



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

[Home](#) [ComPred](#) [ANNPred](#) [References](#) [Help](#) [Matrices](#) [Team](#) [Contact](#)

| | |
|--|-------------------------|
| Antigen Name | Untitled |
| Scanned on | Wed Feb 3 20:00:17 2010 |
| Length of input sequence | 626 amino acids |
| Number of nonamers from input sequence | 618 |
| 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 | SADLDAVVL | 244 | 0.770 |
| ANNs+QM | 2 | MLDKGADVD | 586 | 0.770 |
| ANNs+QM | 3 | SARHEGLSA | 237 | 0.400 |
| ANNs+QM | 4 | LSADLDAVV | 243 | 0.380 |

ALLELE: HLA-A2

Threshold for .5 % with score: .5

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | GLSADLDAV | 242 | 0.940 |
| ANNs+QM | 2 | LLSSAAGNL | 296 | 0.930 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 3 | AVVAVLAVL | 334 | 0.730 |
| ANNs+QM | 4 | FWVDAEPRL | 570 | 0.230 |

| ALLELE: HLA-A*0201 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LLSSAAGNL | 296 | 1.000 |
| ANNs+QM | 2 | SVGRWVAVV | 328 | 1.000 |
| ANNs+QM | 3 | GLSADLDAV | 242 | 0.990 |
| ANNs+QM | 4 | STLTYAEAV | 433 | 0.900 |

| ALLELE: HLA-A*0202 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | SVGRWVAVV | 328 | 1.000 |
| ANNs+QM | 2 | LLSSAAGNL | 296 | 0.990 |
| ANNs+QM | 3 | SIGSVGRWV | 325 | 0.960 |
| ANNs+QM | 4 | AVVAVLAVL | 334 | 0.960 |

| ALLELE: HLA-A*0203 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | SIGSVGRWV | 325 | 1.200 |
| ANNs+QM | 2 | SSADAIATL | 369 | 0.970 |
| ANNs+QM | 3 | SVGRWVAVV | 328 | 0.960 |
| ANNs+QM | 4 | LSADLDAVV | 243 | 0.910 |

| ALLELE: HLA-A*0206 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AVLTVVVTI | 340 | 1.000 |
| ANNs+QM | 2 | SVGRWVAVV | 328 | 0.960 |
| ANNs+QM | 3 | VPVDSVIEL | 545 | 0.960 |
| ANNs+QM | 4 | GLSADLDAV | 242 | 0.890 |

| ALLELE: HLA-A*0205 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 5.950 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AVLTVVVTI | 340 | 11.940 |
| QM | 2 | AVVAVLAVL | 334 | 7.560 |
| QM | 3 | SSADAIATL | 369 | 7.220 |
| QM | 4 | FWVDAEPRL | 570 | 7.090 |

| ALLELE: HLA-A*1101 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVMDFGIAR | 153 | 1.000 |
| ANNs+QM | 2 | ADLDAVLK | 245 | 1.000 |
| ANNs+QM | 3 | WVDAEPRLR | 571 | 0.630 |
| ANNs+QM | 4 | RYQTAAEMR | 262 | 0.530 |

| ALLELE: HLA-A11 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVMDFGIAR | 153 | 1.000 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 2 | ADLDAVVLK | 245 | 1.000 |
| ANNs+QM | 3 | WVDAEPRLR | 571 | 1.000 |
| ANNs+QM | 4 | AVLTVVVTI | 340 | 0.930 |

| ALLELE: HLA-A24 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 7.670 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | REAQNAAAL | 58 | 11.160 |
| QM | 2 | DARSDVYSL | 194 | 10.150 |
| QM | 3 | TYAEAVKKL | 436 | 10.110 |
| QM | 4 | TSAITNVVI | 477 | 10.000 |

| ALLELE: HLA-A*2402 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TYAEAVKKL | 436 | 0.990 |
| ANNs+QM | 2 | RYQTAAEMR | 262 | 0.950 |
| ANNs+QM | 3 | EPPEAPKVL | 280 | 0.890 |
| ANNs+QM | 4 | PPSARHEGL | 235 | 0.810 |

| ALLELE: HLA-A3 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVMDFGIAR | 153 | 1.000 |
| ANNs+QM | 2 | RYQTAAEMR | 262 | 0.990 |
| ANNs+QM | 3 | RFREAAQNA | 55 | 0.960 |
| ANNs+QM | 4 | AQNAAALNH | 60 | 0.910 |

| ALLELE: HLA-A*3101 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KVMDFGIAR | 153 | 3.584 |
| QM | 2 | RYQTAAEMR | 262 | 0.588 |
| QM | 3 | WVDAEPRLR | 571 | -1.609 |

