



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	Thu Feb 25 23:16:16 2010
Length of input sequence	461 amino acids
Number of nonamers from input sequence	453
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	MVDQAALGA	211	1.000
ANNs+QM	2	AALGAAIRY	215	0.990
ANNs+QM	3	AADLGAKVI	190	0.970
ANNs+QM	4	AAIRYAAVD	219	0.770

ALLELE: HLA-A2				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QLAQATLDV	172	1.000
ANNs+QM	2	GLPDAHQKL	327	1.000

ANNs+QM	3	AALSVLVGL	437	1.000
ANNs+QM	4	VLGAIVHA	182	0.960

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QLAQATLDV	172	1.000
ANNs+QM	2	VLGAIVHA	182	1.000
ANNs+QM	3	GVAPAARLL	145	0.990
ANNs+QM	4	AVDKDAVIV	225	0.990

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALGAAIRYA	216	1.000
ANNs+QM	2	GLPDAHQKL	327	1.000
ANNs+QM	3	QLAQATLDV	172	0.990
ANNs+QM	4	AVAALTWQL	393	0.980

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GIAAPGENI	305	2.640
ANNs+QM	2	DCDGHGTLV	122	1.000
ANNs+QM	3	SMPGPWVGI	298	0.990
ANNs+QM	4	QLAQATLDV	172	0.980

ALLELE: HLA-A*0206				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QLAQATLDV	172	1.000
ANNs+QM	2	VLGAIVHA	182	0.970
ANNs+QM	3	WWQPYVLSV	277	0.930
ANNs+QM	4	AVAALTWQL	393	0.910

ALLELE: HLA-A*0205				
Threshold for 4 % with score: 5.950				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AVAALTWQL	393	12.160
QM	2	WVGIAAPGE	303	10.630
QM	3	GHGTLVAGI	125	9.280
QM	4	GVAPAARLL	145	9.210

ALLELE: HLA-A*1101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GLNATEVVR	361	0.880
ANNs+QM	2	LVALSGTSY	335	0.870
ANNs+QM	3	TSYAAGYVS	341	0.780
ANNs+QM	4	GLPDAHQKL	327	0.480

ALLELE: HLA-A11				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GLNATEVVR	361	1.000

ANNs+QM	2	IVAAAGNTG	232	0.960
ANNs+QM	3	GVAPAARLL	145	0.950
ANNs+QM	4	AVDKDAVIV	225	0.900

ALLELE: HLA-A24				
Threshold for 4 % with score: 7.670				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DRMVDQAAL	209	12.110
QM	2	DPQLAQATL	170	10.250
QM	3	MIRAAFACL	1	8.670
QM	4	AGAAALSVL	434	8.520

ALLELE: HLA-A*2402				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RYAAVDKDA	222	0.900
ANNs+QM	2	SMPGPWVGI	298	0.790
ANNs+QM	3	GHGTLVAGI	125	0.720
ANNs+QM	4	GLPDAHQKL	327	0.540

ALLELE: HLA-A3				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RAAFACLAA	3	0.990
ANNs+QM	2	AALGAAIRY	215	0.980
ANNs+QM	3	RNVAFAGAA	429	0.960
ANNs+QM	4	RLTATAHRG	370	0.900

ALLELE: HLA-A*3101				
Threshold for 4 % with score: -1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLNATEVVR	361	0.693
QM	2	AVAALTWQL	393	-2.303
QM	3	AVLAGAIVH	181	-2.526

ALLELE: HLA-A31				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GLNATEVVR	361	0.900
ANNs+QM	2	PAWAIGPPV	22	0.840
ANNs+QM	3	IRAAFACLA	2	0.820
ANNs+QM	4	IRYAAVDKD	221	0.750

ALLELE: HLA-A*0301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QLAQATLDV	172	1.000
ANNs+QM	2	SMPGPWVGI	298	1.000
ANNs+QM	3	ATLDVAVLA	176	0.930
ANNs+QM	4	AVLAGAIVH	181	0.930

ALLELE: HLA-A*3302				
Threshold for 4 % with score: -0.105				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLNATEVVR	361	2.197
QM	2	MIRAAFACL	1	-0.693

QM	3	AIGPPVVDA	25	-0.693
-----------	---	-----------	----	--------

ALLELE: HLA-A68.1				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVAPAARLL	145	2.485
QM	2	AVLAGAIVH	181	2.079
QM	3	AVAALTWQL	393	2.079
QM	4	LVGLTAATV	442	2.079

