



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

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| | |
|--|--------------------------|
| Antigen Name | Untitled |
| Scanned on | Tue Apr 20 23:52:58 2010 |
| Length of input sequence | 314 amino acids |
| Number of nonamers from input sequence | 306 |
| 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 | AADEEAVTE | 17 | 0.680 |
| ANNs+QM | 2 | SDPTTKAAL | 234 | 0.450 |
| ANNs+QM | 3 | VVRGLKALL | 94 | 0.350 |
| ANNs+QM | 4 | VRGLKALLA | 95 | 0.300 |

| ALLELE: HLA-A2 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | GLKALLATV | 97 | 0.970 |
| ANNs+QM | 2 | ALLATVVLA | 100 | 0.920 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 3 | SVASITLTL | 263 | 0.840 |
| ANNs+QM | 4 | KALLATVVL | 99 | 0.420 |

| ALLELE: HLA-A*0201 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ALLATVVLA | 100 | 1.000 |
| ANNs+QM | 2 | VLAVVGIGL | 106 | 1.000 |
| ANNs+QM | 3 | LLQIDTQQV | 154 | 1.000 |
| ANNs+QM | 4 | SVASITLTL | 263 | 0.990 |

| ALLELE: HLA-A*0202 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | GLKALLATV | 97 | 1.000 |
| ANNs+QM | 2 | LLQIDTQQV | 154 | 0.930 |
| ANNs+QM | 3 | AARGVVRGL | 90 | 0.880 |
| ANNs+QM | 4 | IVERVPVVV | 189 | 0.850 |

| ALLELE: HLA-A*0203 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | GLKALLATV | 97 | 0.990 |
| ANNs+QM | 2 | VVRGLKALL | 94 | 0.980 |
| ANNs+QM | 3 | ALLATVVLA | 100 | 0.970 |
| ANNs+QM | 4 | SVASITLTL | 263 | 0.870 |

| ALLELE: HLA-A*0206 | | | | |
|-----------------------------------|------|-----------|-------------|---------------|
| Threshold for .5 % with score: .5 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | IVERVPVVV | 189 | 1.000 |
| ANNs+QM | 2 | SVASITLTL | 263 | 0.990 |
| ANNs+QM | 3 | AVVGIGLGL | 108 | 0.980 |
| ANNs+QM | 4 | LLQIDTQQV | 154 | 0.970 |

| ALLELE: HLA-A*0205 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 5.950 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AARGVVRGL | 90 | 9.780 |
| QM | 2 | EQNPAKPAA | 83 | 9.170 |
| QM | 3 | SDPTTKAAL | 234 | 8.790 |
| QM | 4 | GLKALLATV | 97 | 8.360 |

| ALLELE: HLA-A*1101 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | PGPSDPTTK | 231 | 0.930 |
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.860 |
| ANNs+QM | 3 | ARGVVRGLK | 91 | 0.760 |
| ANNs+QM | 4 | ARRERAERR | 48 | 0.520 |

| ALLELE: HLA-A11 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AERRAAQAR | 53 | 1.000 |

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|----------------|---|-----------|-----|-------|
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.990 |
| ANNs+QM | 3 | TTKAALQVL | 237 | 0.930 |
| ANNs+QM | 4 | GLKALLATV | 97 | 0.810 |

| ALLELE: HLA-A24 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 7.670 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VQRQYPSAL | 177 | 11.760 |
| QM | 2 | AVVGIGLGL | 108 | 8.170 |
| QM | 3 | TVVLAVVGI | 104 | 7.920 |
| QM | 4 | KALLATVVL | 99 | 7.590 |

| ALLELE: HLA-A*2402 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VQRQYPSAL | 177 | 0.700 |
| ANNs+QM | 2 | RCEEKAEKL | 284 | 0.640 |
| ANNs+QM | 3 | SDPTTKAAL | 234 | 0.200 |
| ANNs+QM | 4 | AARGVVRGL | 90 | 0.150 |

| ALLELE: HLA-A3 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ARRERAERR | 48 | 1.000 |
| ANNs+QM | 2 | AERRAAQAR | 53 | 1.000 |
| ANNs+QM | 3 | QARRAAKRR | 67 | 1.000 |
| ANNs+QM | 4 | GVVRGLKAL | 93 | 0.940 |

| ALLELE: HLA-A*3101 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KPAARGVVR | 88 | -0.511 |
| QM | 2 | QARRAAKRR | 67 | -2.303 |
| QM | 3 | ALLATVVLA | 100 | -2.526 |