| ALLELE: HLA-A31 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVMDFGIAR | 153 | 1.000 |
| ANNs+QM | 2 | WVDAEPRLR | 571 | 0.880 |
| ANNs+QM | 3 | RDVAVKVLK | 35 | 0.860 |
| ANNs+QM | 4 | PEAPKVLTD | 282 | 0.830 |

| ALLELE: HLA-A*0301 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ADLDAVVLK | 245 | 1.000 |
| ANNs+QM | 2 | AQNAAALNH | 60 | 0.970 |
| ANNs+QM | 3 | KKLTAAGFG | 442 | 0.920 |
| ANNs+QM | 4 | AVLTVVVTI | 340 | 0.860 |

| ALLELE: HLA-A*3302 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -0.105 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | WVDAEPRLR | 571 | 2.708 |
| QM | 2 | KVMDFGIAR | 153 | 1.504 |

| | | | | |
|-----------|---|-----------|-----|-------|
| QM | 3 | RYQTAAEMR | 262 | 1.504 |
| QM | 4 | DVYSLGCVL | 198 | 0.405 |

| ALLELE: HLA-A68.1 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KVMDFGIAR | 153 | 5.991 |
| QM | 2 | WVDAEPRLR | 571 | 5.298 |
| QM | 3 | DVYSLGCVL | 198 | 2.485 |
| QM | 4 | KVLTDAERT | 286 | 2.079 |

| ALLELE: HLA-A20 Cattle | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.401 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KVMDFGIAR | 153 | 3.689 |
| QM | 2 | WVDAEPRLR | 571 | 3.689 |
| QM | 3 | LLSSAAGNL | 296 | 2.708 |
| QM | 4 | DRYELGEIL | 9 | 2.303 |

| ALLELE: HLA-A2.1 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LLSSAAGNL | 296 | 0.970 |
| ANNs+QM | 2 | TYAEAVKKL | 436 | 0.890 |
| ANNs+QM | 3 | GLSADLDAV | 242 | 0.880 |
| ANNs+QM | 4 | EPPEAPKVL | 280 | 0.860 |

ALLELE: HLA-B14

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | DRYELGEIL | 9 | 1.000 |
| ANNs+QM | 2 | SADLDAVVL | 244 | 0.950 |
| ANNs+QM | 3 | SSADAIATL | 369 | 0.940 |
| ANNs+QM | 4 | REAQNAAAL | 58 | 0.870 |

ALLELE: HLA-B*2702

Threshold for 4 % with score: 0.000

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | DRYELGEIL | 9 | 4.500 |
| QM | 2 | HRDVAVKVL | 34 | 2.890 |
| QM | 3 | KRAIEVIAD | 113 | 1.792 |
| QM | 4 | ERTSLLSSA | 292 | 1.792 |

ALLELE: HLA-B27

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | DRYELGEIL | 9 | 0.960 |
| ANNs+QM | 2 | KRAIEVIAD | 113 | 0.910 |
| ANNs+QM | 3 | HRDVAVKVL | 34 | 0.890 |
| ANNs+QM | 4 | DARSDVYSL | 194 | 0.240 |

ALLELE: HLA-B*2705

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | HRDVAVKVL | 34 | 1.000 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 2 | DRYELGEIL | 9 | 0.950 |
| ANNs+QM | 3 | ERTSLLSSA | 292 | 0.820 |
| ANNs+QM | 4 | KRAIEVIAD | 113 | 0.770 |

| ALLELE: HLA-B*3501 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TPKRAIEVI | 111 | 1.000 |
| ANNs+QM | 2 | EPPEAPKVL | 280 | 1.000 |
| ANNs+QM | 3 | TPELVGKVI | 460 | 1.000 |
| ANNs+QM | 4 | VPVDSVIEL | 545 | 1.000 |

| ALLELE: HLA-B*3701 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | MDFGIARAI | 155 | 4.094 |
| QM | 2 | LDAVVLKAL | 247 | 4.094 |
| QM | 3 | SEVHLARDL | 23 | 2.303 |
| QM | 4 | REAQNAAAL | 58 | 2.303 |

| ALLELE: HLA-B*3801 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.445 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RHEGLSADL | 239 | 5.455 |
| QM | 2 | TYAEAVKKL | 436 | 1.831 |
| QM | 3 | EPPEAPKVL | 280 | 1.649 |
| QM | 4 | FWVDAEPRL | 570 | 1.649 |

