



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

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Antigen Name	Untitled
Scanned on	Sat Apr 24 23:27:37 2010
Length of input sequence	93 amino acids
Number of nonamers from input sequence	85
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	ALDGGVHAL	33	0.600
ANNs+QM	2	DSTTVAALD	27	0.310
ANNs+QM	3	LMISRGLSL	78	0.180
ANNs+QM	4	AEHESNDAL	56	0.170

ALLELE: HLA-A2				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LMISRGLSL	78	0.970
ANNs+QM	2	ALDGGVHAL	33	0.930

ANNs+QM	3	AEHESNDAL	56	0.080
ANNs+QM	4	ADSTTVAAL	26	0.060

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LMISRGLSL	78	1.000
ANNs+QM	2	ALDGGVHAL	33	0.920
ANNs+QM	3	ALGKKLLEE	40	0.080
ANNs+QM	4	RPADSTTVA	24	0.040

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALDGGVHAL	33	0.940
ANNs+QM	2	ALGKKLLEE	40	0.430
ANNs+QM	3	LMISRGLSL	78	0.400
ANNs+QM	4	TFEDLFAEL	9	0.270

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	QQSLAVKTF	2	0.360
ANNs+QM	2	LMISRGLSL	78	0.330
ANNs+QM	3	VAALDGGVH	31	0.310
ANNs+QM	4	GVHALGKKL	37	0.260

ALLELE: HLA-A*0206				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALDGGVHAL	33	0.490
ANNs+QM	2	ALGKKLLEE	40	0.260
ANNs+QM	3	QQSLAVKTF	2	0.150
ANNs+QM	4	RPADSTTVA	24	0.050

ALLELE: HLA-A*0205				
Threshold for 4 % with score: 5.950				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALDGGVHAL	33	12.560
QM	2	ADSTTVAAL	26	10.800
QM	3	AALDGGVHA	32	4.820
QM	4	GVHALGKKL	37	3.680

ALLELE: HLA-A*1101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALGKKLLEE	40	0.710
ANNs+QM	2	TRPADSTTV	23	0.630
ANNs+QM	3	VWLAAEHES	52	0.460
ANNs+QM	4	LMISRGLSL	78	0.240

ALLELE: HLA-A11				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALDGGVHAL	33	0.190

ANNs+QM	2	GVHALGKKL	37	0.170
ANNs+QM	3	VWLAAEHES	52	0.170
ANNs+QM	4	VAALDGGVH	31	0.060

ALLELE: HLA-A24				
Threshold for 4 % with score: 7.670				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LMISRGLSL	78	8.510
QM	2	TFEDLFAEL	9	6.870
QM	3	ADSTTVAAL	26	5.880
QM	4	VHALGKKLL	38	4.730

ALLELE: HLA-A*2402				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TFEDLFAEL	9	1.000
ANNs+QM	2	QQSLAVKTF	2	0.850
ANNs+QM	3	VWLAAEHES	52	0.280
ANNs+QM	4	VHALGKKLL	38	0.180

ALLELE: HLA-A3				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVHALGKKL	37	0.980
ANNs+QM	2	TRPADSTTV	23	0.490
ANNs+QM	3	VAALDGGVH	31	0.440
ANNs+QM	4	AEHESNDAL	56	0.390

ALLELE: HLA-A*3101				
Threshold for 4 % with score: -1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LMISRGLSL	78	-2.526
QM	2	ALDGGVHAL	33	-3.219
QM	3	QQLAVKTF	2	-3.912

ALLELE: HLA-A31				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VAALDGGVH	31	0.870
ANNs+QM	2	TRPADSTTV	23	0.760
ANNs+QM	3	ALGKKLLEE	40	0.660
ANNs+QM	4	VWLAAEHES	52	0.390

ALLELE: HLA-A*0301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALGKKLLEE	40	0.930
ANNs+QM	2	QQLAVKTF	2	0.920
ANNs+QM	3	ADSTTVAAL	26	0.850
ANNs+QM	4	ALDGGVHAL	33	0.670

ALLELE: HLA-A*3302				
Threshold for 4 % with score: -0.105				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	-0.693
QM	2	LMISRGLSL	78	-0.693