| ALLELE: HLA-A31 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ARRERAERR | 48 | 1.000 |
| ANNs+QM | 2 | QARRAAKRR | 67 | 1.000 |
| ANNs+QM | 3 | KPAARGVVR | 88 | 0.990 |
| ANNs+QM | 4 | ARGVVRGLK | 91 | 0.850 |

| ALLELE: HLA-A*0301 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ALLATVVLA | 100 | 0.980 |
| ANNs+QM | 2 | AERRAAQAR | 53 | 0.760 |
| ANNs+QM | 3 | QARATAIEQ | 59 | 0.680 |
| ANNs+QM | 4 | AKPAARGVV | 87 | 0.620 |

| ALLELE: HLA-A*3302 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -0.105 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | QARRAAKRR | 67 | 1.099 |
| QM | 2 | EVASQVGRI | 251 | 0.405 |

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|-----------|---|-----------|----|--------|
| QM | 3 | KPAARGVVR | 88 | -0.105 |
|-----------|---|-----------|----|--------|

| ALLELE: HLA-A68.1 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | EVASQVGRI | 251 | 3.178 |
| QM | 2 | KPAARGVVR | 88 | 2.303 |
| QM | 3 | GVVRGLKAL | 93 | 2.079 |
| QM | 4 | TVVLAVVGI | 104 | 2.079 |

| ALLELE: HLA-A20 Cattle | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.401 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AKPAARGVV | 87 | 5.704 |
| QM | 2 | LKALLATVV | 98 | 5.704 |
| QM | 3 | TKAALQVLT | 238 | 4.605 |
| QM | 4 | ARRERAERR | 48 | 4.382 |

| ALLELE: HLA-A2.1 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VLAVVGIGL | 106 | 1.000 |
| ANNs+QM | 2 | GLKALLATV | 97 | 0.980 |
| ANNs+QM | 3 | VVRGLKALL | 94 | 0.930 |
| ANNs+QM | 4 | GRIAAPSV | 257 | 0.900 |

| ALLELE: HLA-B14 | | | | |
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| Threshold for 4 % with score: 4 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ARRERAERR | 48 | 1.000 |
| ANNs+QM | 2 | VRGLKALLA | 95 | 0.980 |
| ANNs+QM | 3 | VADDAADEE | 13 | 0.910 |
| ANNs+QM | 4 | KALLATVVL | 99 | 0.880 |

| ALLELE: HLA-B*2702 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VRGLKALLA | 95 | 2.996 |
| QM | 2 | GRIAAPSV A | 257 | 2.996 |
| QM | 3 | RRAAQARAT | 55 | 2.890 |
| QM | 4 | VQRQYPSAL | 177 | 1.792 |

| ALLELE: HLA-B27 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | RRAAQARAT | 55 | 0.950 |
| ANNs+QM | 2 | ARGVVRGLK | 91 | 0.730 |
| ANNs+QM | 3 | ARRERAERR | 48 | 0.590 |
| ANNs+QM | 4 | VRGLKALLA | 95 | 0.350 |

| ALLELE: HLA-B*2705 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | ARRERAERR | 48 | 1.000 |
| ANNs+QM | 2 | GRIAAPSV A | 257 | 0.990 |
| ANNs+QM | 3 | RRAAQARAT | 55 | 0.980 |

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|----------------|---|-----------|----|-------|
| ANNs+QM | 4 | KALLATVVL | 99 | 0.940 |
|----------------|---|-----------|----|-------|

| ALLELE: HLA-B*3501 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APSVASITL | 261 | 1.000 |
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.900 |
| ANNs+QM | 3 | KALLATVVL | 99 | 0.700 |
| ANNs+QM | 4 | GPSDPTTKA | 232 | 0.590 |

| ALLELE: HLA-B*3701 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KDFSDGPHL | 198 | 3.689 |
| QM | 2 | SDPTTKAAL | 234 | 3.689 |
| QM | 3 | DEEAVTEPL | 19 | 2.708 |
| QM | 4 | VVRGLKALL | 94 | 1.609 |

| ALLELE: HLA-B*3801 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.445 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RCEEKAEKL | 284 | 1.974 |
| QM | 2 | AVVGIGLGL | 108 | 0.956 |
| QM | 3 | APSVASITL | 261 | 0.956 |
| QM | 4 | KALLATVVL | 99 | 0.262 |

