



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

[Home](#) [ComPred](#) [ANNPred](#) [References](#) [Help](#) [Matrices](#) [Team](#) [Contact](#)

Antigen Name	Untitled
Scanned on	Wed Apr 14 00:06:25 2010
Length of input sequence	358 amino acids
Number of nonamers from input sequence	350
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	SADGAVYTL	171	1.000
<b>ANNs+QM</b>	2	AADPLGRVL	247	0.970
<b>ANNs+QM</b>	3	ALRPGADSA	82	0.860
<b>ANNs+QM</b>	4	SDDHGTAFL	119	0.860

ALLELE: HLA-A2				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SADGAVYTL	171	1.000
<b>ANNs+QM</b>	2	ALRPGADSA	82	0.870

<b>ANNs+QM</b>	3	HVAPRVIFL	102	0.820
<b>ANNs+QM</b>	4	RRFIGLLML	11	0.810

<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	ALRPGADSA	82	1.000
<b>ANNs+QM</b>	2	HVAPRVIFL	102	1.000
<b>ANNs+QM</b>	3	VAGCSSNPL	23	0.990
<b>ANNs+QM</b>	4	FLPGPAAAL	109	0.990

<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	DPASGAATV	186	6.620
<b>ANNs+QM</b>	2	FLPGPAAAL	109	1.000
<b>ANNs+QM</b>	3	ATTMAADPL	243	0.970
<b>ANNs+QM</b>	4	ALTSDDHGT	116	0.960

<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	FLPGPAAAL	109	0.970
<b>ANNs+QM</b>	2	SADGAVYTL	171	0.940
<b>ANNs+QM</b>	3	HVAPRVIFL	102	0.930
<b>ANNs+QM</b>	4	LAARGGYFV	127	0.730

<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	HVAPRVIFL	102	1.000
<b>ANNs+QM</b>	2	AVQRRFIGL	8	0.990
<b>ANNs+QM</b>	3	LAARGGYFV	127	0.980
<b>ANNs+QM</b>	4	SGHTARVNV	140	0.950

<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	FLPGPAAAL	109	14.370
<b>QM</b>	2	ATTMAADPL	243	11.590
<b>QM</b>	3	HVAPRVIFL	102	9.480
<b>QM</b>	4	AADPLGRVL	247	9.330

<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	VRPLSGHPR	61	0.950
<b>ANNs+QM</b>	2	ALTSDDHGT	116	0.610
<b>ANNs+QM</b>	3	PVRQAPYGL	279	0.520
<b>ANNs+QM</b>	4	ADLSSGHTA	136	0.330

<b>ALLELE: HLA-A11</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	TDFTAIARR	154	0.990

<b>ANNs+QM</b>	2	RTKIFARVD	197	0.930
<b>ANNs+QM</b>	3	AVYTLAKNP	175	0.850
<b>ANNs+QM</b>	4	RQLVALRPG	78	0.820

<b>ALLELE: HLA-A24</b>				
Threshold for 4 % with score: 7.670				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	IGLLMLSVL	14	10.660
<b>QM</b>	2	TQGNTTVVL	209	10.480
<b>QM</b>	3	ADGHAQQAL	229	9.220
<b>QM</b>	4	PVRQAPYGL	279	8.140

<b>ALLELE: HLA-A*2402</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	IARRSDGKL	159	0.810
<b>ANNs+QM</b>	2	PVRQAPYGL	279	0.790
<b>ANNs+QM</b>	3	AAHTDFTAI	151	0.750
<b>ANNs+QM</b>	4	SADGAVYTL	171	0.710

<b>ALLELE: HLA-A3</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	VRPLSGHPR	61	0.980
<b>ANNs+QM</b>	2	TIGADGHAQ	226	0.970
<b>ANNs+QM</b>	3	AVYTLAKNP	175	0.950
<b>ANNs+QM</b>	4	RVIFLPGPA	106	0.940

