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

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Antigen Name	Untitled
Scanned on	Mon Mar 15 00:15:07 2010
Length of input sequence	439 amino acids
Number of nonamers from input sequence	431
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	AAEQQSMST	264	1.000
ANNs+QM	2	CSDIGVTGL	317	0.850
ANNs+QM	3	AGALTAASL	15	0.680
ANNs+QM	4	QTFDRADGL	292	0.480

ALLELE: HLA-A2				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SLLRGAGAL	10	1.000
ANNs+QM	2	GLDFDVAPL	299	0.990

ANNs+QM	3	VLLDLNTLL	109	0.980
ANNs+QM	4	RLFVPVLRS	357	0.980

ALLELE: HLA-A*0201

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VLLDLNTLL	109	1.000
ANNs+QM	2	GLDFDVAPL	299	1.000
ANNs+QM	3	LLARDQAFA	116	0.930
ANNs+QM	4	RLFVPVLRS	357	0.920

ALLELE: HLA-A*0202

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SLLRGAGAL	10	1.000
ANNs+QM	2	GLDFDVAPL	299	0.980
ANNs+QM	3	AGALTAASL	15	0.760
ANNs+QM	4	VLLDLNTLL	109	0.600

ALLELE: HLA-A*0203

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ELADRGVLL	103	0.970
ANNs+QM	2	VLLDLNTLL	109	0.960
ANNs+QM	3	GLDFDVAPL	299	0.950
ANNs+QM	4	LLARDQAFA	116	0.930

ALLELE: HLA-A*0206				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VLLDLNTLL	109	0.740
ANNs+QM	2	YPDIKVRAL	63	0.480
ANNs+QM	3	RLFVPVLRS	357	0.470
ANNs+QM	4	ADRGVLLDL	105	0.380

ALLELE: HLA-A*0205				
Threshold for 4 % with score: 5.950				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QTFDRADGL	292	10.760
QM	2	SVGKAGIAL	277	7.720
QM	3	GLDFDVAPL	299	7.480
QM	4	EFLDAAQAL	184	6.940

ALLELE: HLA-A*1101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TADLFSVGK	272	0.990
ANNs+QM	2	RRYPDIKVR	61	0.780
ANNs+QM	3	GFLEAVQFY	243	0.460
ANNs+QM	4	AAEQQSMST	264	0.260

ALLELE: HLA-A11				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TADLFSVGK	272	0.970

ANNs+QM	2	LTAASLAPW	18	0.960
ANNs+QM	3	RRYPDIKVR	61	0.930
ANNs+QM	4	RLFVPVLRS	357	0.600

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AGALTAASL	15	12.660
QM	2	DQAWEFVKF	335	11.180
QM	3	AWELTYAEL	96	10.410
QM	4	RRVGNLAVL	377	10.070

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EFLDAAQAL	184	1.000
ANNs+QM	2	LFSVGKAGI	275	0.980
ANNs+QM	3	RPATSLTGL	420	0.890
ANNs+QM	4	NFLFYNKQL	155	0.880

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRYPDIKVR	61	0.960
ANNs+QM	2	GFLEAVQFY	243	0.950
ANNs+QM	3	NAHRRVGNL	374	0.690
ANNs+QM	4	TADLFSVGK	272	0.670

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRYPDIKVR	61	-1.715
QM	2	RLFVPVLRS	357	-2.631
QM	3	SLLRGAGAL	10	-3.219

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRYPDIKVR	61	1.000
ANNs+QM	2	TADLFSVGK	272	0.710
ANNs+QM	3	RLFVPVLRS	357	0.570
ANNs+QM	4	ELADRGVLL	103	0.530

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QSMSTADLF	268	0.840
ANNs+QM	2	GFLEAVQFY	243	0.730
ANNs+QM	3	AWELTYAEL	96	0.720
ANNs+QM	4	AGALTAASL	15	0.680

