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

Antigen Name	Untitled
Scanned on	Mon Mar 8 00:24:43 2010
Length of input sequence	379 amino acids
Number of nonamers from input sequence	371
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	SMEGAQGVL	250	1.060
ANNs+QM	2	AKDEIEELL	82	0.550
ANNs+QM	3	GETGGAHRI	324	0.430
ANNs+QM	4	DPEVGRKAA	71	0.260

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SLMDAFRSA	175	0.970
ANNs+QM	2	QMGDAAVSL	168	0.840
ANNs+QM	3	GTGGAPVVA	107	0.550
ANNs+QM	4	SIARKLGAL	116	0.550

ALLELE: HLA-A*0201

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QMGDAAVSL	168	1.000
ANNs+QM	2	SLMDAFRSA	175	1.000
ANNs+QM	3	IMSGAGTAL	214	0.960
ANNs+QM	4	SIARKLGAL	116	0.920

ALLELE: HLA-A*0202

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PLHTNGATL	354	0.990
ANNs+QM	2	IMSGAGTAL	214	0.920
ANNs+QM	3	IESAKAGKL	332	0.450
ANNs+QM	4	GIAALRESC	147	0.420

ALLELE: HLA-A*0203

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IMSGAGTAL	214	0.980
ANNs+QM	2	SIARKLGAL	116	0.930
ANNs+QM	3	INTDAQALL	40	0.720
ANNs+QM	4	SMEGAQGVL	250	0.700

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LAVIKVVGI	8	2.040
ANNs+QM	2	LMSDADVKL	48	0.560
ANNs+QM	3	VGRDSTRGL	58	0.410
ANNs+QM	4	GAQGVLMSI	253	0.350

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IMSGAGTAL	214	9.460
QM	2	PLHTNGATL	354	9.220
QM	3	QMGDAAVSL	168	9.000
QM	4	GTGGAPVVA	107	6.210

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RSNQAENGI	140	0.980
ANNs+QM	2	GDEVRVTVI	300	0.800
ANNs+QM	3	INVDFADVK	204	0.630
ANNs+QM	4	ESAKAGKLT	333	0.580

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	INVDFADVK	204	1.000
ANNs+QM	2	LVQDAAHPD	278	0.940
ANNs+QM	3	IGSARGEGR	225	0.750
ANNs+QM	4	ESAKAGKLT	333	0.600

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VVASIARKL	113	11.370
QM	2	QMGDAAVSL	168	10.990
QM	3	AFRSADEVL	179	8.680

QM	4	SMEGAQGVL	250	8.350

ALLELE: HLA-A*2402				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RSNQAENGI	140	0.980
ANNs+QM	2	PLHTNGATL	354	0.930
ANNs+QM	3	LMSDADVKL	48	0.870
ANNs+QM	4	TPGLINVDF	200	0.650

ALLELE: HLA-A3				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VMGETGGAH	322	0.950
ANNs+QM	2	LVQDAAHPD	278	0.910
ANNs+QM	3	HRIESAKAG	330	0.740
ANNs+QM	4	RSNQAENGI	140	0.670

ALLELE: HLA-A*3101				
Threshold for 4 % with score: -1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SIARKLGAL	116	-3.219
QM	2	NTDAQALLM	41	-3.912
QM	3	LMSDADVKL	48	-3.912

ALLELE: HLA-A31				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IGSARGEGR	225	0.970
ANNs+QM	2	VEFIAINTD	35	0.920
ANNs+QM	3	ESAKAGKLT	333	0.920

