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

Antigen Name	Untitled
Scanned on	Sun Feb 14 16:14:43 2010
Length of input sequence	575 amino acids
Number of nonamers from input sequence	567
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	AAEALGMSL	226	1.000
ANNs+QM	2	MREMLAITG	463	1.000
ANNs+QM	3	VFDGERAAL	428	0.900
ANNs+QM	4	RLDVAGRVL	522	0.830

ALLELE: HLA-A2				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RIGSGVPHL	315	1.000

ANNs+QM	2	GVLSKYVKL	556	1.000
ANNs+QM	3	GMLMAAARL	143	0.990
ANNs+QM	4	LMAAARLDL	145	0.990

ALLELE: HLA-A*0201				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SLPGMLMAA	140	1.000
ANNs+QM	2	GMLMAAARL	143	1.000
ANNs+QM	3	SILPGRAKL	162	1.000
ANNs+QM	4	RIGSGVPHL	315	1.000

ALLELE: HLA-A*0202				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALEDGTITV	438	1.000
ANNs+QM	2	LLAGCDKSL	133	0.980
ANNs+QM	3	ALLRNGDRI	513	0.970
ANNs+QM	4	GMLMAAARL	143	0.960

ALLELE: HLA-A*0203				
Threshold for .5 % with score: .5				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	SLPGMLMAA	140	0.970
ANNs+QM	2	STNAVLHLL	290	0.970
ANNs+QM	3	GLGKDVLLL	477	0.960
ANNs+QM	4	VDGGPIALL	507	0.900

ALLELE: HLA-A*0206

Threshold for .5 % with score: .5

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	EITPCNLSL	60	1.000
ANNs+QM	2	SILPGRAKL	162	1.000
ANNs+QM	3	ALEDGTITV	438	1.000
ANNs+QM	4	GVLSKYVKL	556	0.970

ALLELE: HLA-A*0205

Threshold for 4 % with score: 5.950

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GMLMAAARL	143	9.640
QM	2	ALLRNGDRI	513	9.370
QM	3	RIGSGVPHL	315	8.580
QM	4	RLDLAAVFL	150	7.580

ALLELE: HLA-A*1101

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LAPEGAVVK	405	0.950
ANNs+QM	2	IGGVPVVMK	340	0.760
ANNs+QM	3	FSLVSREVI	107	0.580
ANNs+QM	4	PDPDGKVLR	378	0.530

ALLELE: HLA-A11

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TARVFDGER	425	0.980

ANNs+QM	2	IGGVPVVMK	340	0.940
ANNs+QM	3	LAPEGAVVK	405	0.830
ANNs+QM	4	MLMAAARLD	144	0.800

ALLELE: HLA-A24

Threshold for 4 % with score: 7.670

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AERLDGSVL	125	10.550
QM	2	TMASAAEAL	222	10.380
QM	3	NAVLHLLAI	292	10.270
QM	4	TGAIKGAGL	470	8.560

ALLELE: HLA-A*2402

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	VFSAGGYPL	79	1.000
ANNs+QM	2	RFSGGTTGL	489	1.000
ANNs+QM	3	MYTANTMAS	217	0.900
ANNs+QM	4	VFDGERAAL	428	0.650

ALLELE: HLA-A3

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	RVFDGERAA	427	0.950
ANNs+QM	2	LAPEGAVVK	405	0.930
ANNs+QM	3	ACSRGLMSR	189	0.880
ANNs+QM	4	IAHEANVAL	300	0.870

ALLELE: HLA-A*3101

Threshold for 4 % with score: -1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ACSRGLMSR	189	-0.223
QM	2	YAGSILPGR	159	-0.916
QM	3	TARVFDGER	425	-1.609

ALLELE: HLA-A31

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	YAGSILPGR	159	0.980
ANNs+QM	2	NLAAITPPD	371	0.940
ANNs+QM	3	PDPDGKVLR	378	0.930
ANNs+QM	4	TARVFDGER	425	0.880

ALLELE: HLA-A*0301

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALLRNGDRI	513	0.950
ANNs+QM	2	AITGAIKGA	468	0.890
ANNs+QM	3	LAPEGAVVK	405	0.880
ANNs+QM	4	GMLMAAARL	143	0.850

ALLELE: HLA-A*3302

Threshold for 4 % with score: -0.105

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DGLEKAAAR	26	2.197
QM	2	YAGSILPGR	159	1.099

QM	3	ACSRGLMSR	189	1.099
QM	4	TARVFDGER	425	1.099

ALLELE: HLA-A68.1

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	EVVMQAERL	120	3.178
QM	2	DVTDGLEKA	23	2.485
QM	3	RVFDGERAA	427	2.485
QM	4	YAGSILPGR	159	2.303

