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

Antigen Name	Untitled
Scanned on	Tue Mar 9 00:08:33 2010
Length of input sequence	304 amino acids
Number of nonamers from input sequence	296
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	AAAVEAARV	45	0.880
ANNs+QM	2	AAADLAAAI	63	0.860
ANNs+QM	3	AAVEAARVA	46	0.590
ANNs+QM	4	APDTADRVV	150	0.540

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VLASAGLDV	25	0.990
ANNs+QM	2	ALLTQVGKL	159	0.950
ANNs+QM	3	AIALVAEGV	191	0.790

ANNs+QM	4	ELFERLATL	90	0.740

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ILHAAAVEA	42	1.000
ANNs+QM	2	ELFERLATL	90	1.000
ANNs+QM	3	VLATNTSVL	103	1.000
ANNs+QM	4	ALWREAIAL	186	1.000

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ILHAAAVEA	42	1.000
ANNs+QM	2	ATLAPDAVL	96	0.990
ANNs+QM	3	DLAAAIPDA	66	0.980
ANNs+QM	4	VLATNTSVL	103	0.970

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ELFERLATL	90	0.970
ANNs+QM	2	VLASAGLDV	25	0.960
ANNs+QM	3	DYIGLDLTL	227	0.950
ANNs+QM	4	SVAAAADLA	60	0.940

ALLELE: HLA-A*0206
Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VLASAGLDV	25	1.000
ANNs+QM	2	ELFERLATL	90	1.000
ANNs+QM	3	ALLTQVGKL	159	0.990
ANNs+QM	4	LWREAIALV	187	0.990

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DTADRVVAL	152	11.900
QM	2	ALWREAIAL	186	10.960
QM	3	AAADLAAAI	63	10.580
QM	4	ATLAPDAVL	96	10.290

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	MLTSHGFSR	1	0.850
ANNs+QM	2	DPHPSPLLR	248	0.770
ANNs+QM	3	VLASAGLDV	25	0.570
ANNs+QM	4	AIPDADLVI	70	0.440

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LDWPAGARE	273	0.940
ANNs+QM	2	ATLAPDAVL	96	0.880
ANNs+QM	3	MLTSHGFSR	1	0.870
ANNs+QM	4	AVEAARVAG	47	0.860

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VLATNTSVL	103	9.690
QM	2	AIPDADLVI	70	9.680
QM	3	AAAIPDADL	68	9.040
QM	4	ATLAPDAVL	96	8.640

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DYIGLDLTL	227	0.990
ANNs+QM	2	GARTGHGFL	265	0.940
ANNs+QM	3	LWREAIALV	187	0.690
ANNs+QM	4	ALLTQVGKL	159	0.630

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ILHAAAVEA	42	0.970
ANNs+QM	2	TNAEILHAA	38	0.920
ANNs+QM	3	LQHALWREA	183	0.910
ANNs+QM	4	GRRIAGVLA	19	0.890

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MLTSHGFSR	1	1.792

QM	2	ALWREAIAL	186	-2.120
QM	3	DPHPSPLLR	248	-2.120

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RLQHALWRE	182	0.920
ANNs+QM	2	VLASAGLDV	25	0.910
ANNs+QM	3	MLTSHGFSR	1	0.890
ANNs+QM	4	DPHPSPLLR	248	0.840

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AAADLAAAI	63	0.920
ANNs+QM	2	ADLAAAIPD	65	0.910
ANNs+QM	3	ALLTQVGKL	159	0.910
ANNs+QM	4	LQHALWREA	183	0.910

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MLTSHGFSR	1	2.197
QM	2	DPHPSPLLR	248	2.197
QM	3	DYIGLDLTL	227	0.405

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPHPSPLLR	248	3.114
QM	2	SVAAAADLA	60	2.079
QM	3	LVVRNTIGL	207	2.079
QM	4	DTADRVVAL	152	1.792

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VKQELFERL	87	6.215
QM	2	MLTSHGFSR	1	4.787
QM	3	DPHPSPLLR	248	3.689
QM	4	ELFERLATL	90	2.708

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALWREAIAL	186	1.000
ANNs+QM	2	ILHAAAVEA	42	0.990
ANNs+QM	3	GSVAAAADL	59	0.990
ANNs+QM	4	ITDTNAEIL	35	0.970

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ELFERLATL	90	1.000
ANNs+QM	2	DTADRVVAL	152	1.000
ANNs+QM	3	VRNTIGLRL	209	1.000
ANNs+QM	4	TIGLRLATL	212	1.000

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VRNTIGLRL	209	4.094
QM	2	AREATTARL	279	4.094
QM	3	RRIAGVLAS	20	3.401
QM	4	GRRIAGVLA	19	2.996

ALLELE: HLA-B27

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GRRIAGVLA	19	0.980
ANNs+QM	2	RRIAGVLAS	20	0.970
ANNs+QM	3	VRNTIGLRL	209	0.820
ANNs+QM	4	GAGLMGRRI	14	0.360