ANNs+QM	4	FRSADEVLL	180	0.850

<table>
<tr><th colspan="5">ALLELE: HLA-A*0301</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>INVDFADVK</td><td>204</td><td>0.890</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>ADPEVGRKA</td><td>70</td><td>0.860</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>PLHTNGATL</td><td>354</td><td>0.830</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>LVQDAAHPD</td><td>278</td><td>0.790</td></tr>
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<tr><th colspan="5">ALLELE: HLA-A*3302</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: -0.105</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>IGSARGEGR</td><td>225</td><td>1.099</td></tr>
<tr><td>QM</td><td>2</td><td>ESAKAGKLT</td><td>333</td><td>0.405</td></tr>
<tr><td>QM</td><td>3</td><td>NYLAVIKVV</td><td>6</td><td>-0.693</td></tr>
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<tr><th colspan="5">ALLELE: HLA-A68.1</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 1.609</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>VVASIARKL</td><td>113</td><td>2.079</td></tr>
<tr><td>QM</td><td>2</td><td>GTGGAPVVA</td><td>107</td><td>0.693</td></tr>
<tr><td>QM</td><td>3</td><td>ESAKAGKLT</td><td>333</td><td>0.588</td></tr>
<tr><td>QM</td><td>4</td><td>INVDFADVK</td><td>204</td><td>0.182</td></tr>
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<tr><th colspan="5">ALLELE: HLA-A20 Cattle</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 3.401</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>AKDEIEELL</td><td>82</td><td>6.215</td></tr>
<tr><td>QM</td><td>2</td><td>LMSDADVKL</td><td>48</td><td>3.219</td></tr>
<tr><td>QM</td><td>3</td><td>QMGDAAVSL</td><td>168</td><td>3.219</td></tr>
</table>

QM	4	IMSGAGTAL	214	3.219

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QMGDAAVSL	168	1.000
ANNs+QM	2	IMSGAGTAL	214	1.000
ANNs+QM	3	INTDAQALL	40	0.980
ANNs+QM	4	AKDEIEELL	82	0.950

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SIARKLGAL	116	1.000
ANNs+QM	2	GRSLKAAEI	232	0.980
ANNs+QM	3	DAKDEIEEL	81	0.960
ANNs+QM	4	AKDEIEELL	82	0.880

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FRSADEVLL	180	4.094
QM	2	GRSLKAAEI	232	4.094
QM	3	LMSDADVKL	48	0.405
QM	4	QMGDAAVSL	168	0.405

ALLELE: HLA-B27

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FRSADEVLL	180	1.000
ANNs+QM	2	GRSLKAAEI	232	1.000

ANNs+QM	3	RSNQAENGI	140	0.820
ANNs+QM	4	QGLKGVEFI	30	0.600

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FRSADEVLL	180	1.000
ANNs+QM	2	GRSLKAAEI	232	1.000
ANNs+QM	3	RSNQAENGI	140	0.930
ANNs+QM	4	HRIESAKAG	330	0.600

ALLELE: HLA-B*3501				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TPGLINVDF	200	1.000
ANNs+QM	2	FRSADEVLL	180	0.580
ANNs+QM	3	GRSLKAAEI	232	0.570
ANNs+QM	4	LAVIKVVGI	8	0.140

ALLELE: HLA-B*3701				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GDEVRVTVI	300	3.689
QM	2	FEINEAASL	270	2.303
QM	3	GETGGAHRI	324	2.303
QM	4	IESAKAGKL	332	2.303

ALLELE: HLA-B*3801				
Threshold for 4 % with score: 0.445				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SMEGAQGVL	250	2.054

QM	2	LMSDADVKL	48	1.138
QM	3	INTDAQALL	40	0.956
QM	4	QMGDAAVSL	168	0.956

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AKDEIEELL	82	2.197
QM	2	SMEGAQGVL	250	2.197
QM	3	FRSADEVLL	180	2.015
QM	4	INTDAQALL	40	1.792

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AKDEIEELL	82	3.178
QM	2	VVASIARKL	113	0.875
QM	3	FGTVIDDSL	291	0.875
QM	4	INTDAQALL	40	0.693

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FEINEAASL	270	4.382
QM	2	GEGRSLKAA	230	3.689
QM	3	IESAKAGKL	332	2.996
QM	4	GETGGAHRI	324	2.079

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score

QM	1	FEINEAASL	270	3.401
QM	2	IESAKAGKL	332	2.603
QM	3	DEIEELLRG	84	2.197
QM	4	GEGRSLKAA	230	2.197

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QGLKGVEFI	30	1.000
ANNs+QM	2	DAKDEIEEL	81	1.000
ANNs+QM	3	TPGLINVDF	200	0.980
ANNs+QM	4	LAVIKVVGI	8	0.940

