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

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| | |
|---|---|
| Antigen Name | Untitled |
| Scanned on | Fri Mar 26 23:55:55 2010 |
| Length of input sequence | 270 amino acids |
| Number of nonamers from input sequence | 262 |
| 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 |

<table>
<tr><th colspan="5">ALLELE: HLA-A1</th></tr>
<tr><td colspan="5">Threshold for .5 % with score: .5</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td><b>ANNs+QM</b></td><td>1</td><td>GTDLLAKTL</td><td>177</td><td>0.790</td></tr>
<tr><td><b>ANNs+QM</b></td><td>2</td><td>ADAGARLTL</td><td>43</td><td>0.310</td></tr>
<tr><td><b>ANNs+QM</b></td><td>3</td><td>SKAGTDLLA</td><td>174</td><td>0.310</td></tr>
<tr><td><b>ANNs+QM</b></td><td>4</td><td>ALADAGARL</td><td>41</td><td>0.290</td></tr>
</table>

**ALLELE: HLA-A2**

Threshold for .5 % with score: .5

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | ALADAGARL | 41 | 1.000 |
| **ANNs+QM** | 2 | AALGRYGRL | 90 | 0.800 |
| **ANNs+QM** | 3 | ADAGARLTL | 43 | 0.450 |
| **ANNs+QM** | 4 | ILITGATGS | 25 | 0.150 |

**ALLELE: HLA-A*0201**

Threshold for .5 % with score: .5

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | ALADAGARL | 41 | 1.000 |
| **ANNs+QM** | 2 | FVGALIYLL | 241 | 1.000 |
| **ANNs+QM** | 3 | VVTCRPDSL | 73 | 0.940 |
| **ANNs+QM** | 4 | LVSSVRGGL | 154 | 0.450 |

**ALLELE: HLA-A*0202**

Threshold for .5 % with score: .5

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | ALADAGARL | 41 | 1.000 |
| **ANNs+QM** | 2 | LITGATGSL | 26 | 0.980 |
| **ANNs+QM** | 3 | ILITGATGS | 25 | 0.970 |
| **ANNs+QM** | 4 | ADAGARLTL | 43 | 0.630 |

**ALLELE: HLA-A*0203**

Threshold for .5 % with score: .5

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | SKAGTDLLA | 174 | 0.980 |
| **ANNs+QM** | 2 | ALADAGARL | 41 | 0.970 |
| **ANNs+QM** | 3 | ADAGARLTL | 43 | 0.640 |
| **ANNs+QM** | 4 | GNSAGLAEL | 54 | 0.480 |

**ALLELE: HLA-A*0206**

Threshold for .5 % with score: .5

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | VVTCRPDSL | 73 | 1.000 |
| **ANNs+QM** | 2 | ALADAGARL | 41 | 0.990 |
| **ANNs+QM** | 3 | RLTLAGGNS | 48 | 0.460 |
| **ANNs+QM** | 4 | EEMALAQQV | 2 | 0.410 |

**ALLELE: HLA-A*0205**

Threshold for 4 % with score: 5.950

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | ALADAGARL | 41 | 14.840 |
| **QM** | 2 | ADAGARLTL | 43 | 11.160 |
| **QM** | 3 | GHGIRVNAL | 191 | 8.400 |
| **QM** | 4 | AARALADAG | 38 | 8.230 |

**ALLELE: HLA-A*1101**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | MFTDDPKGR | 212 | 0.910 |
| **ANNs+QM** | 2 | GSLGRVAAR | 32 | 0.680 |
| **ANNs+QM** | 3 | RLTLAGGNS | 48 | 0.660 |
| **ANNs+QM** | 4 | EAALGRYGR | 89 | 0.360 |

**ALLELE: HLA-A11**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | RALADAGAR | 40 | 1.000 |
| **ANNs+QM** | 2 | GSLGRVAAR | 32 | 0.850 |
| **ANNs+QM** | 3 | MFTDDPKGR | 212 | 0.850 |
| **ANNs+QM** | 4 | LVNGAGIDD | 62 | 0.710 |