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ESRLFVPVL	355	0.405
QM	2	ELADRGVLL	103	-0.105

QM	3	WSFAEFLDA	180	-0.693

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SVGKAGIAL	277	2.079
QM	2	TADLFSVGK	272	1.099
QM	3	QTFDRADGL	292	0.693

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NKPFERRSL	3	6.215
QM	2	RRYPDIKVR	61	4.382
QM	3	SLLRGAGAL	10	2.708
QM	4	ELADRGVLL	103	2.708

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ELADRGVLL	103	1.000
ANNs+QM	2	GLDFDVAPL	299	1.000
ANNs+QM	3	VLLDLNTLL	109	0.970
ANNs+QM	4	CSDIGVTGL	317	0.870

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SLLRGAGAL	10	1.000
ANNs+QM	2	NAHRRVGNL	374	1.000
ANNs+QM	3	RRVGNLAVL	377	1.000
ANNs+QM	4	PAWEKIAAL	399	1.000

ALLELE: HLA-B*2702				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGNLAVL	377	5.193
QM	2	LRGAGALTA	12	2.996
QM	3	RRYPDIKVR	61	2.890
QM	4	RRSLLRGAG	8	1.792

ALLELE: HLA-B27				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRYPDIKVR	61	1.000
ANNs+QM	2	RRVGNLAVL	377	1.000
ANNs+QM	3	RRSLLRGAG	8	0.880
ANNs+QM	4	TADLFSVGK	272	0.440

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRYPDIKVR	61	1.000
ANNs+QM	2	RRVGNLAVL	377	1.000
ANNs+QM	3	RRSLLRGAG	8	0.980

ANNs+QM	4	ERRSLLRGA	7	0.880

ALLELE: HLA-B*3501

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPWSFAEFL	178	1.000
ANNs+QM	2	RPATSLTGL	420	1.000
ANNs+QM	3	YPDIKVRAL	63	0.930
ANNs+QM	4	RRVGNLAVL	377	0.910

ALLELE: HLA-B*3701

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADRGVLLDL	105	4.094
QM	2	RDQAFAAEL	119	3.689
QM	3	MDRYFGPVL	408	3.689
QM	4	AELADRGVL	102	2.303

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	YPDIKVRAL	63	1.792
QM	2	AWELTYAEL	96	1.792
QM	3	EFLDAAQAL	184	1.649
QM	4	GLDFDVAPL	299	1.099

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGNLAVL	377	3.807
QM	2	YPDIKVRAL	63	2.603
QM	3	GLDFDVAPL	299	2.603
QM	4	CSDIGVTGL	317	2.603

ALLELE: HLA-B*3902				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NKPFERRSL	3	2.996
QM	2	DQAWEFVKF	335	1.609
QM	3	SGPGVMQQL	73	0.875
QM	4	VLLDLNTLL	109	0.875

ALLELE: HLA-B40				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AELADRGVL	102	4.382
QM	2	WELTYAELA	97	3.689
QM	3	ADRGVLLDL	105	0.916
QM	4	RDQAFAAEL	119	0.916

ALLELE: HLA-B*4403				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AELADRGVL	102	2.773
QM	2	WELTYAELA	97	2.485
QM	3	DQAWEFVKF	335	1.504

QM	4	ADRGVLLDL	105	1.216

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YPDIKVRAL	63	0.990
ANNs+QM	2	RPWSFAEFL	178	0.920
ANNs+QM	3	TADLFSVGK	272	0.860
ANNs+QM	4	PAWEKIAAL	399	0.830

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RGSRPATSL	417	8.620
QM	2	NAHRRVGNL	374	8.320
QM	3	AAEQQSMST	264	8.030
QM	4	SGPGVMQQL	73	6.960

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RGSRPATSL	417	8.620
QM	2	NAHRRVGNL	374	8.320
QM	3	AAEQQSMST	264	8.030
QM	4	SGPGVMQQL	73	6.960