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GAQGVLMSI	253	17.850
QM	2	NYLAVIKVV	6	14.670
QM	3	LAVIKVVGI	8	12.950
QM	4	FEPVDAVSV	345	10.590

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GAQGVLMSI	253	17.850
QM	2	NYLAVIKVV	6	14.670
QM	3	LAVIKVVGI	8	12.950
QM	4	FEPVDAVSV	345	10.590

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TGTGGAPVV	106	4.317
QM	2	QGLKGVEFI	30	4.084
QM	3	NYLAVIKVV	6	3.967
QM	4	GDEVRVTVI	300	2.485

ALLELE: HLA-B*5301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	INTDAQALL	40	1.000
ANNs+QM	2	TPGLINVDF	200	1.000
ANNs+QM	3	DPEVGRKAA	71	0.840
ANNs+QM	4	FEINEAASL	270	0.510

ALLELE: HLA-B*5401				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPEVGRKAA	71	0.910
ANNs+QM	2	TPGLINVDF	200	0.840
ANNs+QM	3	IESAKAGKL	332	0.630
ANNs+QM	4	INTDAQALL	40	0.550

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TPGLINVDF	200	0.950
ANNs+QM	2	DPEVGRKAA	71	0.910
ANNs+QM	3	INTDAQALL	40	0.580
ANNs+QM	4	IESAKAGKL	332	0.530

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RSNQAENGI	140	1.887
QM	2	TPGLINVDF	200	1.099
QM	3	NTDAQALLM	41	0.884
QM	4	GTGGAPVVA	107	0.693

ALLELE: HLA-B60				
Threshold for 4 % with score: 1.386				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IESAKAGKL	332	5.864
QM	2	FEINEAASL	270	5.768
QM	3	FEPVDAVSV	345	2.773
QM	4	GETGGAHRI	324	2.175

ALLELE: HLA-B61				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FEPVDAVSV	345	3.689
QM	2	GEGRSLKAA	230	3.091
QM	3	GETGGAHRI	324	2.868
QM	4	FEINEAASL	270	2.773

ALLELE: HLA-B62				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TPGLINVDF	200	2.262
QM	2	SLMDAFRSA	175	0.788
QM	3	SIARKLGAL	116	-0.693

ALLELE: HLA-B7

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TPGLINVDF	200	1.000
ANNs+QM	2	IMSGAGTAL	214	1.000
ANNs+QM	3	AFRSADEVL	179	0.940
ANNs+QM	4	IESAKAGKL	332	0.890

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPEVGRKAA	71	0.950
ANNs+QM	2	INTDAQALL	40	0.890
ANNs+QM	3	TPGLINVDF	200	0.860
ANNs+QM	4	VASIARKLG	114	0.630

ALLELE: HLA-B8

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ESAKAGKLT	333	0.740
ANNs+QM	2	AKDEIEELL	82	0.690
ANNs+QM	3	KAAEIAINS	236	0.680
ANNs+QM	4	NTDAQALLM	41	0.670

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MSIAGGSDL	259	3.178
QM	2	FEINEAASL	270	2.996
QM	3	LAVIKVVGI	8	2.303
QM	4	QGLKGVEFI	30	1.609

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	INTDAQALL	40	7.490
QM	2	SARGEGRSL	227	7.250
QM	3	AFRSADEVL	179	6.580
QM	4	DAKDEIEEL	81	6.370

ALLELE: HLA-Cw*0602

Threshold for 4 % with score: 1.482

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SIARKLGAL	116	2.079
QM	2	VVASIARKL	113	1.887
QM	3	FGTVIDDSL	291	1.887
QM	4	AKDEIEELL	82	1.792

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TPGLINVDF	200	2.667
QM	2	VVASIARKL	113	1.058
QM	3	NYLAVIKVV	6	0.875
QM	4	EAASLVQDA	274	0.748

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FIAINTDAQ	37	1.000
ANNs+QM	2	PLHTNGATL	354	1.000
ANNs+QM	3	VMGETGGAH	322	0.940
ANNs+QM	4	FEINEAASL	270	0.890