ALLELE: HLA-A20 Cattle

Threshold for 4 % with score: 3.401

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	TKEAFENAI	273	5.704
QM	2	SKYVKLVSS	559	4.605
QM	3	YAGSILPGR	159	3.689
QM	4	ACSRGLMSR	189	3.689

ALLELE: HLA-A2.1

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GMLMAAARL	143	1.000
ANNs+QM	2	LMAAARLDL	145	1.000
ANNs+QM	3	RLDLAAVFL	150	1.000
ANNs+QM	4	TMASAAEAL	222	1.000

ALLELE: HLA-B14

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ERLDGSVLL	126	1.000
ANNs+QM	2	PCNLSLDRL	63	0.980
ANNs+QM	3	SILPGRAKL	162	0.960
ANNs+QM	4	STNAVLHLL	290	0.960

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ARRSGQAVV	251	2.996
QM	2	ARVFDGERA	426	2.996
QM	3	IRLDVAGRV	521	2.996
QM	4	ERLDGSVLL	126	2.890

ALLELE: HLA-B27

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ERLDGSVLL	126	1.000
ANNs+QM	2	PRYTTGVLS	551	0.960
ANNs+QM	3	DRLANAVKE	69	0.880
ANNs+QM	4	IRLDVAGRV	521	0.840

ALLELE: HLA-B*2705

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ERLDGSVLL	126	1.000

ANNs+QM	2	ARVFDGERA	426	0.990
ANNs+QM	3	PRYTTGVLS	551	0.990
ANNs+QM	4	ARRSGQAVV	251	0.980

ALLELE: HLA-B*3501

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ERLDGSVLL	126	0.840
ANNs+QM	2	PPDPDGKVL	377	0.800
ANNs+QM	3	ARRSGQAVV	251	0.670
ANNs+QM	4	KPRSRDVTD	18	0.580

ALLELE: HLA-B*3701

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	CDKSLPGML	137	5.298
QM	2	VDGGPIALL	507	5.298
QM	3	HEANVALSL	302	2.708
QM	4	AERLDGSVL	125	2.303

ALLELE: HLA-B*3801

Threshold for 4 % with score: 0.445

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VFDGERAAL	428	2.485
QM	2	RFSGGTTGL	489	1.386
QM	3	RLDLAAVFL	150	1.361
QM	4	AAEALGMSL	226	1.361

ALLELE: HLA-B*3901

Threshold for 4 % with score: 1.792

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ERLDGSVLL	126	4.094
QM	2	IRLDVAGRV	521	2.996
QM	3	RLDLAAVFL	150	2.197
QM	4	AAEALGMSL	226	2.197

ALLELE: HLA-B*3902

Threshold for 4 % with score: 0.693

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AAEALGMSL	226	0.875
QM	2	SGQAVVELL	254	0.875
QM	3	STNAVLHLL	290	0.875
QM	4	GVPVVMKAL	342	0.875

ALLELE: HLA-B40

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HEANVALSL	302	3.689
QM	2	AERLDGSVL	125	2.996
QM	3	GERAALDAL	431	2.996
QM	4	FENAIAVVM	277	2.485

ALLELE: HLA-B*4403

Threshold for 4 % with score: 0.405

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEAASVSTV	6	4.277

QM	2	HEANVALSL	302	2.890
QM	3	GERAALDAL	431	2.197
QM	4	AERLDGSVL	125	2.079

ALLELE: HLA-B*5101				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	NAVLHLLAI	292	1.000
ANNs+QM	2	LAPEGAVVK	405	0.920
ANNs+QM	3	KPRSRDVTD	18	0.910
ANNs+QM	4	DGLEKAAAR	26	0.910

ALLELE: HLA-B*5102				
Threshold for 4 % with score: 9.050				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NAVLHLLAI	292	18.920
QM	2	KGAGLGKDV	474	10.460
QM	3	GGPGMREML	459	10.000
QM	4	NAVKEGVFS	73	9.620

ALLELE: HLA-B*5103				
Threshold for 4 % with score: 9.280				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	NAVLHLLAI	292	18.920
QM	2	KGAGLGKDV	474	10.460
QM	3	GGPGMREML	459	10.000
QM	4	NAVKEGVFS	73	9.620

ALLELE: HLA-B*5201				
Threshold for 4 % with score: 1.974				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	FSLVSREVI	107	3.273
QM	2	FGGSTNAVL	287	2.803
QM	3	ITVGDAVVI	444	2.708
QM	4	KGAGLGKDV	474	2.398

