# MHC Class-II Binding Peptide Prediction Results

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| HELP | HOME | MHC & Prediction Algorithm |

## INPUT & PARAMETER INFORMATION

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| Antigen Name | test |
| Scanned on | Tue Feb 23 17:14:00 2010 |
| Length of input sequence | 99 amino acids |
| Number of nanomers from input sequence | 91 |
| Number of nanomers with obligatory P1 anchor residue | 18 |
| Threshold setting | 3 |
| Number of alleles in query | 51 |
| Number of top scorers to be displayed | 9 |

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|---|---|---|
| ALLELE: DRB1_0101 | Threshold for 3 % with score: 0.14 | Highest Score achievable by any peptide: 6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | WRGAAGTAA | 42 | 2.1900 | 36.50 |
| 2 | VRFQEAANK | 55 | 0.4000 | 6.67 |
| 3 | VVRFQEAAN | 54 | -1.7200 | 0 |
| 4 | MKTDAATLA | 3 | -2.2100 | 0 |
| 5 | LQGQWRGAA | 38 | -2.4000 | 0 |
| 6 | FERISGDLK | 17 | -2.7000 | 0 |
| 7 | FQEAANKQK | 57 | -3.0000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0102 | Threshold for 3 % with score: 0.7 | Highest Score achievable by any peptide: 6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|

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|---|---|---|---|---|
| 1 | VRFQEAANK | 55 | 1.4000 | 23.33 |
| 2 | WRGAAGTAA | 42 | 1.1900 | 19.83 |
| 3 | IRQAGVQYS | 75 | 1.0000 | 16.67 |
| 4 | VVRFQEAAN | 54 | -0.7200 | 0 |
| 5 | MKTDAATLA | 3 | -1.2100 | 0 |
| 6 | LQGQWRGAA | 38 | -1.4000 | 0 |
| 7 | LAQEAGNFE | 10 | -2.5000 | 0 |
| 8 | VQYSRADEE | 80 | -2.6000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0301 | Threshold for 3 % with score: 2.96 | Highest Score achievable by any peptide: 9.5 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.4000 | 46.32 |
| 2 | ISGDLKTQI | 20 | 4.0000 | 42.11 |
| 3 | MKTDAATLA | 3 | 3.3000 | 34.74 |
| 4 | VRFQEAANK | 55 | 2.8000 | 29.47 |
| 5 | LQGQWRGAA | 38 | 2.5000 | 26.32 |
| 6 | VQYSRADEE | 80 | 1.8000 | 18.95 |
| 7 | ISTNIRQAG | 71 | 1.2000 | 12.63 |
| 8 | WRGAAGTAA | 42 | 0.6000 | 6.32 |

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|---|---|---|
| ALLELE: DRB1_0305 | Threshold for 3 % with score: 1.7 | Highest Score achievable by any peptide: 9.1 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.0000 | 32.97 |
| 2 | MKTDAATLA | 3 | 2.3000 | 25.27 |
| 3 | ISGDLKTQI | 20 | 2.1000 | 23.08 |
| 4 | VRFQEAANK | 55 | 1.7000 | 18.68 |
| 5 | WRGAAGTAA | 42 | 1.6000 | 17.58 |
| 6 | LQGQWRGAA | 38 | 1.5000 | 16.48 |
| 7 | FERISGDLK | 17 | -0.3000 | 0 |
| 8 | VQYSRADEE | 80 | -0.6000 | 0 |