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

| Threshold for 4 % with score: 1.792 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RCEEKAEKL | 284 | 2.890 |
| QM | 2 | GVVRGLKAL | 93 | 2.197 |
| QM | 3 | KALLATVVL | 99 | 1.792 |
| QM | 4 | AVVGIGLGL | 108 | 1.792 |

| ALLELE: HLA-B*3902 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.693 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VQRQYPSAL | 177 | 1.974 |
| QM | 2 | VLAVVGIGL | 106 | 0.875 |
| QM | 3 | AVVGIGLGL | 108 | 0.875 |
| QM | 4 | SVASITLTL | 263 | 0.875 |

| ALLELE: HLA-B*40 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SEQNPAKPA | 82 | 3.401 |
| QM | 2 | DEEAVTEPL | 19 | 2.303 |
| QM | 3 | KDFSDGPHL | 198 | 2.303 |
| QM | 4 | CEEKAEKLA | 285 | 2.303 |

| ALLELE: HLA-B*4403 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DEEAVTEPL | 19 | 3.296 |
| QM | 2 | SEQNPAKPA | 82 | 2.890 |
| QM | 3 | CEEKAEKLA | 285 | 2.197 |

| | | | | |
|-----------|---|-----------|---|-------|
| QM | 4 | NEDPQIERV | 5 | 2.079 |
|-----------|---|-----------|---|-------|

| ALLELE: HLA-B*5101 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VGRIAAPSV | 256 | 1.000 |
| ANNs+QM | 2 | AADEEAVTE | 17 | 0.950 |
| ANNs+QM | 3 | KALLATVVL | 99 | 0.920 |
| ANNs+QM | 4 | RCEEKAEKL | 284 | 0.910 |

| ALLELE: HLA-B*5102 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 9.050 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VGRIAAPSV | 256 | 13.960 |
| QM | 2 | VASQVGRIA | 252 | 13.660 |
| QM | 3 | IVERVPVVV | 189 | 9.400 |
| QM | 4 | NEDPQIERV | 5 | 8.950 |

| ALLELE: HLA-B*5103 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 9.280 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VGRIAAPSV | 256 | 13.960 |
| QM | 2 | VASQVGRIA | 252 | 13.660 |
| QM | 3 | IVERVPVVV | 189 | 9.400 |
| QM | 4 | NEDPQIERV | 5 | 8.950 |

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

| Threshold for 4 % with score: 1.974 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | IVERVPVVV | 189 | 3.401 |
| QM | 2 | MSAREIVII | 124 | 2.708 |
| QM | 3 | KALLATVVL | 99 | 2.069 |
| QM | 4 | AKPAARGVV | 87 | 1.974 |

| ALLELE: HLA-B*5301 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APSVASITL | 261 | 1.000 |
| ANNs+QM | 2 | GPSDPTTKA | 232 | 0.920 |
| ANNs+QM | 3 | KPAARGVVR | 88 | 0.790 |
| ANNs+QM | 4 | AERRAAQAR | 53 | 0.230 |

| ALLELE: HLA-B*5401 | | | | |
|---------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APSVASITL | 261 | 1.000 |
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.970 |
| ANNs+QM | 3 | GPSDPTTKA | 232 | 0.940 |
| ANNs+QM | 4 | GRIAAPSVVA | 257 | 0.830 |

| ALLELE: HLA-B*51 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | RCEEKAEKL | 284 | 0.950 |
| ANNs+QM | 2 | GPSDPTTKA | 232 | 0.920 |
| ANNs+QM | 3 | APSVASITL | 261 | 0.780 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 4 | VGRIAAPSV | 256 | 0.710 |
|----------------|---|-----------|-----|-------|

| ALLELE: HLA-B*5801 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: -0.223 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KALLATVVV | 99 | 1.099 |
| QM | 2 | MSAREIVII | 124 | 0.875 |
| QM | 3 | TTKAALQVL | 237 | 0.875 |
| QM | 4 | TAIEQARRA | 63 | 0.788 |

| ALLELE: HLA-B60 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.386 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DEEAVTEPL | 19 | 5.170 |
| QM | 2 | KDFSDGPHL | 198 | 2.996 |
| QM | 3 | SDPTTKAAL | 234 | 2.996 |
| QM | 4 | KALLATVVV | 99 | 2.773 |

| ALLELE: HLA-B61 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | NEDPQIERV | 5 | 4.382 |
| QM | 2 | SEQNPAKPA | 82 | 2.996 |
| QM | 3 | CEEKAEKLA | 285 | 2.996 |
| QM | 4 | EEKAEKLAA | 286 | 2.996 |