**ALLELE: HLA-A24**

Threshold for 4 % with score: 7.670

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | AQQVPNLGL | 7 | 10.560 |
| **QM** | 2 | GHGIRVNAL | 191 | 9.960 |
| **QM** | 3 | AELVNGAGI | 60 | 8.860 |
| **QM** | 4 | ALADAGARL | 41 | 5.310 |

**ALLELE: HLA-A*2402**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | MFTDDPKGR | 212 | 0.850 |
| **ANNs+QM** | 2 | AELVNGAGI | 60 | 0.580 |
| **ANNs+QM** | 3 | AQQVPNLGL | 7 | 0.420 |
| **ANNs+QM** | 4 | LAGGNSAGL | 51 | 0.300 |

**ALLELE: HLA-A3**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | RALADAGAR | 40 | 0.970 |
| **ANNs+QM** | 2 | SAYCPSKAG | 169 | 0.970 |
| **ANNs+QM** | 3 | RVAARALAD | 36 | 0.950 |
| **ANNs+QM** | 4 | GSLGRVAAR | 32 | 0.890 |

**ALLELE: HLA-A*3101**

Threshold for 4 % with score: -1.609

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | RALADAGAR | 40 | 0.182 |
| **QM** | 2 | EAALGRYGR | 89 | -1.204 |
| **QM** | 3 | MFTDDPKGR | 212 | -1.204 |

**ALLELE: HLA-A31**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | VRGAWLVCR | 129 | 0.980 |
| **ANNs+QM** | 2 | EAALGRYGR | 89 | 0.950 |
| **ANNs+QM** | 3 | PSKAGTDLL | 173 | 0.940 |
| **ANNs+QM** | 4 | FVGALIYLL | 241 | 0.900 |

**ALLELE: HLA-A*0301**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | ATGSLGRVA | 30 | 0.950 |
| **ANNs+QM** | 2 | ADAQQMVEA | 82 | 0.950 |
| **ANNs+QM** | 3 | ALADAGARL | 41 | 0.880 |
| **ANNs+QM** | 4 | AELVNGAGI | 60 | 0.850 |

**ALLELE: HLA-A*3302**

Threshold for 4 % with score: -0.105

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | GSLGRVAAR | 32 | 2.708 |
| **QM** | 2 | EAALGRYGR | 89 | 2.197 |
| **QM** | 3 | MFTDDPKGR | 212 | 1.099 |

**ALLELE: HLA-A68.1**

Threshold for 4 % with score: 1.609

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | GSLGRVAAR | 32 | 3.401 |
| **QM** | 2 | EAALGRYGR | 89 | 3.401 |
| **QM** | 3 | RALADAGAR | 40 | 2.303 |
| **QM** | 4 | FVGALIYLL | 241 | 2.079 |

**ALLELE: HLA-A20 Cattle**

Threshold for 4 % with score: 3.401

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | SKAGTDLLA | 174 | 4.605 |
| **QM** | 2 | VRGAWLVCR | 129 | 4.382 |
| **QM** | 3 | GSLGRVAAR | 32 | 3.689 |
| **QM** | 4 | RALADAGAR | 40 | 3.689 |

**ALLELE: HLA-A2.1**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | ALADAGARL | 41 | 1.000 |
| **ANNs+QM** | 2 | ILITGATGS | 25 | 0.990 |
| **ANNs+QM** | 3 | GTDLLAKTL | 177 | 0.940 |
| **ANNs+QM** | 4 | CRAAGRVLL | 136 | 0.910 |

**ALLELE: HLA-B14**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | AALGRYGRL | 90 | 1.000 |
| **ANNs+QM** | 2 | CRAAGRVLL | 136 | 1.000 |
| **ANNs+QM** | 3 | GHGIRVNAL | 191 | 1.000 |
| **ANNs+QM** | 4 | ARALADAGA | 39 | 0.910 |

**ALLELE: HLA-B*2702**

Threshold for 4 % with score: 0.000

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | CRAAGRVLL | 136 | 4.094 |
| **QM** | 2 | ARALADAGA | 39 | 2.996 |
| **QM** | 3 | ARLTLAGGN | 47 | 2.303 |
| **QM** | 4 | AQQVPNLGL | 7 | 1.792 |

