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

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Antigen Name	Untitled
Scanned on	Tue Mar 30 23:38:08 2010
Length of input sequence	414 amino acids
Number of nonamers from input sequence	406
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
ANNs+QM	1	HVECAAIAL	230	1.000
ANNs+QM	2	SKSRGNLVL	293	0.440
ANNs+QM	3	ALPAGPAAV	350	0.430
ANNs+QM	4	YQDIYFRAD	159	0.360

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALSRIGSGL	237	0.980
ANNs+QM	2	ALPAGPAAV	350	0.970

ANNs+QM	3	DIDDPLFER	84	0.940
ANNs+QM	4	AQAEVALFC	104	0.430

ALLELE: HLA-A*0201

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALSRIGSGL	237	1.000
ANNs+QM	2	SKSRGNLVL	293	1.000
ANNs+QM	3	ALPAGPAAV	350	1.000
ANNs+QM	4	KLVATAIDA	400	0.770

ALLELE: HLA-A*0202

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALPAGPAAV	350	1.000
ANNs+QM	2	KLVATAIDA	400	0.990
ANNs+QM	3	ALSRIGSGL	237	0.980
ANNs+QM	4	HVECAAIAL	230	0.660

ALLELE: HLA-A*0203

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HDAGAPKLV	394	0.980
ANNs+QM	2	ALSRIGSGL	237	0.930
ANNs+QM	3	GAPKLVATA	397	0.760
ANNs+QM	4	APKLVATAI	398	0.480

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALPAGPAAV	350	0.980
ANNs+QM	2	DVEPSAVRL	309	0.800
ANNs+QM	3	HDAGAPKLV	394	0.430
ANNs+QM	4	DDLDTPKAI	370	0.250

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GAPKLVATA	397	10.850
QM	2	ALPAGPAAV	350	10.300
QM	3	LWLDLGHEL	68	9.290
QM	4	DVEPSAVRL	309	9.280

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LADDLDTPK	368	0.990
ANNs+QM	2	LGLLAGHYR	317	0.710
ANNs+QM	3	DIDDPLFER	84	0.280
ANNs+QM	4	SRGNLVLVS	295	0.150

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LGLLAGHYR	317	0.990

ANNs+QM	2	LADDLDTPK	368	0.990
ANNs+QM	3	DIDDPLFER	84	0.470
ANNs+QM	4	AGAPKLVAT	396	0.430

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LFCEDMAAL	110	10.760
QM	2	DDLDTPKAI	370	10.030
QM	3	HRWRTATAL	343	8.720
QM	4	APKLVATAI	398	7.200

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LFCEDMAAL	110	1.000
ANNs+QM	2	RWRTATALP	344	0.940
ANNs+QM	3	GWHVECAAI	228	0.840
ANNs+QM	4	LWLDLGHEL	68	0.830

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HVECAAIAL	230	0.960
ANNs+QM	2	HRWRTATAL	343	0.900
ANNs+QM	3	VVARVRRYL	360	0.840
ANNs+QM	4	LFCEDMAAL	110	0.770

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DIDDPLFER	84	1.281
QM	2	KLVATAIDA	400	-1.427
QM	3	LVLVSALRA	299	-2.526

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DIDDPLFER	84	0.950
ANNs+QM	2	LGLLAGHYR	317	0.850
ANNs+QM	3	LADDLDTPK	368	0.840
ANNs+QM	4	RPGKSDELD	196	0.820

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DDLDTPKAI	370	0.960
ANNs+QM	2	LADDLDTPK	368	0.920
ANNs+QM	3	ALSRIGSGL	237	0.840
ANNs+QM	4	AALDGWVTD	379	0.810

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DIDDPLFER	84	3.807
QM	2	LGLLAGHYR	317	1.099

QM	3	EVALFCEDM	107	0.405
QM	4	DVEPSAVRL	309	0.405

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	EVALFCEDM	107	3.178
QM	2	DVEPSAVRL	309	2.890
QM	3	DIDDPLFER	84	2.708
QM	4	LVLVSALRA	299	2.079