| ALLELE: HLA-B*3901 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.792 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RHEGLSADL | 239 | 5.598 |
| QM | 2 | HRDVAVKVL | 34 | 4.212 |
| QM | 3 | DRYELGEIL | 9 | 4.094 |
| QM | 4 | VPVDSVIEL | 545 | 2.890 |

| ALLELE: HLA-B*3902 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.693 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DRYELGEIL | 9 | 0.875 |
| QM | 2 | DVYSLGCVL | 198 | 0.875 |
| QM | 3 | LGCVLYEVL | 202 | 0.875 |
| QM | 4 | RHEGLSADL | 239 | 0.875 |

| ALLELE: HLA-B*40 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SEVHLARDL | 23 | 4.382 |
| QM | 2 | REAQNAAAL | 58 | 3.689 |
| QM | 3 | MEYVDGVTI | 92 | 3.689 |
| QM | 4 | LDAVVLKAL | 247 | 1.609 |

| ALLELE: HLA-B*4403 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SEVHLARDL | 23 | 3.178 |

| | | | | |
|-----------|---|-----------|-----|-------|
| QM | 2 | REAQNAAAL | 58 | 2.485 |
| QM | 3 | AERTSLLSS | 291 | 2.485 |
| QM | 4 | MEYVDGVTL | 92 | 1.386 |

| ALLELE: HLA-B*5101 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TPKRAIEVI | 111 | 1.000 |
| ANNs+QM | 2 | TPELVGKVI | 460 | 1.000 |
| ANNs+QM | 3 | EPPEAPKVL | 280 | 0.950 |
| ANNs+QM | 4 | YAEAVKKLT | 437 | 0.880 |

| ALLELE: HLA-B*5102 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 9.050 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TPELVGKVI | 460 | 17.960 |
| QM | 2 | TPKRAIEVI | 111 | 12.400 |
| QM | 3 | RGQSSADAI | 366 | 11.350 |
| QM | 4 | VPDVRGQSS | 362 | 10.070 |

| ALLELE: HLA-B*5103 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 9.280 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TPELVGKVI | 460 | 17.960 |
| QM | 2 | TPKRAIEVI | 111 | 12.400 |
| QM | 3 | RGQSSADAI | 366 | 11.350 |
| QM | 4 | VPDVRGQSS | 362 | 10.070 |

| ALLELE: HLA-B*5201 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.974 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TPELVGKVI | 460 | 4.883 |
| QM | 2 | TPKRAIEVI | 111 | 4.413 |
| QM | 3 | LGCVLYEVL | 202 | 3.679 |
| QM | 4 | EPPEAPKVL | 280 | 3.679 |

| ALLELE: HLA-B*5301 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | EPPEAPKVL | 280 | 1.000 |
| ANNs+QM | 2 | VPVDSVIEL | 545 | 1.000 |
| ANNs+QM | 3 | PPSARHEGL | 235 | 0.980 |
| ANNs+QM | 4 | TPKRAIEVI | 111 | 0.970 |

| ALLELE: HLA-B*5401 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TPKRAIEVI | 111 | 1.000 |
| ANNs+QM | 2 | VPVDSVIEL | 545 | 1.000 |
| ANNs+QM | 3 | EPPEAPKVL | 280 | 0.990 |
| ANNs+QM | 4 | PPSARHEGL | 235 | 0.980 |

| ALLELE: HLA-B*51 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | FWVDAEPRL | 570 | 1.000 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 2 | EPPEAPKVL | 280 | 0.990 |
| ANNs+QM | 3 | TPKRAIEVI | 111 | 0.980 |
| ANNs+QM | 4 | TPELVGKVI | 460 | 0.980 |

| ALLELE: HLA-B*5801 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -0.223 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RTSLLSSAA | 293 | 2.197 |
| QM | 2 | ISATNAVKV | 146 | 1.194 |
| QM | 3 | LSADLDAVV | 243 | 1.099 |
| QM | 4 | SSADAIATL | 369 | 0.971 |

| ALLELE: HLA-B60 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.386 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SEVHLARDL | 23 | 5.864 |
| QM | 2 | REAQNAAAL | 58 | 5.768 |
| QM | 3 | MEYVDGVTL | 92 | 5.768 |
| QM | 4 | LDAVVLKAL | 247 | 3.784 |

| ALLELE: HLA-B61 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | REAQNAAAL | 58 | 2.868 |
| QM | 2 | SEVHLARDL | 23 | 2.773 |
| QM | 3 | MEYVDGVTL | 92 | 2.773 |
| QM | 4 | MDFGIARAI | 155 | 1.099 |

