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

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Antigen Name	Untitled
Scanned on	Sun Jan 31 12:31:30 2010
Length of input sequence	640 amino acids
Number of nonamers from input sequence	632
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	ATEQLAVSL	316	1.000
ANNs+QM	2	LADDVARSF	433	1.000
ANNs+QM	3	AAGPDGTTA	123	0.410
ANNs+QM	4	AQPSARLVL	114	0.390

ALLELE: HLA-A2

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GMLSSVVGL	498	1.000
ANNs+QM	2	QLLNSLLNL	85	0.990
ANNs+QM	3	ILSQVNDNL	616	0.990
ANNs+QM	4	LLRSHAVTL	267	0.970

ALLELE: HLA-A*0201

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QLLNSLLNL	85	1.000
ANNs+QM	2	HLSATLGLL	186	1.000
ANNs+QM	3	GMLSSVVGL	498	1.000
ANNs+QM	4	ILSQVNDNL	616	1.000

ALLELE: HLA-A*0202

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QICPVGAVV	223	1.000
ANNs+QM	2	NLAGLEPTL	623	0.990
ANNs+QM	3	LLRSHAVTL	267	0.980
ANNs+QM	4	ILSQVNDNL	616	0.980

ALLELE: HLA-A*0203

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NLAGLEPTL	623	1.000
ANNs+QM	2	HLSATLGLL	186	0.980
ANNs+QM	3	ATLGLLPEA	189	0.960
ANNs+QM	4	QICPVGAVV	223	0.950

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QLLNSLLNL	85	1.000
ANNs+QM	2	QICPVGAVV	223	0.990
ANNs+QM	3	GSYGGVVMI	489	0.930
ANNs+QM	4	ILSQVNDNL	616	0.850

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NLAGLEPTL	623	12.060
QM	2	NDPNLRDRL	332	10.970
QM	3	AQPSARLVL	114	10.360
QM	4	GQPHLSATL	183	9.280

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LSRATERVR	298	0.920
ANNs+QM	2	SYSAQPSAR	111	0.480
ANNs+QM	3	WAYQRSEAL	425	0.460
ANNs+QM	4	TDPQVRVVI	67	0.390

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EALADDVAR	431	0.980
ANNs+QM	2	LSRATERVR	298	0.970
ANNs+QM	3	KQNRLLRVR	529	0.890
ANNs+QM	4	IVNANAAHL	244	0.870

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QTALWQQVL	357	10.680
QM	2	AQPSARLVL	114	9.070
QM	3	GMLSSVVGL	498	8.920
QM	4	WQQVLGDGF	361	8.770

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NFPAIVKFL	285	1.000
ANNs+QM	2	SYSAQPSAR	111	0.970
ANNs+QM	3	WQQVLGDGF	361	0.700
ANNs+QM	4	QLLNSLLNL	85	0.670

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	MVPAGLCAY	1	0.990
ANNs+QM	2	KQNRLLRVR	529	0.990
ANNs+QM	3	SYSAQPSAR	111	0.940
ANNs+QM	4	RIRELQRQL	606	0.930

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	KQNRLLRVR	529	0.182
QM	2	SYSAQPSAR	111	-0.511
QM	3	QLLNSLLNL	85	-1.833

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VVNDPNLRD	330	0.930
ANNs+QM	2	EALADDVAR	431	0.920
ANNs+QM	3	LSRATERVR	298	0.890
ANNs+QM	4	KQNRLLRVR	529	0.770

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	AQPSARLVL	114	0.830
ANNs+QM	2	ATLGLLPEA	189	0.800
ANNs+QM	3	KQNRLLRVR	529	0.770
ANNs+QM	4	ADAGLDSVL	442	0.700

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	SYSAQPSAR	111	2.708
QM	2	LSRATERVR	298	2.708
QM	3	EALADDVAR	431	2.197
QM	4	EVGAPSPLL	159	0.405

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	EALADDVAR	431	3.807
QM	2	EVGAPSPLL	159	3.178
QM	3	LSRATERVR	298	3.114
QM	4	IVELIDHTI	36	1.792

