7	LLNAPVSVS	122	1.5000	17.24
8	MLRHVVVLI	79	1.3000	14.94
9	VNQLPRVGL	0	1.2600	14.48
10	VIGNRPKIG	101	1.0000	11.49
11	LAAIATALV	146	1.0000	11.49
12	LVGLLFPSA	23	0.9500	10.92
13	VLITQHGYR	85	0.9000	10.34
14	LGLTGRGEG	137	0.9000	10.34
15	VHPIEPGRP	12	0.8000	9.20

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	MLRHVVVLI	79	4.9000	55.68
2	VVVLITQHG	83	3.8000	43.18
3	LLNAPVSVS	122	2.9000	32.95
4	VVLITQHGY	84	2.8000	31.82
5	LEAQAVLSR	113	2.8000	31.82
6	LRHVVVLIT	80	2.6000	29.55
7	VGNAVVQVI	94	2.4000	27.27
8	VIGNRPKIG	101	2.3000	26.14
9	VAVHALCDA	42	2.2000	25.00
10	WRRLEAQAV	110	2.2000	25.00
11	VNQLPRVGL	0	2.0600	23.41
12	ITQHGYRVG	87	1.7000	19.32
13	VQVIGNRPK	99	1.5000	17.05
14	VLSRLLNAP	118	1.4000	15.91
15	LITQHGYRV	86	1.1000	12.50

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	MLRHVVVLI	79	3.9000	44.32
2	WRRLEAQAV	110	3.2000	36.36
3	VVVLITQHG	83	2.8000	31.82
4	WLVGLLFPS	22	1.9000	21.59
5	LLNAPVSVS	122	1.9000	21.59
6	VVLITQHGY	84	1.8000	20.45
7	LEAQAVLSR	113	1.8000	20.45
8	LRHVVVLIT	80	1.6000	18.18
9	VGNAVVQVI	94	1.4000	15.91
10	VIGNRPKIG	101	1.3000	14.77
11	VAVHALCDA	42	1.2000	13.64
12	FGVDDPRWQ	64	1.1000	12.50
13	VNQLPRVGL	0	1.0600	12.05
14	WQGVSGADM	71	0.9000	10.23
15	YRVGNAVVQ	92	0.9000	10.23

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	MLRHVVVLI	79	4.2000	46.67
2	VVVLITQHG	83	3.7000	41.11
3	LRHVVVLIT	80	2.8000	31.11
4	VVLITQHGY	84	2.6000	28.89
5	VGLLFPSAD	24	2.5000	27.78
6	LLNAPVSVS	122	2.5000	27.78
7	VAVHALCDA	42	2.2000	24.44
8	VIGNRPKIG	101	2.2000	24.44
9	VNQLPRVGL	0	2.1000	23.33
10	VLSAAGLGD	51	1.9000	21.11

11	IGNRPKIGW	102	1.9000	21.11
12	VGNAVVQVI	94	1.7000	18.89
13	FGVDDPRWQ	64	1.6000	17.78
14	ITQHGYRVG	87	1.6000	17.78
15	WRRLEAQAV	110	1.5000	16.67

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	LRHVVVLIT	80	4.0000	45.98
2	WRRLEAQAV	110	3.2000	36.78
3	VVVLITQHG	83	2.8000	32.18
4	VVLITQHGY	84	2.8000	32.18
5	WQGVSGADM	71	2.2000	25.29
6	LEAQAVLSR	113	1.9000	21.84
7	LLNAPVSVS	122	1.5000	17.24
8	MLRHVVVLI	79	1.3000	14.94
9	VNQLPRVGL	0	1.2600	14.48
10	VIGNRPKIG	101	1.0000	11.49
11	LAAIATALV	146	1.0000	11.49
12	LVGLLFPSA	23	0.9500	10.92
13	VLITQHGYR	85	0.9000	10.34
14	LGLTGRGEG	137	0.9000	10.34
15	VHPIEPGRP	12	0.8000	9.20

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	WRRLEAQAV	110	2.1000	30.88
2	LRHVVVLIT	80	1.5000	22.06
3	VVVLITQHG	83	1.3000	19.12