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| ALLELE: DRB1_0306 | Threshold for 3 % with score: 2.08 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | MKTDAATLA | 3 | 3.3000 | 37.50 |
| 3 | ISGDLKTQI | 20 | 3.1000 | 35.23 |
| 4 | VRFQEAANK | 55 | 2.7000 | 30.68 |
| 5 | LQGQWRGAA | 38 | 1.1000 | 12.50 |
| 6 | VQYSRADEE | 80 | 0.7000 | 7.95 |
| 7 | WRGAAGTAA | 42 | 0.6000 | 6.82 |
| 8 | ISTNIRQAG | 71 | -0.1000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0307 | Threshold for 3 % with score: 2.08 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | MKTDAATLA | 3 | 3.3000 | 37.50 |
| 3 | ISGDLKTQI | 20 | 3.1000 | 35.23 |
| 4 | VRFQEAANK | 55 | 2.7000 | 30.68 |
| 5 | LQGQWRGAA | 38 | 1.1000 | 12.50 |
| 6 | VQYSRADEE | 80 | 0.7000 | 7.95 |
| 7 | WRGAAGTAA | 42 | 0.6000 | 6.82 |
| 8 | ISTNIRQAG | 71 | -0.1000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0308 | Threshold for 3 % with score: 2.08 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | MKTDAATLA | 3 | 3.3000 | 37.50 |
| 3 | ISGDLKTQI | 20 | 3.1000 | 35.23 |
| 4 | VRFQEAANK | 55 | 2.7000 | 30.68 |
| 5 | LQGQWRGAA | 38 | 1.1000 | 12.50 |

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|---|---|---|---|---|
| 6 | VQYSRADEE | 80 | 0.7000 | 7.95 |
| 7 | WRGAAGTAA | 42 | 0.6000 | 6.82 |
| 8 | ISTNIRQAG | 71 | -0.1000 | 0 |

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| ALLELE:<br>DRB1_0309 | Threshold for 3 % with score:<br>2.4 | Highest Score achievable by any peptide: 9.5 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.4000 | 35.79 |
| 2 | ISGDLKTQI | 20 | 3.0000 | 31.58 |
| 3 | MKTDAATLA | 3 | 2.3000 | 24.21 |
| 4 | VRFQEAANK | 55 | 1.8000 | 18.95 |
| 5 | WRGAAGTAA | 42 | 1.6000 | 16.84 |
| 6 | LQGQWRGAA | 38 | 1.5000 | 15.79 |
| 7 | VQYSRADEE | 80 | 0.8000 | 8.42 |
| 8 | ISTNIRQAG | 71 | 0.2000 | 2.11 |

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|---|---|---|
| ALLELE:<br>DRB1_0311 | Threshold for 3 % with score:<br>2.08 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | MKTDAATLA | 3 | 3.3000 | 37.50 |
| 3 | ISGDLKTQI | 20 | 3.1000 | 35.23 |
| 4 | VRFQEAANK | 55 | 2.7000 | 30.68 |
| 5 | LQGQWRGAA | 38 | 1.1000 | 12.50 |
| 6 | VQYSRADEE | 80 | 0.7000 | 7.95 |
| 7 | WRGAAGTAA | 42 | 0.6000 | 6.82 |
| 8 | ISTNIRQAG | 71 | -0.1000 | 0 |

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|---|---|---|
| ALLELE:<br>DRB1_0401 | Threshold for 3 % with score:<br>1.48 | Highest Score achievable by any peptide: 8.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|