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SKSRGNLVL	293	6.215
QM	2	DIDDPLFER	84	3.689
QM	3	LGLLAGHYR	317	2.996
QM	4	ALSRIGSGL	237	2.708

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALPAGPAAV	350	1.000
ANNs+QM	2	GHDAGAPKL	393	0.990
ANNs+QM	3	KLVATAIDA	400	0.970
ANNs+QM	4	HVECAAIAL	230	0.960

<table>
<tr><th colspan="5">ALLELE: HLA-B14</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 4</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>ANNs+QM</td><td>1</td><td>HRWRTATAL</td><td>343</td><td>1.000</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>RRPGKSDEL</td><td>195</td><td>0.980</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>VRRYLADDL</td><td>364</td><td>0.960</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>SKSRGNLVL</td><td>293</td><td>0.930</td></tr>
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<tr><th colspan="5">ALLELE: HLA-B*2702</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 0.000</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>QM</td><td>1</td><td>HRWRTATAL</td><td>343</td><td>5.704</td></tr>
<tr><td>QM</td><td>2</td><td>RRPGKSDEL</td><td>195</td><td>5.193</td></tr>
<tr><td>QM</td><td>3</td><td>VRRYLADDL</td><td>364</td><td>4.094</td></tr>
<tr><td>QM</td><td>4</td><td>SRGNLVLVS</td><td>295</td><td>2.303</td></tr>
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<tr><th colspan="5">ALLELE: HLA-B27</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 4</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>ANNs+QM</td><td>1</td><td>RRPGKSDEL</td><td>195</td><td>1.000</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>HRWRTATAL</td><td>343</td><td>1.000</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>SRGNLVLVS</td><td>295</td><td>0.900</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>VRRYLADDL</td><td>364</td><td>0.850</td></tr>
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<tr><th colspan="5">ALLELE: HLA-B*2705</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 4</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>ANNs+QM</td><td>1</td><td>RRPGKSDEL</td><td>195</td><td>1.000</td></tr>
</table>

ANNs+QM	2	HRWRTATAL	343	1.000
ANNs+QM	3	VRRYLADDL	364	0.950
ANNs+QM	4	SRGNLVLVS	295	0.870

ALLELE: HLA-B*3501

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APKLVATAI	398	0.970
ANNs+QM	2	RRPGKSDEL	195	0.530
ANNs+QM	3	AALDGWVTD	379	0.500
ANNs+QM	4	SKSRGNLVL	293	0.250

ALLELE: HLA-B*3701

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RDGVDWRDL	95	3.689
QM	2	DDLDTPKAI	370	3.689
QM	3	HDAGAPKLV	394	3.689
QM	4	MVELIEKML	136	2.015

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GHDAGAPKL	393	4.682
QM	2	LWLDLGHEL	68	1.649
QM	3	LFCEDMAAL	110	1.386
QM	4	MVELIEKML	136	1.361

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GHDAGAPKL	393	5.598
QM	2	HRWRTATAL	343	3.401
QM	3	RRPGKSDEL	195	2.708
QM	4	LWLDLGHEL	68	2.485

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SKSRGNLVL	293	2.996
QM	2	LWLDLGHEL	68	0.875
QM	3	MVELIEKML	136	0.875
QM	4	ALSRIGSGL	237	0.875

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LDTPKAIAA	372	1.609
QM	2	VECAAIALS	231	1.386
QM	3	ATALPAGPA	348	1.099
QM	4	RDGVDWRDL	95	0.916

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VECAAIALS	231	1.792

QM	2	DDLDTPKAI	370	1.504
QM	3	HDAGAPKLV	394	1.216
QM	4	LDTPKAIAA	372	0.811

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APKLVATAI	398	1.000
ANNs+QM	2	DPRRPGKSD	193	0.870
ANNs+QM	3	GAPKLVATA	397	0.830
ANNs+QM	4	DDLDTPKAI	370	0.800

