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

Antigen Name	Untitled
Scanned on	Sat Feb 20 00:20:50 2010
Length of input sequence	168 amino acids
Number of nonamers from input sequence	160
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	EATGNRGKL	126	0.350
ANNs+QM	2	NRGKLEALL	130	0.170
ANNs+QM	3	KPGVLARVA	15	0.110
ANNs+QM	4	RSRMTIVVS	46	0.110

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KLEALLRVL	133	0.660
ANNs+QM	2	KTHTLSVLV	4	0.320

ANNs+QM	3	LVEDKPGVL	11	0.080
ANNs+QM	4	PLEQITKQL	59	0.080

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KTHTLSVLV	4	1.000
ANNs+QM	2	VIDVSPESL	115	0.990
ANNs+QM	3	IAQSGMVSL	149	0.670
ANNs+QM	4	KLEALLRVL	133	0.340

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KLEALLRVL	133	1.000
ANNs+QM	2	DKPGVLARV	14	0.930
ANNs+QM	3	PLEQITKQL	59	0.930
ANNs+QM	4	DEHSVSREL	81	0.450

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DKPGVLARV	14	0.980
ANNs+QM	2	KTHTLSVLV	4	0.970
ANNs+QM	3	VEDKPGVLA	12	0.730
ANNs+QM	4	ATGNRGKLE	127	0.350

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DKPGVLARV	14	0.990
ANNs+QM	2	KTHTLSVLV	4	0.780
ANNs+QM	3	SRMTIVVSA	47	0.380
ANNs+QM	4	LVEDKPGVL	11	0.350

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KLEALLRVL	133	7.700
QM	2	DKPGVLARV	14	5.230
QM	3	NRGKLEALL	130	4.420
QM	4	KTHTLSVLV	4	3.810

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ATGNRGKLE	127	0.770
ANNs+QM	2	VSPESLTVE	118	0.500
ANNs+QM	3	VIDVSPESL	115	0.270
ANNs+QM	4	KTHTLSVLV	4	0.200

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ATGNRGKLE	127	0.640

ANNs+QM	2	RSRMTIVVS	46	0.590
ANNs+QM	3	HTLSVLVED	6	0.290
ANNs+QM	4	KTHTLSVLV	4	0.250

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NRGKLEALL	130	8.860
QM	2	SQVIEAVNL	102	8.230
QM	3	IAQSGMVSL	149	6.310
QM	4	VIDVSPESL	115	5.770

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EATGNRGKL	126	0.900
ANNs+QM	2	PLEQITKQL	59	0.270
ANNs+QM	3	IAQSGMVSL	149	0.130
ANNs+QM	4	SQVIEAVNL	102	0.070

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RSRMTIVVS	46	0.840
ANNs+QM	2	KTHTLSVLV	4	0.680
ANNs+QM	3	VIEAVNLFR	104	0.550
ANNs+QM	4	ATGNRGKLE	127	0.250

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VIEAVNLFR	104	1.386
QM	2	SQVIEAVNL	102	-3.219
QM	3	KTHTLSVLV	4	-3.507

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VIEAVNLFR	104	0.980
ANNs+QM	2	VEDKPGVLA	12	0.800
ANNs+QM	3	NRGKLEALL	130	0.800
ANNs+QM	4	ATGNRGKLE	127	0.650

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KTHTLSVLV	4	0.720
ANNs+QM	2	ATGNRGKLE	127	0.510
ANNs+QM	3	RSRMTIVVS	46	0.380
ANNs+QM	4	DEHSVSREL	81	0.270

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VIEAVNLFR	104	2.708
QM	2	LVEDKPGVL	11	-0.693

QM	3	VIDVSPESL	115	-0.693

ALLELE: HLA-A68.1				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VIEAVNLFR	104	1.609
QM	2	LVEDKPGVL	11	1.386
QM	3	KTHTLSVLV	4	0.000

ALLELE: HLA-A20 Cattle				
Threshold for 4 % with score: 3.401				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DKPGVLARV	14	5.704
QM	2	VIEAVNLFR	104	3.689
QM	3	KLEALLRVL	133	2.708
QM	4	RRGFNIESL	28	2.303

ALLELE: HLA-A2.1				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KLEALLRVL	133	0.990
ANNs+QM	2	KTHTLSVLV	4	0.950
ANNs+QM	3	IAQSGMVSL	149	0.770
ANNs+QM	4	FNIESLAVG	31	0.580

ALLELE: HLA-B14
Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRGFNIESL	28	1.000
ANNs+QM	2	DKPGVLARV	14	0.910
ANNs+QM	3	EATGNRGKL	126	0.910
ANNs+QM	4	NRGKLEALL	130	0.880

ALLELE: HLA-B*2702				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRGFNIESL	28	5.193
QM	2	NRGKLEALL	130	4.094
QM	3	SRMTIVVSA	47	2.996
QM	4	SQVIEAVNL	102	1.792

ALLELE: HLA-B27				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRGFNIESL	28	1.000
ANNs+QM	2	SRMTIVVSA	47	0.950
ANNs+QM	3	KTHTLSVLV	4	0.340
ANNs+QM	4	NRGKLEALL	130	0.300