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|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.8000 | 32.56 |
| 2 | VRFQEAANK | 55 | 2.5000 | 29.07 |
| 3 | MKTDAATLA | 3 | 1.4000 | 16.28 |
| 4 | WRGAAGTAA | 42 | 0.8000 | 9.30 |
| 5 | FQEAANKQK | 57 | 0.7000 | 8.14 |
| 6 | MAEMKTDAA | 0 | 0.3000 | 3.49 |
| 7 | VQYSRADEE | 80 | -0.2000 | 0 |
| 8 | FERISGDLK | 17 | -0.5000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0402 | Threshold for 3 % with score: 1.8 | Highest Score achievable by any peptide: 9.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.9000 | 51.04 |
| 2 | VRFQEAANK | 55 | 2.3000 | 23.96 |
| 3 | VVRFQEAAN | 54 | -0.7000 | 0 |
| 4 | MAEMKTDAA | 0 | -0.8000 | 0 |
| 5 | LDEISTNIR | 68 | -0.9200 | 0 |
| 6 | LKTQIDQVE | 24 | -1.0000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0404 | Threshold for 3 % with score: 1.8 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.6000 | 40.91 |
| 2 | VRFQEAANK | 55 | 2.7000 | 30.68 |
| 3 | MAEMKTDAA | 0 | 1.3000 | 14.77 |
| 4 | MKTDAATLA | 3 | 0.4000 | 4.55 |
| 5 | WRGAAGTAA | 42 | 0.3000 | 3.41 |
| 6 | LDEISTNIR | 68 | 0.2000 | 2.27 |
| 7 | IDQVESTAG | 28 | -0.4000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0405 | Threshold for 3 % with score: 2.0 | Highest Score achievable by any peptide: 9.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.6000 | 27.66 |
| 2 | WRGAAGTAA | 42 | 1.3000 | 13.83 |
| 3 | VVRFQEAAN | 54 | 1.0000 | 10.64 |
| 4 | VRFQEAANK | 55 | 1.0000 | 10.64 |
| 5 | VQYSRADEE | 80 | 0.4000 | 4.26 |
| 6 | MAEMKTDAA | 0 | 0.3000 | 3.19 |
| 7 | LKTQIDQVE | 24 | 0.1000 | 1.06 |
| 8 | IDQVESTAG | 28 | -0.1000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0408 | Threshold for 3 % with score: 1.2 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.6000 | 29.55 |
| 2 | VRFQEAANK | 55 | 1.7000 | 19.32 |
| 3 | WRGAAGTAA | 42 | 1.3000 | 14.77 |
| 4 | MAEMKTDAA | 0 | 0.3000 | 3.41 |
| 5 | FQEAANKQK | 57 | -0.3000 | 0 |
| 6 | MKTDAATLA | 3 | -0.6000 | 0 |
| 7 | LDEISTNIR | 68 | -0.8000 | 0 |
| 8 | VVRFQEAAN | 54 | -1.0000 | 0 |

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| ALLELE: DRB1_0410 | Threshold for 3 % with score: 2.6 | Highest Score achievable by any peptide: 9.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.6000 | 38.30 |
| 2 | VVRFQEAAN | 54 | 2.0000 | 21.28 |
| 3 | VRFQEAANK | 55 | 2.0000 | 21.28 |
| 4 | VQYSRADEE | 80 | 1.4000 | 14.89 |
| 5 | MAEMKTDAA | 0 | 1.3000 | 13.83 |
| 6 | LKTQIDQVE | 24 | 1.1000 | 11.70 |
| 7 | IDQVESTAG | 28 | 0.9000 | 9.57 |
| 8 | MKTDAATLA | 3 | 0.4000 | 4.26 |
| 9 | WRGAAGTAA | 42 | 0.3000 | 3.19 |

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| ALLELE:<br>DRB1_0421 | Threshold for 3 % with score:<br>2.3 | Highest Score achievable by any peptide: 9 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.2000 | 35.56 |
| 2 | VRFQEAANK | 55 | 2.6000 | 28.89 |
| 3 | MKTDAATLA | 3 | 1.4000 | 15.56 |
| 4 | VQYSRADEE | 80 | 1.2000 | 13.33 |
| 5 | WRGAAGTAA | 42 | 0.8000 | 8.89 |
| 6 | FQEAANKQK | 57 | 0.8000 | 8.89 |
| 7 | MAEMKTDAA | 0 | 0.3000 | 3.33 |
| 8 | LDEISTNIR | 68 | 0.3000 | 3.33 |

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| ALLELE:<br>DRB1_0423 | Threshold for 3 % with score:<br>1.68 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.6000 | 40.91 |
| 2 | VRFQEAANK | 55 | 2.7000 | 30.68 |
| 3 | MAEMKTDAA | 0 | 1.3000 | 14.77 |
| 4 | MKTDAATLA | 3 | 0.4000 | 4.55 |
| 5 | WRGAAGTAA | 42 | 0.3000 | 3.41 |
| 6 | LDEISTNIR | 68 | 0.2000 | 2.27 |
| 7 | IDQVESTAG | 28 | -0.4000 | 0 |

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|---|---|---|
| ALLELE:<br>DRB1_0426 | Threshold for 3 % with score:<br>1.6 | Highest Score achievable by any peptide: 8.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.8000 | 32.56 |
| 2 | VRFQEAANK | 55 | 2.5000 | 29.07 |
| 3 | MKTDAATLA | 3 | 1.4000 | 16.28 |
| 4 | WRGAAGTAA | 42 | 0.8000 | 9.30 |
| 5 | FQEAANKQK | 57 | 0.7000 | 8.14 |