ALLELE: HLA-B62

Threshold for 4 % with score: 0.693

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | GLSADLDAV | 242 | 0.693 |
| QM | 2 | LLSSAAGNL | 296 | 0.693 |
| QM | 3 | SIGSVGRWV | 325 | 0.693 |

ALLELE: HLA-B7

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | PPSARHEGL | 235 | 1.000 |
| ANNs+QM | 2 | EPPEAPKVL | 280 | 1.000 |
| ANNs+QM | 3 | AVVAVLAVL | 334 | 1.000 |
| ANNs+QM | 4 | VPVDSVIEL | 545 | 1.000 |

ALLELE: HLA-B*0702

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | TPKRAIEVI | 111 | 1.000 |
| ANNs+QM | 2 | PPSARHEGL | 235 | 1.000 |
| ANNs+QM | 3 | EPPEAPKVL | 280 | 1.000 |
| ANNs+QM | 4 | VPVDSVIEL | 545 | 1.000 |

ALLELE: HLA-B8

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | TSAITNVVI | 477 | 0.770 |
| ANNs+QM | 2 | EPPEAPKVL | 280 | 0.680 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 3 | RYQTAAEMR | 262 | 0.670 |
| ANNs+QM | 4 | HRDVAVKVL | 34 | 0.660 |

| ALLELE: HLA-Cw*0301 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 2.015 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DRYELGEIL | 9 | 4.094 |
| QM | 2 | MEYVDGVTL | 92 | 3.178 |
| QM | 3 | SEVHLARDL | 23 | 2.996 |
| QM | 4 | DVYSLGCVL | 198 | 2.996 |

| ALLELE: HLA-Cw*0401 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4.370 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | EPPEAPKVL | 280 | 15.550 |
| QM | 2 | TYAEAVKKL | 436 | 11.640 |
| QM | 3 | HRDVAVKVL | 34 | 9.840 |
| QM | 4 | VPVDSVIEL | 545 | 8.370 |

| ALLELE: HLA-Cw*0602 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.482 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DRYELGEIL | 9 | 1.887 |
| QM | 2 | SEVHLARDL | 23 | 1.887 |
| QM | 3 | DVYSLGCVL | 198 | 1.792 |
| QM | 4 | LGCVLYEVL | 202 | 1.792 |

ALLELE: HLA-Cw*0702

Threshold for 4 % with score: 1.212

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | LDAVVLKAL | 247 | 2.444 |
| QM | 2 | TYAEAVKKL | 436 | 2.156 |
| QM | 3 | VPVDSVIEL | 545 | 1.800 |
| QM | 4 | EPPEAPKVL | 280 | 1.281 |

ALLELE: H2-Db

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | REAQNAAAL | 58 | 1.000 |
| ANNs+QM | 2 | ISATNAVKV | 146 | 0.960 |
| ANNs+QM | 3 | SEVHLARDL | 23 | 0.880 |
| ANNs+QM | 4 | SSADAIATL | 369 | 0.880 |

ALLELE: H2-Dd

Threshold for 4 % with score: 11.800

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | RGQSSADAI | 366 | 20.550 |
| QM | 2 | FGGMSEVHL | 19 | 19.600 |
| QM | 3 | LGCVLYEVL | 202 | 15.600 |
| QM | 4 | FWVDAEPRL | 570 | 15.580 |

ALLELE: H2-Kb

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| ANNs+QM | 1 | SSADAIATL | 369 | 0.990 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 2 | LGCVLYEVL | 202 | 0.980 |
| ANNs+QM | 3 | REAQNAAAL | 58 | 0.970 |
| ANNs+QM | 4 | EPPEAPKVL | 280 | 0.920 |

| ALLELE: H2-Kd | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TYAEAVKKL | 436 | 1.000 |
| ANNs+QM | 2 | EPPEAPKVL | 280 | 0.990 |
| ANNs+QM | 3 | PPSARHEGL | 235 | 0.980 |
| ANNs+QM | 4 | STLTYAEAV | 433 | 0.960 |

| ALLELE: H2-Kk | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | MDFGIARAI | 155 | 5.298 |
| QM | 2 | SEVHLARDL | 23 | 3.689 |
| QM | 3 | MEYVDGRTL | 92 | 2.996 |
| QM | 4 | REAQNAAAL | 58 | 2.303 |

| ALLELE: H2-Ld | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | PPSARHEGL | 235 | 1.000 |
| ANNs+QM | 2 | EPPEAPKVL | 280 | 1.000 |
| ANNs+QM | 3 | DARSDVYSL | 194 | 0.740 |
| ANNs+QM | 4 | LLSSAAGNL | 296 | 0.690 |