ALLELE: HLA-A20 Cattle				
Threshold for 4 % with score: 3.401				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLNATEVVR	361	4.787
QM	2	DKDAVIVAA	227	4.605
QM	3	PKDTTPRNV	423	3.401
QM	4	SMPGPWVGI	298	2.708

ALLELE: HLA-A2.1				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SMPGPWVGI	298	1.000
ANNs+QM	2	GIAAPGENI	305	1.000
ANNs+QM	3	GVAPAARLL	145	0.990
ANNs+QM	4	GAIVHAADL	185	0.990

ALLELE: HLA-B14				
------------------------	--	--	--	--

Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GAIVHAADL	185	1.000
ANNs+QM	2	DAHQKLVAL	330	1.000
ANNs+QM	3	DPQLAQATL	170	0.930
ANNs+QM	4	QATLDVAVL	175	0.930

ALLELE: HLA-B*2702				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SRPDDPRNW	258	3.401
QM	2	IRAAFACLA	2	2.996
QM	3	DRMVDQAAL	209	2.890
QM	4	IRYAAVDKD	221	2.303

ALLELE: HLA-B27				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IRAAFACLA	2	0.850
ANNs+QM	2	IRYAAVDKD	221	0.850
ANNs+QM	3	PRNVAFAGA	428	0.740
ANNs+QM	4	DRMVDQAAL	209	0.660

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IRAAFACLA	2	0.950
ANNs+QM	2	DRMVDQAAL	209	0.890
ANNs+QM	3	PRNVAFAGA	428	0.830

ANNs+QM	4	SRPDDPRNW	258	0.770
----------------	---	-----------	-----	-------

ALLELE: HLA-B*3501				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPQLAQATL	170	1.000
ANNs+QM	2	LPADRMVDQ	206	0.990
ANNs+QM	3	AADLGAKVI	190	0.540
ANNs+QM	4	SASCDSNPL	246	0.470

ALLELE: HLA-B*3701				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TDCDGHGTL	121	3.689
QM	2	GDGALANGL	320	3.689
QM	3	GVAPAARLL	145	1.609
QM	4	GDPQLAQAT	169	1.386

ALLELE: HLA-B*3801				
Threshold for 4 % with score: 0.445				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GHGTLVAGI	125	2.460
QM	2	GLPDAHQKL	327	1.138
QM	3	DPQLAQATL	170	0.956
QM	4	GNLDAVAAL	389	0.956

ALLELE: HLA-B*3901				
---------------------------	--	--	--	--

Threshold for 4 % with score: 1.792				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GHGTLVAGI	125	3.807
QM	2	DRMVDQAAL	209	3.401
QM	3	GNLDAVAAL	389	2.890
QM	4	AALSVLVGL	437	2.197

ALLELE: HLA-B*3902				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AVAALTWQL	393	0.875
QM	2	AALSVLVGL	437	0.875
QM	3	TGVQPGPRL	96	0.693
QM	4	GVAPAARLL	145	0.693

ALLELE: HLA-B*40				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RESSNIVGA	380	2.996
QM	2	GDGALANGL	320	1.609
QM	3	GAIVHAADL	185	1.386
QM	4	TGVQPGPRL	96	1.099

ALLELE: HLA-B*4403				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AALGAAIRY	215	3.701
QM	2	DTTPRNVAF	425	1.792
QM	3	RESSNIVGA	380	1.386

QM	4	VDKDAVIVA	226	0.811
-----------	---	-----------	-----	-------

ALLELE: HLA-B*5101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AADLGAKVI	190	1.000
ANNs+QM	2	DAHQKLVAL	330	0.980
ANNs+QM	3	AAPAKPVAD	409	0.950
ANNs+QM	4	DPQLAQATL	170	0.940

ALLELE: HLA-B*5102				
Threshold for 4 % with score: 9.050				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GGAAPAKPV	407	15.330
QM	2	PAWAIGPPV	22	13.270
QM	3	FAGAAALSV	433	13.110
QM	4	AADLGAKVI	190	11.010

ALLELE: HLA-B*5103				
Threshold for 4 % with score: 9.280				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GGAAPAKPV	407	15.330
QM	2	PAWAIGPPV	22	13.270
QM	3	FAGAAALSV	433	13.110
QM	4	AADLGAKVI	190	11.010

ALLELE: HLA-B*5201				
---------------------------	--	--	--	--

Threshold for 4 % with score: 1.974				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	WQPYVLSVA	278	3.784
QM	2	ACLAATVVV	7	3.679
QM	3	AADLGAKVI	190	3.679
QM	4	DQAALGAAI	213	3.178