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|---|---|---|---|---|
| 6 | MAEMKTDAA | 0 | 0.3000 | 3.49 |
| 7 | VQYSRADEE | 80 | -0.2000 | 0 |
| 8 | FERISGDLK | 17 | -0.5000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0701 | Threshold for 3 % with score: 4.1 | Highest Score achievable by any peptide: 11.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | WRGAAGTAA | 42 | 2.7000 | 23.28 |
| 2 | IRQAGVQYS | 75 | 2.1000 | 18.10 |
| 3 | VQYSRADEE | 80 | 0.9000 | 7.76 |
| 4 | ISGDLKTQI | 20 | 0.5000 | 4.31 |
| 5 | VESTAGSLQ | 31 | -0.4000 | 0 |
| 6 | IDQVESTAG | 28 | -0.5000 | 0 |
| 7 | MKTDAATLA | 3 | -0.6000 | 0 |
| 8 | VRFQEAANK | 55 | -0.6000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0703 | Threshold for 3 % with score: 4.0 | Highest Score achievable by any peptide: 11.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | WRGAAGTAA | 42 | 2.7000 | 23.28 |
| 2 | IRQAGVQYS | 75 | 2.1000 | 18.10 |
| 3 | VQYSRADEE | 80 | 0.9000 | 7.76 |
| 4 | ISGDLKTQI | 20 | 0.5000 | 4.31 |
| 5 | VESTAGSLQ | 31 | -0.4000 | 0 |
| 6 | IDQVESTAG | 28 | -0.5000 | 0 |
| 7 | MKTDAATLA | 3 | -0.6000 | 0 |
| 8 | VRFQEAANK | 55 | -0.6000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0801 | Threshold for 3 % with score: 1.8 | Highest Score achievable by any peptide: 8.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|

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|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 1.9000 | 22.09 |
| 2 | VVRFQEAAN | 54 | 1.5000 | 17.44 |
| 3 | LQGQWRGAA | 38 | -0.1000 | 0 |
| 4 | WRGAAGTAA | 42 | -0.7000 | 0 |
| 5 | VQYSRADEE | 80 | -1.1000 | 0 |
| 6 | ISTNIRQAG | 71 | -1.2000 | 0 |
| 7 | YSRADEEQQ | 82 | -2.1000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0802 | Threshold for 3 % with score: 1.0 | Highest Score achievable by any peptide: 8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 1.9000 | 23.75 |
| 2 | VRFQEAANK | 55 | 0.7000 | 8.75 |
| 3 | LQGQWRGAA | 38 | -0.1000 | 0 |
| 4 | VVRFQEAAN | 54 | -0.5000 | 0 |
| 5 | WRGAAGTAA | 42 | -0.7000 | 0 |
| 6 | FQEAANKQK | 57 | -1.7000 | 0 |
| 7 | FERISGDLK | 17 | -2.3000 | 0 |
| 8 | MAEMKTDAA | 0 | -2.4000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0804 | Threshold for 3 % with score: 1.6 | Highest Score achievable by any peptide: 8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.9000 | 36.25 |
| 2 | VRFQEAANK | 55 | 1.7000 | 21.25 |
| 3 | LQGQWRGAA | 38 | 0.9000 | 11.25 |
| 4 | VVRFQEAAN | 54 | 0.5000 | 6.25 |
| 5 | MAEMKTDAA | 0 | -1.4000 | 0 |
| 6 | ISTNIRQAG | 71 | -1.5000 | 0 |
| 7 | WRGAAGTAA | 42 | -1.7000 | 0 |
| 8 | VESTAGSLQ | 31 | -2.2000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0806 | Threshold for 3 % with score: 2.4 | Highest Score achievable by any peptide: 8.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.9000 | 33.72 |
| 2 | VVRFQEAAN | 54 | 2.5000 | 29.07 |
| 3 | VRFQEAANK | 55 | 1.0000 | 11.63 |
| 4 | LQGQWRGAA | 38 | 0.9000 | 10.47 |
| 5 | VQYSRADEE | 80 | -0.1000 | 0 |
| 6 | ISTNIRQAG | 71 | -0.2000 | 0 |
| 7 | MAEMKTDAA | 0 | -1.4000 | 0 |
| 8 | VESTAGSLQ | 31 | -1.4000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0813 | Threshold for 3 % with score: 1.9 | Highest Score achievable by any peptide: 8.7 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.9000 | 33.33 |
| 2 | WRGAAGTAA | 42 | 2.1000 | 24.14 |
| 3 | VRFQEAANK | 55 | 0.7000 | 8.05 |
| 4 | MKTDAATLA | 3 | -0.5000 | 0 |
| 5 | VVRFQEAAN | 54 | -0.5000 | 0 |
| 6 | ISGDLKTQI | 20 | -0.7000 | 0 |
| 7 | LQGQWRGAA | 38 | -0.8000 | 0 |
| 8 | FERISGDLK | 17 | -1.1000 | 0 |