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VGRDSTRGL	58	19.940
QM	2	QMGDAAVSL	168	15.440
QM	3	GAPVVASIA	110	13.030
QM	4	RSNQAENGI	140	12.640

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PLHTNGATL	354	1.000
ANNs+QM	2	AKDEIEELL	82	0.980
ANNs+QM	3	IMSGAGTAL	214	0.980
ANNs+QM	4	VVASIARKL	113	0.920

ALLELE: H2-Kd

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PLHTNGATL	354	0.990
ANNs+QM	2	RSNQAENGI	140	0.980
ANNs+QM	3	FEINEAASL	270	0.970
ANNs+QM	4	SARGEGRSL	227	0.940

ALLELE: H2-Kk

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GETGGAHRI	324	6.908
QM	2	GDEVRVTVI	300	4.605
QM	3	FEPVDAVSV	345	4.317
QM	4	FEINEAASL	270	3.401

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TPGLINVDF	200	1.000
ANNs+QM	2	MSIAGGSDL	259	1.000
ANNs+QM	3	IESAKAGKL	332	0.910
ANNs+QM	4	IMSGAGTAL	214	0.710

ALLELE: HLA-G				
Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VVASIARKL	113	10.780
QM	2	FRSADEVLL	180	9.980
QM	3	PLHTNGATL	354	9.510
QM	4	DAKDEIEEL	81	9.450

ALLELE: H-2Qa				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GETGGAHRI	324	8.000
QM	2	FGTVIDDSL	291	7.970
QM	3	VVASIARKL	113	6.900
QM	4	MSIAGGSDL	259	6.570

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GEGRSLKAA	230	6.250
QM	2	FRSADEVLL	180	5.330
QM	3	SARGEGRSL	227	4.540

QM	4	SIARKLGAL	116	4.360

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PVDAVSVPL	347	10.610
QM	2	GAQGVLMSI	253	9.350
QM	3	PLHTNGATL	354	7.410
QM	4	VVASIARKL	113	7.230

ALLELE: Mamu-A*01

Threshold for 4 % with score: 3.650

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QGLKGVEFI	30	4.720
QM	2	SLMDAFRSA	175	2.820
QM	3	AKDEIEELL	82	2.120
QM	4	INTDAQALL	40	1.870

ALLELE: HLA-A*0204

Threshold for 4 % with score: 12.070

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VASIARKLG	114	14.430
QM	2	INTDAQALL	40	13.750
QM	3	PLHTNGATL	354	12.430
QM	4	IMSGAGTAL	214	12.060

ALLELE: HLA-B*2703

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FRSADEVLL	180	10.700
QM	2	HRIESAKAG	330	6.370

QM	3	GRSLKAAEI	232	6.160
QM	4	AKDEIEELL	82	2.500

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GRSLKAAEI	232	10.460
QM	2	FRSADEVLL	180	8.300
QM	3	MSIAGGSDL	259	8.260
QM	4	GEGRSLKAA	230	8.220

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEIEELLRG	84	12.700
QM	2	IMSGAGTAL	214	12.510
QM	3	EGGGTGTGG	102	10.460
QM	4	FEINEAASL	270	10.010

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FIAINTDAQ	37	3.170
QM	2	DTLIVIPND	156	2.600
QM	3	VSVPLHTNG	351	1.510
QM	4	LVQDAAHPD	278	0.920

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FEINEAASL	270	8.810

QM	2	GETGGAHRI	324	8.190
QM	3	GEGRSLKAA	230	5.990
QM	4	DAKDEIEEL	81	5.910

ALLELE: HLA-A*6801

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LVQDAAHPD	278	0.980
ANNs+QM	2	ESAKAGKLT	333	0.920
ANNs+QM	3	VVASIARKL	113	0.850
ANNs+QM	4	PVDAVSVPL	347	0.730

ALLELE: HLA-A*6802

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VASIARKLG	114	1.000
ANNs+QM	2	VVASIARKL	113	0.970
ANNs+QM	3	QGLKGVEFI	30	0.960
ANNs+QM	4	VFVTAGEGG	96	0.960