



**nHLAPred**  
**A neural network based MHC Class-I Binding Peptide Prediction Server**

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Antigen Name	Untitled
Scanned on	Wed Apr 28 23:41:24 2010
Length of input sequence	111 amino acids
Number of nonamers from input sequence	103
Threshold setting	.5
Number of alleles in query	67
Number of top scorers to be displayed	4
Number of top scorers to be displayed	4
Proteosome Filter	on at 5 threshold
ImmunoProteosome Filter	on at 5 threshold

ALLELE: HLA-A1				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	YETDRNHDL	16	0.050
<b>ANNs+QM</b>	2	DRVLRGSRL	3	0.010
<b>ANNs+QM</b>	3	SIEELEELL	90	0.010
<b>ANNs+QM</b>	4	LEELLKERL	94	0.010

ALLELE: HLA-A2				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	LERRSIEEL	86	0.100
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.010

<b>ANNs+QM</b>	3	MADRVLGRS	1	0.000
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<b>ALLELE: HLA-A*0201</b>				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.980
<b>ANNs+QM</b>	2	LERRSIEEL	86	0.010
<b>ANNs+QM</b>	3	MADRVLGRS	1	0.000

<b>ALLELE: HLA-A*0202</b>				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	YETDRNHDL	16	0.420
<b>ANNs+QM</b>	2	LEELLKERL	94	0.170
<b>ANNs+QM</b>	3	LERRSIEEL	86	0.060
<b>ANNs+QM</b>	4	DRVLGRSRL	3	0.030

<b>ALLELE: HLA-A*0203</b>				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	YETDRNHDL	16	0.460
<b>ANNs+QM</b>	2	SIEELEELL	90	0.460
<b>ANNs+QM</b>	3	NGEEFEVPF	36	0.060
<b>ANNs+QM</b>	4	LERRSIEEL	86	0.040

<b>ALLELE: HLA-A*0206</b>				
Threshold for .5 % with score: .5				

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	0.420
<b>ANNs+QM</b>	2	LERRSIEEL	86	0.060
<b>ANNs+QM</b>	3	LEELLKERL	94	0.030

<b>ALLELE: HLA-A*0205</b>				
Threshold for 4 % with score: 5.950				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	LEELLKERL	94	5.500
<b>QM</b>	2	DRVLRGSRL	3	2.250
<b>QM</b>	3	YETDRNHDL	16	-0.480

<b>ALLELE: HLA-A*1101</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.120
<b>ANNs+QM</b>	2	DRVLRGSRL	3	0.020
<b>ANNs+QM</b>	3	YETDRNHDL	16	0.010
<b>ANNs+QM</b>	4	NGEEFEVPF	36	0.010

<b>ALLELE: HLA-A11</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	MADRVLGRS	1	0.000
<b>ANNs+QM</b>	2	ADRVLGRSR	2	0.000
<b>ANNs+QM</b>	3	DRVLRGSRL	3	0.000

**ALLELE: HLA-A24**

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	7.660
<b>QM</b>	2	NGEEFEVPF	36	3.930
<b>QM</b>	3	SIEELEELL	90	2.250

**ALLELE: HLA-A\*2402**

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	NGEEFEVPF	36	0.230
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.090
<b>ANNs+QM</b>	3	SIEELEELL	90	0.090
<b>ANNs+QM</b>	4	LERRSIEEL	86	0.020

**ALLELE: HLA-A3**

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	0.030
<b>ANNs+QM</b>	2	LERRSIEEL	86	0.030
<b>ANNs+QM</b>	3	NGEEFEVPF	36	0.020
<b>ANNs+QM</b>	4	SIEELEELL	90	0.020

**ALLELE: HLA-A\*3101**

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELEELL	90	-3.912
<b>QM</b>	2	LERRSIEEL	86	-7.824

<b>QM</b>	3	YETDRNHDL	16	-8.517
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<b>ALLELE: HLA-A31</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.150
<b>ANNs+QM</b>	2	DRVLRGSRL	3	0.140
<b>ANNs+QM</b>	3	NGEEFEVPF	36	0.060
<b>ANNs+QM</b>	4	YETDRNHDL	16	0.040

<b>ALLELE: HLA-A*0301</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	NGEEFEVPF	36	0.030
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.010
<b>ANNs+QM</b>	3	SIEELEELL	90	0.010

<b>ALLELE: HLA-A*3302</b>				
Threshold for 4 % with score: -0.105				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELEELL	90	-0.693
<b>QM</b>	2	DRVLRGSRL	3	-3.507
<b>QM</b>	3	YETDRNHDL	16	-4.605