ALLELE: HLA-B*5301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPQLAQATL	170	1.000
ANNs+QM	2	LPAEPGGGA	401	0.950
ANNs+QM	3	TDCDGHGTL	121	0.790
ANNs+QM	4	LPADRMVDQ	206	0.730

ALLELE: HLA-B*5401				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPQLAQATL	170	1.000
ANNs+QM	2	LPAEPGGGA	401	0.980
ANNs+QM	3	LPADRMVDQ	206	0.890
ANNs+QM	4	DCDGHGTLV	122	0.760

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SASCDSNPL	246	1.000
ANNs+QM	2	WWQPYVLSV	277	1.000
ANNs+QM	3	DPQLAQATL	170	0.990

ANNs+QM	4	DAHQKLVAL	330	0.960
----------------	---	-----------	-----	-------

ALLELE: HLA-B*5801				
Threshold for 4 % with score: -0.223				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DTTPRNVAF	425	3.178
QM	2	RTSGGDPQL	165	1.792
QM	3	AGWWTPPAW	16	1.386
QM	4	LSVLVGLTA	439	1.289

ALLELE: HLA-B60				
Threshold for 4 % with score: 1.386				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GDGALANGL	320	3.091
QM	2	TDCDGHGTL	121	2.996
QM	3	AALSVLVGL	437	2.868
QM	4	RESSNIVGA	380	2.773

ALLELE: HLA-B61				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RESSNIVGA	380	3.784
QM	2	VDKDAVIVA	226	0.916
QM	3	GGAAPAKPV	407	0.788
QM	4	ACLAATVVV	7	0.693

ALLELE: HLA-B62				
------------------------	--	--	--	--

Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	WQPYVLSVA	278	2.175
QM	2	DQAALGAAI	213	2.079
QM	3	AQATLDVAV	174	1.569
QM	4	ALGAAIRYA	216	1.482

ALLELE: HLA-B7				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	MIRAAFACL	1	1.000
ANNs+QM	2	DPQLAQATL	170	1.000
ANNs+QM	3	LVRSRYPGL	354	1.000
ANNs+QM	4	AVLAGAIVH	181	0.930

ALLELE: HLA-B*0702				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPQLAQATL	170	1.000
ANNs+QM	2	LPAEPGGGA	401	0.990
ANNs+QM	3	LPADRMVDQ	206	0.910
ANNs+QM	4	TPRNVAFAG	427	0.870

ALLELE: HLA-B8				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DCDGHGTLV	122	0.750
ANNs+QM	2	IRAAFACLA	2	0.680
ANNs+QM	3	FAGAAALSV	433	0.680

ANNs+QM	4	AADLGAKVI	190	0.650
----------------	---	-----------	-----	-------

ALLELE: HLA-Cw*0301				
Threshold for 4 % with score: 2.015				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GAIVHAADL	185	3.689
QM	2	DRMVDQAAL	209	3.689
QM	3	AALSVLVGL	437	3.689
QM	4	TGVQPGPRL	96	2.996

ALLELE: HLA-Cw*0401				
Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLPDAHQKL	327	9.430
QM	2	GNLDAVAAL	389	7.370
QM	3	QATLDVAVL	175	4.640
QM	4	SNIVGAGNL	383	4.310

ALLELE: HLA-Cw*0602				
Threshold for 4 % with score: 1.482				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DAHQKLVAL	330	2.175
QM	2	GDGALANGL	320	1.887
QM	3	GHGTLVAGI	125	1.792
QM	4	AVAALTWQL	393	1.792

ALLELE: HLA-Cw*0702				
----------------------------	--	--	--	--

Threshold for 4 % with score: 1.212				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LVALSGTSY	335	2.079
QM	2	GDGALANGL	320	1.569
QM	3	AALGAAIRY	215	1.482
QM	4	RYAAVDKDA	222	1.058

ALLELE: H2-Db				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVAPAARLL	145	0.980
ANNs+QM	2	VSNSGDGAL	316	0.950
ANNs+QM	3	RAAFACLAA	3	0.880
ANNs+QM	4	MIRAAFACL	1	0.860

ALLELE: H2-Dd				
Threshold for 4 % with score: 11.800				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLPDAHQKL	327	17.420
QM	2	PGPRLPNVD	100	15.030
QM	3	SMPGPWVGI	298	14.510
QM	4	DPQLAQATL	170	13.920

