



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 | Sat Mar 13 00:41:35 2010 |
| Length of input sequence | 291 amino acids |
| Number of nonamers from input sequence | 283 |
| 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 | AVDVPESRI | 259 | 0.680 |
| ANNs+QM | 2 | APELLPASI | 33 | 0.300 |
| ANNs+QM | 3 | AVIIDADGA | 251 | 0.200 |
| ANNs+QM | 4 | RGNLAAAMQ | 145 | 0.170 |

| ALLELE: HLA-A2 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | NLAAAMQGL | 147 | 1.000 |
| ANNs+QM | 2 | GLRVAVEAL | 220 | 0.980 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 3 | FLRRQAPEL | 28 | 0.960 |
| ANNs+QM | 4 | AAMQGLLAL | 150 | 0.670 |

| ALLELE: HLA-A*0201 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VTWPLPDRL | 1 | 1.000 |
| ANNs+QM | 2 | FLRRQAPEL | 28 | 1.000 |
| ANNs+QM | 3 | NLAAAMQGL | 147 | 0.990 |
| ANNs+QM | 4 | AAMQGLLAL | 150 | 0.970 |

| ALLELE: HLA-A*0202 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | FLRRQAPEL | 28 | 0.990 |
| ANNs+QM | 2 | ASISGGAPL | 39 | 0.990 |
| ANNs+QM | 3 | NLAAAMQGL | 147 | 0.980 |
| ANNs+QM | 4 | IAGTAAVAV | 102 | 0.930 |

| ALLELE: HLA-A*0203 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | FLRRQAPEL | 28 | 0.950 |
| ANNs+QM | 2 | NLAAAMQGL | 147 | 0.940 |
| ANNs+QM | 3 | QGLLALPLL | 153 | 0.940 |
| ANNs+QM | 4 | FARLYAVEL | 112 | 0.460 |

| ALLELE: HLA-A*0206 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVYITDDYT | 90 | 1.000 |
| ANNs+QM | 2 | EHYEKLEGV | 121 | 0.990 |
| ANNs+QM | 3 | TDGDSGLRV | 215 | 0.880 |
| ANNs+QM | 4 | QVTDGDSGL | 213 | 0.850 |

| ALLELE: HLA-A*0205 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 5.950 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VTWPLPDRL | 1 | 15.510 |
| QM | 2 | IAGTAAVAV | 102 | 9.710 |
| QM | 3 | FLRRQAPEL | 28 | 9.430 |
| QM | 4 | MQGLLALPL | 152 | 8.920 |

| ALLELE: HLA-A*1101 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LRRQAPPELL | 29 | 0.650 |
| ANNs+QM | 2 | DSGLRVAVE | 218 | 0.500 |
| ANNs+QM | 3 | VPLTFAGKI | 129 | 0.270 |
| ANNs+QM | 4 | AAMQGLLAL | 150 | 0.220 |

| ALLELE: HLA-A11 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVYITDDYT | 90 | 0.970 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 2 | AVDVPESRI | 259 | 0.900 |
| ANNs+QM | 3 | YTATGIAGT | 97 | 0.610 |
| ANNs+QM | 4 | LLPASISGG | 36 | 0.590 |

| ALLELE: HLA-A24 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 7.670 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | APELLPASI | 33 | 10.040 |
| QM | 2 | NLAAAMQGL | 147 | 7.320 |
| QM | 3 | VPLTFAGKI | 129 | 5.770 |
| QM | 4 | TDDYTATGI | 94 | 5.720 |

| ALLELE: HLA-A*2402 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TFAGKINRL | 132 | 1.000 |
| ANNs+QM | 2 | VPLTFAGKI | 129 | 0.890 |
| ANNs+QM | 3 | LRRQAPPELL | 29 | 0.690 |
| ANNs+QM | 4 | VTWPLPDRL | 1 | 0.400 |