<b>ALLELE: HLA-A68.1</b>				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score

<b>QM</b>	1	SIEELEELL	90	-1.897
<b>QM</b>	2	DRVLRGSRL	3	-2.813
<b>QM</b>	3	YETDRNHDL	16	-3.507

<b>ALLELE: HLA-A20 Cattle</b>				
Threshold for 4 % with score: 3.401				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	2.303
<b>QM</b>	2	SIEELEELL	90	1.609
<b>QM</b>	3	NGEEFEVPF	36	0.916

<b>ALLELE: HLA-A2.1</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.950
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.440
<b>ANNs+QM</b>	3	LEELLKERL	94	0.160
<b>ANNs+QM</b>	4	NGEEFEVPF	36	0.030

<b>ALLELE: HLA-B14</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	1.000
<b>ANNs+QM</b>	2	YETDRNHDL	16	1.000
<b>ANNs+QM</b>	3	SIEELEELL	90	0.330
<b>ANNs+QM</b>	4	LERRSIEEL	86	0.090

<b>ALLELE: HLA-B*2702</b>				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	2.890
<b>QM</b>	2	YETDRNHDL	16	-0.105
<b>QM</b>	3	LERRSIEEL	86	-0.105

<b>ALLELE: HLA-B27</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	0.770
<b>ANNs+QM</b>	2	MADRVLGRS	1	0.000
<b>ANNs+QM</b>	3	ADRVLGRSR	2	0.000

<b>ALLELE: HLA-B*2705</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	1.000
<b>ANNs+QM</b>	2	LERRSIEEL	86	0.100
<b>ANNs+QM</b>	3	SIEELEELL	90	0.010
<b>ANNs+QM</b>	4	LEELKERL	94	0.010

<b>ALLELE: HLA-B*3501</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	0.750
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.110
<b>ANNs+QM</b>	3	NGEEFEVPF	36	0.030

<b>ALLELE: HLA-B*3701</b>				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	YETDRNHDL	16	2.303
<b>QM</b>	2	LERRSIEEL	86	2.303
<b>QM</b>	3	LEELLKERL	94	2.303
<b>QM</b>	4	SIEELEELL	90	1.609

<b>ALLELE: HLA-B*3801</b>				
Threshold for 4 % with score: 0.445				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELEELL	90	2.054
<b>QM</b>	2	NGEEFEVPF	36	1.792
<b>QM</b>	3	LEELLKERL	94	-0.942

<b>ALLELE: HLA-B*3901</b>				
Threshold for 4 % with score: 1.792				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	3.401
<b>QM</b>	2	SIEELEELL	90	2.197
<b>QM</b>	3	YETDRNHDL	16	-0.511

<b>ALLELE: HLA-B*3902</b>				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELEELL	90	0.875
<b>QM</b>	2	DRVLRGSRL	3	0.693



<b>QM</b>	3	NGEEFEVVPF	36	-0.511
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<b>ALLELE: HLA-B40</b>				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	YETDRNHDL	16	2.996
<b>QM</b>	2	LERRSIEEL	86	2.303
<b>QM</b>	3	LEELLKERL	94	2.303

<b>ALLELE: HLA-B*4403</b>				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	YETDRNHDL	16	1.386
<b>QM</b>	2	LERRSIEEL	86	1.386
<b>QM</b>	3	LEELLKERL	94	1.386

<b>ALLELE: HLA-B*5101</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	NGEEFEVVPF	36	0.650
<b>ANNs+QM</b>	2	SIEELEELL	90	0.220
<b>ANNs+QM</b>	3	DRVLRGSRL	3	0.210
<b>ANNs+QM</b>	4	LEELLKERL	94	0.160

<b>ALLELE: HLA-B*5102</b>				
Threshold for 4 % with score: 9.050				
Prediction method	Rank	Sequence	Residue No.	Peptide Score

<b>QM</b>	1	NGEEFEVPF	36	3.030
<b>QM</b>	2	LERRSIEEL	86	2.710
<b>QM</b>	3	LEELLKERL	94	0.450

<b>ALLELE: HLA-B*5103</b>				
Threshold for 4 % with score: 9.280				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGEEFEVPF	36	8.030
<b>QM</b>	2	LERRSIEEL	86	2.710
<b>QM</b>	3	LEELLKERL	94	0.450

<b>ALLELE: HLA-B*5201</b>				
Threshold for 4 % with score: 1.974				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGEEFEVPF	36	1.504
<b>QM</b>	2	LEELLKERL	94	-0.138
<b>QM</b>	3	SIEELEELL	90	-0.639