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APKLVATAI	398	12.820
QM	2	DPRRPGKSD	193	11.080
QM	3	DDLDTPKAI	370	7.390
QM	4	LGLLAGHYR	317	6.230

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APKLVATAI	398	12.820
QM	2	DPRRPGKSD	193	11.080
QM	3	DDLDTPKAI	370	7.390
QM	4	LGLLAGHYR	317	6.230

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APKLVATAI	398	2.485
QM	2	AQAEVALFC	104	1.974
QM	3	ALPAGPAAV	350	1.281
QM	4	DDLDTPKAI	370	1.194

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APKLVATAI	398	0.910
ANNs+QM	2	DPRRPGKSD	193	0.870
ANNs+QM	3	RPGKSDELD	196	0.640
ANNs+QM	4	SKSRGNLVL	293	0.400

ALLELE: HLA-B*5401

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPRRPGKSD	193	0.940
ANNs+QM	2	APKLVATAI	398	0.900
ANNs+QM	3	RPGKSDELD	196	0.740
ANNs+QM	4	ATALPAGPA	348	0.500

ALLELE: HLA-B*51

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LWLDLGHEL	68	1.000

ANNs+QM	2	DPRRPGKSD	193	0.970
ANNs+QM	3	APKLVATAI	398	0.820
ANNs+QM	4	RRPGKSDEL	195	0.630

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RADRDGVDW	92	4.883
QM	2	GAPKLVATA	397	1.376
QM	3	ATALPAGPA	348	0.693
QM	4	TALPAGPAA	349	0.693

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RDGVDWRDL	95	2.996
QM	2	GNLVLVSAL	297	2.175
QM	3	DDLDTPKAI	370	0.693
QM	4	HDAGAPKLV	394	0.693

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HDAGAPKLV	394	2.303
QM	2	LDTPKAIAA	372	1.609
QM	3	DDLDTPKAI	370	0.693
QM	4	VECAAIALS	231	0.470

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AQAEVALFC	104	2.357
QM	2	ALSRIGSGL	237	1.386
QM	3	ALPAGPAAV	350	1.386
QM	4	KLVATAIDA	400	0.875

ALLELE: HLA-B7

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APKLVATAI	398	1.000
ANNs+QM	2	ALPAGPAAV	350	0.770
ANNs+QM	3	RRPGKSDEL	195	0.670
ANNs+QM	4	DPRRPGKSD	193	0.650

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPRRPGKSD	193	0.980
ANNs+QM	2	RPGKSDELD	196	0.940
ANNs+QM	3	APKLVATAI	398	0.680
ANNs+QM	4	VVARVRRYL	360	0.360

ALLELE: HLA-B8

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VECAAIALS	231	0.670

ANNs+QM	2	YQDIYFRAD	159	0.620
ANNs+QM	3	VRRYLADDL	364	0.610
ANNs+QM	4	RPGKSDELD	196	0.590

ALLELE: HLA-Cw*0301				
Threshold for 4 % with score: 2.015				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GNLVLVSAL	297	3.178
QM	2	LWLDLGHEL	68	2.996
QM	3	DVEPSAVRL	309	2.303
QM	4	TALPAGPAA	349	2.303

ALLELE: HLA-Cw*0401				
Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LFCEDMAAL	110	6.760
QM	2	SKSRGNLVL	293	3.640
QM	3	LWLDLGHEL	68	3.370
QM	4	GHDAGAPKL	393	2.990

ALLELE: HLA-Cw*0602				
Threshold for 4 % with score: 1.482				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GNLVLVSAL	297	2.485
QM	2	MVELIEKML	136	1.887
QM	3	VRRYLADDL	364	1.887
QM	4	LWLDLGHEL	68	1.792

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SRGNLVLVS	295	1.163
QM	2	GNLVLVSAL	297	1.058
QM	3	VRRYLADDL	364	1.058
QM	4	VVARVRRYL	360	0.875

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RDGVDWRDL	95	0.980
ANNs+QM	2	GAPKLVATA	397	0.960
ANNs+QM	3	AALDGWVTD	379	0.900
ANNs+QM	4	TALPAGPAA	349	0.860