4	LLNAPVSVS	122	1.1000	16.18
5	VVLITQHGY	84	0.8000	11.76
6	WQGVSGADM	71	0.7000	10.29
7	YRVGNAVVQ	92	0.4000	5.88
8	VQVIGNRPK	99	0.1000	1.47
9	MLRHVVVLI	79	-0.1000	0
10	VNQLPRVGL	0	-0.2000	0
11	WLVGLLFPS	22	-0.2000	0
12	LVGLLFPSA	23	-0.2000	0
13	VHPIEPGRP	12	-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	LRHVVVLIT	80	4.3000	51.81
2	VVLITQHGY	84	2.5000	30.12
3	VVVLITQHG	83	2.4000	28.92
4	LLNAPVSVS	122	2.1000	25.30
5	LVGLLFPSA	23	1.9500	23.49
6	MLRHVVVLI	79	1.4000	16.87
7	IGNRPKIGW	102	1.4000	16.87
8	LEAQAVLSR	113	1.4000	16.87
9	VNQLPRVGL	0	1.3000	15.66
10	VQVIGNRPK	99	1.3000	15.66
11	WRRLEAQAV	110	1.2000	14.46
12	LAAIATALV	146	1.0000	12.05
13	VHPIEPGRP	12	0.8000	9.64
14	VGNAVVQVI	94	0.8000	9.64
15	VIGNRPKIG	101	0.6000	7.23

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	LRHVVVLIT	80	4.2000	47.19
2	VVVLITQHG	83	2.7000	30.34
3	VVLITQHGY	84	2.6000	29.21
4	WRRLEAQAV	110	2.5000	28.09
5	VLSAAGLGD	51	2.0000	22.47
6	VGLLFPSAD	24	1.8000	20.22
7	WQGVSGADM	71	1.8000	20.22
8	YRVGNAVVQ	92	1.7000	19.10
9	VNQLPRVGL	0	1.3000	14.61
10	IGNRPKIGW	102	1.3000	14.61
11	LLNAPVSVS	122	1.1000	12.36
12	LVGLLFPSA	23	0.9500	10.67
13	VIGNRPKIG	101	0.9000	10.11
14	VSGADMLRH	74	0.8000	8.99
15	LGLTGRGEG	137	0.8000	8.99

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	MLRHVVVLI	79	4.0000	47.62
2	LLNAPVSVS	122	2.5000	29.76
3	VVVLITQHG	83	2.4000	28.57
4	VAVHALCDA	42	2.2000	26.19
5	LRHVVVLIT	80	1.9000	22.62
6	VVLITQHGY	84	1.5000	17.86
7	VGNAVVQVI	94	1.5000	17.86
8	VQVIGNRPK	99	1.4000	16.67
9	LEAQAVLSR	113	1.3000	15.48
10	WRRLEAQAV	110	1.2000	14.29
11	VNQLPRVGL	0	1.1000	13.10
12	IGNRPKIGW	102	1.0000	11.90
13	VIGNRPKIG	101	0.9000	10.71

14	LVGLLFPSA	23	0.8000	9.52
15	FGVDDPRWQ	64	0.8000	9.52

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	MLRHVVVLI	79	3.0000	35.71
2	WRRLEAQAV	110	2.2000	26.19
3	FGVDDPRWQ	64	1.8000	21.43
4	YRVGNAVVQ	92	1.6000	19.05
5	WLVGLLFPS	22	1.5000	17.86
6	LLNAPVSVS	122	1.5000	17.86
7	VVVLITQHG	83	1.4000	16.67
8	VAVHALCDA	42	1.2000	14.29
9	LRHVVVLIT	80	0.9000	10.71
10	VVLITQHGY	84	0.5000	5.95
11	VGNAVVQVI	94	0.5000	5.95
12	VQVIGNRPK	99	0.4000	4.76
13	LEAQAVLSR	113	0.3000	3.57
14	VNQLPRVGL	0	0.1000	1.19

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	MLRHVVVLI	79	4.9000	55.68
2	VVVLITQHG	83	3.8000	43.18
3	LLNAPVSVS	122	2.9000	32.95
4	VVLITQHGY	84	2.8000	31.82
5	LEAQAVLSR	113	2.8000	31.82
6	LRHVVVLIT	80	2.6000	29.55
7	VGNAVVQVI	94	2.4000	27.27

8	VIGNRPKIG	101	2.3000	26.14
9	VAVHALCDA	42	2.2000	25.00
10	WRRLEAQAV	110	2.2000	25.00
11	VNQLPRVGL	0	2.0600	23.41
12	ITQHGYRVG	87	1.7000	19.32
13	VQVIGNRPK	99	1.5000	17.05
14	VLSRLLNAP	118	1.4000	15.91
15	LITQHGYRV	86	1.1000	12.50

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	MLRHVVVLI	79	4.9000	55.68
2	VVVLITQHG	83	3.8000	43.18
3	LLNAPVSVS	122	2.9000	32.95
4	VVLITQHGY	84	2.8000	31.82
5	LEAQAVLSR	113	2.8000	31.82
6	LRHVVVLIT	80	2.6000	29.55
7	VGNAVVQVI	94	2.4000	27.27
8	VIGNRPKIG	101	2.3000	26.14
9	VAVHALCDA	42	2.2000	25.00
10	WRRLEAQAV	110	2.2000	25.00
11	VNQLPRVGL	0	2.0600	23.41
12	ITQHGYRVG	87	1.7000	19.32
13	VQVIGNRPK	99	1.5000	17.05
14	VLSRLLNAP	118	1.4000	15.91
15	LITQHGYRV	86	1.1000	12.50

