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

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Antigen Name	Untitled
Scanned on	Wed Feb 24 13:30:14 2010
Length of input sequence	314 amino acids
Number of nonamers from input sequence	306
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	PTDPASPYA	139	0.370
ANNs+QM	2	EAGVVAIFA	186	0.330
ANNs+QM	3	LGDLKRSCL	272	0.270
ANNs+QM	4	GFIGSTLVD	10	0.200

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HRPEVVFHL	69	0.600
ANNs+QM	2	SVADPQFDA	86	0.600

ANNs+QM	3	VVAIFAQAL	189	0.440
ANNs+QM	4	VNVIGTVRL	96	0.270

ALLELE: HLA-A*0201

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVAIFAQAL	189	0.990
ANNs+QM	2	AQIDVRRSV	79	0.950
ANNs+QM	3	HRPEVVFHL	69	0.580
ANNs+QM	4	GKVAGEIYL	149	0.120

ALLELE: HLA-A*0202

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FATGRATNL	33	0.940
ANNs+QM	2	AGVVAIFAQ	187	0.450
ANNs+QM	3	HRPEVVFHL	69	0.440
ANNs+QM	4	DPHGEAGVV	182	0.440

ALLELE: HLA-A*0203

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FATGRATNL	33	0.970
ANNs+QM	2	SVADPQFDA	86	0.820
ANNs+QM	3	KRSCLDIGL	276	0.770
ANNs+QM	4	LGWRPQIEL	289	0.490

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AQIDVRRSV	79	0.910
ANNs+QM	2	ADGHSVVGL	22	0.490
ANNs+QM	3	GFIGSTLVD	10	0.380
ANNs+QM	4	HRPEVVFHL	69	0.290

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IGSTLVDRL	12	13.510
QM	2	DPEFHPPRL	264	6.960
QM	3	VVAIFAQAL	189	6.920
QM	4	ADGHSVVGL	22	6.540

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVDAFVRVS	221	0.650
ANNs+QM	2	GPRQDPHGE	178	0.580
ANNs+QM	3	APTDPASPY	138	0.480
ANNs+QM	4	PTDPASPYA	139	0.240

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVDAFVRVS	221	0.780

ANNs+QM	2	YVFVDDVVD	215	0.720
ANNs+QM	3	PTDPASPYA	139	0.620
ANNs+QM	4	SAVAAAVGG	253	0.400

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VVAIFAQAL	189	11.970
QM	2	HRPEVVFHL	69	7.260
QM	3	DPEFHPPRL	264	6.970
QM	4	ADGHSVVGL	22	6.310

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KRSCLDIGL	276	0.620
ANNs+QM	2	GSTLVDRLL	13	0.150
ANNs+QM	3	GPRQDPHGE	178	0.140
ANNs+QM	4	VFVEADIVT	51	0.100

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SPYAAGKVA	144	0.930
ANNs+QM	2	APTDPASPY	138	0.550
ANNs+QM	3	VVAIFAQAL	189	0.480
ANNs+QM	4	DPHGEAGVV	182	0.440

ALLELE: HLA-A*3101				
Threshold for 4 % with score: -1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RQLHSAVAA	249	-2.120
QM	2	SVADPQFDA	86	-2.813
QM	3	FVEADIVTA	52	-3.219

ALLELE: HLA-A31				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YVFVDDVVD	215	0.880
ANNs+QM	2	SPYAAGKVA	144	0.550
ANNs+QM	3	FVEADIVTA	52	0.530
ANNs+QM	4	PTDPASPYA	139	0.410

ALLELE: HLA-A*0301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AQIDVRRSV	79	1.000
ANNs+QM	2	APTDPASPY	138	0.950
ANNs+QM	3	SPYAAGKVA	144	0.650
ANNs+QM	4	RQLHSAVAA	249	0.280

ALLELE: HLA-A*3302				
Threshold for 4 % with score: -0.105				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GSTLVDRLL	13	-0.693
QM	2	NSAHVFVEA	47	-0.693