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

| Threshold for 4 % with score: 0.693 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GLKALLATV | 97 | 2.580 |
| QM | 2 | VQRQYPSAL | 177 | 2.485 |
| QM | 3 | VLAVVGIGL | 106 | 1.569 |
| QM | 4 | EQNPAKPAA | 83 | 0.875 |

| ALLELE: HLA-B7 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | AARGVVRGL | 90 | 1.000 |
| ANNs+QM | 2 | APSVASITL | 261 | 1.000 |
| ANNs+QM | 3 | AKPAARGVV | 87 | 0.980 |
| ANNs+QM | 4 | VVRGLKALL | 94 | 0.950 |

| ALLELE: HLA-B*0702 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APSVASITL | 261 | 1.000 |
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.990 |
| ANNs+QM | 3 | GPSDPTTKA | 232 | 0.870 |
| ANNs+QM | 4 | VVRGLKALL | 94 | 0.450 |

| ALLELE: HLA-B8 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | VRGLKALLA | 95 | 0.730 |
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.690 |
| ANNs+QM | 3 | AKPAARGVV | 87 | 0.680 |

| | | | | |
|----------------|---|-----------|-----|-------|
| ANNs+QM | 4 | CEEKAEKLA | 285 | 0.680 |
|----------------|---|-----------|-----|-------|

| ALLELE: HLA-Cw*0301 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 2.015 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | KALLATVVL | 99 | 3.689 |
| QM | 2 | GVVRGLKAL | 93 | 3.584 |
| QM | 3 | AVVGIGLGL | 108 | 2.996 |
| QM | 4 | GAVSREEVL | 135 | 2.996 |

| ALLELE: HLA-Cw*0401 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4.370 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | TTKAALQVL | 237 | 6.490 |
| QM | 2 | APSVASITL | 261 | 3.910 |
| QM | 3 | SDPTTKAAL | 234 | 3.760 |
| QM | 4 | VQRQYPSAL | 177 | 2.430 |

| ALLELE: HLA-Cw*0602 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.482 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VVRGLKALL | 94 | 1.792 |
| QM | 2 | GLKALLATV | 97 | 1.792 |
| QM | 3 | AVVGIGLGL | 108 | 1.792 |
| QM | 4 | SVASITLTL | 263 | 1.792 |

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

| Threshold for 4 % with score: 1.212 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SDPTTKAAL | 234 | 1.058 |
| QM | 2 | AARGVVRGL | 90 | 0.971 |
| QM | 3 | VLAVVGIGL | 106 | 0.875 |
| QM | 4 | SVASITLTL | 263 | 0.875 |

| ALLELE: H2-Db | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | SDPTTKAAL | 234 | 0.920 |
| ANNs+QM | 2 | AADEEAVTE | 17 | 0.780 |
| ANNs+QM | 3 | CEEKAEKLA | 285 | 0.760 |
| ANNs+QM | 4 | GVVRGLKAL | 93 | 0.710 |

| ALLELE: H2-Dd | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 11.800 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VGRIAAPSV | 256 | 13.890 |
| QM | 2 | SDPTTKAAL | 234 | 12.320 |
| QM | 3 | GAVSREEVL | 135 | 12.240 |
| QM | 4 | PGPSDPTTK | 231 | 12.200 |

| ALLELE: H2-Kb | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APSVASITL | 261 | 0.990 |
| ANNs+QM | 2 | VVRGLKALL | 94 | 0.920 |
| ANNs+QM | 3 | AADEEAVTE | 17 | 0.880 |

| | | | | |
|----------------|---|-----------|----|-------|
| ANNs+QM | 4 | AARGVVRGL | 90 | 0.830 |
|----------------|---|-----------|----|-------|

| ALLELE: H2-Kd | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | SDPTTKAAL | 234 | 0.990 |
| ANNs+QM | 2 | VQRQYPSAL | 177 | 0.980 |
| ANNs+QM | 3 | AARGVVRGL | 90 | 0.960 |
| ANNs+QM | 4 | ARGVVRGLK | 91 | 0.950 |

| ALLELE: H2-Kk | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 1.609 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DEEAVTEPL | 19 | 4.382 |
| QM | 2 | NEDPQIERV | 5 | 3.912 |
| QM | 3 | EEKAEKLAA | 286 | 3.689 |
| QM | 4 | CEEKAEKLA | 285 | 2.996 |

| ALLELE: H2-Ld | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | APSVASITL | 261 | 1.000 |
| ANNs+QM | 2 | KPAARGVVR | 88 | 0.660 |
| ANNs+QM | 3 | KALLATVVL | 99 | 0.260 |
| ANNs+QM | 4 | RCEEKAEKL | 284 | 0.230 |