<b>ALLELE: HLA-A*3101</b>				
Threshold for 4 % with score: -1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	RVIFLPGPA	106	-2.120
<b>QM</b>	2	TDFTAIARR	154	-2.120
<b>QM</b>	3	AVQRRFIGL	8	-2.526

<b>ALLELE: HLA-A31</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	VRPLSGHPR	61	1.000
<b>ANNs+QM</b>	2	TDFTAIARR	154	1.000
<b>ANNs+QM</b>	3	LAARGGYFV	127	0.860
<b>ANNs+QM</b>	4	RRFIGLLML	11	0.850

<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	AVYTLAKNP	175	0.980
<b>ANNs+QM</b>	2	ADLSSGHTA	136	0.920
<b>ANNs+QM</b>	3	AFDETSDTL	330	0.860
<b>ANNs+QM</b>	4	AAHTDFTAI	151	0.850

<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	AVQRRFIGL	8	-0.693
<b>QM</b>	2	HVAPRVIFL	102	-0.693

<b>QM</b>	3	VIFLPGPAA	107	-0.693
-----------	---	-----------	-----	--------

<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	HVAPRVIFL	102	2.485
<b>QM</b>	2	RVIFLPGPA	106	2.079
<b>QM</b>	3	AVQRRFIGL	8	1.386

<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	VRPLSGHPR	61	4.382
<b>QM</b>	2	FLPGPAAAL	109	2.708
<b>QM</b>	3	RRFIGLLML	11	2.303
<b>QM</b>	4	RRSDGKLVL	161	2.303

<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	FLPGPAAAL	109	1.000
<b>ANNs+QM</b>	2	ALTSDDHGT	116	0.970
<b>ANNs+QM</b>	3	ATTMAADPL	243	0.930
<b>ANNs+QM</b>	4	TTMAADPLG	244	0.900

<b>ALLELE: HLA-B14</b>				
Threshold for 4 % with score: 4				

Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	RRFIGLLML	11	1.000
<b>ANNs+QM</b>	2	IGLLMLSVL	14	0.980
<b>ANNs+QM</b>	3	RRSDGKLVL	161	0.960
<b>ANNs+QM</b>	4	SADGAVYTL	171	0.960

<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	RRFIGLLML	11	6.802
<b>QM</b>	2	RRSDGKLVL	161	5.193
<b>QM</b>	3	TQGNTTVVL	209	1.792
<b>QM</b>	4	VRPLSGHPR	61	1.386

<b>ALLELE: HLA-B*27</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	RRFIGLLML	11	1.000
<b>ANNs+QM</b>	2	RRSDGKLVL	161	1.000
<b>ANNs+QM</b>	3	RTKIFARVD	197	0.400
<b>ANNs+QM</b>	4	LAARGGYFV	127	0.330

<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	RRFIGLLML	11	1.000
<b>ANNs+QM</b>	2	RRSDGKLVL	161	1.000
<b>ANNs+QM</b>	3	VRPLSGHPR	61	0.970

<b>ANNs+QM</b>	4	TDFTAIARR	154	0.610
----------------	---	-----------	-----	-------

<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	DPASGAATV	186	0.970
<b>ANNs+QM</b>	2	RPLSGHPRA	62	0.920
<b>ANNs+QM</b>	3	RRSDGKLVL	161	0.880
<b>ANNs+QM</b>	4	AFDETSDTL	330	0.840

<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	SDDHGTAFL	119	5.298
<b>QM</b>	2	ADPLGRVLI	248	5.298
<b>QM</b>	3	ADGHAQQAL	229	3.689
<b>QM</b>	4	RRFIGLLML	11	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	AFDETSDTL	330	2.485
<b>QM</b>	2	SADGAVYTL	171	2.054
<b>QM</b>	3	DHGTAFLAA	121	1.361
<b>QM</b>	4	AADPLGRVL	247	1.361