QM	3	FVEADIVTA	52	-0.693

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SVADPQFDA	86	2.079
QM	2	VVAIFAQAL	189	2.079
QM	3	FVEADIVTA	52	1.386
QM	4	YVFVDDVVD	215	0.182

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GKVAGEIYL	149	6.215
QM	2	GKETSDRQL	243	6.215
QM	3	GRATNLEHL	36	2.303
QM	4	HRPEVVFHL	69	2.303

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GRATNLEHL	36	0.960
ANNs+QM	2	GSTLVDRLL	13	0.910
ANNs+QM	3	KRSCLDIGL	276	0.880
ANNs+QM	4	SAVAAAVGG	253	0.870

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FATGRATNL	33	1.000
ANNs+QM	2	GRATNLEHL	36	1.000
ANNs+QM	3	DRQLHSAVA	248	1.000
ANNs+QM	4	DPEFHPPRL	264	1.000

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KRSCLDIGL	276	5.193
QM	2	GRATNLEHL	36	4.094
QM	3	HRPEVVFHL	69	4.094
QM	4	DRQLHSAVA	248	1.792

ALLELE: HLA-B27

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GRATNLEHL	36	0.660
ANNs+QM	2	HRPEVVFHL	69	0.550
ANNs+QM	3	KRSCLDIGL	276	0.490
ANNs+QM	4	DRQLHSAVA	248	0.260

ALLELE: HLA-B*2705

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KRSCLDIGL	276	1.000
ANNs+QM	2	GRATNLEHL	36	0.830
ANNs+QM	3	DRQLHSAVA	248	0.730

ANNs+QM	4	RQLHSAVAA	249	0.450

ALLELE: HLA-B*3501

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPEFHPPRL	264	1.000
ANNs+QM	2	APTDPASPY	138	0.970
ANNs+QM	3	DPHGEAGVV	182	0.690
ANNs+QM	4	LGDLKRSCL	272	0.400

ALLELE: HLA-B*3701

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADGHSVVGL	22	3.689
QM	2	GSTLVDRLL	13	2.015
QM	3	HRPEVVFHL	69	0.405

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPEFHPPRL	264	1.792
QM	2	LGDLKRSCL	272	1.099
QM	3	FATGRATNL	33	0.693
QM	4	IGSTLVDRL	12	0.262

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HRPEVVFHL	69	3.807
QM	2	GRATNLEHL	36	3.114
QM	3	DPEFHPPRL	264	2.197
QM	4	KRSCLDIGL	276	2.015

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GKVAGEIYL	149	2.996
QM	2	GKETSDRQL	243	2.996
QM	3	IGSTLVDRL	12	0.875
QM	4	GSTLVDRLL	13	0.875

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADGHSVVGL	22	1.609
QM	2	VNVIGTVRL	96	0.693
QM	3	LGWRPQIEL	289	0.405

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APTDPASPY	138	2.197
QM	2	ADGHSVVGL	22	1.099
QM	3	AQIDVRRSV	79	-0.288

ALLELE: HLA-B*5101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPHGEAGVV	182	1.000
ANNs+QM	2	APTDPASPY	138	0.850
ANNs+QM	3	SPYAAGKVA	144	0.790
ANNs+QM	4	LGDLKRSCL	272	0.770

ALLELE: HLA-B*5102				
Threshold for 4 % with score: 9.050				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPHGEAGVV	182	15.090
QM	2	HGEAGVVAI	184	11.500
QM	3	DPEFHPPRL	264	9.740
QM	4	LGWRPQIEL	289	7.090

ALLELE: HLA-B*5103				
Threshold for 4 % with score: 9.280				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPHGEAGVV	182	15.090
QM	2	HGEAGVVAI	184	11.500
QM	3	DPEFHPPRL	264	9.740
QM	4	LGWRPQIEL	289	7.090