ALLELE: HLA-B*5301				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PPDPDGKVL	377	0.950
ANNs+QM	2	KPRSRDVTD	18	0.750
ANNs+QM	3	GITILHGSL	397	0.460
ANNs+QM	4	TMASAAEAL	222	0.440

ALLELE: HLA-B*5401				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PPDPDGKVL	377	0.980
ANNs+QM	2	KPRSRDVTD	18	0.940
ANNs+QM	3	GITILHGSL	397	0.690
ANNs+QM	4	ARRSGQAVV	251	0.560

ALLELE: HLA-B*51				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PPDPDGKVL	377	0.990

ANNs+QM	2	TGAIKGAGL	470	0.850
ANNs+QM	3	KPRSRDVTD	18	0.810
ANNs+QM	4	ARRSGQAVV	251	0.790

ALLELE: HLA-B*5801

Threshold for 4 % with score: -0.223

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	STNAVLHLL	290	1.281
QM	2	VTDGLEKAA	24	1.194
QM	3	IAHEANVAL	300	1.099
QM	4	ITVGDAVVI	444	1.099

ALLELE: HLA-B60

Threshold for 4 % with score: 1.386

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	HEANVALSL	302	6.557
QM	2	AERLDGSVL	125	5.075
QM	3	GERAALDAL	431	5.075
QM	4	FENAIAVVM	277	3.784

ALLELE: HLA-B61

Threshold for 4 % with score: 0.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEAASVSTV	6	4.382
QM	2	HEANVALSL	302	2.773
QM	3	GERAALDAL	431	2.175
QM	4	AERLDGSVL	125	2.079

ALLELE: HLA-B62				
Threshold for 4 % with score: 0.693				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLGKDVLLL	477	1.569
QM	2	SLPGMLMAA	140	0.875
QM	3	RIGSGVPHL	315	0.693
QM	4	ALLRNGDRI	513	0.693

ALLELE: HLA-B7				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PPDPDGKVL	377	1.000
ANNs+QM	2	KPRSRDVTD	18	0.970
ANNs+QM	3	ARRSGQAVV	251	0.930
ANNs+QM	4	RLDVAGRVL	522	0.840

ALLELE: HLA-B*0702				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	PPDPDGKVL	377	0.990
ANNs+QM	2	KPRSRDVTD	18	0.950
ANNs+QM	3	GITILHGSL	397	0.700
ANNs+QM	4	LMAAARLDL	145	0.690

ALLELE: HLA-B8				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	DILTKEAFE	270	0.740

ANNs+QM	2	PPDPDGKVL	377	0.720
ANNs+QM	3	RLDVAGRVL	522	0.720
ANNs+QM	4	LMAAARLDL	145	0.670

ALLELE: HLA-Cw*0301

Threshold for 4 % with score: 2.015

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVLSKYVKL	556	4.605
QM	2	SILPGRAKL	162	3.912
QM	3	ERLDGSVLL	126	3.689
QM	4	EVVMQAERL	120	2.996

ALLELE: HLA-Cw*0401

Threshold for 4 % with score: 4.370

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	VFSAGGYPL	79	12.640
QM	2	PPDPDGKVL	377	10.840
QM	3	VFDGERAAL	428	10.170
QM	4	STNAVLHLL	290	8.430

ALLELE: HLA-Cw*0602

Threshold for 4 % with score: 1.482

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	AAEALGMSL	226	1.887
QM	2	CDKSLPGML	137	1.792
QM	3	TGHTMAENL	364	1.792
QM	4	GITILHGSL	397	1.792

ALLELE: HLA-Cw*0702				
Threshold for 4 % with score: 1.212				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GVPVVMKAL	342	1.751
QM	2	VAGRVLDVL	525	1.664
QM	3	VDGGPIALL	507	1.569
QM	4	CDKSLPGML	137	0.875

ALLELE: H2-Db				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	ALLRNGDRI	513	1.000
ANNs+QM	2	GGSTNAVLH	288	0.990
ANNs+QM	3	RIGSGVPHL	315	0.980
ANNs+QM	4	SILPGRAKL	162	0.970

ALLELE: H2-Dd				
Threshold for 4 % with score: 11.800				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GGPGMREML	459	21.440
QM	2	GVPVVMKAL	342	20.750
QM	3	SGQAVVELL	254	17.800
QM	4	FGGSTNAVL	287	17.600

ALLELE: H2-Kb				
Threshold for 4 % with score: 4				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	GGPGMREML	459	1.000