<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	RRFIGLLML	11	3.807
<b>QM</b>	2	AFDETSDTL	330	2.890
<b>QM</b>	3	RRSDGKLVL	161	2.708
<b>QM</b>	4	SADGAVYTL	171	2.603

<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	TQGNTTVVL	209	2.996
<b>QM</b>	2	IGLLMLSVL	14	0.875
<b>QM</b>	3	AADPLGRVL	247	0.875
<b>QM</b>	4	SNTVIGYDL	301	0.875

<b>ALLELE: HLA-B*40</b>				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	ADLSSGHTA	136	2.303
<b>QM</b>	2	ADGHAQQAL	229	1.609
<b>QM</b>	3	SDDHGTAFL	119	0.223

<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	SDGKLVLS	163	1.099
<b>QM</b>	2	LGSADGAVY	169	1.099
<b>QM</b>	3	ADLSSGHTA	136	0.693

<b>QM</b>	4	SDDHGTAFL	119	0.405
-----------	---	-----------	-----	-------

<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	DPASGAATV	186	1.000
<b>ANNs+QM</b>	2	AAHTDFTAI	151	0.920
<b>ANNs+QM</b>	3	IQLLMLSVL	14	0.890
<b>ANNs+QM</b>	4	LAARGGYFV	127	0.850

<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	AAHTDFTAI	151	13.360
<b>QM</b>	2	LAARGGYFV	127	11.260
<b>QM</b>	3	DPASGAATV	186	11.000
<b>QM</b>	4	SGHTARVNV	140	10.620

<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	AAHTDFTAI	151	13.360
<b>QM</b>	2	LAARGGYFV	127	11.260
<b>QM</b>	3	DPASGAATV	186	11.000
<b>QM</b>	4	SGHTARVNV	140	10.620

<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	IGLLMLSVL	14	4.084
<b>QM</b>	2	TQGNTTVVL	209	3.497
<b>QM</b>	3	AADPLGRVL	247	2.262
<b>QM</b>	4	LGSADGAVY	169	2.197

<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	RPLSGHPRA	62	1.000
<b>ANNs+QM</b>	2	DPASGAATV	186	0.990
<b>ANNs+QM</b>	3	NPAVDPASG	182	0.430
<b>ANNs+QM</b>	4	RRSDGKLVL	161	0.420

<b>ALLELE: HLA-B*5401</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	RPLSGHPRA	62	1.000
<b>ANNs+QM</b>	2	DPASGAATV	186	0.990
<b>ANNs+QM</b>	3	NPAVDPASG	182	0.790
<b>ANNs+QM</b>	4	IARRSDGKL	159	0.560

<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	VAGCSSNPL	23	1.000
<b>ANNs+QM</b>	2	DPASGAATV	186	0.990
<b>ANNs+QM</b>	3	RRFIGLLML	11	0.960

<b>ANNs+QM</b>	4	RPLSGHPRA	62	0.960
----------------	---	-----------	----	-------

<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	RAGQGATTM	238	1.194
<b>QM</b>	2	AADPLGRVL	247	1.194
<b>QM</b>	3	ATTMAADPL	243	0.693
<b>QM</b>	4	IARRSDGKL	159	0.501

<b>ALLELE: HLA-B60</b>				
Threshold for 4 % with score: 1.386				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SDDHGTAFL	119	2.996
<b>QM</b>	2	ADGHAQQAL	229	2.996
<b>QM</b>	3	SNTVIGYDL	301	2.175
<b>QM</b>	4	IGLLMLSVL	14	2.079

<b>ALLELE: HLA-B61</b>				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	ADLSSGHTA	136	1.609
<b>QM</b>	2	LAARGGYFV	127	1.099
<b>QM</b>	3	DPASGAATV	186	0.693
<b>QM</b>	4	RPLSGHPRA	62	0.095

<b>ALLELE: HLA-B62</b>				
------------------------	--	--	--	--

Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	ALRPGADSA	82	2.667
<b>QM</b>	2	TQGNTTVVL	209	2.357
<b>QM</b>	3	FLPGPAAAL	109	0.875
<b>QM</b>	4	LGSADGAVY	169	0.788