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|---|---|---|
| ALLELE: DRB1_0817 | Threshold for 3 % with score: 2.8 | Highest Score achievable by any peptide: 10.1 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.0000 | 19.80 |
| 2 | VVRFQEAAN | 54 | 1.5000 | 14.85 |
| 3 | WRGAAGTAA | 42 | 0.4000 | 3.96 |
| 4 | YSRADEEQQ | 82 | -1.0000 | 0 |
| 5 | ISTNIRQAG | 71 | -1.1000 | 0 |
| 6 | VQYSRADEE | 80 | -1.4000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1101 | Threshold for 3 % with score: 1.1 | Highest Score achievable by any peptide: 8.3 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.0000 | 24.10 |
| 2 | VRFQEAANK | 55 | 1.3000 | 15.66 |
| 3 | LQGQWRGAA | 38 | 0.6000 | 7.23 |
| 4 | WRGAAGTAA | 42 | 0.4000 | 4.82 |
| 5 | VVRFQEAAN | 54 | -0.6000 | 0 |
| 6 | FQEAANKQK | 57 | -1.1000 | 0 |
| 7 | YSRADEEQQ | 82 | -1.8000 | 0 |
| 8 | FERISGDLK | 17 | -2.0000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1102 | Threshold for 3 % with score: 1.8 | Highest Score achievable by any peptide: 8.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.7000 | 44.05 |
| 2 | VRFQEAANK | 55 | 3.3000 | 39.29 |
| 3 | LQGQWRGAA | 38 | 1.5000 | 17.86 |
| 4 | VVRFQEAAN | 54 | 0.8000 | 9.52 |
| 5 | WRGAAGTAA | 42 | -0.2000 | 0 |
| 6 | ISTNIRQAG | 71 | -0.6000 | 0 |
| 7 | MAEMKTDAA | 0 | -1.1000 | 0 |
| 8 | MKTDAATLA | 3 | -1.2000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1104 | Threshold for 3 % with score: 2.0 | Highest Score achievable by any peptide: 8.3 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.0000 | 36.14 |
| 2 | VRFQEAANK | 55 | 2.3000 | 27.71 |
| 3 | LQGQWRGAA | 38 | 1.6000 | 19.28 |
| 4 | VVRFQEAAN | 54 | 0.4000 | 4.82 |