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GWHVECAAI	228	15.570
QM	2	AGAPKLVAT	396	12.400
QM	3	GAPKLVATA	397	11.510
QM	4	VVARVRRYL	360	10.580

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GAPKLVATA	397	1.000

ANNs+QM	2	YQDIYFRAD	159	0.980
ANNs+QM	3	TALPAGPAA	349	0.970
ANNs+QM	4	VRRYLADDL	364	0.900

ALLELE: H2-Kd

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRPGKSDEL	195	0.880
ANNs+QM	2	GWHVECAAI	228	0.730
ANNs+QM	3	VVARVRRYL	360	0.650
ANNs+QM	4	APKLVATAI	398	0.500

ALLELE: H2-Kk

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DDLDTPKAI	370	5.298
QM	2	VECAAIALS	231	2.708
QM	3	HDAGAPKLV	394	2.303
QM	4	APKLVATAI	398	2.303

ALLELE: H2-Ld

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SKSRGNLVL	293	0.950
ANNs+QM	2	VRRYLADDL	364	0.640
ANNs+QM	3	GHDAGAPKL	393	0.370
ANNs+QM	4	DVEPSAVRL	309	0.250

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DVEPSAVRL	309	12.650
QM	2	RRPGKSDEL	195	12.370
QM	3	GAPKLVATA	397	12.060
QM	4	VRRYLADDL	364	10.780

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LWLDLGHEL	68	12.710
QM	2	ALSRIGSGL	237	10.260
QM	3	DDLDTPKAI	370	8.580
QM	4	HRWRTATAL	343	8.470

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRPGKSDEL	195	13.870
QM	2	LWLDLGHEL	68	6.130
QM	3	RPGKSDELD	196	5.600
QM	4	DPRRPGKSD	193	4.400

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APKLVATAI	398	12.320

QM	2	ALSRIGSGL	237	11.070
QM	3	HVECAAIAL	230	9.390
QM	4	DPRRPGKSD	193	9.340

ALLELE: Mamu-A*01				
Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HVECAAIAL	230	6.490
QM	2	DVEPSAVRL	309	5.240
QM	3	YQDIYFRAD	159	3.760
QM	4	GAPKLVATA	397	3.570

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALPAGPAAV	350	14.590
QM	2	VVARVRRYL	360	14.200
QM	3	HDAGAPKLV	394	13.760
QM	4	ALSRIGSGL	237	12.940

ALLELE: HLA-B*2703				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRPGKSDEL	195	13.190
QM	2	SRGNLVLVS	295	5.060
QM	3	VRRYLADDL	364	3.230
QM	4	HRWRTATAL	343	2.830

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRPGKSDEL	195	17.790
QM	2	VRRYLADDL	364	16.110
QM	3	RDGVDWRDL	95	11.590
QM	4	GNLVLVSAL	297	10.930

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HVECAAIAL	230	5.080
QM	2	LFCEDMAAL	110	5.030
QM	3	DAVEYGGHD	387	4.610
QM	4	SRGNLVLVS	295	4.220

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DIDDPLFER	84	6.330
QM	2	LADDLDTPK	368	3.430
QM	3	QDVEPSAVR	308	2.670
QM	4	LVLVSALRA	299	2.260

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VECAAIALS	231	5.110

QM	2	GHDAGAPKL	393	4.010
QM	3	APKLVATAI	398	3.930
QM	4	LGLLAGHYR	317	2.570

ALLELE: HLA-A*6801

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LADDLDTPK	368	0.970
ANNs+QM	2	LGLLAGHYR	317	0.880
ANNs+QM	3	APKLVATAI	398	0.840
ANNs+QM	4	QDVEPSAVR	308	0.650

ALLELE: HLA-A*6802

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EVALFCEDM	107	1.000
ANNs+QM	2	TATALPAGP	347	0.960
ANNs+QM	3	HDAGAPKLV	394	0.960
ANNs+QM	4	VVARVRRYL	360	0.940