QM	3	ALDGGVHAL	33	-1.204
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ALLELE: HLA-A68.1				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	1.386
QM	2	AALDGGVHA	32	-1.204
QM	3	RPADSTTVA	24	-1.609

ALLELE: HLA-A20 Cattle				
Threshold for 4 % with score: 3.401				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LMISRGLSL	78	3.219
QM	2	ALDGGVHAL	33	2.708
QM	3	QQLAVKTF	2	2.303
QM	4	KKLLEEAGE	43	2.303

ALLELE: HLA-A2.1				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALDGGVHAL	33	1.000
ANNs+QM	2	LMISRGLSL	78	1.000
ANNs+QM	3	GVHALGKKL	37	0.950
ANNs+QM	4	VHALGKKLL	38	0.800

ALLELE: HLA-B14				
Threshold for 4 % with score: 4				

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VHALGKKLL	38	0.890
ANNs+QM	2	ALGKKLLEE	40	0.850
ANNs+QM	3	AEHESNDAL	56	0.640
ANNs+QM	4	VAALDGGVH	31	0.550

ALLELE: HLA-B*2702				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRPADSTTV	23	2.996
QM	2	QQLAVKTF	2	1.792
QM	3	LMISRGLSL	78	0.405

ALLELE: HLA-B27				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TRPADSTTV	23	1.000
ANNs+QM	2	VAALDGGVH	31	0.030
ANNs+QM	3	QQLAVKTF	2	0.020
ANNs+QM	4	ALDGGVHAL	33	0.020

ALLELE: HLA-B*2705				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TRPADSTTV	23	0.950
ANNs+QM	2	VAALDGGVH	31	0.310
ANNs+QM	3	VHALGKKLL	38	0.210
ANNs+QM	4	ALGKKLLEE	40	0.090

ALLELE: HLA-B*3501				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.970
ANNs+QM	2	TRPADSTTV	23	0.940
ANNs+QM	3	VHALGKKLL	38	0.130
ANNs+QM	4	VAALDGGVH	31	0.120

ALLELE: HLA-B*3701				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADSTTVAAL	26	3.689
QM	2	LEEAGEVWL	46	2.303
QM	3	AEHESNDAL	56	2.303
QM	4	VHALGKKLL	38	1.609

ALLELE: HLA-B*3801				
Threshold for 4 % with score: 0.445				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VHALGKKLL	38	3.401
QM	2	TFEDLFAEL	9	2.747
QM	3	ALDGGVHAL	33	1.792
QM	4	GVHALGKKL	37	0.445

ALLELE: HLA-B*3901				
Threshold for 4 % with score: 1.792				
Prediction method	Rank	Sequence	Residue No.	Peptide Score

QM	1	VHALGKKLL	38	3.807
QM	2	TFEDLFAEL	9	2.890
QM	3	ALDGGVHAL	33	2.603
QM	4	LMISRGLSL	78	1.792

ALLELE: HLA-B*3902				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QQLAVKTF	2	1.609
QM	2	TFEDLFAEL	9	0.875
QM	3	GVHALGKKL	37	0.875
QM	4	ALDGGVHAL	33	0.693

ALLELE: HLA-B*40				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEHESNDAL	56	3.689
QM	2	LEEAGEVWL	46	2.303
QM	3	ADSTTVAAL	26	1.609
QM	4	AALDGGVHA	32	0.693

ALLELE: HLA-B*4403				
Threshold for 4 % with score: 0.405				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AEHESNDAL	56	2.079
QM	2	LEEAGEVWL	46	1.386
QM	3	QQLAVKTF	2	1.216
QM	4	ADSTTVAAL	26	1.099

ALLELE: HLA-B*5101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VAALDGGVH	31	0.730
ANNs+QM	2	QQSLAVKTF	2	0.700
ANNs+QM	3	TRPADSTTV	23	0.580
ANNs+QM	4	LMISRGLSL	78	0.370

ALLELE: HLA-B*5102				
Threshold for 4 % with score: 9.050				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRPADSTTV	23	5.610
QM	2	VAALDGGVH	31	4.910
QM	3	LMISRGLSL	78	3.610
QM	4	PADSTTVAA	25	3.540