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LKQGKSQLL	79	6.215
QM	2	GKSQLLNSL	82	6.215
QM	3	KQNRLLRVR	529	4.382
QM	4	LSRATERVR	298	3.689

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	HLSATLGLL	186	1.000
ANNs+QM	2	VMGTDFGRL	458	1.000
ANNs+QM	3	ILSQVNDNL	616	1.000
ANNs+QM	4	NLPAARVGD	92	0.960

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRVGVIVEL	31	1.000
ANNs+QM	2	GKSQLLNSL	82	1.000
ANNs+QM	3	WAYQRSEAL	425	1.000
ANNs+QM	4	TDFGRLKAL	461	1.000

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGVIVEL	31	5.193
QM	2	SRATERVRA	299	2.996
QM	3	WQQVLGDGF	361	2.996
QM	4	LRVEVGAPS	156	2.303

ALLELE: HLA-B27

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRVGVIVEL	31	1.000
ANNs+QM	2	GSYGGVVMI	489	0.950
ANNs+QM	3	SRATERVRA	299	0.940
ANNs+QM	4	LRVEVGAPS	156	0.250

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RRVGVIVEL	31	1.000
ANNs+QM	2	KQNRLLRVR	529	0.960
ANNs+QM	3	SRATERVRA	299	0.950
ANNs+QM	4	GSYGGVVMI	489	0.620

ALLELE: HLA-B*3501				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NPLSVGAGL	510	1.000
ANNs+QM	2	QPSARLVLA	115	0.920
ANNs+QM	3	DPQVRVVIA	68	0.830
ANNs+QM	4	RRVGVIVEL	31	0.730

ALLELE: HLA-B*3701				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TDPQVRVVI	67	4.094
QM	2	NDPNLRDRL	332	3.689
QM	3	ADAGLDSVL	442	3.689
QM	4	LDSVLSAEL	446	3.689

ALLELE: HLA-B*3801				
Threshold for 4 % with score: 0.445				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LADDVARSF	433	2.054
QM	2	PHAGGREVL	148	1.792
QM	3	ATEQLAVSL	316	1.361
QM	4	NFPAIVKFL	285	0.956

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGVIVEL	31	3.807
QM	2	QLLNSLLNL	85	2.197
QM	3	ATEQLAVSL	316	2.197
QM	4	GMLSSVVGL	498	2.197

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GKSQLLNSL	82	3.178
QM	2	GQPHLSATL	183	3.178
QM	3	LKQGKSQLL	79	2.996
QM	4	AQPSARLVL	114	2.996

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TESLQATIA	586	2.996
QM	2	TERVRAGVL	302	2.303
QM	3	ADAGLDSVL	442	2.303
QM	4	TDFGRLKAL	461	2.303

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEIGNDVEN	405	2.890
QM	2	VENAIATAV	411	2.197
QM	3	TESLQATIA	586	2.197
QM	4	TERVRAGVL	302	1.792

ALLELE: HLA-B*5101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DGTTAAVDI	127	1.000
ANNs+QM	2	IGNDVENAI	407	1.000
ANNs+QM	3	LADDVARSF	433	0.860
ANNs+QM	4	NAIATAVGD	413	0.850

ALLELE: HLA-B*5102

Threshold for 4 % with score: 9.050

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DGTTAAVDI	127	12.300
QM	2	NPLSVGAGL	510	10.330
QM	3	DPQVRVVIA	68	9.730
QM	4	VGLGLFNPL	504	9.370

ALLELE: HLA-B*5103

Threshold for 4 % with score: 9.280

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LADDVARSF	433	14.060
QM	2	DGTTAAVDI	127	12.300
QM	3	NPLSVGAGL	510	10.330
QM	4	DPQVRVVIA	68	9.730

ALLELE: HLA-B*5201

Threshold for 4 % with score: 1.974

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AQPSARLVL	114	4.094
QM	2	TDPQVRVVI	67	3.689
QM	3	QICPVGAVV	223	3.178
QM	4	GSYGGVVMI	489	3.114