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRGFNIESL	28	1.000
ANNs+QM	2	SRMTIVVSA	47	0.940
ANNs+QM	3	NRGKLEALL	130	0.840

ANNs+QM	4	RSRMTIVVS	46	0.780

ALLELE: HLA-B*3501

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SPESLTVEA	119	0.850
ANNs+QM	2	KPGVLARVA	15	0.440
ANNs+QM	3	IAQSGMVSL	149	0.400
ANNs+QM	4	KTHTLSVLV	4	0.160

ALLELE: HLA-B*3701

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	2.708
QM	2	VEDKPGVLA	12	1.609
QM	3	NRGKLEALL	130	1.609

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LVEDKPGVL	11	1.792
QM	2	KLEALLRVL	133	1.361
QM	3	VIDVSPESL	115	1.099
QM	4	EATGNRGKL	126	0.875

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRGFNIESL	28	3.114
QM	2	LVEDKPGVL	11	2.890
QM	3	KLEALLRVL	133	2.603
QM	4	VIDVSPESL	115	2.197

ALLELE: HLA-B*3902				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SQVIEAVNL	102	2.996
QM	2	NRGKLEALL	130	0.875
QM	3	KLEALLRVL	133	0.875
QM	4	LVEDKPGVL	11	0.693

ALLELE: HLA-B40				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	2.996
QM	2	VEDKPGVLA	12	2.708
QM	3	SQVIEAVNL	102	0.000

ALLELE: HLA-B*4403				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	2.890
QM	2	VEDKPGVLA	12	1.386
QM	3	RELALIKVQ	87	0.182

ALLELE: HLA-B*5101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KTHTLSVLV	4	0.770
ANNs+QM	2	KPGVLARVA	15	0.650
ANNs+QM	3	DKPGVLARV	14	0.510
ANNs+QM	4	IAQSGMVSL	149	0.390

ALLELE: HLA-B*5102				
Threshold for 4 % with score: 9.050				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IAQSGMVSL	149	10.170
QM	2	KTHTLSVLV	4	8.200
QM	3	VIDVSPESL	115	6.650
QM	4	DKPGVLARV	14	6.350

ALLELE: HLA-B*5103				
Threshold for 4 % with score: 9.280				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IAQSGMVSL	149	10.170
QM	2	KTHTLSVLV	4	8.200
QM	3	VIDVSPESL	115	6.650
QM	4	DKPGVLARV	14	6.350

ALLELE: HLA-B*5201				
Threshold for 4 % with score: 1.974				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KPGVLARVA	15	2.485

QM	2	KLEALLRVL	133	1.664
QM	3	LVEDKPGVL	11	1.099
QM	4	SQVIEAVNL	102	0.875

ALLELE: HLA-B*5301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KPGVLARVA	15	0.970
ANNs+QM	2	FNIESLAVG	31	0.360
ANNs+QM	3	SPESLTVEA	119	0.310
ANNs+QM	4	SQVIEAVNL	102	0.100

ALLELE: HLA-B*5401				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KPGVLARVA	15	1.000
ANNs+QM	2	SPESLTVEA	119	1.000
ANNs+QM	3	FNIESLAVG	31	0.590
ANNs+QM	4	KTHTLSVLV	4	0.460

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KPGVLARVA	15	0.940
ANNs+QM	2	LVEDKPGVL	11	0.870
ANNs+QM	3	EATGNRGKL	126	0.490
ANNs+QM	4	DKPGVLARV	14	0.470

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KTHTLSVLV	4	2.197
QM	2	IAQSGMVSL	149	0.405
QM	3	RSRMTIVVS	46	0.365

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	5.170
QM	2	VEDKPGVLA	12	2.079
QM	3	SQVIEAVNL	102	2.079
QM	4	IAQSGMVSL	149	2.079

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEDKPGVLA	12	2.996
QM	2	DEHSVSREL	81	2.079
QM	3	RELALIKVQ	87	0.565

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SQVIEAVNL	102	1.569
QM	2	KLEALLRVL	133	0.278
QM	3	KPGVLARVA	15	-0.821

ALLELE: HLA-B7

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KPGVLARVA	15	0.910
ANNs+QM	2	KLEALLRVL	133	0.780
ANNs+QM	3	DKPGVLARV	14	0.610
ANNs+QM	4	EATGNRGKL	126	0.470

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KPGVLARVA	15	0.990
ANNs+QM	2	SPESLTVEA	119	0.890
ANNs+QM	3	KTHTLSVLV	4	0.710
ANNs+QM	4	VIEAVNLFR	104	0.440

ALLELE: HLA-B8

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VEDKPGVLA	12	0.670
ANNs+QM	2	KPGVLARVA	15	0.670
ANNs+QM	3	VIEAVNLFR	104	0.670
ANNs+QM	4	RSRMTIVVS	46	0.610

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SQVIEAVNL	102	2.996
QM	2	IAQSGMVSL	149	2.079
QM	3	RRGFNIESL	28	1.569
QM	4	EATGNRGKL	126	0.875