| | | | | |
|---|---|---|---|---|
| 5 | WRGAAGTAA | 42 | -0.6000 | 0 |
| 6 | ISTNIRQAG | 71 | -1.4000 | 0 |
| 7 | VESTAGSLQ | 31 | -1.8000 | 0 |
| 8 | MKTDAATLA | 3 | -1.9000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1106 | Threshold for 3 % with score: 2.0 | Highest Score achievable by any peptide: 8.3 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.0000 | 36.14 |
| 2 | VRFQEAANK | 55 | 2.3000 | 27.71 |
| 3 | LQGQWRGAA | 38 | 1.6000 | 19.28 |
| 4 | VVRFQEAAN | 54 | 0.4000 | 4.82 |
| 5 | WRGAAGTAA | 42 | -0.6000 | 0 |
| 6 | ISTNIRQAG | 71 | -1.4000 | 0 |
| 7 | VESTAGSLQ | 31 | -1.8000 | 0 |
| 8 | MKTDAATLA | 3 | -1.9000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1107 | Threshold for 3 % with score: 2.1 | Highest Score achievable by any peptide: 9.1 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.0000 | 43.96 |
| 2 | MKTDAATLA | 3 | 3.3000 | 36.26 |
| 3 | ISGDLKTQI | 20 | 3.1000 | 34.07 |
| 4 | VRFQEAANK | 55 | 2.7000 | 29.67 |
| 5 | LQGQWRGAA | 38 | 2.5000 | 27.47 |
| 6 | WRGAAGTAA | 42 | 0.6000 | 6.59 |
| 7 | VQYSRADEE | 80 | 0.4000 | 4.40 |
| 8 | ISTNIRQAG | 71 | -0.2000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1114 | Threshold for 3 % with score: 1.3 | Highest Score achievable by any peptide: 8.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.7000 | 32.14 |
| 2 | VRFQEAANK | 55 | 2.3000 | 27.38 |
| 3 | WRGAAGTAA | 42 | 0.8000 | 9.52 |
| 4 | LQGQWRGAA | 38 | 0.5000 | 5.95 |
| 5 | VVRFQEAAN | 54 | -0.2000 | 0 |
| 6 | FQEAANKQK | 57 | -0.9000 | 0 |
| 7 | YSRADEEQQ | 82 | -1.5000 | 0 |
| 8 | ISTNIRQAG | 71 | -1.6000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1120 | Threshold for 3 % with score: 2.1 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.1000 | 35.23 |
| 2 | VRFQEAANK | 55 | 2.4000 | 27.27 |
| 3 | WRGAAGTAA | 42 | 0.8000 | 9.09 |
| 4 | VVRFQEAAN | 54 | 0.6000 | 6.82 |
| 5 | LQGQWRGAA | 38 | 0.5000 | 5.68 |
| 6 | ISTNIRQAG | 71 | -0.2000 | 0 |
| 7 | FQEAANKQK | 57 | -0.8000 | 0 |
| 8 | VQYSRADEE | 80 | -1.4000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1121 | Threshold for 3 % with score: 1.8 | Highest Score achievable by any peptide: 8.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.7000 | 44.05 |
| 2 | VRFQEAANK | 55 | 3.3000 | 39.29 |
| 3 | LQGQWRGAA | 38 | 1.5000 | 17.86 |
| 4 | VVRFQEAAN | 54 | 0.8000 | 9.52 |
| 5 | WRGAAGTAA | 42 | -0.2000 | 0 |
| 6 | ISTNIRQAG | 71 | -0.6000 | 0 |
| 7 | MAEMKTDAA | 0 | -1.1000 | 0 |
| 8 | MKTDAATLA | 3 | -1.2000 | 0 |

| ALLELE: DRB1_1128 | Threshold for 3 % with score: 2.15 | Highest Score achievable by any peptide: 8.7 |
|---|---|---|

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.4000 | 27.59 |
| 2 | VRFQEAANK | 55 | 1.4000 | 16.09 |
| 3 | LQGQWRGAA | 38 | 0.6000 | 6.90 |
| 4 | WRGAAGTAA | 42 | 0.4000 | 4.60 |
| 5 | VVRFQEAAN | 54 | 0.2000 | 2.30 |
| 6 | FQEAANKQK | 57 | -1.0000 | 0 |
| 7 | ISTNIRQAG | 71 | -1.0000 | 0 |
| 8 | FERISGDLK | 17 | -1.9000 | 0 |

| ALLELE: DRB1_1301 | Threshold for 3 % with score: 2.6 | Highest Score achievable by any peptide: 8.8 |
|---|---|---|

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | VRFQEAANK | 55 | 3.4000 | 38.64 |
| 3 | VVRFQEAAN | 54 | 1.6000 | 18.18 |
| 4 | LQGQWRGAA | 38 | 1.5000 | 17.05 |
| 5 | ISTNIRQAG | 71 | 0.8000 | 9.09 |
| 6 | WRGAAGTAA | 42 | -0.2000 | 0 |
| 7 | VQYSRADEE | 80 | -0.4000 | 0 |
| 8 | ISGDLKTQI | 20 | -0.5000 | 0 |

| ALLELE: DRB1_1302 | Threshold for 3 % with score: 2.1 | Highest Score achievable by any peptide: 8.8 |
|---|---|---|