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

| Threshold for 4 % with score: 9.260 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SDPTTKAAL | 234 | 11.840 |
| QM | 2 | TTKAALQVL | 237 | 10.780 |
| QM | 3 | VVRGLKALL | 94 | 10.110 |
| QM | 4 | GLKALLATV | 97 | 10.060 |

| ALLELE: H-2Qa | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 6.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | VLAVVGIGL | 106 | 13.840 |
| QM | 2 | VQRQYPSAL | 177 | 9.800 |
| QM | 3 | EVASQVGRI | 251 | 7.000 |
| QM | 4 | DEEAVTEPL | 19 | 6.920 |

| ALLELE: HLA-B*2706 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 5.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | RCEEKAEKL | 284 | 6.000 |
| QM | 2 | GRIAAPPSVA | 257 | 4.220 |
| QM | 3 | SEQNPAKPA | 82 | 4.000 |
| QM | 4 | GVVRGLKAL | 93 | 3.580 |

| ALLELE: HLA-B35 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 8.350 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | APSVASITL | 261 | 13.790 |
| QM | 2 | RCEEKAEKL | 284 | 11.790 |
| QM | 3 | VLAVVGIGL | 106 | 9.630 |

| | | | | |
|-----------|---|-----------|-----|-------|
| QM | 4 | AVVGIGLGL | 108 | 9.050 |
|-----------|---|-----------|-----|-------|

| ALLELE: Mamu-A*01 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.650 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | SVASITLTL | 263 | 5.120 |
| QM | 2 | TAIEQARRA | 63 | 3.170 |
| QM | 3 | APSVASITL | 261 | 3.070 |
| QM | 4 | TKAALQVLT | 238 | 1.980 |

| ALLELE: HLA-A*0204 | | | | |
|--------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 12.070 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | ALLATVVLA | 100 | 18.740 |
| QM | 2 | VLAVVGIGL | 106 | 17.460 |
| QM | 3 | GLKALLATV | 97 | 15.670 |
| QM | 4 | KALLATVVL | 99 | 15.610 |

| ALLELE: HLA-B*2703 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Threshold for 4 % with score: 5.130 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | ARRERAERR | 48 | 7.780 |
| QM | 2 | GRIAAPSVVA | 257 | 7.210 |
| QM | 3 | VRGLKALLA | 95 | 5.070 |
| QM | 4 | ARGVVRGLK | 91 | 4.730 |

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

| Threshold for 4 % with score: 8.790 | | | | |
|-------------------------------------|------|------------|-------------|---------------|
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | GRIAAPSV A | 257 | 13.660 |
| QM | 2 | VQRQYPSAL | 177 | 13.600 |
| QM | 3 | VVRGLKALL | 94 | 11.680 |
| QM | 4 | APSVASITL | 261 | 10.800 |

| ALLELE: HLA-B*2902 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 7.750 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | DEEAVTEPL | 19 | 10.980 |
| QM | 2 | SDPTTKAAL | 234 | 9.030 |
| QM | 3 | AARGVVRGL | 90 | 7.700 |
| QM | 4 | TVVLAVVGI | 104 | 7.350 |

| ALLELE: HLA-A*3301 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 3.840 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | LLQIDTQQV | 154 | 1.760 |
| QM | 2 | GLKALLATV | 97 | 1.520 |
| QM | 3 | QARRAAKRR | 67 | 1.170 |
| QM | 4 | ARGVVRGLK | 91 | 1.160 |

| ALLELE: HLA-B44 | | | | |
|-------------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4.900 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| QM | 1 | AERRAAQAR | 53 | 11.470 |
| QM | 2 | EKAEKLAA | 286 | 9.570 |
| QM | 3 | NEDPQIERV | 5 | 5.580 |

| | | | | |
|-----------|---|-----------|-----|-------|
| QM | 4 | AVVGIGLGL | 108 | 5.110 |
|-----------|---|-----------|-----|-------|

| ALLELE: HLA-A*6801 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | KPAARGVVR | 88 | 0.920 |
| ANNs+QM | 2 | EVASQVGRI | 251 | 0.890 |
| ANNs+QM | 3 | QARRAAKRR | 67 | 0.870 |
| ANNs+QM | 4 | AERRAAQAR | 53 | 0.860 |

| ALLELE: HLA-A*6802 | | | | |
|---------------------------------|------|-----------|-------------|---------------|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| ANNs+QM | 1 | TVVLAVVGI | 104 | 1.000 |
| ANNs+QM | 2 | GAVSREEVL | 135 | 0.970 |
| ANNs+QM | 3 | VVRGLKALL | 94 | 0.960 |
| ANNs+QM | 4 | IVERVPVVV | 189 | 0.960 |