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

Antigen Name	Untitled
Scanned on	Wed Mar 3 20:17:40 2010
Length of input sequence	624 amino acids
Number of nonamers from input sequence	616
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	AKEQKAKVL	374	0.830
ANNs+QM	2	VALEGALKL	490	0.830
ANNs+QM	3	ASDTDTEVA	124	0.730
ANNs+QM	4	IAEQPAAVA	269	0.730

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GYDSSGIAL	28	1.000
ANNs+QM	2	YLLGLALAQ	424	1.000
ANNs+QM	3	YMHAEGFAA	503	1.000
ANNs+QM	4	VLDRSTLVV	348	0.990

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VLDRSTLVV	348	1.000
ANNs+QM	2	ELEAMPDLV	448	1.000
ANNs+QM	3	VALEGALKL	490	1.000
ANNs+QM	4	HLIEIPAVS	576	1.000

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VLDRSTLVV	348	0.970
ANNs+QM	2	RVIAATGPV	458	0.970
ANNs+QM	3	HLIEIPAVS	576	0.970
ANNs+QM	4	FVGSVLAVL	149	0.930

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVASTKTFL	409	0.990
ANNs+QM	2	STIPLQVFA	592	0.960
ANNs+QM	3	FVGSVLAVL	149	0.850
ANNs+QM	4	IQTRGAVTI	552	0.830

ALLELE: HLA-A*0206				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EIAEQPAAV	268	1.000
ANNs+QM	2	REIDKVFVV	302	0.990

ANNs+QM	3	VLDRSTLVV	348	0.990
ANNs+QM	4	GVASTKTFL	409	0.990

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AVSTLLQPL	582	12.480
QM	2	QPAAVADTL	272	10.950
QM	3	AATGPVAEL	461	9.980
QM	4	FVGSVLAVL	149	7.900

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EAMPDLVAR	450	1.000
ANNs+QM	2	QVFAASVAR	597	1.000
ANNs+QM	3	VVMPSPKGS	530	0.730
ANNs+QM	4	AISQSGETA	357	0.670

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QVFAASVAR	597	1.000
ANNs+QM	2	GTLVAARRS	175	0.970
ANNs+QM	3	GQDQAVVIT	215	0.970
ANNs+QM	4	RVIAATGPV	458	0.930

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ARRSTPLVL	180	14.310
QM	2	LAQIAANYL	417	9.570
QM	3	RHVGYPVAL	484	8.830
QM	4	ANYLLGLAL	422	8.350

ALLELE: HLA-A*2402				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NFAVLRREL	108	1.000
ANNs+QM	2	LYTRAGPEI	400	0.990
ANNs+QM	3	GYDSSGIAL	28	0.920
ANNs+QM	4	RPFHIDWDL	245	0.880

ALLELE: HLA-A3				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PVAELAHRF	465	1.000
ANNs+QM	2	QVFAASVAR	597	1.000
ANNs+QM	3	TVRRRAGRL	43	0.990
ANNs+QM	4	VRRRAGRLA	44	0.980

ALLELE: HLA-A*3101				
Threshold for 4 % with score: -1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QVFAASVAR	597	1.792
QM	2	EAMPDLVAR	450	-1.022
QM	3	KLKELAYMH	497	-1.204

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QVFAASVAR	597	1.000
ANNs+QM	2	EAMPDLVAR	450	0.970
ANNs+QM	3	RGYDVDKPR	607	0.970
ANNs+QM	4	DGGTLTVRR	38	0.960

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IQTRGAVTI	552	1.000
ANNs+QM	2	AKEQKAKVL	374	0.990
ANNs+QM	3	AISQSGETA	357	0.930
ANNs+QM	4	YLLGLALAQ	424	0.890

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QVFAASVAR	597	2.708
QM	2	DGGTLTVRR	38	2.197
QM	3	EAMPDLVAR	450	2.197
QM	4	GGTLTVRRR	39	1.099

