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

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Antigen Name	Untitled
Scanned on	Wed Apr 14 00:45:05 2010
Length of input sequence	486 amino acids
Number of nonamers from input sequence	478
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	MAEYTAAKA	199	1.000
ANNs+QM	2	VLDALAAAA	281	1.000
ANNs+QM	3	HAEVAAMAS	362	1.000
ANNs+QM	4	AGETVGAAV	429	1.000

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AQVRVGFRL	233	1.000
ANNs+QM	2	SLHAEVAAM	360	1.000

ANNs+QM	3	VLDEPAELL	155	0.980
ANNs+QM	4	FQLHWAPSL	170	0.970

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PLGPGAPVL	4	1.000
ANNs+QM	2	VLDEPAELL	155	1.000
ANNs+QM	3	FQLHWAPSL	170	1.000
ANNs+QM	4	VLDALAAAA	281	1.000

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PVPGPVGVL	274	4.660
ANNs+QM	2	PLGPGAPVL	4	1.000
ANNs+QM	3	PLLAAAAAA	81	0.960
ANNs+QM	4	LAAAAAAGV	83	0.940

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LGPGAPVLV	5	0.990
ANNs+QM	2	AFSDDLTLL	260	0.970
ANNs+QM	3	VLDPLGPGA	1	0.950
ANNs+QM	4	AQPGDTVLL	449	0.930

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NIGSAVLDV	147	1.000
ANNs+QM	2	RVLTGGVAV	208	1.000
ANNs+QM	3	IPVPGPVGV	273	0.970
ANNs+QM	4	EPAARELGV	243	0.900

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PLGPGAPVL	4	11.490
QM	2	ATPLLAAAA	79	10.740
QM	3	AVLIGRDRA	375	10.340
QM	4	AQVRVGFRL	233	9.930

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALAAAALAR	284	1.000
ANNs+QM	2	AMLIAGGRR	133	0.810
ANNs+QM	3	GLLKGASLH	354	0.770
ANNs+QM	4	KTTTTSMLH	124	0.740

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AMLIAGGRR	133	1.000

ANNs+QM	2	ALAAAALAR	284	1.000
ANNs+QM	3	MTAAVAAAR	438	1.000
ANNs+QM	4	AEYTAAKAR	200	0.960

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VQQITGYAL	61	13.760
QM	2	FQLHWAPSL	170	9.610
QM	3	RVVWIAGGL	347	9.470
QM	4	DVLDEPAEL	154	9.290

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GFSPATPLL	75	1.000
ANNs+QM	2	AFSDDLTLL	260	1.000
ANNs+QM	3	GYADRGEAF	469	0.990
ANNs+QM	4	LRPHAERGL	44	0.470

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALAAAALAR	284	1.000
ANNs+QM	2	TSFRVGRHR	306	1.000
ANNs+QM	3	AEYTAAKAR	200	0.990
ANNs+QM	4	MTAAVAAAR	438	0.990

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AMLIAGGRR	133	1.386
QM	2	ALAAAALAR	284	1.386
QM	3	MTAAVAAAR	438	0.000

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TSFRVGRHR	306	0.990
ANNs+QM	2	AMLIAGGRR	133	0.970
ANNs+QM	3	MTAAVAAAR	438	0.900
ANNs+QM	4	GAVLIGRDR	374	0.890

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AMLIAGGRR	133	0.980
ANNs+QM	2	AVMTAAVAA	436	0.940
ANNs+QM	3	GLLKGASLH	354	0.920
ANNs+QM	4	AGLDDSRAA	217	0.900

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AMLIAGGRR	133	2.708
QM	2	TSFRVGRHR	306	2.708

QM	3	ALAAAALAR	284	2.197
QM	4	APVLVAGGR	9	1.099

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MTAAVAAAR	438	4.605
QM	2	TSFRVGRHR	306	3.807
QM	3	DVLDEPAEL	154	3.178
QM	4	EVAAMASRL	364	3.178

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AMLIAGGRR	133	5.298
QM	2	ALAAAALAR	284	4.787
QM	3	DKAGETVGA	427	4.605
QM	4	APVLVAGGR	9	3.689

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PLGPGAPVL	4	1.000
ANNs+QM	2	VLDEPAELL	155	1.000
ANNs+QM	3	GFSPATPLL	75	0.990
ANNs+QM	4	VLDALAAAA	281	0.990

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LRPEAGAVL	178	1.000
ANNs+QM	2	LDDSRAAAL	219	1.000
ANNs+QM	3	DRAAVAEAL	381	1.000
ANNs+QM	4	PAELLAVEL	159	0.960

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LRPEAGAVL	178	4.094
QM	2	GRVTGQAVA	16	2.996
QM	3	SRHAPDVPV	390	2.996
QM	4	LRPHAERGL	44	2.890

ALLELE: HLA-B27

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GRDRAAVAE	379	0.900
ANNs+QM	2	LRPHAERGL	44	0.800
ANNs+QM	3	LRPEAGAVL	178	0.790
ANNs+QM	4	DRAAVAEAL	381	0.790