| ALLELE: HLA-A3 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVYITDDYT | 90 | 0.810 |
| ANNs+QM | 2 | VRGNLAAAM | 144 | 0.750 |
| ANNs+QM | 3 | TFAGKINRL | 132 | 0.650 |
| ANNs+QM | 4 | TATGIAGTA | 98 | 0.410 |

| ALLELE: HLA-A*3101 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | NLAAAMQGL | 147 | -3.219 |
| QM | 2 | MQGLLALPL | 152 | -3.219 |
| QM | 3 | GLRVAVEAL | 220 | -3.219 |

| ALLELE: HLA-A31 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AVDVPEMRI | 259 | 0.760 |
| ANNs+QM | 2 | TGIAGTAAV | 100 | 0.630 |
| ANNs+QM | 3 | VAVEALYDA | 223 | 0.570 |
| ANNs+QM | 4 | LKYPGGVVM | 63 | 0.550 |

| ALLELE: HLA-A*0301 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KVYITDDYT | 90 | 0.830 |
| ANNs+QM | 2 | ADDDSATGG | 232 | 0.830 |
| ANNs+QM | 3 | ASISGGAPL | 39 | 0.750 |
| ANNs+QM | 4 | AAMQGLLAL | 150 | 0.650 |

| ALLELE: HLA-A*3302 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -0.105 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LSGTPAVDL | 14 | -0.693 |
| QM | 2 | ASISGGAPL | 39 | -0.693 |

| | | | | |
|-----------|---|-----------|-----|--------|
| QM | 3 | QVTDGDSGL | 213 | -0.693 |
|-----------|---|-----------|-----|--------|

| ALLELE: HLA-A68.1 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AVIIDADGA | 251 | 2.079 |
| QM | 2 | KVYITDDYT | 90 | 1.792 |
| QM | 3 | QVTDGDSGL | 213 | 1.792 |
| QM | 4 | AVDVPESRI | 259 | 1.792 |

| ALLELE: HLA-A20 Cattle | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.401 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LKYPGGVVM | 63 | 5.704 |
| QM | 2 | FLRRQAPEL | 28 | 2.708 |
| QM | 3 | NLAAAMQGL | 147 | 2.708 |
| QM | 4 | GLRVAVEAL | 220 | 2.708 |

| ALLELE: HLA-A2.1 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | FLRRQAPEL | 28 | 1.000 |
| ANNs+QM | 2 | NLAAAMQGL | 147 | 1.000 |
| ANNs+QM | 3 | GLRVAVEAL | 220 | 1.000 |
| ANNs+QM | 4 | ASISGGAPL | 39 | 0.970 |

| ALLELE: HLA-B14 | | | | |
|------------------------|--|--|--|--|
|------------------------|--|--|--|--|

| Threshold for 4 % with score: 4 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AAMQGLLAL | 150 | 1.000 |
| ANNs+QM | 2 | VPESRIAEL | 262 | 1.000 |
| ANNs+QM | 3 | QGLLALPLL | 153 | 0.980 |
| ANNs+QM | 4 | FARLYAVEL | 112 | 0.960 |

| ALLELE: HLA-B*2702 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LRRQAPPELL | 29 | 4.094 |
| QM | 2 | VRGNLAAAM | 144 | 2.996 |
| QM | 3 | MQGLLALPL | 152 | 1.792 |
| QM | 4 | VTWPLPDRL | 1 | 0.405 |

| ALLELE: HLA-B27 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LRRQAPPELL | 29 | 1.000 |
| ANNs+QM | 2 | TFAGKINRL | 132 | 0.150 |
| ANNs+QM | 3 | GTA AVAVEF | 104 | 0.120 |
| ANNs+QM | 4 | KVYITDDYT | 90 | 0.070 |

| ALLELE: HLA-B*2705 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LRRQAPPELL | 29 | 0.970 |
| ANNs+QM | 2 | TFAGKINRL | 132 | 0.850 |
| ANNs+QM | 3 | FARLYAVEL | 112 | 0.480 |