<b>ALLELE: HLA-B*5301</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	YETDRNHDL	16	0.240
<b>ANNs+QM</b>	2	LEELLKERL	94	0.130
<b>ANNs+QM</b>	3	SIEELEELL	90	0.080
<b>ANNs+QM</b>	4	DRVLRGSRL	3	0.060

<b>ALLELE: HLA-B*5401</b>				
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Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	LEELLKERL	94	0.190
<b>ANNs+QM</b>	2	NGEEFEVPF	36	0.150
<b>ANNs+QM</b>	3	DRVLRGSRL	3	0.090
<b>ANNs+QM</b>	4	SIEELEELL	90	0.090

<b>ALLELE: HLA-B*51</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DRVLRGSRL	3	0.770
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.400
<b>ANNs+QM</b>	3	NGEEFEVPF	36	0.150
<b>ANNs+QM</b>	4	LEELLKERL	94	0.110

<b>ALLELE: HLA-B*5801</b>				
Threshold for 4 % with score: -0.223				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGEEFEVPF	36	1.792
<b>QM</b>	2	SIEELEELL	90	-2.813
<b>QM</b>	3	LEELLKERL	94	-3.411

<b>ALLELE: HLA-B60</b>				
Threshold for 4 % with score: 1.386				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	LEELLKERL	94	5.266
<b>QM</b>	2	YETDRNHDL	16	5.075
<b>QM</b>	3	LERRSIEEL	86	5.075

<b>ALLELE: HLA-B61</b>				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	YETDRNHDL	16	2.773
<b>QM</b>	2	LERRSIEEL	86	2.773
<b>QM</b>	3	LEELLKERL	94	2.079

<b>ALLELE: HLA-B62</b>				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGEEFEVPF	36	-0.233
<b>QM</b>	2	SIEELEELL	90	-1.802
<b>QM</b>	3	LERRSIEEL	86	-3.507

<b>ALLELE: HLA-B7</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	YETDRNHDL	16	0.210
<b>ANNs+QM</b>	2	LERRSIEEL	86	0.150
<b>ANNs+QM</b>	3	SIEELEELL	90	0.100
<b>ANNs+QM</b>	4	DRVLRGSRL	3	0.030

<b>ALLELE: HLA-B*0702</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.340
<b>ANNs+QM</b>	2	LEELLKERL	94	0.050

<b>ANNs+QM</b>	3	LERRSIEEL	86	0.040
<b>ANNs+QM</b>	4	YETDRNHDL	16	0.020

<b>ALLELE: HLA-B8</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.600
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.540
<b>ANNs+QM</b>	3	DRVLRGSRL	3	0.530
<b>ANNs+QM</b>	4	LEELKERL	94	0.520

<b>ALLELE: HLA-Cw*0301</b>				
Threshold for 4 % with score: 2.015				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	3.871
<b>QM</b>	2	YETDRNHDL	16	0.693
<b>QM</b>	3	SIEELEELL	90	0.405

<b>ALLELE: HLA-Cw*0401</b>				
Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	YETDRNHDL	16	4.900
<b>QM</b>	2	SIEELEELL	90	2.370
<b>QM</b>	3	DRVLRGSRL	3	-1.010

<b>ALLELE: HLA-Cw*0602</b>				
Threshold for 4 % with score: 1.482				

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELEELL	90	1.792
<b>QM</b>	2	LEELLKERL	94	1.792
<b>QM</b>	3	LERRSIEEL	86	1.386
<b>QM</b>	4	DRVLRGSRL	3	0.788

<b>ALLELE: HLA-Cw*0702</b>				
Threshold for 4 % with score: 1.212				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGEEFEVPF	36	0.693
<b>QM</b>	2	LERRSIEEL	86	0.365
<b>QM</b>	3	SIEELEELL	90	0.182
<b>QM</b>	4	LEELLKERL	94	0.182

<b>ALLELE: H2-Db</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.390
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.010
<b>ANNs+QM</b>	3	MADRVLGRS	1	0.000

<b>ALLELE: H2-Dd</b>				
Threshold for 4 % with score: 11.800				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGEEFEVPF	36	18.920
<b>QM</b>	2	YETDRNHDL	16	9.910
<b>QM</b>	3	SIEELEELL	90	8.470
<b>QM</b>	4	LERRSIEEL	86	8.160

<b>ALLELE: H2-Kb</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.830
<b>ANNs+QM</b>	2	YETDRNHDL	16	0.200
<b>ANNs+QM</b>	3	DRVLRGSRL	3	0.060
<b>ANNs+QM</b>	4	NGEEFEVPF	36	0.030