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	LRHVVVLIT	80	4.0000	40.82
2	MLRHVVVLI	79	3.5000	35.71
3	VNQLPRVGL	0	3.1000	31.63
4	LVGLLFPSA	23	2.8000	28.57
5	VVLITQHGY	84	2.6000	26.53
6	VVQVIGNRP	98	2.4000	24.49
7	WRRLEAQAV	110	2.4000	24.49
8	VVVLITQHG	83	1.9600	20.00
9	LSRLLNAPV	119	1.9000	19.39
10	WLVGLLFPS	22	1.8000	18.37
11	VAVHALCDA	42	1.8000	18.37
12	LITQHGYRV	86	1.8000	18.37
13	VLSAAGLGD	51	1.7000	17.35
14	VHALCDAVL	44	1.4000	14.29
15	LNAPVSVSA	123	1.4000	14.29

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	WRRLEAQAV	110	3.4000	34.69
2	LRHVVVLIT	80	3.0000	30.61
3	WLVGLLFPS	22	2.8000	28.57
4	MLRHVVVLI	79	2.5000	25.51
5	WQGVSGADM	71	2.1800	22.24
6	VNQLPRVGL	0	2.1000	21.43
7	LVGLLFPSA	23	1.8000	18.37
8	VVLITQHGY	84	1.6000	16.33
9	YRVGNAVVQ	92	1.4000	14.29
10	VVQVIGNRP	98	1.4000	14.29
11	VVVLITQHG	83	0.9600	9.80
12	LSRLLNAPV	119	0.9000	9.18
13	VAVHALCDA	42	0.8000	8.16
14	LITQHGYRV	86	0.8000	8.16

15	VLSAAGLGD	51	0.7000	7.14

ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRHVVVLIT	80	4.0000	40.82
2	MLRHVVVLI	79	3.5000	35.71
3	VNQLPRVGL	0	3.1000	31.63
4	LVGLLFPSA	23	2.8000	28.57
5	VVLITQHGY	84	2.6000	26.53
6	VVQVIGNRP	98	2.4000	24.49
7	WRRLEAQAV	110	2.4000	24.49
8	VVVLITQHG	83	1.9600	20.00
9	LSRLLNAPV	119	1.9000	19.39
10	WLVGLLFPS	22	1.8000	18.37
11	VAVHALCDA	42	1.8000	18.37
12	LITQHGYRV	86	1.8000	18.37
13	VLSAAGLGD	51	1.7000	17.35
14	VHALCDAVL	44	1.4000	14.29
15	LNAPVSVSA	123	1.4000	14.29

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VQVIGNRPK	99	4.7000	47.96
2	VVLITQHGY	84	4.5000	45.92
3	WRRLEAQAV	110	4.0000	40.82
4	VLITQHGYR	85	3.7000	37.76
5	WQGVSGADM	71	2.7000	27.55
6	VVVLITQHG	83	2.5000	25.51
7	LRHVVVLIT	80	1.6000	16.33

8	VVQVIGNRP	98	1.6000	16.33
9	YRVGNAVVQ	92	1.5000	15.31
10	VHPIEPGRP	12	1.4000	14.29
11	FGVDDPRWQ	64	1.3000	13.27
12	WLVGLLFPS	22	1.1000	11.22
13	VGNAVVQVI	94	0.6000	6.12
14	LGLTGRGEG	137	0.5000	5.10
15	LEAQAVLSR	113	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	VQVIGNRPK	99	4.7000	47.96
2	VVLITQHGY	84	4.5000	45.92
3	WRRLEAQAV	110	4.0000	40.82
4	VLITQHGYR	85	3.7000	37.76
5	WQGVSGADM	71	2.7000	27.55
6	VVVLITQHG	83	2.5000	25.51
7	LRHVVVLIT	80	1.6000	16.33
8	VVQVIGNRP	98	1.6000	16.33
9	YRVGNAVVQ	92	1.5000	15.31
10	VHPIEPGRP	12	1.4000	14.29
11	FGVDDPRWQ	64	1.3000	13.27
12	WLVGLLFPS	22	1.1000	11.22
13	VGNAVVQVI	94	0.6000	6.12
14	LGLTGRGEG	137	0.5000	5.10
15	LEAQAVLSR	113	0.2000	2.04