ALLELE: HLA-B*2705

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GRRIAGVLA	19	1.000
ANNs+QM	2	AREATTARL	279	1.000
ANNs+QM	3	RRIAGVLAS	20	0.990
ANNs+QM	4	VRNTIGLRL	209	0.920

ALLELE: HLA-B*3501

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HPSPLLREL	250	1.000

ANNs+QM	2	IPDADLVIE	71	0.970
ANNs+QM	3	SPLLRELVA	252	0.950
ANNs+QM	4	APDTADRVV	150	0.770

ALLELE: HLA-B*3701

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HDPHPSPLL	247	5.298
QM	2	RELVAAGQL	256	2.303
QM	3	GARTGHGFL	265	1.609
QM	4	RAAVVGAGL	9	0.405

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QHALWREAI	184	2.197
QM	2	DYIGLDLTL	227	1.649
QM	3	LHAAAVEAA	43	1.361
QM	4	VIEAVVENL	77	1.361

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AREATTARL	279	3.807
QM	2	ELFERLATL	90	2.890
QM	3	QHALWREAI	184	2.708
QM	4	VRNTIGLRL	209	2.708

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VKQELFERL	87	3.178
QM	2	RAAVVGAGL	9	0.875
QM	3	VIEAVVENL	77	0.875
QM	4	IGNRLQHAL	179	0.875

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEAARVAGA	48	3.689
QM	2	RELVAAGQL	256	3.689
QM	3	AGVLASAGL	23	1.386
QM	4	AAVEAARVA	46	1.386

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEAARVAGA	48	3.178
QM	2	RELVAAGQL	256	2.890
QM	3	DTADRVVAL	152	0.588

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IGLDLTLAI	229	1.000
ANNs+QM	2	GAGLMGRRI	14	0.970
ANNs+QM	3	APDTADRVV	150	0.960

ANNs+QM	4	SPLLRELVA	252	0.940

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GAGLMGRRI	14	12.740
QM	2	DPHPSPLLR	248	12.320
QM	3	IGLDLTLAI	229	11.370
QM	4	VAGAGRGSV	53	11.060

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GAGLMGRRI	14	12.740
QM	2	DPHPSPLLR	248	12.320
QM	3	IGLDLTLAI	229	11.370
QM	4	VAGAGRGSV	53	11.060

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APDTADRVV	150	5.011
QM	2	IGLDLTLAI	229	3.497
QM	3	AIPDADLVI	70	3.401
QM	4	SPLLRELVA	252	2.485

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IGNRLQHAL	179	1.000
ANNs+QM	2	HPSPLLREL	250	1.000
ANNs+QM	3	APDTADRVV	150	0.990
ANNs+QM	4	DPHPSPLLR	248	0.980

ALLELE: HLA-B*5401				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APDTADRVV	150	0.990
ANNs+QM	2	DPHPSPLLR	248	0.970
ANNs+QM	3	HPSPLLREL	250	0.920
ANNs+QM	4	SPLLRELVA	252	0.920

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IGNRLQHAL	179	1.000
ANNs+QM	2	LWREAIALV	187	1.000
ANNs+QM	3	HPSPLLREL	250	1.000
ANNs+QM	4	TARLAQHIA	284	1.000

ALLELE: HLA-B*5801				
Threshold for 4 % with score: -0.223				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RAAVVGAGL	9	1.504
QM	2	ITDTNAEIL	35	1.194
QM	3	ASAGLDVAI	27	1.099
QM	4	TTARLAQHI	283	1.099

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RELVAAGQL	256	5.864
QM	2	HDPHPSPLL	247	2.996
QM	3	DTADRVVAL	152	2.773
QM	4	RAAVVGAGL	9	2.175

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEAARVAGA	48	3.689
QM	2	RELVAAGQL	256	2.868
QM	3	AAAVEAARV	45	0.693

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LQHALWREA	183	2.079
QM	2	RLATLAPDA	94	1.386
QM	3	ILHAAAVEA	42	1.138
QM	4	ELFERLATL	90	0.884

ALLELE: HLA-B7

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RAAVVGAGL	9	1.000
ANNs+QM	2	HPSPLLREL	250	1.000

ANNs+QM	3	ATLAPDAVL	96	0.990
ANNs+QM	4	APDTADRVV	150	0.990

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HPSPLLREL	250	1.000
ANNs+QM	2	APDTADRVV	150	0.980
ANNs+QM	3	DPHPSPLLR	248	0.970
ANNs+QM	4	SPLLRELVA	252	0.930

ALLELE: HLA-B8

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APDTADRVV	150	0.730
ANNs+QM	2	SPLLRELVA	252	0.730
ANNs+QM	3	PSPLLRELV	251	0.720
ANNs+QM	4	GARTGHGFL	265	0.720

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LVVRNTIGL	207	3.584
QM	2	AGVLASAGL	23	2.996
QM	3	GSVAAAADL	59	2.996
QM	4	ALLTQVGKL	159	2.996