| | | | | |
|----------------|---|-----------|----|-------|
| ANNs+QM | 4 | YTATGIAGT | 97 | 0.380 |
|----------------|---|-----------|----|-------|

| ALLELE: HLA-B*3501 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APELLPASI | 33 | 1.000 |
| ANNs+QM | 2 | VPLTFAGKI | 129 | 1.000 |
| ANNs+QM | 3 | VPESRIAEL | 262 | 1.000 |
| ANNs+QM | 4 | LAAAMQGLL | 148 | 0.690 |

| ALLELE: HLA-B*3701 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TDDYTATGI | 94 | 3.689 |
| QM | 2 | YEKLEGVPL | 123 | 2.303 |
| QM | 3 | TDGDSGLRV | 215 | 2.079 |
| QM | 4 | LRRQAPPELL | 29 | 1.609 |

| ALLELE: HLA-B*3801 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.445 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | EHYEKLEGV | 121 | 2.485 |
| QM | 2 | VPESRIAEL | 262 | 1.792 |
| QM | 3 | TFAGKINRL | 132 | 1.386 |
| QM | 4 | PHGTTIVAL | 55 | 1.099 |

| ALLELE: HLA-B*3901 | | | | |
|---------------------------|--|--|--|--|
|---------------------------|--|--|--|--|

| Threshold for 4 % with score: 1.792 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | EHYEKLEGV | 121 | 5.193 |
| QM | 2 | PHGTTIVAL | 55 | 2.603 |
| QM | 3 | VPESRIAEL | 262 | 2.603 |
| QM | 4 | AAMQGLLAL | 150 | 2.197 |

| ALLELE: HLA-B*3902 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.693 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | MQGLLALPL | 152 | 3.178 |
| QM | 2 | LKYPGGVVM | 63 | 2.303 |
| QM | 3 | VTWPLPDRL | 1 | 0.875 |
| QM | 4 | LAIMVRGNL | 140 | 0.875 |

| ALLELE: HLA-B*40 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | YEKLEGVPL | 123 | 2.303 |
| QM | 2 | DDYTATGIA | 95 | 1.609 |
| QM | 3 | ASISGGAPL | 39 | 1.386 |
| QM | 4 | EEGYQAVGS | 190 | 1.386 |

| ALLELE: HLA-B*4403 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | EEGYQAVGS | 190 | 1.792 |
| QM | 2 | GTA AVAVEF | 104 | 1.504 |
| QM | 3 | YEKLEGVPL | 123 | 1.386 |

| | | | | |
|-----------|---|-----------|----|-------|
| QM | 4 | DDYTATGIA | 95 | 1.216 |
|-----------|---|-----------|----|-------|

| ALLELE: HLA-B*5101 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | IAGTAAVAV | 102 | 1.000 |
| ANNs+QM | 2 | VPLTFAGKI | 129 | 1.000 |
| ANNs+QM | 3 | FARLYAVEL | 112 | 0.950 |
| ANNs+QM | 4 | DPQSAGRIV | 170 | 0.950 |

| ALLELE: HLA-B*5102 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 9.050 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DPQSAGRIV | 170 | 18.780 |
| QM | 2 | VPLTFAGKI | 129 | 13.380 |
| QM | 3 | APELLPASI | 33 | 12.900 |
| QM | 4 | IAGTAAVAV | 102 | 11.430 |

| ALLELE: HLA-B*5103 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 9.280 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DPQSAGRIV | 170 | 18.780 |
| QM | 2 | VPLTFAGKI | 129 | 13.380 |
| QM | 3 | APELLPASI | 33 | 12.900 |
| QM | 4 | IAGTAAVAV | 102 | 11.430 |

| ALLELE: HLA-B*5201 | | | | |
|---------------------------|--|--|--|--|
|---------------------------|--|--|--|--|

| Threshold for 4 % with score: 1.974 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DPQSAGRIV | 170 | 4.317 |
| QM | 2 | VPLTFAGKI | 129 | 3.114 |
| QM | 3 | TGIAGTAAV | 100 | 2.986 |
| QM | 4 | APELLPASI | 33 | 2.485 |