**ALLELE: HLA-B27**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | CRAAGRVLL | 136 | 0.890 |
| **ANNs+QM** | 2 | ARLTLAGGN | 47 | 0.630 |
| **ANNs+QM** | 3 | VRGAWLVCR | 129 | 0.560 |
| **ANNs+QM** | 4 | RALADAGAR | 40 | 0.320 |

**ALLELE: HLA-B*2705**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | VRGAWLVCR | 129 | 1.000 |
| **ANNs+QM** | 2 | CRAAGRVLL | 136 | 0.990 |
| **ANNs+QM** | 3 | ARALADAGA | 39 | 0.980 |
| **ANNs+QM** | 4 | ARLTLAGGN | 47 | 0.980 |

**ALLELE: HLA-B*3501**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | EPEDFVGAL | 237 | 1.000 |
| **ANNs+QM** | 2 | CRAAGRVLL | 136 | 0.820 |
| **ANNs+QM** | 3 | FVGALIYLL | 241 | 0.140 |
| **ANNs+QM** | 4 | GTDLLAKTL | 177 | 0.120 |

**ALLELE: HLA-B*3701**

Threshold for 4 % with score: 0.405

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | ADAGARLTL | 43 | 3.689 |
| **QM** | 2 | AELVNGAGI | 60 | 2.303 |
| **QM** | 3 | CRAAGRVLL | 136 | 1.609 |
| **QM** | 4 | FVGALIYLL | 241 | 1.609 |

**ALLELE: HLA-B*3801**

Threshold for 4 % with score: 0.445

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | GHGIRVNAL | 191 | 3.401 |
| **QM** | 2 | EPEDFVGAL | 237 | 2.485 |
| **QM** | 3 | GTDLLAKTL | 177 | 1.361 |
| **QM** | 4 | LITGATGSL | 26 | 0.956 |

**ALLELE: HLA-B*3901**

Threshold for 4 % with score: 1.792

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | GHGIRVNAL | 191 | 4.905 |
| **QM** | 2 | EPEDFVGAL | 237 | 3.296 |
| **QM** | 3 | GTDLLAKTL | 177 | 2.197 |
| **QM** | 4 | CRAAGRVLL | 136 | 2.015 |

**ALLELE: HLA-B*3902**

Threshold for 4 % with score: 0.693

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | AQQVPNLGL | 7 | 2.996 |
| **QM** | 2 | LVSSVRGGL | 154 | 0.875 |
| **QM** | 3 | GTDLLAKTL | 177 | 0.875 |
| **QM** | 4 | EPEDFVGAL | 237 | 0.875 |

| **ALLELE: HLA-B40** | | | | |
|---|---|---|---|---|
| Threshold for 4 % with score: 0.000 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| **QM** | 1 | AEPEDFVGA | 236 | 3.689 |
| **QM** | 2 | AELVNGAGI | 60 | 2.773 |
| **QM** | 3 | ADAGARLTL | 43 | 2.303 |
| **QM** | 4 | ADAQQMVEA | 82 | 2.303 |

| **ALLELE: HLA-B*4403** | | | | |
|---|---|---|---|---|
| Threshold for 4 % with score: 0.405 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| **QM** | 1 | AELVNGAGI | 60 | 2.773 |
| **QM** | 2 | EEMALAQQV | 2 | 2.485 |
| **QM** | 3 | AEPEDFVGA | 236 | 2.079 |
| **QM** | 4 | ADAGARLTL | 43 | 1.504 |

| **ALLELE: HLA-B*5101** | | | | |
|---|---|---|---|---|
| Threshold for 4 % with score: 4 | | | | |
| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
| **ANNs+QM** | 1 | YGRLDGVLV | 95 | 1.000 |
| **ANNs+QM** | 2 | YCPSKAGTD | 171 | 0.910 |
| **ANNs+QM** | 3 | GTDLLAKTL | 177 | 0.820 |
| **ANNs+QM** | 4 | RALADAGAR | 40 | 0.790 |