ALLELE: HLA-B*5201				
Threshold for 4 % with score: 1.974				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DPHGEAGVV	182	3.912

QM	2	SPYAAGKVA	144	3.902
QM	3	AQIDVRRSV	79	3.689
QM	4	HGEAGVVAI	184	2.197

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPEFHPPRL	264	1.000
ANNs+QM	2	LGWRPQIEL	289	1.000
ANNs+QM	3	APTDPASPY	138	0.980
ANNs+QM	4	DPHGEAGVV	182	0.980

ALLELE: HLA-B*5401

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APTDPASPY	138	1.000
ANNs+QM	2	DPEFHPPRL	264	1.000
ANNs+QM	3	SPYAAGKVA	144	0.990
ANNs+QM	4	DPHGEAGVV	182	0.980

ALLELE: HLA-B*51

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APTDPASPY	138	0.990
ANNs+QM	2	DPEFHPPRL	264	0.990
ANNs+QM	3	GPRQDPHGE	178	0.970
ANNs+QM	4	DPHGEAGVV	182	0.970

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NSAHVFVEA	47	1.281
QM	2	GSTLVDRLL	13	1.099
QM	3	FATGRATNL	33	0.095

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADGHSVVGL	22	3.689
QM	2	VNVIGTVRL	96	2.868
QM	3	IGSTLVDRL	12	2.270
QM	4	LGWRPQIEL	289	2.079

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADGHSVVGL	22	0.000
QM	2	NSAHVFVEA	47	0.000
QM	3	AQIDVRRSV	79	0.000

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RQLHSAVAA	249	1.569
QM	2	AQIDVRRSV	79	1.482
QM	3	APTDPASPY	138	0.788

ALLELE: HLA-B7				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPHGEAGVV	182	0.940
ANNs+QM	2	KRSCLDIGL	276	0.930
ANNs+QM	3	FATGRATNL	33	0.920
ANNs+QM	4	DPEFHPPRL	264	0.840

ALLELE: HLA-B*0702				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPEFHPPRL	264	1.000
ANNs+QM	2	LGWRPQIEL	289	1.000
ANNs+QM	3	SPYAAGKVA	144	0.990
ANNs+QM	4	DPHGEAGVV	182	0.950

ALLELE: HLA-B8				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SPYAAGKVA	144	0.660
ANNs+QM	2	GSTLVDRLL	13	0.640
ANNs+QM	3	LGDLKRSCL	272	0.640
ANNs+QM	4	KRSCLDIGL	276	0.610

ALLELE: HLA-Cw*0301
Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VNVIGTVRL	96	2.996
QM	2	GKVAGEIYL	149	2.303
QM	3	HRPEVVFHL	69	1.792
QM	4	GRATNLEHL	36	1.569

ALLELE: HLA-Cw*0401				
Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SPYAAGKVA	144	10.640
QM	2	HRPEVVFHL	69	6.430
QM	3	DPEFHPPRL	264	5.370
QM	4	VNVIGTVRL	96	4.370

ALLELE: HLA-Cw*0602				
Threshold for 4 % with score: 1.482				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IGSTLVDRL	12	2.580
QM	2	KRSCLDIGL	276	1.982
QM	3	VVAIFAQAL	189	1.887
QM	4	GRATNLEHL	36	1.482

ALLELE: HLA-Cw*0702				
Threshold for 4 % with score: 1.212				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	APTDPASPY	138	2.821
QM	2	HRPEVVFHL	69	2.262
QM	3	ADGHSVVGL	22	1.569

QM	4	GRATNLEHL	36	1.569

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GRATNLEHL	36	1.000
ANNs+QM	2	GKVAGEIYL	149	0.690
ANNs+QM	3	VVAIFAQAL	189	0.660
ANNs+QM	4	FATGRATNL	33	0.270

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HGEAGVVAI	184	17.890
QM	2	HRPEVVFHL	69	17.640
QM	3	AGVVAIFAQ	187	14.470
QM	4	VNVIGTVRL	96	12.580