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HPSPLLREL	250	6.090
QM	2	DTADRVVAL	152	4.900
QM	3	VRNTIGLRL	209	4.250
QM	4	AREATTARL	279	2.970

ALLELE: HLA-Cw*0602				
Threshold for 4 % with score: 1.482				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HPSPLLREL	250	2.676
QM	2	IGNRLQHAL	179	1.887
QM	3	VRNTIGLRL	209	1.887
QM	4	LAQHIAAQL	287	1.887

ALLELE: HLA-Cw*0702				
Threshold for 4 % with score: 1.212				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HPSPLLREL	250	2.493
QM	2	DYIGLDLTL	227	1.281
QM	3	RAAVVGAGL	9	0.971
QM	4	VIEAVVENL	77	0.875

ALLELE: H2-Db				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ITDTNAEIL	35	1.000
ANNs+QM	2	AAADLAAAI	63	0.940
ANNs+QM	3	TIGLRLATL	212	0.860
ANNs+QM	4	AAAIPDADL	68	0.850

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IGNRLQHAL	179	20.540
QM	2	IGLDLTLAI	229	19.500
QM	3	AGVLASAGL	23	13.720
QM	4	RGSVAAAAD	58	13.550

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HDPHPSPLL	247	1.000
ANNs+QM	2	AAAIPDADL	68	0.980
ANNs+QM	3	AAAVEAARV	45	0.940
ANNs+QM	4	AAADLAAAI	63	0.940

ALLELE: H2-Kd

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DYIGLDLTL	227	1.000
ANNs+QM	2	ITDTNAEIL	35	0.970
ANNs+QM	3	GARTGHGFL	265	0.970
ANNs+QM	4	RAAVVGAGL	9	0.930

ALLELE: H2-Kk

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score

QM	1	VEAARVAGA	48	2.708
QM	2	GAGLMGRRI	14	2.303
QM	3	ASAGLDVAI	27	2.303
QM	4	AAADLAAAI	63	2.303

ALLELE: H2-Ld

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GSVAAAADL	59	1.000
ANNs+QM	2	HPSPLLREL	250	1.000
ANNs+QM	3	LTSHGFSRA	2	0.870
ANNs+QM	4	GARTGHGFL	265	0.830

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALLTQVGKL	159	16.180
QM	2	VIEAVVENL	77	14.780
QM	3	VLPIGAVTE	110	14.660
QM	4	GSVAAAADL	59	14.110

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IGNRLQHAL	179	14.330
QM	2	RAAVVGAGL	9	10.220
QM	3	TNAEILHAA	38	9.030
QM	4	ALWREAIAL	186	7.760

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ARTAPDTAD	147	6.140
QM	2	LQHALWREA	183	6.000
QM	3	HPSPLLREL	250	4.290
QM	4	DWPAGAREA	274	4.000

ALLELE: HLA-B35				
Threshold for 4 % with score: 8.350				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HPSPLLREL	250	10.410
QM	2	RAAVVGAGL	9	8.770
QM	3	ELFERLATL	90	8.750
QM	4	IPDADLVIE	71	8.580

ALLELE: Mamu-A*01				
Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HDPHPSPLL	247	6.770
QM	2	DTADRVVAL	152	4.950
QM	3	AAAIPDADL	68	3.780
QM	4	AAADLAAAI	63	1.950

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ILHAAAVEA	42	20.400
QM	2	ELFERLATL	90	19.270

QM	3	RAAVVGAGL	9	17.260
QM	4	GFSRAAVVG	6	15.730

ALLELE: HLA-B*2703

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AREATTARL	279	7.230
QM	2	GRRIAGVLA	19	6.580
QM	3	ARTAPDTAD	147	5.470
QM	4	ARVAGAGRG	51	5.000

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AGVLASAGL	23	13.340
QM	2	VRNTIGLRL	209	13.160
QM	3	AREATTARL	279	11.980
QM	4	GRGSVAAAA	57	11.660

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GARTGHGFL	265	8.510
QM	2	HPSPLLREL	250	6.820
QM	3	DYIGLDLTL	227	6.420
QM	4	RELVAAGQL	256	5.930

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPHPSPLLR	248	3.680
QM	2	HDPHPSPLL	247	3.460
QM	3	MLTSHGFSR	1	1.810
QM	4	LQHALWREA	183	1.700

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AGVLASAGL	23	7.440
QM	2	GSVAAAADL	59	6.870
QM	3	VEAARVAGA	48	6.260
QM	4	RELVAAGQL	256	5.350

ALLELE: HLA-A*6801

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SVAAAADLA	60	0.930
ANNs+QM	2	AAADLAAAI	63	0.920
ANNs+QM	3	ASAGLDVAI	27	0.830
ANNs+QM	4	AVEAARVAG	47	0.700

ALLELE: HLA-A*6802

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AAAIPDADL	68	0.990
ANNs+QM	2	PSPLLRELV	251	0.990
ANNs+QM	3	AAAVEAARV	45	0.980
ANNs+QM	4	VEAARVAGA	48	0.980