ALLELE: H2-Kb				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVAPAARLL	145	0.990
ANNs+QM	2	GAIVHAADL	185	0.980
ANNs+QM	3	DCDGHGTLV	122	0.940

ANNs+QM	4	AALGAAIRY	215	0.940
----------------	---	-----------	-----	-------

ALLELE: H2-Kd				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SNIVGAGNL	383	0.990
ANNs+QM	2	DRMVDQAAL	209	0.950
ANNs+QM	3	GHGTLVAGI	125	0.940
ANNs+QM	4	PKDTTPRNV	423	0.930

ALLELE: H2-Kk				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DQAALGAAI	213	2.996
QM	2	GHGTLVAGI	125	2.303
QM	3	AADLGAKVI	190	2.303
QM	4	TDCDGHGTL	121	2.079

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPQLAQATL	170	1.000
ANNs+QM	2	LPADRMVDQ	206	1.000
ANNs+QM	3	VSNSGDGAL	316	1.000
ANNs+QM	4	TDCDGHGTL	121	0.790

ALLELE: HLA-G				
----------------------	--	--	--	--

Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLPDAHQKL	327	24.910
QM	2	GVAPAARLL	145	17.450
QM	3	MIRAAFACL	1	16.780
QM	4	VLGAIVHA	182	14.600

ALLELE: H-2Qa				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DQAALGAAI	213	9.500
QM	2	DRMVDQAAL	209	8.470
QM	3	AALSVLVGL	437	8.330
QM	4	RLTATAHRG	370	6.790

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SRPDDPRNW	258	9.000
QM	2	QLPAEPGGG	400	8.010
QM	3	SMPGPWVGI	298	6.530
QM	4	LPAEPGGGA	401	6.330

ALLELE: HLA-B35				
Threshold for 4 % with score: 8.350				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPQLAQATL	170	11.910
QM	2	AALSVLVGL	437	9.160
QM	3	TPRNVAFAG	427	8.910

QM	4	AVDKDAVIV	225	8.810
-----------	---	-----------	-----	-------

ALLELE: Mamu-A*01				
Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SASCDSNPL	246	6.080
QM	2	TDCDGHGTL	121	5.650
QM	3	WWQPYVLSV	277	4.390
QM	4	ITCLPADRM	203	3.020

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VAFAGAAAL	431	18.040
QM	2	GNLDAVAAL	389	17.690
QM	3	GLPDAHQKL	327	17.370
QM	4	RLTATAHRG	370	17.150

ALLELE: HLA-B*2703				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SRPDDPRNW	258	11.530
QM	2	IRYAAVDKD	221	3.000
QM	3	VLGAIVHA	182	2.540
QM	4	IRAAFACLA	2	2.340

ALLELE: HLA-B*2704				
---------------------------	--	--	--	--

Threshold for 4 % with score: 8.790				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DRMVDQAAL	209	16.490
QM	2	AGAAALSVL	434	11.340
QM	3	DPQLAQATL	170	11.050
QM	4	VAFAGAAAL	431	10.550

ALLELE: HLA-B*2902				
Threshold for 4 % with score: 7.750				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEPGGGAAP	403	10.840
QM	2	TDCDGHGTL	121	9.750
QM	3	GHGTLVAGI	125	8.510
QM	4	SNIVGAGNL	383	6.880

ALLELE: HLA-A*3301				
Threshold for 4 % with score: 3.840				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AVAALTWQL	393	5.730
QM	2	AIGPPVVDA	25	3.800
QM	3	GLNATEVVR	361	2.360
QM	4	GALANGLPD	322	2.180

ALLELE: HLA-B44				
Threshold for 4 % with score: 4.900				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEPGGGAAP	403	10.370
QM	2	GDGALANGL	320	6.020
QM	3	GAIVHAADL	185	5.240

QM	4	AGNLDAVAA	388	4.670
-----------	---	-----------	-----	-------

ALLELE: HLA-A*6801				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVAPAARLL	145	0.970
ANNs+QM	2	GGAAPAKPV	407	0.910
ANNs+QM	3	RAAFACLAA	3	0.900
ANNs+QM	4	SMPGPWVGI	298	0.880

ALLELE: HLA-A*6802				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	WAIGPPVVD	24	0.980
ANNs+QM	2	GVAPAARLL	145	0.980
ANNs+QM	3	LVGLTAATV	442	0.980
ANNs+QM	4	QATLDVAVL	175	0.970