<b>ALLELE: H2-Kd</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.850
<b>ANNs+QM</b>	2	DRVLRGSRL	3	0.350
<b>ANNs+QM</b>	3	LEELLKERL	94	0.100
<b>ANNs+QM</b>	4	NGEEFEVPF	36	0.060

<b>ALLELE: H2-Kk</b>				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	LEELLKERL	94	4.382
<b>QM</b>	2	YETDRNHDL	16	3.689
<b>QM</b>	3	LERRSIEEL	86	2.996

<b>ALLELE: H2-Ld</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	YETDRNHDL	16	0.910

<b>ANNs+QM</b>	2	DRVLRGSRL	3	0.380
<b>ANNs+QM</b>	3	LEELLKERL	94	0.040
<b>ANNs+QM</b>	4	LERRSIEEL	86	0.030

<b>ALLELE: HLA-G</b>				
Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELELL	90	9.780
<b>QM</b>	2	DRVLRGSRL	3	4.780
<b>QM</b>	3	YETDRNHDL	16	4.780
<b>QM</b>	4	LEELLKERL	94	2.780

<b>ALLELE: H-2Qa</b>				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	YETDRNHDL	16	13.470
<b>QM</b>	2	DRVLRGSRL	3	7.470
<b>QM</b>	3	LERRSIEEL	86	3.130
<b>QM</b>	4	LEELLKERL	94	1.800

<b>ALLELE: HLA-B*2706</b>				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	7.330
<b>QM</b>	2	LEELLKERL	94	5.000
<b>QM</b>	3	SIEELELL	90	4.330
<b>QM</b>	4	LERRSIEEL	86	2.400



**ALLELE: HLA-B35**

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	9.710
<b>QM</b>	2	NGEEFEVPF	36	5.130
<b>QM</b>	3	LEELLKERL	94	3.530
<b>QM</b>	4	YETDRNHDL	16	2.250

**ALLELE: Mamu-A\*01**

Threshold for 4 % with score: 3.650

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELELL	90	2.950
<b>QM</b>	2	LEELLKERL	94	-2.390
<b>QM</b>	3	YETDRNHDL	16	-2.660

**ALLELE: HLA-A\*0204**

Threshold for 4 % with score: 12.070

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELELL	90	6.010
<b>QM</b>	2	YETDRNHDL	16	5.090
<b>QM</b>	3	LERRSIEEL	86	0.560
<b>QM</b>	4	DRVLRGSRL	3	0.320

**ALLELE: HLA-B\*2703**

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	5.420
<b>QM</b>	2	NGEEFEVPF	36	2.340

<b>QM</b>	3	SIEELEELL	90	2.230
<b>QM</b>	4	LERRSIEEL	86	0.830

<b>ALLELE: HLA-B*2704</b>				
Threshold for 4 % with score: 8.790				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	DRVLRGSRL	3	19.050
<b>QM</b>	2	LEELLKERL	94	6.130
<b>QM</b>	3	YETDRNHDL	16	5.450
<b>QM</b>	4	LERRSIEEL	86	4.650

<b>ALLELE: HLA-B*2902</b>				
Threshold for 4 % with score: 7.750				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	LEELLKERL	94	11.420
<b>QM</b>	2	LERRSIEEL	86	8.430
<b>QM</b>	3	YETDRNHDL	16	6.600
<b>QM</b>	4	SIEELEELL	90	5.420

<b>ALLELE: HLA-A*3301</b>				
Threshold for 4 % with score: 3.840				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SIEELEELL	90	-2.540
<b>QM</b>	2	LERRSIEEL	86	-2.830
<b>QM</b>	3	YETDRNHDL	16	-3.320

<b>ALLELE: HLA-B44</b>				
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Threshold for 4 % with score: 4.900				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	LERRSIEEL	86	9.800
<b>QM</b>	2	LEELLKERL	94	5.650
<b>QM</b>	3	YETDRNHDL	16	2.390

<b>ALLELE: HLA-A*6801</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	NGEEFEVPF	36	0.010
<b>ANNs+QM</b>	2	SIEELEELL	90	0.010
<b>ANNs+QM</b>	3	MADRVLGRS	1	0.000

<b>ALLELE: HLA-A*6802</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SIEELEELL	90	0.970
<b>ANNs+QM</b>	2	DRVLRGSRL	3	0.490
<b>ANNs+QM</b>	3	LEELLKERL	94	0.290
<b>ANNs+QM</b>	4	YETDRNHDL	16	0.130