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QVFAASVAR	597	5.991
QM	2	EAMPDLVAR	450	3.807
QM	3	FVGSVLAVL	149	2.079
QM	4	GVASTKTFL	409	2.079

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AKEQKAKVL	374	6.215
QM	2	TKTFLAQIA	413	4.605
QM	3	EAMPDLVAR	450	3.689
QM	4	QVFAASVAR	597	3.689

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AQIAANYLL	418	0.990
ANNs+QM	2	KLKELAYMH	497	0.990
ANNs+QM	3	GTAYHSGLL	313	0.980
ANNs+QM	4	GYPVALEGA	487	0.980

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TVRRRAGRL	43	1.000
ANNs+QM	2	DRNAHPHRD	85	1.000
ANNs+QM	3	TRLPVEVEL	330	1.000
ANNs+QM	4	VALEGALKL	490	1.000

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	YRGYDSSGI	26	4.094
QM	2	ARRSTPLVL	180	4.094

QM	3	TRLPVEVEL	330	4.094
QM	4	VRRRAGRLA	44	1.792

ALLELE: HLA-B27				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YRGYDSSGI	26	1.000
ANNs+QM	2	TRLPVEVEL	330	1.000
ANNs+QM	3	GQDQAVVIT	215	0.600
ANNs+QM	4	DRNAHPHRD	85	0.590

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ARRSTPLVL	180	1.000
ANNs+QM	2	TRLPVEVEL	330	1.000
ANNs+QM	3	YRGYDSSGI	26	0.990
ANNs+QM	4	VRRRAGRLA	44	0.970

ALLELE: HLA-B*3501				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPFHIDWDL	245	1.000
ANNs+QM	2	QPAAVADTL	272	1.000
ANNs+QM	3	MPDLVARVI	452	1.000
ANNs+QM	4	YPVALEGAL	488	1.000

ALLELE: HLA-B*3701
Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADDFVGSVL	146	4.094
QM	2	SDFDGNDGL	230	3.689
QM	3	YDVDKPRNL	609	3.689
QM	4	HELEAMPDL	447	2.303

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VHNGIIENF	101	4.357
QM	2	RHVGYPVAL	484	4.094
QM	3	EHTREAVEL	206	3.401
QM	4	GYDSSGIAL	28	1.792

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RHVGYPVAL	484	5.193
QM	2	EHTREAVEL	206	4.500
QM	3	TRLPVEVEL	330	2.708
QM	4	VALEGALKL	490	2.485

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AKEQKAKVL	374	2.996
QM	2	AQIAANYLL	418	2.996
QM	3	NFAVLRREL	108	0.875
QM	4	FVGSVLAVL	149	0.875

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HELEAMPDL	447	3.689
QM	2	AEGFAAGEL	506	3.689
QM	3	REYHELEAM	444	3.178
QM	4	LETAGVEFA	116	2.996

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	REIDKVFVV	302	4.905
QM	2	AEGFAAGEL	506	2.890
QM	3	LETAGVEFA	116	2.485
QM	4	HELEAMPDL	447	2.485

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	MPDLVARVI	452	1.000
ANNs+QM	2	LGRHVGYPV	482	1.000
ANNs+QM	3	RPFHIDWDL	245	0.940
ANNs+QM	4	IQTRGAVTI	552	0.920

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MPDLVARVI	452	15.410
QM	2	LGRHVGYPV	482	14.220
QM	3	VLDRSTLVV	348	8.390
QM	4	SATLHAKLL	538	7.870

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MPDLVARVI	452	15.410
QM	2	LGRHVGYPV	482	14.220
QM	3	LAYMHAEGF	501	12.480
QM	4	VHNGIIENF	101	8.500

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MPDLVARVI	452	5.886
QM	2	VLDRSTLVV	348	3.497
QM	3	GQDQAVVIT	215	3.401
QM	4	IQTRGAVTI	552	3.114