ALLELE: HLA-B*5301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LLRSHAVTL	267	1.000
ANNs+QM	2	QPSARLVLA	115	0.740
ANNs+QM	3	NPLSVGAGL	510	0.740
ANNs+QM	4	ATIAAAQVA	591	0.540

ALLELE: HLA-B*5401

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DPQVRVVIA	68	1.000
ANNs+QM	2	QPSARLVLA	115	0.940
ANNs+QM	3	NPLSVGAGL	510	0.890
ANNs+QM	4	ATIAAAQVA	591	0.790

ALLELE: HLA-B*51

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NPLSVGAGL	510	0.950
ANNs+QM	2	DPQVRVVIA	68	0.800
ANNs+QM	3	LADDVARSF	433	0.720
ANNs+QM	4	VMGTDFGRL	458	0.560

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LADDVARSF	433	3.497
QM	2	KSQLLNSLL	83	2.197
QM	3	RSEALADDV	429	2.197
QM	4	RSATEQLAV	314	1.887

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TERVRAGVL	302	5.075
QM	2	ADAGLDSVL	442	3.784
QM	3	LDSVLSAEL	446	3.784
QM	4	NDPNLRDRL	332	3.186

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VENAIATAV	411	3.689
QM	2	TESLQATIA	586	2.996
QM	3	TERVRAGVL	302	2.079
QM	4	TDFGRLKAL	461	1.099

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	WQQVLGDGF	361	5.075
QM	2	GQPHLSATL	183	2.175
QM	3	LLRSHAVTL	267	2.069
QM	4	ILSQVNDNL	616	1.649

ALLELE: HLA-B7

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NPLSVGAGL	510	1.000
ANNs+QM	2	TERVRAGVL	302	0.960
ANNs+QM	3	RIRELQRQL	606	0.930
ANNs+QM	4	AQPSARLVL	114	0.920

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NPLSVGAGL	510	0.960
ANNs+QM	2	QPSARLVLA	115	0.890
ANNs+QM	3	LSRATERVR	298	0.570
ANNs+QM	4	PIIAVSSLL	260	0.510

ALLELE: HLA-B8

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LSRATERVR	298	0.740
ANNs+QM	2	KSQLLNSLL	83	0.710
ANNs+QM	3	RSATEQLAV	314	0.670
ANNs+QM	4	PSPLLRGGL	163	0.660

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VGLGLFNPL	504	4.605
QM	2	LAVSLGSEL	320	3.871
QM	3	RRVGVIVEL	31	3.689
QM	4	WAYQRSEAL	425	3.689

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NFPAIVKFL	285	13.250
QM	2	IVNANAAHL	244	5.640
QM	3	QTALWQQVL	357	4.490
QM	4	WAYQRSEAL	425	4.170

ALLELE: HLA-Cw*0602

Threshold for 4 % with score: 1.482

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GKSQLLNSL	82	2.580
QM	2	NFPAIVKFL	285	2.580
QM	3	KSQLLNSLL	83	1.887
QM	4	GQPHLSATL	183	1.887

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MVPAGLCAY	1	2.955
QM	2	RRVGVIVEL	31	1.751
QM	3	NFPAIVKFL	285	1.751
QM	4	NDPNLRDRL	332	1.569

ALLELE: H2-Db

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	IVNANAAHL	244	1.000
ANNs+QM	2	LSVVNDPNL	328	1.000
ANNs+QM	3	WAYQRSEAL	425	1.000
ANNs+QM	4	RIRELQRQL	606	0.960

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IGNDVENAI	407	20.130
QM	2	NDPNLRDRL	332	18.750
QM	3	VGGLGQPHL	179	16.610
QM	4	AQPSARLVL	114	16.200

ALLELE: H2-Kb

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GQPHLSATL	183	1.000
ANNs+QM	2	NLAGLEPTL	623	1.000
ANNs+QM	3	VGLGLFNPL	504	0.990
ANNs+QM	4	WAYQRSEAL	425	0.960