| ALLELE: HLA-B*5301 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VPESRIAEL | 262 | 1.000 |
| ANNs+QM | 2 | DPQSAGRIV | 170 | 0.970 |
| ANNs+QM | 3 | VPLTFAGKI | 129 | 0.930 |
| ANNs+QM | 4 | APELLPASI | 33 | 0.910 |

| ALLELE: HLA-B*5401 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | DPQSAGRIV | 170 | 0.980 |
| ANNs+QM | 2 | APELLPASI | 33 | 0.950 |
| ANNs+QM | 3 | VPLTFAGKI | 129 | 0.940 |
| ANNs+QM | 4 | VPESRIAEL | 262 | 0.930 |

| ALLELE: HLA-B*51 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VPLTFAGKI | 129 | 0.990 |
| ANNs+QM | 2 | VPESRIAEL | 262 | 0.980 |
| ANNs+QM | 3 | DPQSAGRIV | 170 | 0.960 |

| | | | | |
|----------------|---|-----------|----|-------|
| ANNs+QM | 4 | APELLPASI | 33 | 0.790 |
|----------------|---|-----------|----|-------|

| ALLELE: HLA-B*5801 | | | | |
|--------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: -0.223 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GTA AVAVEF | 104 | 4.094 |
| QM | 2 | VTWPLPDL | 1 | 1.887 |
| QM | 3 | VAVEALYDA | 223 | 0.971 |
| QM | 4 | YTATGIAGT | 97 | 0.875 |

| ALLELE: HLA-B60 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.386 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | YEKLEGVPL | 123 | 5.768 |
| QM | 2 | AAMQGLLAL | 150 | 2.773 |
| QM | 3 | LAIMVRGNL | 140 | 2.175 |
| QM | 4 | LSGTPAVDL | 14 | 2.079 |

| ALLELE: HLA-B61 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | YEKLEGVPL | 123 | 2.079 |
| QM | 2 | DDYTATGIA | 95 | 1.609 |
| QM | 3 | TDGDSGLRV | 215 | 1.609 |
| QM | 4 | TGIAGTAAV | 100 | 0.693 |

| ALLELE: HLA-B62 | | | | |
|------------------------|--|--|--|--|
|------------------------|--|--|--|--|

| Threshold for 4 % with score: 0.693 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | MQGLLALPL | 152 | 2.955 |
| QM | 2 | FLRRQAPEL | 28 | 1.792 |
| QM | 3 | GLRVAVEAL | 220 | 1.792 |
| QM | 4 | GTA AVAVEF | 104 | 1.569 |

| ALLELE: HLA-B7 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AAMQGLLAL | 150 | 1.000 |
| ANNs+QM | 2 | VPESRIAEL | 262 | 1.000 |
| ANNs+QM | 3 | ASISGGAPL | 39 | 0.970 |
| ANNs+QM | 4 | DPQSAGRIV | 170 | 0.880 |

| ALLELE: HLA-B*0702 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VPESRIAEL | 262 | 1.000 |
| ANNs+QM | 2 | VPLTFAGKI | 129 | 0.900 |
| ANNs+QM | 3 | DPQSAGRIV | 170 | 0.890 |
| ANNs+QM | 4 | APELLPASI | 33 | 0.870 |

| ALLELE: HLA-B8 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LAAAMQGLL | 148 | 0.660 |
| ANNs+QM | 2 | TAAVAVEFA | 105 | 0.650 |
| ANNs+QM | 3 | KVYITDDYT | 90 | 0.640 |

| | | | | |
|----------------|---|-----------|----|-------|
| ANNs+QM | 4 | YTATGIAGT | 97 | 0.640 |
|----------------|---|-----------|----|-------|

| ALLELE: HLA-Cw*0301 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 2.015 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AAMQGLLAL | 150 | 3.689 |
| QM | 2 | LKYPGGVVM | 63 | 3.219 |
| QM | 3 | ASISGGAPL | 39 | 2.996 |
| QM | 4 | LAIMVRGNL | 140 | 2.996 |