ALLELE: HLA-B*5103				
Threshold for 4 % with score: 9.280				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRPADSTTV	23	5.610
QM	2	VAALDGGVH	31	4.910
QM	3	QQSLAVKTF	2	4.160
QM	4	LMISRGLSL	78	3.610

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

QM	1	QQSLAVKTF	2	2.293
QM	2	RPADSTTVA	24	1.705
QM	3	ALDGGVHAL	33	-0.511

ALLELE: HLA-B*5301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.940
ANNs+QM	2	LMISRGLSL	78	0.350
ANNs+QM	3	VHALGKKLL	38	0.340
ANNs+QM	4	AEHESNDAL	56	0.170

ALLELE: HLA-B*5401				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.970
ANNs+QM	2	PADSTTVAA	25	0.230
ANNs+QM	3	LMISRGLSL	78	0.130
ANNs+QM	4	VAALDGGVH	31	0.080

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.920
ANNs+QM	2	VAALDGGVH	31	0.370
ANNs+QM	3	LMISRGLSL	78	0.360
ANNs+QM	4	VHALGKKLL	38	0.250

ALLELE: HLA-B*5801				
Threshold for 4 % with score: -0.223				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AALDGGVHA	32	0.000
QM	2	QQLAVKTF	2	-0.639
QM	3	RPADSTTVA	24	-1.204

ALLELE: HLA-B60				
Threshold for 4 % with score: 1.386				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LEEAGEVWL	46	5.768
QM	2	AEHESNDAL	56	5.075
QM	3	ADSTTVAAL	26	3.689
QM	4	LMISRGLSL	78	0.470

ALLELE: HLA-B61				
Threshold for 4 % with score: 0.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LEEAGEVWL	46	2.079
QM	2	AEHESNDAL	56	2.079
QM	3	RPADSTTVA	24	0.095

ALLELE: HLA-B62				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	QQLAVKTF	2	4.477
QM	2	ALDGGVHAL	33	0.365
QM	3	ALGKKLLEE	40	-0.734

ALLELE: HLA-B7

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.610
ANNs+QM	2	LMISRGLSL	78	0.600
ANNs+QM	3	TRPADSTTV	23	0.590
ANNs+QM	4	ADSTTVAAL	26	0.260

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.980
ANNs+QM	2	LMISRGLSL	78	0.420
ANNs+QM	3	VAALDGGVH	31	0.360
ANNs+QM	4	VHALGKKLL	38	0.290

ALLELE: HLA-B8

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VAALDGGVH	31	0.720
ANNs+QM	2	VHALGKKLL	38	0.700
ANNs+QM	3	DSTTVAALD	27	0.620
ANNs+QM	4	KKLLEEAGE	43	0.570

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LMISRGLSL	78	2.996
QM	2	TFEDLFAEL	9	2.303
QM	3	AEHESNDAL	56	1.099
QM	4	GVHALGKKL	37	0.875

ALLELE: HLA-Cw*0401				
Threshold for 4 % with score: 4.370				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALDGGVHAL	33	9.230
QM	2	VHALGKKLL	38	6.430
QM	3	QQSLAVKTF	2	5.790
QM	4	TFEDLFAEL	9	3.580

ALLELE: HLA-Cw*0602				
Threshold for 4 % with score: 1.482				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	1.887
QM	2	TFEDLFAEL	9	1.792
QM	3	ADSTTVAAL	26	1.386
QM	4	ALDGGVHAL	33	1.386

ALLELE: HLA-Cw*0702				
Threshold for 4 % with score: 1.212				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ADSTTVAAL	26	1.058
QM	2	TFEDLFAEL	9	0.701
QM	3	QQSLAVKTF	2	0.693

QM	4	RPADSTTVA	24	0.519
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ALLELE: H2-Db				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ADSTTVAAL	26	0.710
ANNs+QM	2	AEHESNDAL	56	0.570
ANNs+QM	3	AALDGGVHA	32	0.520
ANNs+QM	4	GVHALGKKL	37	0.490

ALLELE: H2-Dd				
Threshold for 4 % with score: 11.800				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	11.600
QM	2	AEHESNDAL	56	9.250
QM	3	LMISRGLSL	78	8.400
QM	4	LEEAGEVWL	46	8.110