<table>
<tr><th colspan="5"><b>ALLELE: HLA-B*5102</b></th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 9.050</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td><b>QM</b></td><td>1</td><td>YGRLDGVLV</td><td>95</td><td>13.490</td></tr>
<tr><td><b>QM</b></td><td>2</td><td>QGQGGSVVL</td><td>146</td><td>6.060</td></tr>
<tr><td><b>QM</b></td><td>3</td><td>LGRVAARAL</td><td>34</td><td>5.920</td></tr>
<tr><td><b>QM</b></td><td>4</td><td>SAYCPSKAG</td><td>169</td><td>5.330</td></tr>
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<tr><th colspan="5"><b>ALLELE: HLA-B*5103</b></th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 9.280</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td><b>QM</b></td><td>1</td><td>YGRLDGVLV</td><td>95</td><td>13.490</td></tr>
<tr><td><b>QM</b></td><td>2</td><td>QGQGGSVVL</td><td>146</td><td>6.060</td></tr>
<tr><td><b>QM</b></td><td>3</td><td>LGRVAARAL</td><td>34</td><td>5.920</td></tr>
<tr><td><b>QM</b></td><td>4</td><td>SAYCPSKAG</td><td>169</td><td>5.330</td></tr>
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<tr><th colspan="5"><b>ALLELE: HLA-B*5201</b></th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 1.974</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td><b>QM</b></td><td>1</td><td>QGQGGSVVL</td><td>146</td><td>2.803</td></tr>
<tr><td><b>QM</b></td><td>2</td><td>EEMALAQQV</td><td>2</td><td>0.971</td></tr>
<tr><td><b>QM</b></td><td>3</td><td>AQQVPNLGL</td><td>7</td><td>0.971</td></tr>
<tr><td><b>QM</b></td><td>4</td><td>AELVNGAGI</td><td>60</td><td>0.875</td></tr>
</table>

**ALLELE: HLA-B*5301**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | EPEDFVGAL | 237 | 1.000 |
| **ANNs+QM** | 2 | YCPSKAGTD | 171 | 0.500 |
| **ANNs+QM** | 3 | VCRAAGRVL | 135 | 0.430 |
| **ANNs+QM** | 4 | ALADAGARL | 41 | 0.360 |

**ALLELE: HLA-B*5401**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | EPEDFVGAL | 237 | 1.000 |
| **ANNs+QM** | 2 | VCRAAGRVL | 135 | 0.630 |
| **ANNs+QM** | 3 | YCPSKAGTD | 171 | 0.580 |
| **ANNs+QM** | 4 | ATGSLGRVA | 30 | 0.560 |

**ALLELE: HLA-B*51**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | EPEDFVGAL | 237 | 0.880 |
| **ANNs+QM** | 2 | YCPSKAGTD | 171 | 0.850 |
| **ANNs+QM** | 3 | VCRAAGRVL | 135 | 0.500 |
| **ANNs+QM** | 4 | VVTCRPDSL | 73 | 0.490 |

**ALLELE: HLA-B*5801**

Threshold for 4 % with score: -0.223

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | GTDLLAKTL | 177 | 1.289 |
| **QM** | 2 | ATGSLGRVA | 30 | 1.099 |
| **QM** | 3 | LTLAGGNSA | 49 | 0.788 |
| **QM** | 4 | AALGRYGRL | 90 | 0.095 |

**ALLELE: HLA-B60**

Threshold for 4 % with score: 1.386

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | ADAGARLTL | 43 | 4.382 |
| **QM** | 2 | EEMALAQQV | 2 | 2.963 |
| **QM** | 3 | AELVNGAGI | 60 | 2.773 |
| **QM** | 4 | AALGRYGRL | 90 | 2.175 |

**ALLELE: HLA-B61**

Threshold for 4 % with score: 0.000

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | EEMALAQQV | 2 | 4.382 |
| **QM** | 2 | AEPEDFVGA | 236 | 2.996 |
| **QM** | 3 | AELVNGAGI | 60 | 2.773 |
| **QM** | 4 | ADAQQMVEA | 82 | 1.609 |