ALLELE: HLA-B*2705

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LRPHAERGL	44	1.000

ANNs+QM	2	GRDRAAVAE	379	0.980
ANNs+QM	3	LRPEAGAVL	178	0.940
ANNs+QM	4	GRVTGQAVA	16	0.910

ALLELE: HLA-B*3501				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VPIWGDVEL	91	1.000
ANNs+QM	2	GPVGVLDAL	277	1.000
ANNs+QM	3	APVLVAGGR	9	0.970
ANNs+QM	4	MPATVEVPV	409	0.970

ALLELE: HLA-B*3701				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LDDSRAAAL	219	3.689
QM	2	VDRAFSDDL	257	3.689
QM	3	LDALAAAAL	282	3.689
QM	4	VEVPVACVL	413	2.708

ALLELE: HLA-B*3801				
Threshold for 4 % with score: 0.445				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LHAEVAAMA	361	2.054
QM	2	VLDEPAELL	155	1.792
QM	3	GPVGVLDAL	277	1.649
QM	4	WHATMAEYT	195	1.543

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LRPEAGAVL	178	3.401
QM	2	VLDEPAELL	155	2.890
QM	3	DRAAVAEAL	381	2.708
QM	4	RHRAEVVAV	312	2.603

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FQLHWAPSL	170	3.178
QM	2	AQVRVGFRL	233	3.178
QM	3	VQQITGYAL	61	2.996
QM	4	AQPGDTVLL	449	2.996

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEVPVACVL	413	5.075
QM	2	GETVGAAVM	430	3.178
QM	3	DDLTLLPVA	263	1.609
QM	4	LDALAAAAL	282	1.609

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEVPVACVL	413	3.584

QM	2	DAVQQITGY	59	3.296
QM	3	GETVGAAVM	430	1.792
QM	4	DDLTLLPVA	263	1.504

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EPAARELGV	243	1.000
ANNs+QM	2	VGRHRAEVV	310	1.000
ANNs+QM	3	LAYPRVVWI	343	1.000
ANNs+QM	4	MPATVEVPV	409	1.000

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IPVPGPVGV	273	15.340
QM	2	LGPGAPVLV	5	14.440
QM	3	MPATVEVPV	409	14.080
QM	4	AALARSVGV	288	13.520

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IPVPGPVGV	273	15.340
QM	2	LGPGAPVLV	5	14.440
QM	3	MPATVEVPV	409	14.080
QM	4	AALARSVGV	288	13.520

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IGSAVLDVL	148	3.679
QM	2	VGRHRAEVV	310	3.209
QM	3	TGQAVAAVL	19	3.178
QM	4	LGPGAPVLV	5	3.114

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SPATPLLAA	77	1.000
ANNs+QM	2	VPIWGDVEL	91	1.000
ANNs+QM	3	IPVPGPVGV	273	1.000
ANNs+QM	4	GPVGVLDAL	277	1.000

ALLELE: HLA-B*5401

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SPATPLLAA	77	1.000
ANNs+QM	2	TPLLAAAAA	80	1.000
ANNs+QM	3	IPVPGPVGV	273	1.000
ANNs+QM	4	MPATVEVPV	409	1.000

ALLELE: HLA-B*51

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VPIWGDVEL	91	1.000

ANNs+QM	2	IWGDVELAW	93	1.000
ANNs+QM	3	LAYPRVVWI	343	1.000
ANNs+QM	4	EPAARELGV	243	0.980

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ATVEVPVAC	411	1.792
QM	2	ITGYALVVA	64	1.281
QM	3	ASPGFSPAT	72	1.099
QM	4	ATPLLAAAA	79	1.099

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEVPVACVL	413	5.864
QM	2	LDALAAAAL	282	3.689
QM	3	LDDSRAAAL	219	2.996
QM	4	VDRAFSDDL	257	2.996

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GETVGAAVM	430	2.868
QM	2	VEVPVACVL	413	2.773
QM	3	DDLTLLPVA	263	1.609
QM	4	LAAAAAAGV	83	0.693

ALLELE: HLA-B62				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AQVRVGFRL	233	2.079
QM	2	AQPGDTVLL	449	1.751
QM	3	VLVAGGRVT	11	1.482
QM	4	VQQITGYAL	61	1.386

ALLELE: HLA-B7				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GPVGVLDAL	277	1.000
ANNs+QM	2	YTAAKARVL	202	0.990
ANNs+QM	3	VPIWGDVEL	91	0.940
ANNs+QM	4	ASRLVGAVL	369	0.930

ALLELE: HLA-B*0702				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SPATPLLAA	77	1.000
ANNs+QM	2	VPIWGDVEL	91	1.000
ANNs+QM	3	GPVGVLDAL	277	1.000
ANNs+QM	4	MPATVEVPV	409	1.000

ALLELE: HLA-B8				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EPAARELGV	243	0.750