ALLELE: H2-Kd

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PSPLLRGGL	163	0.990
ANNs+QM	2	PHAGGREVL	148	0.930
ANNs+QM	3	NPLSVGAGL	510	0.920
ANNs+QM	4	SYSAQPSAR	111	0.910

ALLELE: H2-Kk

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TDPQVRVVI	67	5.298
QM	2	VENAIATAV	411	5.011
QM	3	TERVRAGVL	302	2.996
QM	4	IGNDVENAI	407	2.996

ALLELE: H2-Ld

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LSVVNDPNL	328	1.000
ANNs+QM	2	PHAGGREVL	148	0.810
ANNs+QM	3	AQPSARLVL	114	0.760
ANNs+QM	4	QPSARLVLA	115	0.710

ALLELE: HLA-G				
Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VMGTDFGRL	458	16.780
QM	2	AQPSARLVL	114	13.840
QM	3	RIRELQRQL	606	13.640
QM	4	LLRSHAVTL	267	13.380

ALLELE: H-2Qa				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IVELIDHTI	36	12.830
QM	2	NPLSVGAGL	510	10.800
QM	3	GMLSSVVGL	498	10.380
QM	4	WQQVLGDGF	361	8.000

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AVTLNDKEL	272	8.800
QM	2	RRVGVIVEL	31	8.530
QM	3	SYSAQPSAR	111	5.560
QM	4	PSPLLRGGL	163	4.670

ALLELE: HLA-B35				
Threshold for 4 % with score: 8.350				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NPLSVGAGL	510	17.300
QM	2	TDFGRLKAL	461	9.250
QM	3	LADDVARSF	433	9.160
QM	4	DPQVRVVIA	68	7.870

ALLELE: Mamu-A*01

Threshold for 4 % with score: 3.650

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	WAYQRSEAL	425	7.860
QM	2	LTESLQATI	585	5.520
QM	3	ATEQLAVSL	316	4.030
QM	4	ITRSLTESL	581	3.950

ALLELE: HLA-A*0204

Threshold for 4 % with score: 12.070

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HLSATLGLL	186	19.530
QM	2	ILSQVNDNL	616	18.290
QM	3	LLRSHAVTL	267	16.290
QM	4	GLFNPLSVG	507	16.070

ALLELE: HLA-B*2703

Threshold for 4 % with score: 5.130

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RRVGVIVEL	31	14.300
QM	2	SRATERVRA	299	8.330
QM	3	PHAGGREVL	148	3.390
QM	4	VMGTDFGRL	458	2.360

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GQPHLSATL	183	14.810
QM	2	TDFGRLKAL	461	13.690
QM	3	VGGLGQPHL	179	13.470
QM	4	RRVGVIVEL	31	13.310

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PHAGGREVL	148	11.600
QM	2	PSPLLRGGL	163	8.320
QM	3	TERVRAGVL	302	7.980
QM	4	VMGTDFGRL	458	7.650

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	IVNANAAHL	244	5.930
QM	2	VVNDPNLRD	330	4.930
QM	3	QLLNSLLNL	85	4.110
QM	4	QICPVGAVV	223	4.040

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEIGNDVEN	405	9.560
QM	2	VENAIATAV	411	8.280
QM	3	ATIAAAQVA	591	5.510
QM	4	ATEQLAVSL	316	4.580

ALLELE: HLA-A*6801

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	FVWAYQRSE	423	0.950
ANNs+QM	2	GLFNPLSVG	507	0.810
ANNs+QM	3	EALADDVAR	431	0.790
ANNs+QM	4	TDFGRLKAL	461	0.790

<table>
<tr><th colspan="5">ALLELE: HLA-A*6802</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 4</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>ANNs+QM</td><td>1</td><td>RRVGVIVEL</td><td>31</td><td>1.000</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>NAIATAVGD</td><td>413</td><td>0.990</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>NFPAIVKFL</td><td>285</td><td>0.970</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>NLPAARVGD</td><td>92</td><td>0.960</td></tr>
</table>