<table>
<tr><th colspan="5">ALLELE: HLA-B62</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 0.693</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>**QM**</td><td>1</td><td>AQQVPNLGL</td><td>7</td><td>1.569</td></tr>
<tr><td>**QM**</td><td>2</td><td>ALADAGARL</td><td>41</td><td>0.788</td></tr>
<tr><td>**QM**</td><td>3</td><td>ILITGATGS</td><td>25</td><td>0.222</td></tr>
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<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>EPEDFVGAL</td><td>237</td><td>1.000</td></tr>
<tr><td>**ANNs+QM**</td><td>2</td><td>FVGALIYLL</td><td>241</td><td>1.000</td></tr>
<tr><td>**ANNs+QM**</td><td>3</td><td>VCRAAGRVL</td><td>135</td><td>0.990</td></tr>
<tr><td>**ANNs+QM**</td><td>4</td><td>AQQVPNLGL</td><td>7</td><td>0.880</td></tr>
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<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>VCRAAGRVL</td><td>135</td><td>0.860</td></tr>
<tr><td>**ANNs+QM**</td><td>2</td><td>CRAAGRVLL</td><td>136</td><td>0.850</td></tr>
<tr><td>**ANNs+QM**</td><td>3</td><td>EPEDFVGAL</td><td>237</td><td>0.750</td></tr>
<tr><td>**ANNs+QM**</td><td>4</td><td>TEMAVEDFD</td><td>114</td><td>0.470</td></tr>
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<tr><th colspan="5">ALLELE: HLA-B8</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>VCRAAGRVL</td><td>135</td><td>0.740</td></tr>
<tr><td>ANNs+QM</td><td>2</td><td>SKAGTDLLA</td><td>174</td><td>0.690</td></tr>
<tr><td>ANNs+QM</td><td>3</td><td>EAALGRYGR</td><td>89</td><td>0.660</td></tr>
<tr><td>ANNs+QM</td><td>4</td><td>ILITGATGS</td><td>25</td><td>0.650</td></tr>
</table>

<table>
<tr><th colspan="5">ALLELE: HLA-Cw*0301</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 2.015</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>QM</td><td>1</td><td>AALGRYGRL</td><td>90</td><td>5.298</td></tr>
<tr><td>QM</td><td>2</td><td>AELVNGAGI</td><td>60</td><td>1.792</td></tr>
<tr><td>QM</td><td>3</td><td>LAGGNSAGL</td><td>51</td><td>1.569</td></tr>
<tr><td>QM</td><td>4</td><td>AQQVPNLGL</td><td>7</td><td>0.693</td></tr>
</table>

<table>
<tr><th colspan="5">ALLELE: HLA-Cw*0401</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 4.370</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>QM</td><td>1</td><td>ALADAGARL</td><td>41</td><td>12.700</td></tr>
<tr><td>QM</td><td>2</td><td>EPEDFVGAL</td><td>237</td><td>11.160</td></tr>
<tr><td>QM</td><td>3</td><td>VCRAAGRVL</td><td>135</td><td>8.430</td></tr>
<tr><td>QM</td><td>4</td><td>VVTCRPDSL</td><td>73</td><td>5.230</td></tr>
</table>

**ALLELE: HLA-Cw*0602**

Threshold for 4 % with score: 1.482

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | EPEDFVGAL | 237 | 2.580 |
| **QM** | 2 | FVGALIYLL | 241 | 2.580 |
| **QM** | 3 | GTDLLAKTL | 177 | 1.887 |
| **QM** | 4 | GHGIRVNAL | 191 | 1.482 |

**ALLELE: HLA-Cw*0702**

Threshold for 4 % with score: 1.212

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | EPEDFVGAL | 237 | 2.493 |
| **QM** | 2 | FVGALIYLL | 241 | 1.569 |
| **QM** | 3 | ADAGARLTL | 43 | 0.875 |
| **QM** | 4 | CRAAGRVLL | 136 | 0.875 |