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PLEQITKQL	59	2.310
QM	2	VIDVSPESL	115	1.840
QM	3	IAQSGMVSL	149	1.310
QM	4	EATGNRGKL	126	0.640

ALLELE: HLA-Cw*0602

Threshold for 4 % with score: 1.482

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KLEALLRVL	133	2.676
QM	2	NRGKLEALL	130	1.887
QM	3	RRGFNIESL	28	1.482
QM	4	LVEDKPGVL	11	1.386

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRGFNIESL	28	1.569
QM	2	NRGKLEALL	130	1.569
QM	3	KPGVLARVA	15	0.875

QM	4	KLEALLRVL	133	0.875

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRGFNIESL	28	1.000
ANNs+QM	2	EATGNRGKL	126	0.890
ANNs+QM	3	ATGNRGKLE	127	0.810
ANNs+QM	4	NRGKLEALL	130	0.720

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IAQSGMVSL	149	14.380
QM	2	RRGFNIESL	28	13.240
QM	3	NRGKLEALL	130	11.910
QM	4	DEHSVSREL	81	8.830

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KPGVLARVA	15	0.950
ANNs+QM	2	VIDVSPESL	115	0.900
ANNs+QM	3	NRGKLEALL	130	0.830
ANNs+QM	4	VEDKPGVLA	12	0.560

ALLELE: H2-Kd

Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EATGNRGKL	126	0.990
ANNs+QM	2	NRGKLEALL	130	0.950
ANNs+QM	3	VIDVSPESL	115	0.920
ANNs+QM	4	RRGFNIESL	28	0.910

ALLELE: H2-Kk				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	4.382
QM	2	VEDKPGVLA	12	2.708
QM	3	RELALIKVQ	87	0.000

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IAQSGMVSL	149	0.810
ANNs+QM	2	EATGNRGKL	126	0.340
ANNs+QM	3	KPGVLARVA	15	0.170
ANNs+QM	4	LVEDKPGVL	11	0.150

ALLELE: HLA-G				
Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KLEALLRVL	133	14.180
QM	2	RRGFNIESL	28	6.970
QM	3	VSPESLTVE	118	6.730

QM	4	LVEDKPGVL	11	6.110

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	9.550
QM	2	VIDVSPESL	115	5.800
QM	3	RRGFNIESL	28	4.140
QM	4	SQVIEAVNL	102	2.470

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRGFNIESL	28	10.670
QM	2	SPESLTVEA	119	7.040
QM	3	LVEDKPGVL	11	5.330
QM	4	KLEALLRVL	133	4.960

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VIDVSPESL	115	5.890
QM	2	IAQSGMVSL	149	5.330
QM	3	LVEDKPGVL	11	4.360
QM	4	DEHSVSREL	81	4.040

ALLELE: Mamu-A*01

Threshold for 4 % with score: 3.650

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KTHTLSVLV	4	2.220
QM	2	VIDVSPESL	115	2.190
QM	3	SRMTIVVSA	47	0.730
QM	4	VEDKPGVLA	12	0.100

ALLELE: HLA-A*0204

Threshold for 4 % with score: 12.070

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KLEALLRVL	133	14.700
QM	2	HTLSVLVED	6	11.160
QM	3	VEDKPGVLA	12	10.530
QM	4	IAQSGMVSL	149	9.100

ALLELE: HLA-B*2703

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRGFNIESL	28	8.890
QM	2	NRGKLEALL	130	7.830
QM	3	SRMTIVVSA	47	2.040
QM	4	HTLSVLVED	6	0.580

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRGFNIESL	28	17.570
QM	2	NRGKLEALL	130	13.720
QM	3	DEHSVSREL	81	10.800

QM	4	VIDVSPESL	115	5.990

ALLELE: HLA-B*2902				
Threshold for 4 % with score: 7.750				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEHSVSREL	81	8.100
QM	2	LVEDKPGVL	11	7.750
QM	3	SQVIEAVNL	102	5.860
QM	4	IAQSGMVSL	149	4.350

ALLELE: HLA-A*3301				
Threshold for 4 % with score: 3.840				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VIEAVNLFR	104	3.690
QM	2	FNIESLAVG	31	1.890
QM	3	ATGNRGKLE	127	0.780

ALLELE: HLA-B44				
Threshold for 4 % with score: 4.900				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RELALIKVQ	87	2.320
QM	2	EATGNRGKL	126	1.980
QM	3	VEDKPGVLA	12	1.560
QM	4	DEHSVSREL	81	0.970

ALLELE: HLA-A*6801
Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ATGNRGKLE	127	0.830
ANNs+QM	2	DEHSVSREL	81	0.300
ANNs+QM	3	KTHTLSVLV	4	0.250
ANNs+QM	4	RSRMTIVVS	46	0.180

ALLELE: HLA-A*6802				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RSRMTIVVS	46	1.000
ANNs+QM	2	SRMTIVVSA	47	1.000
ANNs+QM	3	EATGNRGKL	126	0.970
ANNs+QM	4	ATGNRGKLE	127	0.970