| ALLELE: HLA-Cw*0401 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4.370 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TFAGKINRL | 132 | 7.370 |
| QM | 2 | AAMQGLLAL | 150 | 6.700 |
| QM | 3 | VPESRIAEL | 262 | 4.830 |
| QM | 4 | VTWPLPDR | 1 | 4.490 |

| ALLELE: HLA-Cw*0602 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.482 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TFAGKINRL | 132 | 2.175 |
| QM | 2 | LAAAMQGLL | 148 | 1.887 |
| QM | 3 | MQGLLALPL | 152 | 1.887 |
| QM | 4 | VTWPLPDR | 1 | 1.792 |

| ALLELE: HLA-Cw*0702 | | | | |
|----------------------------|--|--|--|--|
|----------------------------|--|--|--|--|

| Threshold for 4 % with score: 1.212 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GTA AVAVEF | 104 | 1.569 |
| QM | 2 | LAAAMQGLL | 148 | 0.971 |
| QM | 3 | NLAAAMQGL | 147 | 0.875 |
| QM | 4 | MQGLLALPL | 152 | 0.875 |

| ALLELE: H2-Db | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AAMQGLLAL | 150 | 1.000 |
| ANNs+QM | 2 | VRGNLAAAM | 144 | 0.870 |
| ANNs+QM | 3 | PHGTTIVAL | 55 | 0.790 |
| ANNs+QM | 4 | IAGTAAVAV | 102 | 0.690 |

| ALLELE: H2-Dd | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 11.800 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GLRVAVEAL | 220 | 15.910 |
| QM | 2 | PHGTTIVAL | 55 | 12.910 |
| QM | 3 | VRGNLAAAM | 144 | 12.860 |
| QM | 4 | VPESRIAEL | 262 | 11.830 |

| ALLELE: H2-Kb | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TFAGKINRL | 132 | 0.970 |
| ANNs+QM | 2 | ASISGGAPL | 39 | 0.960 |
| ANNs+QM | 3 | TATGIAGTA | 98 | 0.900 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 4 | LAAAMQGLL | 148 | 0.820 |
|----------------|---|-----------|-----|-------|

| ALLELE: H2-Kd | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LRRQAPELL | 29 | 0.980 |
| ANNs+QM | 2 | VPLTFAGKI | 129 | 0.970 |
| ANNs+QM | 3 | LAIMVRGNL | 140 | 0.950 |
| ANNs+QM | 4 | ASISGGAPL | 39 | 0.910 |

| ALLELE: H2-Kk | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TDDYTATGI | 94 | 4.605 |
| QM | 2 | YEKLEGVPL | 123 | 2.996 |
| QM | 3 | EEGYQAVGS | 190 | 2.996 |
| QM | 4 | APELLPASI | 33 | 2.303 |

| ALLELE: H2-Ld | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | LSGTPAVDL | 14 | 1.000 |
| ANNs+QM | 2 | PQSAGRIVS | 171 | 0.810 |
| ANNs+QM | 3 | TFAGKINRL | 132 | 0.760 |
| ANNs+QM | 4 | ASISGGAPL | 39 | 0.470 |

| ALLELE: HLA-G | | | | |
|----------------------|--|--|--|--|
|----------------------|--|--|--|--|

| Threshold for 4 % with score: 9.260 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | NLAAAMQGL | 147 | 14.850 |
| QM | 2 | FLRRQAPEL | 28 | 12.180 |
| QM | 3 | LSGTPAVDL | 14 | 11.310 |
| QM | 4 | GLRVAVEAL | 220 | 10.180 |

| ALLELE: H-2Qa | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 6.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GLRVAVEAL | 220 | 6.760 |
| QM | 2 | NLAAAMQGL | 147 | 5.930 |
| QM | 3 | LAIMVRGNL | 140 | 5.150 |
| QM | 4 | QVTDGDSGL | 213 | 5.140 |