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.1000 | 35.23 |
| 2 | VRFQEAANK | 55 | 2.4000 | 27.27 |
| 3 | WRGAAGTAA | 42 | 0.8000 | 9.09 |
| 4 | VVRFQEAAN | 54 | 0.6000 | 6.82 |
| 5 | LQGQWRGAA | 38 | 0.5000 | 5.68 |

| | | | | |
|---|---|---|---|---|
| 6 | ISTNIRQAG | 71 | -0.2000 | 0 |
| 7 | FQEAANKQK | 57 | -0.8000 | 0 |
| 8 | VQYSRADEE | 80 | -1.4000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1304 | Threshold for 3 % with score: 2.6 | Highest Score achievable by any peptide: 9 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.7000 | 41.11 |
| 2 | VVRFQEAAN | 54 | 2.8000 | 31.11 |
| 3 | VRFQEAANK | 55 | 2.6000 | 28.89 |
| 4 | LQGQWRGAA | 38 | 1.5000 | 16.67 |
| 5 | VQYSRADEE | 80 | 1.2000 | 13.33 |
| 6 | ISTNIRQAG | 71 | 0.7000 | 7.78 |
| 7 | LKTQIDQVE | 24 | 0.2000 | 2.22 |
| 8 | WRGAAGTAA | 42 | -0.2000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1305 | Threshold for 3 % with score: 2.2 | Highest Score achievable by any peptide: 8.7 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.4000 | 27.59 |
| 2 | VRFQEAANK | 55 | 1.4000 | 16.09 |
| 3 | LQGQWRGAA | 38 | 0.6000 | 6.90 |
| 4 | WRGAAGTAA | 42 | 0.4000 | 4.60 |
| 5 | VVRFQEAAN | 54 | 0.2000 | 2.30 |
| 6 | FQEAANKQK | 57 | -1.0000 | 0 |
| 7 | ISTNIRQAG | 71 | -1.0000 | 0 |
| 8 | FERISGDLK | 17 | -1.9000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1307 | Threshold for 3 % with score: 0.6 | Highest Score achievable by any peptide: 6.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|

| | | | | |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 1.9000 | 27.94 |
| 2 | VRFQEAANK | 55 | 1.3000 | 19.12 |
| 3 | LQGQWRGAA | 38 | 0.5000 | 7.35 |
| 4 | VVRFQEAAN | 54 | -0.6000 | 0 |
| 5 | WRGAAGTAA | 42 | -0.7000 | 0 |
| 6 | FERISGDLK | 17 | -1.7000 | 0 |
| 7 | FQEAANKQK | 57 | -1.7000 | 0 |
| 8 | ISTNIRQAG | 71 | -2.5000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1311 | Threshold for 3 % with score: 2.0 | Highest Score achievable by any peptide: 8.3 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.0000 | 36.14 |
| 2 | VRFQEAANK | 55 | 2.3000 | 27.71 |
| 3 | LQGQWRGAA | 38 | 1.6000 | 19.28 |
| 4 | VVRFQEAAN | 54 | 0.4000 | 4.82 |
| 5 | WRGAAGTAA | 42 | -0.6000 | 0 |
| 6 | ISTNIRQAG | 71 | -1.4000 | 0 |
| 7 | VESTAGSLQ | 31 | -1.8000 | 0 |
| 8 | MKTDAATLA | 3 | -1.9000 | 0 |