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPFHIDWDL	245	1.000
ANNs+QM	2	QPAAVADTL	272	1.000
ANNs+QM	3	YPVALEGAL	488	1.000
ANNs+QM	4	MPDLVARVI	452	0.990

ALLELE: HLA-B*5401

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPFHIDWDL	245	1.000
ANNs+QM	2	MPDLVARVI	452	0.990

ANNs+QM	3	YPVALEGAL	488	0.980
ANNs+QM	4	SPKGSATLH	534	0.940

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPFHIDWDL	245	1.000
ANNs+QM	2	MPDLVARVI	452	1.000
ANNs+QM	3	QPAAVADTL	272	0.950
ANNs+QM	4	VALEGALKL	490	0.890

ALLELE: HLA-B*5801				
Threshold for 4 % with score: -0.223				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LAYMHAEGF	501	2.996
QM	2	STIPLQVFA	592	1.792
QM	3	QSGETADTL	360	1.482
QM	4	GSATLHAKL	537	1.194

ALLELE: HLA-B60				
Threshold for 4 % with score: 1.386				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HELEAMPDL	447	5.768
QM	2	AEGFAAGEL	506	5.075
QM	3	YDVDKPRNL	609	3.689
QM	4	ADDFVGSVL	146	3.091

ALLELE: HLA-B61
Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	REIDKVFVV	302	4.477
QM	2	LETAGVEFA	116	3.689
QM	3	REYHELEAM	444	2.868
QM	4	HELEAMPDL	447	2.773

ALLELE: HLA-B62				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IQTRGAVTI	552	2.619
QM	2	AQIAANYLL	418	1.386
QM	3	LAYMHAEGF	501	0.693
QM	4	GQDQAVVIT	215	0.365

ALLELE: HLA-B7				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPFHIDWDL	245	1.000
ANNs+QM	2	QPAAVADTL	272	1.000
ANNs+QM	3	AQIAANYLL	418	1.000
ANNs+QM	4	YPVALEGAL	488	1.000

ALLELE: HLA-B*0702				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FVGSVLAVL	149	1.000
ANNs+QM	2	RPFHIDWDL	245	1.000
ANNs+QM	3	QPAAVADTL	272	1.000
ANNs+QM	4	YPVALEGAL	488	1.000

ALLELE: HLA-B8				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KLKELAYMH	497	1.000
ANNs+QM	2	AQIAANYLL	418	0.700
ANNs+QM	3	RPFHIDWDL	245	0.670
ANNs+QM	4	REIDKVFVV	302	0.670

ALLELE: HLA-Cw*0301				
Threshold for 4 % with score: 2.015				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRLPVEVEL	330	4.605
QM	2	HELEAMPDL	447	4.094
QM	3	VALEGALKL	490	4.094
QM	4	AQIAANYLL	418	2.996

ALLELE: HLA-Cw*0401				
Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QPAAVADTL	272	7.370
QM	2	AKEQKAKVL	374	5.700
QM	3	YPVALEGAL	488	5.430
QM	4	RPFHIDWDL	245	5.370

ALLELE: HLA-Cw*0602				
Threshold for 4 % with score: 1.482				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AVSTLLQPL	582	2.580
QM	2	EGALKLKEL	493	2.175
QM	3	YPVALEGAL	488	1.982
QM	4	NFAVLRREL	108	1.887

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QPAAVADTL	272	1.974
QM	2	FVGSVLAVL	149	1.569
QM	3	YPVALEGAL	488	1.559
QM	4	RPFHIDWDL	245	1.463

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QSGETADTL	360	1.000
ANNs+QM	2	AEGFAAGEL	506	0.930
ANNs+QM	3	QPAAVADTL	272	0.910
ANNs+QM	4	YPVALEGAL	488	0.830

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DGGTLTVRR	38	15.360
QM	2	GYPVALEGA	487	14.840
QM	3	PHRDAAGKI	90	14.530
QM	4	PVAELAHRF	465	12.090