| ALLELE: HLA-B*2706 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 5.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | QVTDGDSGL | 213 | 7.200 |
| QM | 2 | LLPASISGG | 36 | 5.340 |
| QM | 3 | EHYEKLEGV | 121 | 5.290 |
| QM | 4 | TFAGKINRL | 132 | 4.870 |

| ALLELE: HLA-B35 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 8.350 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VPLTFAGKI | 129 | 15.900 |
| QM | 2 | AVDVPEsRI | 259 | 12.410 |
| QM | 3 | VPESRIAEL | 262 | 11.860 |

| | | | | |
|-----------|---|-----------|----|--------|
| QM | 4 | APELLPASI | 33 | 10.470 |
|-----------|---|-----------|----|--------|

| ALLELE: Mamu-A*01 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.650 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AAMQGLLAL | 150 | 3.720 |
| QM | 2 | RAIIESRSG | 272 | 3.350 |
| QM | 3 | TGIAGTAAV | 100 | 3.260 |
| QM | 4 | AVDVPEPRI | 259 | 2.680 |

| ALLELE: HLA-A*0204 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 12.070 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GLRVAVEAL | 220 | 20.290 |
| QM | 2 | FLRRQAPEL | 28 | 17.930 |
| QM | 3 | NLAAAMQGL | 147 | 17.420 |
| QM | 4 | FARLYAVEL | 112 | 14.290 |

| ALLELE: HLA-B*2703 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 5.130 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LRRQAPPELL | 29 | 8.030 |
| QM | 2 | TFAGKINRL | 132 | 4.680 |
| QM | 3 | GTA AVAVEF | 104 | 3.160 |
| QM | 4 | VRGNLAAAM | 144 | 2.070 |

| ALLELE: HLA-B*2704 | | | | |
|---------------------------|--|--|--|--|
|---------------------------|--|--|--|--|

| Threshold for 4 % with score: 8.790 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LRRQAPPELL | 29 | 14.230 |
| QM | 2 | QGLLALPLL | 153 | 13.470 |
| QM | 3 | VPESRIAEL | 262 | 12.680 |
| QM | 4 | VRGNLAAAM | 144 | 9.660 |

| ALLELE: HLA-B*2902 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 7.750 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | PHGTTIVAL | 55 | 10.530 |
| QM | 2 | LAIMVRGNL | 140 | 9.650 |
| QM | 3 | YEKLEGVPL | 123 | 8.060 |
| QM | 4 | PQSAGRIVS | 171 | 6.980 |

| ALLELE: HLA-A*3301 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.840 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LAIMVRGNL | 140 | 2.130 |
| QM | 2 | LSGTPAVDL | 14 | 1.270 |
| QM | 3 | GNLAAAMQG | 146 | 1.270 |
| QM | 4 | LAAAMQGLL | 148 | 0.540 |

| ALLELE: HLA-B44 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4.900 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | YEKLEGVPL | 123 | 10.960 |
| QM | 2 | EEGYQAVGS | 190 | 8.890 |
| QM | 3 | GTA AVAVEF | 104 | 4.650 |

| | | | | |
|-----------|---|-----------|-----|-------|
| QM | 4 | GLRVAVEAL | 220 | 4.060 |
|-----------|---|-----------|-----|-------|

| ALLELE: HLA-A*6801 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ASISGGAPL | 39 | 0.480 |
| ANNs+QM | 2 | GTA AVAVEF | 104 | 0.480 |
| ANNs+QM | 3 | AVDVPE SRI | 259 | 0.460 |
| ANNs+QM | 4 | ADDDSATGG | 232 | 0.440 |

| ALLELE: HLA-A*6802 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VTWPLPDRL | 1 | 0.990 |
| ANNs+QM | 2 | IAGTAAVAV | 102 | 0.990 |
| ANNs+QM | 3 | TAAVAVEFA | 105 | 0.990 |
| ANNs+QM | 4 | AVIIDADGA | 251 | 0.980 |