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RPWSFAEFL	178	3.209
QM	2	IGVTGLAIA	320	2.516
QM	3	DQAWEFVKF	335	1.609
QM	4	AELADRGVL	102	1.569

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YPDIKVRAL	63	1.000
ANNs+QM	2	RPWSFAEFL	178	1.000
ANNs+QM	3	RPATSLTGL	420	1.000
ANNs+QM	4	APWAAGCAA	24	0.840

ALLELE: HLA-B*5401

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	APWAAGCAA	24	1.000
ANNs+QM	2	RPWSFAEFL	178	1.000
ANNs+QM	3	YPDIKVRAL	63	0.980
ANNs+QM	4	RPATSLTGL	420	0.920

ALLELE: HLA-B*51

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YPDIKVRAL	63	1.000
ANNs+QM	2	RPATSLTGL	420	0.960
ANNs+QM	3	RPWSFAEFL	178	0.950

ANNs+QM	4	ESRLFVPVL	355	0.600

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LTAASLAPW	18	4.564
QM	2	QSMSTADLF	268	3.689
QM	3	RSLLRGAGA	9	1.792
QM	4	WSFAEFLDA	180	0.971

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AELADRGVL	102	5.768
QM	2	ADRGVLLDL	105	3.784
QM	3	RDQAFAAEL	119	2.996
QM	4	MDRYFGPVL	408	2.996

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	WELTYAELA	97	3.689
QM	2	AELADRGVL	102	2.773
QM	3	WSFAEFLDA	180	0.405
QM	4	RSLLRGAGA	9	0.095

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DQAWEFVKF	335	4.564
QM	2	VLLDLNTLL	109	1.664
QM	3	SLLRGAGAL	10	1.386
QM	4	ELADRGVLL	103	0.971

ALLELE: HLA-B7				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YPDIKVRAL	63	1.000
ANNs+QM	2	RDQAFAAEL	119	1.000
ANNs+QM	3	RPWSFAEFL	178	1.000
ANNs+QM	4	MDRYFGPVL	408	1.000

ALLELE: HLA-B*0702				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YPDIKVRAL	63	1.000
ANNs+QM	2	RPWSFAEFL	178	1.000
ANNs+QM	3	RPATSLTGL	420	1.000
ANNs+QM	4	APWAAGCAA	24	0.840

ALLELE: HLA-B8				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QTFDRADGL	292	1.000
ANNs+QM	2	CSDIGVTGL	317	0.690
ANNs+QM	3	YPDIKVRAL	63	0.650

ANNs+QM	4	QSMSTADLF	268	0.650

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGNLAVL	377	3.871
QM	2	SLLRGAGAL	10	3.401
QM	3	NFLFYNKQL	155	3.178
QM	4	EFLDAAQAL	184	3.178

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	YPDIKVRAL	63	13.020
QM	2	EFLDAAQAL	184	11.100
QM	3	RPWSFAEFL	178	7.370
QM	4	ELADRGVLL	103	6.960

ALLELE: HLA-Cw*0602

Threshold for 4 % with score: 1.482

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ESRLFVPVL	355	2.485
QM	2	YPDIKVRAL	63	2.365
QM	3	RPWSFAEFL	178	1.887
QM	4	VLLDLNTLL	109	1.792

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GFLEAVQFY	243	2.262
QM	2	RPATSLTGL	420	1.974
QM	3	ADRGVLLDL	105	1.751
QM	4	SGPGVMQQL	73	1.569

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRVGNLAVL	377	1.000
ANNs+QM	2	SVGKAGIAL	277	0.900
ANNs+QM	3	NAHRRVGNL	374	0.860
ANNs+QM	4	EFLDAAQAL	184	0.810

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SGPGVMQQL	73	21.440
QM	2	RGSRPATSL	417	15.460
QM	3	PAWEKIAAL	399	15.400
QM	4	NKPFERRSL	3	13.320