ALLELE: HLA-G

Threshold for 4 % with score: 9.260

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | EPPEAPKVL | 280 | 13.510 |
| QM | 2 | SSADAIATL | 369 | 13.110 |
| QM | 3 | TYAEAVKKL | 436 | 12.780 |
| QM | 4 | LLSSAAGNL | 296 | 10.180 |

ALLELE: H-2Qa

Threshold for 4 % with score: 6.000

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | DRYELGEIL | 9 | 8.800 |
| QM | 2 | LDAVVLKAL | 247 | 8.750 |
| QM | 3 | RGQSSADAI | 366 | 8.000 |
| QM | 4 | REAQNAAAL | 58 | 7.470 |

ALLELE: HLA-B*2706

Threshold for 4 % with score: 5.000

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | PPSARHEGL | 235 | 6.670 |
| QM | 2 | EPPEAPKVL | 280 | 6.000 |
| QM | 3 | ERTSLLSSA | 292 | 5.870 |
| QM | 4 | RHEGLSADL | 239 | 5.200 |

ALLELE: HLA-B35

Threshold for 4 % with score: 8.350

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|-------------------|------|-----------|-------------|---------------|
| QM | 1 | TPELVGKVI | 460 | 14.660 |

| | | | | |
|-----------|---|-----------|-----|--------|
| QM | 2 | PPSARHEGL | 235 | 13.780 |
| QM | 3 | VPDVRGQSS | 362 | 12.200 |
| QM | 4 | TPKRAIEVI | 111 | 10.690 |

| ALLELE: Mamu-A*01 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.650 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KVMDFGIAR | 153 | 3.820 |
| QM | 2 | STLTYAEAV | 433 | 3.020 |
| QM | 3 | TSAITNVVI | 477 | 2.670 |
| QM | 4 | DARSDVYSL | 194 | 2.160 |

| ALLELE: HLA-A*0204 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 12.070 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | MLDKGADVD | 586 | 21.640 |
| QM | 2 | LDAVVLKAL | 247 | 18.860 |
| QM | 3 | GLSADLDAV | 242 | 17.000 |
| QM | 4 | LLSSAAGNL | 296 | 16.860 |

| ALLELE: HLA-B*2703 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 5.130 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | ARHEGLSAD | 238 | 8.250 |
| QM | 2 | HRDVAVKVL | 34 | 6.430 |
| QM | 3 | KRAIEVIAD | 113 | 5.390 |
| QM | 4 | VPVDSVIEL | 545 | 4.400 |

| ALLELE: HLA-B*2704 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 8.790 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RHEGLSADL | 239 | 13.560 |
| QM | 2 | ARHEGLSAD | 238 | 12.450 |
| QM | 3 | ERTSLLSSA | 292 | 11.650 |
| QM | 4 | SEVHLARDL | 23 | 10.670 |

| ALLELE: HLA-B*2902 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 7.750 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SEVHLARDL | 23 | 12.700 |
| QM | 2 | MEYVDGVTL | 92 | 11.110 |
| QM | 3 | PEAPKVLTD | 282 | 10.700 |
| QM | 4 | PPSARHEGL | 235 | 8.930 |

| ALLELE: HLA-A*3301 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.840 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AQNAAALNH | 60 | 2.900 |
| QM | 2 | DVSTLTAE | 431 | 1.510 |
| QM | 3 | SIGSVGRWV | 325 | 1.230 |
| QM | 4 | ADLDAVVLK | 245 | 1.060 |

| ALLELE: HLA-B44 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4.900 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | REAQNAAAL | 58 | 9.390 |

| | | | | |
|-----------|---|-----------|-----|-------|
| QM | 2 | SEVHLARDL | 23 | 8.520 |
| QM | 3 | AQNAAALNH | 60 | 7.450 |
| QM | 4 | HEGLSADLD | 240 | 4.880 |

| ALLELE: HLA-A*6801 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVMDFGIAR | 153 | 0.990 |
| ANNs+QM | 2 | MDFGIARAI | 155 | 0.970 |
| ANNs+QM | 3 | ADLDAVVLK | 245 | 0.940 |
| ANNs+QM | 4 | WVDAEPRLR | 571 | 0.900 |

| ALLELE: HLA-A*6802 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | GGMSEVHLA | 20 | 1.000 |
| ANNs+QM | 2 | STLTYAEAV | 433 | 1.000 |
| ANNs+QM | 3 | TYAEAVKKL | 436 | 1.000 |
| ANNs+QM | 4 | ISATNAVKV | 146 | 0.990 |