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVAIFAQAL	189	1.000
ANNs+QM	2	FATGRATNL	33	0.990
ANNs+QM	3	PTDPASPYA	139	0.840
ANNs+QM	4	EAGVVAIFA	186	0.770

ALLELE: H2-Kd

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	KRSCLDIGL	276	0.990
ANNs+QM	2	GRATNLEHL	36	0.950
ANNs+QM	3	FATGRATNL	33	0.860
ANNs+QM	4	DPHGEAGVV	182	0.850

ALLELE: H2-Kk

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HGEAGVVAI	184	2.303
QM	2	ADGHSVVGL	22	1.386
QM	3	AQIDVRRSV	79	0.000

ALLELE: H2-Ld

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPEFHPPRL	264	0.930
ANNs+QM	2	DPHGEAGVV	182	0.800
ANNs+QM	3	KRSCLDIGL	276	0.750
ANNs+QM	4	FATGRATNL	33	0.740

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HRPEVVFHL	69	18.510
QM	2	FATGRATNL	33	10.780
QM	3	GRATNLEHL	36	10.780

QM	4	IGSTLVDRL	12	9.780

ALLELE: H-2Qa				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HRPEVVFHL	69	8.550
QM	2	GRATNLEHL	36	7.380
QM	3	KRSCLDIGL	276	6.470
QM	4	GSTLVDRLL	13	5.220

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SPYAAGKVA	144	6.670
QM	2	KRSCLDIGL	276	6.000
QM	3	DPEFHPPRL	264	5.330
QM	4	GKETSDRQL	243	4.890

ALLELE: HLA-B35				
Threshold for 4 % with score: 8.350				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LGDLKRSCL	272	11.220
QM	2	DPEFHPPRL	264	11.110
QM	3	APTDPASPY	138	9.420
QM	4	HRPEVVFHL	69	7.640

ALLELE: Mamu-A*01

Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VVAIFAQAL	189	8.050
QM	2	VNVIGTVRL	96	3.590
QM	3	HGEAGVVAI	184	3.300
QM	4	SVADPQFDA	86	2.820

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VVAIFAQAL	189	14.390
QM	2	RQLHSAVAA	249	11.760
QM	3	FATGRATNL	33	9.860
QM	4	NLEHLADNS	40	9.820

ALLELE: HLA-B*2703				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HRPEVVFHL	69	10.500
QM	2	KRSCLDIGL	276	9.000
QM	3	GRATNLEHL	36	6.700
QM	4	GKVAGEIYL	149	4.670

ALLELE: HLA-B*2704				
Threshold for 4 % with score: 8.790				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GRATNLEHL	36	15.570
QM	2	KRSCLDIGL	276	14.780
QM	3	DRQLHSAVA	248	11.910

QM	4	DPEFHPPRL	264	11.470

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PHGEAGVVA	183	8.060
QM	2	SAVAAAVGG	253	7.860
QM	3	IGSTLVDRL	12	6.370
QM	4	KRSCLDIGL	276	6.370

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SVADPQFDA	86	2.350
QM	2	APTDPASPY	138	1.130
QM	3	HRPEVVFHL	69	0.910
QM	4	VIGTVRLAE	98	0.710

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AGVVAIFAQ	187	4.250
QM	2	SAVAAAVGG	253	3.720
QM	3	HGEAGVVAI	184	2.910
QM	4	GKVAGEIYL	149	2.290

ALLELE: HLA-A*6801

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVDAFVRVS	221	0.770
ANNs+QM	2	SAVAAAVGG	253	0.720
ANNs+QM	3	PTDPASPYA	139	0.590
ANNs+QM	4	VVAIFAQAL	189	0.590

ALLELE: HLA-A*6802

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVAIFAQAL	189	0.980
ANNs+QM	2	IGSTLVDRL	12	0.970
ANNs+QM	3	SAVAAAVGG	253	0.970
ANNs+QM	4	VVDAFVRVS	221	0.960