ANNs+QM	2	FSPATPLLA	76	0.730
ANNs+QM	3	YTAAKARVL	202	0.730
ANNs+QM	4	VLDEPAELL	155	0.690

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEVPVACVL	413	4.605
QM	2	LAYPRVVWI	343	3.912
QM	3	AQVRVGFRL	233	3.401
QM	4	DVLDEPAEL	154	2.996

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VPIWGDVEL	91	8.760
QM	2	SLHAEVAAM	360	7.970
QM	3	AFSDDLTLL	260	7.700
QM	4	GFSPATPLL	75	6.640

ALLELE: HLA-Cw*0602

Threshold for 4 % with score: 1.482

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VDRAFSDDL	257	1.792
QM	2	RVVWIAGGL	347	1.792
QM	3	EVAAMASRL	364	1.792
QM	4	YTAAKARVL	202	1.577

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DAVQQITGY	59	2.175
QM	2	GPVGVLDAL	277	2.156
QM	3	DRAAVAEAL	381	1.751
QM	4	SPATPLLAA	77	1.058

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PLGPGAPVL	4	1.000
ANNs+QM	2	CGNIGSAVL	145	1.000
ANNs+QM	3	MAQPGDTVL	448	0.970
ANNs+QM	4	RVLTGGVAV	208	0.830

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TGGVAVAGL	211	19.270
QM	2	TGQAVAAVL	19	17.660
QM	3	GGLLKGASL	353	15.690
QM	4	LRPEAGAVL	178	14.460

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ASPGFSPAT	72	1.000

ANNs+QM	2	YTAAKARVL	202	0.980
ANNs+QM	3	AFSDDLTLL	260	0.980
ANNs+QM	4	LRPHAERGL	44	0.970

ALLELE: H2-Kd				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LRPHAERGL	44	1.000
ANNs+QM	2	GFSPATPLL	75	1.000
ANNs+QM	3	YTAAKARVL	202	0.980
ANNs+QM	4	TGGVAVAGL	211	0.970

ALLELE: H2-Kk				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEVPVACVL	413	4.094
QM	2	GETVGAAVM	430	2.996
QM	3	DDLTLLPVA	263	2.079
QM	4	VDRAFSDDL	257	1.792

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APSLRPEAG	175	1.000
ANNs+QM	2	ASRLVGAVL	369	1.000
ANNs+QM	3	MAQPGDTVL	448	1.000
ANNs+QM	4	YTAAKARVL	202	0.990

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LRPEAGAVL	178	14.840
QM	2	PVPGPVGVL	274	14.840
QM	3	EVAAMASRL	364	14.780
QM	4	AQPGDTVLL	449	14.710

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DRAAVAEAL	381	11.720
QM	2	AQVRVGFRL	233	11.220
QM	3	FQLHWAPSL	170	8.050
QM	4	VEVPVACVL	413	7.550

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SRHAPDVPV	390	11.000
QM	2	IAGGLLKGA	351	9.490
QM	3	LRPHAERGL	44	6.330
QM	4	IPVPGPVGV	273	6.330

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GPVGVLDAL	277	15.830

QM	2	FQLHWAPSL	170	12.700
QM	3	AQVRVGFRL	233	11.220
QM	4	GGLLKGASL	353	9.640

ALLELE: Mamu-A*01				
Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ASPGFSPAT	72	6.860
QM	2	SVGVPAGAI	293	4.320
QM	3	VLDEPAELL	155	3.830
QM	4	AGLDDSRAA	217	3.120

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VLDEPAELL	155	22.490
QM	2	PLLAAAAAA	81	17.400
QM	3	LDALAAAAL	282	16.890
QM	4	VLDALAAAA	281	16.600

ALLELE: HLA-B*2703				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LRPHAERGL	44	10.830
QM	2	LRPEAGAVL	178	7.500
QM	3	VPIWGDVEL	91	5.940
QM	4	ARSVGVPAG	291	5.340

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VDRAFSDDL	257	15.350
QM	2	SRHAPDVPV	390	12.250
QM	3	DRAAVAEAL	381	11.560
QM	4	LRPHAERGL	44	11.430

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VEVPVACVL	413	13.930
QM	2	GPVGVLDAL	277	10.560
QM	3	AEYTAAKAR	200	9.930
QM	4	MAQPGDTVL	448	9.750

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TSFRVGRHR	306	5.970
QM	2	HWAPSLRPE	173	5.940
QM	3	DSKATNPHA	329	4.610
QM	4	MTAAVAAAR	438	4.370

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEYTAAKAR	200	9.890

QM	2	GETVGAAVM	430	6.040
QM	3	GYADRGEAF	469	5.860
QM	4	LDALAAAAL	282	5.590

ALLELE: HLA-A*6801				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	MTAAVAAAR	438	1.000
ANNs+QM	2	ALAAAALAR	284	0.980
ANNs+QM	3	AMLIAGGRR	133	0.950
ANNs+QM	4	AEYTAAKAR	200	0.950

ALLELE: HLA-A*6802				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LAAAAAAGV	83	0.990
ANNs+QM	2	YTAAKARVL	202	0.980
ANNs+QM	3	EPAARELGV	243	0.980
ANNs+QM	4	IPVPGPVGV	273	0.980