<b>ALLELE: HLA-B7</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	AVQRRFIGL	8	1.000
<b>ANNs+QM</b>	2	FLPGPAAAL	109	1.000
<b>ANNs+QM</b>	3	PVRQAPYGL	279	1.000
<b>ANNs+QM</b>	4	DPASGAATV	186	0.980

<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	DPASGAATV	186	1.000
<b>ANNs+QM</b>	2	RPLSGHPRA	62	0.980
<b>ANNs+QM</b>	3	NPAVDPASG	182	0.960
<b>ANNs+QM</b>	4	FTAIARRSD	156	0.840

<b>ALLELE: HLA-B8</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	RRFIGLLML	11	0.660
<b>ANNs+QM</b>	2	AADPLGRVL	247	0.640
<b>ANNs+QM</b>	3	LAARGGYFV	127	0.630

<b>ANNs+QM</b>	4	FTAIARRSD	156	0.620
----------------	---	-----------	-----	-------

<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	IPLLMLSVL	14	3.178
<b>QM</b>	2	YGLAGSREL	285	2.996
<b>QM</b>	3	AVQRRFIGL	8	2.708
<b>QM</b>	4	RRFIGLLML	11	2.485

<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	SDDHGTAFL	119	11.170
<b>QM</b>	2	SADGAVYTL	171	8.780
<b>QM</b>	3	SNTVIGYDL	301	8.370
<b>QM</b>	4	AFDETSDTL	330	8.230

<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	IPLLMLSVL	14	2.580
<b>QM</b>	2	AADPLGRVL	247	1.982
<b>QM</b>	3	SNTVIGYDL	301	1.792
<b>QM</b>	4	RRFIGLLML	11	1.482

<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	SDGKLVLS	163	1.163
<b>QM</b>	2	ADGHAQQAL	229	1.058
<b>QM</b>	3	RRFIGLLML	11	0.875
<b>QM</b>	4	IGLLMLSVL	14	0.875

<b>ALLELE: H2-Db</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	FLPGPAAAL	109	1.000
<b>ANNs+QM</b>	2	AAHTDFTAI	151	1.000
<b>ANNs+QM</b>	3	ADGHAQQAL	229	1.000
<b>ANNs+QM</b>	4	RAGQGATTM	238	1.000

<b>ALLELE: H2-Dd</b>				
Threshold for 4 % with score: 11.800				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	NGTRQLVAL	75	17.930
<b>QM</b>	2	FLPGPAAAL	109	14.610
<b>QM</b>	3	SGHTARVNV	140	14.090
<b>QM</b>	4	ADPLGRVLI	248	12.290

<b>ALLELE: H2-Kb</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	SADGAVYTL	171	1.000
<b>ANNs+QM</b>	2	AADPLGRVL	247	0.990
<b>ANNs+QM</b>	3	AFDETSDTL	330	0.960

<b>ANNs+QM</b>	4	AAHTDFTAI	151	0.950
----------------	---	-----------	-----	-------

<b>ALLELE: H2-Kd</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	DPASGAATV	186	0.920
<b>ANNs+QM</b>	2	FLPGPAAAL	109	0.880
<b>ANNs+QM</b>	3	AADPLGRVL	247	0.880
<b>ANNs+QM</b>	4	PVRQAPYGL	279	0.840

<b>ALLELE: H2-Kk</b>				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	ADPLGRVLI	248	5.298
<b>QM</b>	2	SDDHGTAFL	119	2.079
<b>QM</b>	3	AAHTDFTAI	151	1.609
<b>QM</b>	4	SDGKLVLS	163	1.386

<b>ALLELE: H2-Ld</b>				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>ANNs+QM</b>	1	RRSDGKLVL	161	0.950
<b>ANNs+QM</b>	2	RPLSGHPRA	62	0.940
<b>ANNs+QM</b>	3	DPASGAATV	186	0.890
<b>ANNs+QM</b>	4	RRFIGLLML	11	0.770