**ALLELE: H2-Db**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | LAGGNSAGL | 51 | 1.000 |
| **ANNs+QM** | 2 | AELVNGAGI | 60 | 1.000 |
| **ANNs+QM** | 3 | CRAAGRVLL | 136 | 0.940 |
| **ANNs+QM** | 4 | GHGIRVNAL | 191 | 0.770 |

**ALLELE: H2-Dd**

Threshold for 4 % with score: 11.800

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | LGRVAARAL | 34 | 19.460 |
| **QM** | 2 | GHGIRVNAL | 191 | 14.410 |
| **QM** | 3 | GGNSAGLAE | 53 | 11.980 |
| **QM** | 4 | ALADAGARL | 41 | 11.510 |

**ALLELE: H2-Kb**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | AALGRYGRL | 90 | 0.990 |
| **ANNs+QM** | 2 | LGRVAARAL | 34 | 0.980 |
| **ANNs+QM** | 3 | ALADAGARL | 41 | 0.900 |
| **ANNs+QM** | 4 | VCRAAGRVL | 135 | 0.890 |

**ALLELE: H2-Kd**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | AQQVPNLGL | 7 | 0.930 |
| **ANNs+QM** | 2 | ILITGATGS | 25 | 0.900 |
| **ANNs+QM** | 3 | LAGGNSAGL | 51 | 0.900 |
| **ANNs+QM** | 4 | AELVNGAGI | 60 | 0.900 |

**ALLELE: H2-Kk**

Threshold for 4 % with score: 1.609

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | AELVNGAGI | 60 | 6.215 |
| **QM** | 2 | EEMALAQQV | 2 | 5.298 |
| **QM** | 3 | AEPEDFVGA | 236 | 2.303 |
| **QM** | 4 | ADAGARLTL | 43 | 1.386 |

**ALLELE: H2-Ld**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | CRAAGRVLL | 136 | 0.960 |
| **ANNs+QM** | 2 | VCRAAGRVL | 135 | 0.640 |
| **ANNs+QM** | 3 | YCPSKAGTD | 171 | 0.620 |
| **ANNs+QM** | 4 | AQQVPNLGL | 7 | 0.530 |

**ALLELE: HLA-G**

Threshold for 4 % with score: 9.260

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | ALADAGARL | 41 | 15.510 |
| **QM** | 2 | FVGALIYLL | 241 | 12.780 |
| **QM** | 3 | ADAGARLTL | 43 | 11.110 |
| **QM** | 4 | CRAAGRVLL | 136 | 10.640 |

<table>
<tr><th colspan="5">**ALLELE: H-2Qa**</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 6.000</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>**QM**</td><td>1</td><td>AELVNGAGI</td><td>60</td><td>8.910</td></tr>
<tr><td>**QM**</td><td>2</td><td>AQQVPNLGL</td><td>7</td><td>5.800</td></tr>
<tr><td>**QM**</td><td>3</td><td>LVSSVRGGL</td><td>154</td><td>4.880</td></tr>
<tr><td>**QM**</td><td>4</td><td>LGRVAARAL</td><td>34</td><td>3.800</td></tr>
</table>

<table>
<tr><th colspan="5">**ALLELE: HLA-B*2706**</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 5.000</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>**QM**</td><td>1</td><td>ARALADAGA</td><td>39</td><td>4.600</td></tr>
<tr><td>**QM**</td><td>2</td><td>MFTDDPKGR</td><td>212</td><td>4.420</td></tr>
<tr><td>**QM**</td><td>3</td><td>FVGALIYLL</td><td>241</td><td>4.000</td></tr>
<tr><td>**QM**</td><td>4</td><td>EPEDFVGAL</td><td>237</td><td>3.670</td></tr>
</table>