ALLELE: H2-Kb				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TFEDLFAEL	9	0.600
ANNs+QM	2	VAALDGGVH	31	0.490
ANNs+QM	3	VHALGKKLL	38	0.470
ANNs+QM	4	TRPADSTTV	23	0.340

ALLELE: H2-Kd				
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Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TFEDLFAEL	9	1.000
ANNs+QM	2	ADSTTVAAL	26	0.950
ANNs+QM	3	LMISRGLSL	78	0.910
ANNs+QM	4	VHALGKKLL	38	0.780

ALLELE: H2-Kk				
Threshold for 4 % with score: 1.609				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LEEAGEVWL	46	4.382
QM	2	AEHESNDAL	56	3.689
QM	3	ADSTTVAAL	26	1.386
QM	4	VHALGKKLL	38	0.182

ALLELE: H2-Ld				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RPADSTTVA	24	0.710
ANNs+QM	2	QQSLAVKTF	2	0.690
ANNs+QM	3	VHALGKKLL	38	0.640
ANNs+QM	4	LEEAGEVWL	46	0.570

ALLELE: HLA-G				
Threshold for 4 % with score: 9.260				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRPADSTTV	23	14.060
QM	2	ALDGGVHAL	33	9.510
QM	3	GVHALGKKL	37	8.780

QM	4	VHALGKKLL	38	8.110
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ALLELE: H-2Qa				
Threshold for 4 % with score: 6.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALDGGVHAL	33	9.760
QM	2	LMISRGLSL	78	8.400
QM	3	VWLAAEHES	52	3.400
QM	4	AEHESNDAL	56	3.130

ALLELE: HLA-B*2706				
Threshold for 4 % with score: 5.000				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	6.890
QM	2	VHALGKKLL	38	3.330
QM	3	LEEAGEVWL	46	2.330
QM	4	RPADSTTVA	24	1.670

ALLELE: HLA-B35				
Threshold for 4 % with score: 8.350				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	10.760
QM	2	LMISRGLSL	78	8.210
QM	3	ALDGGVHAL	33	7.390
QM	4	ADSTTVAAL	26	5.550

ALLELE: Mamu-A*01				
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Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRPADSTTV	23	5.100
QM	2	TFEDLFAEL	9	3.450
QM	3	AEHESNDAL	56	-0.120

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALDGGVHAL	33	20.910
QM	2	ADSTTVAAL	26	15.170
QM	3	VHALGKKLL	38	12.100
QM	4	GVHALGKKL	37	9.270

ALLELE: HLA-B*2703				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TRPADSTTV	23	7.400
QM	2	ALDGGVHAL	33	2.500
QM	3	VHALGKKLL	38	1.720
QM	4	VWLAAEHES	52	1.340

ALLELE: HLA-B*2704				
Threshold for 4 % with score: 8.790				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVHALGKKL	37	14.280
QM	2	TRPADSTTV	23	10.570
QM	3	QQSLAVKTF	2	10.010

QM	4	VHALGKKLL	38	9.870
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ALLELE: HLA-B*2902				
Threshold for 4 % with score: 7.750				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LEEAGEVWL	46	9.180
QM	2	ADSTTVAAL	26	8.930
QM	3	AEHESNDAL	56	8.700
QM	4	QQSLAVKTF	2	3.700

ALLELE: HLA-A*3301				
Threshold for 4 % with score: 3.840				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AALDGGVHA	32	-0.250
QM	2	ADSTTVAAL	26	-0.460
QM	3	DSTTVAALD	27	-0.530

ALLELE: HLA-B44				
Threshold for 4 % with score: 4.900				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	LEEAGEVWL	46	7.830
QM	2	ALDGGVHAL	33	5.370
QM	3	ADSTTVAAL	26	4.380
QM	4	AEHESNDAL	56	1.950

ALLELE: HLA-A*6801				
Threshold for 4 % with score: 4				

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GVHALGKKL	37	0.920
ANNs+QM	2	ALDGGVHAL	33	0.900
ANNs+QM	3	VWLAAEHES	52	0.420
ANNs+QM	4	VAALDGGVH	31	0.210

ALLELE: HLA-A*6802				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VAALDGGVH	31	0.990
ANNs+QM	2	QQSLAVKTF	2	0.970
ANNs+QM	3	GVHALGKKL	37	0.970
ANNs+QM	4	ADSTTVAAL	26	0.950