<b>ALLELE: HLA-G</b>				
----------------------	--	--	--	--



Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	FLPGPAAAL	109	17.570
<b>QM</b>	2	HVAPRVIFL	102	11.780
<b>QM</b>	3	AVQRRFIGL	8	10.110
<b>QM</b>	4	RRSDGKLVL	161	9.970

ALLELE: H-2Qa				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SNTVIGYDL	301	10.970
<b>QM</b>	2	NGTRQLVAL	75	8.340
<b>QM</b>	3	ALTSDDHGT	116	8.290
<b>QM</b>	4	VRPLSGHPR	61	6.530

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	VRPLSGHPR	61	8.890
<b>QM</b>	2	RRSDGKLVL	161	5.000
<b>QM</b>	3	RPLSGHPRA	62	4.510
<b>QM</b>	4	ALTSDDHGT	116	3.510

ALLELE: HLA-B35				
Threshold for 4 % with score: 8.350				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	AVQRRFIGL	8	14.360
<b>QM</b>	2	AAHTDFTAI	151	12.400
<b>QM</b>	3	NPAVDPASG	182	8.600

<b>QM</b>	4	HVAPRVIFL	102	8.250
-----------	---	-----------	-----	-------

<b>ALLELE: Mamu-A*01</b>				
Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	VAGCSSNPL	23	5.160
<b>QM</b>	2	AAHTDFTAI	151	4.390
<b>QM</b>	3	HVAPRVIFL	102	4.120
<b>QM</b>	4	AVQRRFIGL	8	3.080

<b>ALLELE: HLA-A*0204</b>				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	FLPGPAAAL	109	22.000
<b>QM</b>	2	SADGAVYTL	171	17.890
<b>QM</b>	3	AFDETSDTL	330	14.270
<b>QM</b>	4	NVADAAHTD	147	12.560

<b>ALLELE: HLA-B*2703</b>				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	VRPLSGHPR	61	9.980
<b>QM</b>	2	RRFIGLLML	11	9.610
<b>QM</b>	3	RRSDGKLVL	161	8.360
<b>QM</b>	4	SDDHGTAFL	119	5.830

<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	VRPLSGHPR	61	13.380
<b>QM</b>	2	RRFIGLLML	11	13.310
<b>QM</b>	3	ADGHAQQAL	229	11.470
<b>QM</b>	4	YGLAGSREL	285	10.920

<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	PVRQAPYGL	279	10.100
<b>QM</b>	2	SADGAVYTL	171	9.650
<b>QM</b>	3	TQGNTTVVL	209	7.300
<b>QM</b>	4	SDGKLVLS	163	6.320

<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	LAKNPAVDP	179	4.270
<b>QM</b>	2	TDFTAIARR	154	3.200
<b>QM</b>	3	VIFLPGPAA	107	3.170
<b>QM</b>	4	VAGCSSNPL	23	1.700

<b>ALLELE: HLA-B*44</b>				
Threshold for 4 % with score: 4.900				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
<b>QM</b>	1	SADGAVYTL	171	6.560
<b>QM</b>	2	ADGHAQQAL	229	3.540
<b>QM</b>	3	FLPGPAAAL	109	1.950

<b>QM</b>	4	SDDHGTAFL	119	1.150
-----------	---	-----------	-----	-------

<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	NVADAAHTD	147	0.970
<b>ANNs+QM</b>	2	VRPLSGHPR	61	0.950
<b>ANNs+QM</b>	3	RQLVALRPG	78	0.780
<b>ANNs+QM</b>	4	SADGAVYTL	171	0.760

<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	FTAIARRSD	156	1.000
<b>ANNs+QM</b>	2	HVAPRVIFL	102	0.990
<b>ANNs+QM</b>	3	SGHTARVNV	140	0.990
<b>ANNs+QM</b>	4	SADGAVYTL	171	0.960