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GTLVAARRS	175	0.920
ANNs+QM	2	AQIAANYLL	418	0.920

ANNs+QM	3	QPAAVADTL	272	0.900
ANNs+QM	4	ANADDPGTL	169	0.890

ALLELE: H2-Kd				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NFAVLRREL	108	1.000
ANNs+QM	2	GYDSSGIAL	28	0.990
ANNs+QM	3	GSATLHAKL	537	0.980
ANNs+QM	4	YDVDKPRNL	609	0.980

ALLELE: H2-Kk				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	REIDKVFVV	302	3.219
QM	2	LETAGVEFA	116	2.996
QM	3	HELEAMPDL	447	2.996
QM	4	AEGFAAGEL	506	2.996

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPFHIDWDL	245	1.000
ANNs+QM	2	QPAAVADTL	272	1.000
ANNs+QM	3	YPVALEGAL	488	1.000
ANNs+QM	4	RNAHPHRDA	86	0.950

ALLELE: HLA-G
Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GSATLHAKL	537	14.110
QM	2	GVASTKTFL	409	12.780
QM	3	TVRRRAGRL	43	12.110
QM	4	KLKELAYMH	497	11.400

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRLPVEVEL	330	9.790
QM	2	RPFHIDWDL	245	9.640
QM	3	DRNAHPHRD	85	9.360
QM	4	GYDSSGIAL	28	7.470

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	EGALKLKEL	493	7.290
QM	2	RHVGYPVAL	484	7.200
QM	3	DRNAHPHRD	85	6.670
QM	4	YMHAEGFAA	503	6.010

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RPFHIDWDL	245	14.980
QM	2	QPAAVADTL	272	13.550
QM	3	MPDLVARVI	452	13.320
QM	4	YPVALEGAL	488	10.970

ALLELE: Mamu-A*01

Threshold for 4 % with score: 3.650

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LIEIPAVST	577	6.060
QM	2	GTAYHSGLL	313	5.250
QM	3	STIPLQVFA	592	3.570
QM	4	TVRRRAGRL	43	3.090

ALLELE: HLA-A*0204

Threshold for 4 % with score: 12.070

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FVGSVLAVL	149	14.510
QM	2	AATGPVAEL	461	14.030
QM	3	QPAAVADTL	272	13.960
QM	4	RHVGYPVAL	484	13.690

ALLELE: HLA-B*2703

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRLPVEVEL	330	11.500
QM	2	DRNAHPHRD	85	8.200
QM	3	VRRRAGRLA	44	6.780
QM	4	ARRSTPLVL	180	6.690

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DRNAHPHRD	85	14.710
QM	2	RPFHIDWDL	245	13.060
QM	3	YRGYDSSGI	26	12.700
QM	4	ARRSTPLVL	180	12.640

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEGFAAGEL	506	11.280
QM	2	GETADDFVG	143	10.840
QM	3	HELEAMPDL	447	10.750
QM	4	REYHELEAM	444	10.700

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QVFAASVAR	597	4.110
QM	2	AVSTLLQPL	582	2.930
QM	3	VVMPSPKGS	530	2.620
QM	4	LVFANADDP	166	2.340

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEGFAAGEL	506	14.240
QM	2	AEQPAAVAD	270	9.110
QM	3	LETAGVEFA	116	7.480
QM	4	VHNGIIENF	101	6.310

ALLELE: HLA-A*6801

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QVFAASVAR	597	1.000
ANNs+QM	2	RGYDVDKPR	607	0.970

ANNs+QM	3	SPKGSATLH	534	0.940
ANNs+QM	4	EAMPDLVAR	450	0.910

ALLELE: HLA-A*6802				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVASTKTFL	409	1.000
ANNs+QM	2	RHVGYPVAL	484	1.000
ANNs+QM	3	VVMPSPKGS	530	1.000
ANNs+QM	4	HLIEIPAVS	576	1.000