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<tr><th colspan="5">**ALLELE: HLA-B35**</th></tr>
<tr><td colspan="5">Threshold for 4 % with score: 8.350</td></tr>
<tr><td>Prediction method</td><td>Rank</td><td>Sequence</td><td>Residue No.</td><td>Peptide Score</td></tr>
<tr><td>**QM**</td><td>1</td><td>EPEDFVGAL</td><td>237</td><td>12.600</td></tr>
<tr><td>**QM**</td><td>2</td><td>AALGRYGRL</td><td>90</td><td>8.640</td></tr>
<tr><td>**QM**</td><td>3</td><td>VVTCRPDSL</td><td>73</td><td>7.720</td></tr>
<tr><td>**QM**</td><td>4</td><td>AQQVPNLGL</td><td>7</td><td>6.710</td></tr>
</table>

**ALLELE: Mamu-A*01**

Threshold for 4 % with score: 3.650

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | SAYCPSKAG | 169 | 5.350 |
| **QM** | 2 | EPEDFVGAL | 237 | 5.250 |
| **QM** | 3 | FVGALIYLL | 241 | 2.120 |
| **QM** | 4 | AVMDANVRG | 123 | 1.910 |

**ALLELE: HLA-A*0204**

Threshold for 4 % with score: 12.070

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | ALADAGARL | 41 | 17.320 |
| **QM** | 2 | GNSAGLAEL | 54 | 15.870 |
| **QM** | 3 | ADAGARLTL | 43 | 14.340 |
| **QM** | 4 | CRAAGRVLL | 136 | 13.870 |

**ALLELE: HLA-B*2703**

Threshold for 4 % with score: 5.130

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | ARALADAGA | 39 | 7.130 |
| **QM** | 2 | CRAAGRVLL | 136 | 6.730 |
| **QM** | 3 | VRGAWLVCR | 129 | 6.170 |
| **QM** | 4 | ALADAGARL | 41 | 1.850 |

**ALLELE: HLA-B*2704**

Threshold for 4 % with score: 8.790

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | VRGAWLVCR | 129 | 16.800 |
| **QM** | 2 | CRAAGRVLL | 136 | 14.430 |
| **QM** | 3 | GNSAGLAEL | 54 | 14.020 |
| **QM** | 4 | VVTCRPDSL | 73 | 12.670 |

**ALLELE: HLA-B*2902**

Threshold for 4 % with score: 7.750

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | LVSSVRGGL | 154 | 10.650 |
| **QM** | 2 | EPEDFVGAL | 237 | 9.700 |
| **QM** | 3 | AEPEDFVGA | 236 | 8.200 |
| **QM** | 4 | EAALGRYGR | 89 | 5.750 |

**ALLELE: HLA-A*3301**

Threshold for 4 % with score: 3.840

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | LAGGNSAGL | 51 | 2.910 |
| **QM** | 2 | GSLGRVAAR | 32 | 2.450 |
| **QM** | 3 | FVGALIYLL | 241 | 2.360 |
| **QM** | 4 | SAYCPSKAG | 169 | 1.530 |

**ALLELE: HLA-B44**

Threshold for 4 % with score: 4.900

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **QM** | 1 | AELVNGAGI | 60 | 8.090 |
| **QM** | 2 | EEMALAQQV | 2 | 7.030 |
| **QM** | 3 | GGNSAGLAE | 53 | 6.560 |
| **QM** | 4 | ADAGARLTL | 43 | 4.760 |

**ALLELE: HLA-A*6801**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | GSLGRVAAR | 32 | 0.980 |
| **ANNs+QM** | 2 | RALADAGAR | 40 | 0.970 |
| **ANNs+QM** | 3 | SAYCPSKAG | 169 | 0.970 |
| **ANNs+QM** | 4 | RVAARALAD | 36 | 0.950 |

**ALLELE: HLA-A*6802**

Threshold for 4 % with score: 4

| Prediction method | Rank | Sequence | Residue No. | Peptide Score |
|---|---|---|---|---|
| **ANNs+QM** | 1 | ILITGATGS | 25 | 0.980 |
| **ANNs+QM** | 2 | ARALADAGA | 39 | 0.980 |
| **ANNs+QM** | 3 | EAALGRYGR | 89 | 0.960 |
| **ANNs+QM** | 4 | YGRLDGVLV | 95 | 0.950 |