ANNs+QM	2	TMASAAEAL	222	0.990
ANNs+QM	3	TGHTMAENL	364	0.990
ANNs+QM	4	TGAIKGAGL	470	0.970

ALLELE: H2-Kd

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	TGHTMAENL	364	1.000
ANNs+QM	2	RFSGGTTGL	489	1.000
ANNs+QM	3	CDKSLPGML	137	0.990
ANNs+QM	4	TGAIKGAGL	470	0.990

ALLELE: H2-Kk

Threshold for 4 % with score: 1.609

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	DEAASVSTV	6	4.605
QM	2	PEAVDGGPI	504	3.912
QM	3	HEANVALSL	302	3.689
QM	4	FENAIAVVM	277	3.401

ALLELE: H2-Ld

Threshold for 4 % with score: 4

Prediction method	Rank	Sequence	Residue No.	Peptide Score
ANNs+QM	1	LMAAARLDL	145	1.000
ANNs+QM	2	GSTNAVLHL	289	1.000
ANNs+QM	3	TGHTMAENL	364	1.000
ANNs+QM	4	PPDPDGKVL	377	0.920

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GLGKDVLLL	477	21.180
QM	2	GGPGMREML	459	13.840
QM	3	LMAAARLDL	145	13.110
QM	4	RIGSGVPHL	315	12.970

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	STNAVLHLL	290	13.780
QM	2	TMASAAEAL	222	12.470
QM	3	ALLRNGDRI	513	8.200
QM	4	NAVLHLLAI	292	6.870

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PPDPDGKVL	377	7.670
QM	2	ARVFDGERA	426	7.270
QM	3	PCNLSLDRL	63	6.970
QM	4	AAEALGMSL	226	6.940

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	PPDPDGKVL	377	17.430

QM	2	GVLSKYVKL	556	11.100
QM	3	TGHTMAENL	364	9.320
QM	4	AAEALGMSL	226	9.070

ALLELE: Mamu-A*01				
Threshold for 4 % with score: 3.650				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ALEDGTITV	438	3.920
QM	2	TKEAFENAI	273	3.150
QM	3	GITILHGSL	397	2.710
QM	4	IAHEANVAL	300	2.550

ALLELE: HLA-A*0204				
Threshold for 4 % with score: 12.070				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	RLDVAGRVL	522	21.200
QM	2	RLDLAAVFL	150	20.760
QM	3	IAHEANVAL	300	18.260
QM	4	VFDGERAAL	428	16.860

ALLELE: HLA-B*2703				
Threshold for 4 % with score: 5.130				
Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	ARVFDGERA	426	11.770
QM	2	GRVLDVLAD	527	7.060
QM	3	ERLDGSVLL	126	5.770
QM	4	ARRSGQAVV	251	4.730

ALLELE: HLA-B*2704

Threshold for 4 % with score: 8.790

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GERAALDAL	431	15.350
QM	2	ARRSGQAVV	251	11.110
QM	3	VDGGPIALL	507	11.010
QM	4	ARVFDGERA	426	10.700

ALLELE: HLA-B*2902

Threshold for 4 % with score: 7.750

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GERAALDAL	431	12.890
QM	2	SERDVTIID	174	10.750
QM	3	HEANVALSL	302	9.930
QM	4	PEGAVVKTA	407	9.930

ALLELE: HLA-A*3301

Threshold for 4 % with score: 3.840

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	MYTANTMAS	217	4.600
QM	2	NLAAITPPD	371	2.300
QM	3	YAGSILPGR	159	2.050
QM	4	STNAVLHLL	290	1.910

ALLELE: HLA-B44

Threshold for 4 % with score: 4.900

Prediction method	Rank	Sequence	Residue No.	Peptide Score
QM	1	GERAALDAL	431	8.840

QM	2	AERLDGSVL	125	8.630
QM	3	FENAIAVVM	277	8.110
QM	4	SGQAVVELL	254	4.000

<table>
<tr><th colspan="5">ALLELE: HLA-A*6801</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>YAGSILPGR</td><td>159</td><td>0.980</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>RVFDGERAA</td><td>427</td><td>0.860</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>VMAFGGSTN</td><td>284</td><td>0.830</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>MLMAAARLD</td><td>144</td><td>0.800</td></tr>
</table>

<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>HGSLAPEGA</td><td>402</td><td>1.000</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>VALSLQDFS</td><td>306</td><td>0.990</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>RLDLAAVFL</td><td>150</td><td>0.980</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>DILTKEAFE</td><td>270</td><td>0.980</td></tr>
</table>