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPWSFAEFL	178	1.000
ANNs+QM	2	YPDIKVRAL	63	0.990
ANNs+QM	3	TAASLAPWA	19	0.950

ANNs+QM	4	PAWEKIAAL	399	0.940

ALLELE: H2-Kd				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NFLFYNKQL	155	1.000
ANNs+QM	2	LFSVGKAGI	275	1.000
ANNs+QM	3	YPDIKVRAL	63	0.990
ANNs+QM	4	RPWSFAEFL	178	0.980

ALLELE: H2-Kk				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AELADRGVL	102	2.996
QM	2	LFSVGKAGI	275	2.996
QM	3	WELTYAELA	97	2.303
QM	4	ADRGVLLDL	105	2.079

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YPDIKVRAL	63	1.000
ANNs+QM	2	CSDIGVTGL	317	1.000
ANNs+QM	3	RPATSLTGL	420	1.000
ANNs+QM	4	DQAWEFVKF	335	0.930

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ELADRGVLL	103	15.380
QM	2	GLDFDVAPL	299	13.510
QM	3	VLLDLNTLL	109	12.180
QM	4	SGPGVMQQL	73	11.510

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SLLRGAGAL	10	8.670
QM	2	RPATSLTGL	420	8.380
QM	3	DQAWEFVKF	335	6.600
QM	4	ELADRGVLL	103	5.430

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRYPDIKVR	61	9.220
QM	2	RRVGNLAVL	377	5.490
QM	3	RRSLLRGAG	8	5.340
QM	4	RSLLRGAGA	9	4.130

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	YPDIKVRAL	63	14.600
QM	2	RPATSLTGL	420	13.000
QM	3	RPWSFAEFL	178	11.820

QM	4	NAHRRVGNL	374	10.970

ALLELE: Mamu-A*01

Threshold for 4 % with score: 3.650

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	YPDIKVRAL	63	7.150
QM	2	AAEQQSMST	264	5.230
QM	3	CSDIGVTGL	317	4.820
QM	4	SVGKAGIAL	277	3.070

ALLELE: HLA-A*0204

Threshold for 4 % with score: 12.070

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLDFDVAPL	299	18.320
QM	2	SLLRGAGAL	10	17.970
QM	3	ELADRGVLL	103	16.270
QM	4	RLFVPVLRS	357	15.820

ALLELE: HLA-B*2703

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRYPDIKVR	61	10.580
QM	2	RRVGNLAVL	377	8.210
QM	3	DQAWEFVKF	335	4.290
QM	4	RRSLLRGAG	8	4.060

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGNLAVL	377	16.450
QM	2	SVGKAGIAL	277	14.690
QM	3	RRSLLRGAG	8	13.600
QM	4	RDQAFAAEL	119	12.810

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AELADRGVL	102	11.880
QM	2	SVGKAGIAL	277	10.560
QM	3	PAWEKIAAL	399	6.360
QM	4	RRSLLRGAG	8	6.270

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LTAASLAPW	18	6.350
QM	2	FANAHRRVG	372	2.180
QM	3	RLFVPVLRS	357	2.040
QM	4	VNAWVSFYA	207	2.020

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AWELTYAEL	96	7.900
QM	2	AGALTAASL	15	6.740
QM	3	WELTYAELA	97	6.490

QM	4	AELADRGVL	102	6.050

ALLELE: HLA-A*6801				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LTAASLAPW	18	0.960
ANNs+QM	2	TADLFSVGK	272	0.880
ANNs+QM	3	RRYPDIKVR	61	0.800
ANNs+QM	4	SVGKAGIAL	277	0.760

ALLELE: HLA-A*6802				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GFLEAVQFY	243	1.000
ANNs+QM	2	QTFDRADGL	292	0.970
ANNs+QM	3	CSDIGVTGL	317	0.970
ANNs+QM	4	ESRLFVPVL	355	0.960