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|---|---|---|
| ALLELE: DRB1_1321 | Threshold for 3 % with score: 2.2 | Highest Score achievable by any peptide: 8.9 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.0000 | 22.47 |
| 2 | VVRFQEAAN | 54 | 1.4000 | 15.73 |
| 3 | LQGQWRGAA | 38 | 0.6000 | 6.74 |
| 4 | VRFQEAANK | 55 | 0.6000 | 6.74 |
| 5 | WRGAAGTAA | 42 | 0.4000 | 4.49 |
| 6 | YSRADEEQQ | 82 | -1.0000 | 0 |
| 7 | ISTNIRQAG | 71 | -1.1000 | 0 |
| 8 | VQYSRADEE | 80 | -1.1000 | 0 |

| | | |
|---|---|---|
| ALLELE:<br>DRB1_1322 | Threshold for 3 % with score:<br>1.8 | Highest Score achievable by any peptide: 8.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 3.7000 | 44.05 |
| 2 | VRFQEAANK | 55 | 3.3000 | 39.29 |
| 3 | LQGQWRGAA | 38 | 1.5000 | 17.86 |
| 4 | VVRFQEAAN | 54 | 0.8000 | 9.52 |
| 5 | WRGAAGTAA | 42 | -0.2000 | 0 |
| 6 | ISTNIRQAG | 71 | -0.6000 | 0 |
| 7 | MAEMKTDAA | 0 | -1.1000 | 0 |
| 8 | MKTDAATLA | 3 | -1.2000 | 0 |

| | | |
|---|---|---|
| ALLELE:<br>DRB1_1323 | Threshold for 3 % with score:<br>1.3 | Highest Score achievable by any peptide: 8.4 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 2.7000 | 32.14 |
| 2 | VRFQEAANK | 55 | 2.3000 | 27.38 |
| 3 | WRGAAGTAA | 42 | 0.8000 | 9.52 |
| 4 | LQGQWRGAA | 38 | 0.5000 | 5.95 |
| 5 | VVRFQEAAN | 54 | -0.2000 | 0 |
| 6 | FQEAANKQK | 57 | -0.9000 | 0 |
| 7 | YSRADEEQQ | 82 | -1.5000 | 0 |
| 8 | ISTNIRQAG | 71 | -1.6000 | 0 |

| | | |
|---|---|---|
| ALLELE:<br>DRB1_1327 | Threshold for 3 % with score:<br>2.6 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | VRFQEAANK | 55 | 3.4000 | 38.64 |
| 3 | VVRFQEAAN | 54 | 1.6000 | 18.18 |
| 4 | LQGQWRGAA | 38 | 1.5000 | 17.05 |
| 5 | ISTNIRQAG | 71 | 0.8000 | 9.09 |

| | | | | |
|---|---|---|---|---|
| 6 | WRGAAGTAA | 42 | -0.2000 | 0 |
| 7 | VQYSRADEE | 80 | -0.4000 | 0 |
| 8 | ISGDLKTQI | 20 | -0.5000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1328 | Threshold for 3 % with score: 2.6 | Highest Score achievable by any peptide: 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | IRQAGVQYS | 75 | 4.1000 | 46.59 |
| 2 | VRFQEAANK | 55 | 3.4000 | 38.64 |
| 3 | VVRFQEAAN | 54 | 1.6000 | 18.18 |
| 4 | LQGQWRGAA | 38 | 1.5000 | 17.05 |
| 5 | ISTNIRQAG | 71 | 0.8000 | 9.09 |
| 6 | WRGAAGTAA | 42 | -0.2000 | 0 |
| 7 | VQYSRADEE | 80 | -0.4000 | 0 |
| 8 | ISGDLKTQI | 20 | -0.5000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1501 | Threshold for 3 % with score: 3.25 | Highest Score achievable by any peptide: 9.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VVRFQEAAN | 54 | 3.0000 | 30.61 |
| 2 | WRGAAGTAA | 42 | 2.1000 | 21.43 |
| 3 | LQGQWRGAA | 38 | 1.6000 | 16.33 |
| 4 | IRQAGVQYS | 75 | 1.3000 | 13.27 |
| 5 | MKTDAATLA | 3 | 0.9000 | 9.18 |
| 6 | VRFQEAANK | 55 | 0.5000 | 5.10 |
| 7 | ISGDLKTQI | 20 | 0.1000 | 1.02 |
| 8 | ISTNIRQAG | 71 | -0.6000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1502 | Threshold for 3 % with score: 3.25 | Highest Score achievable by any peptide: 9.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|

| | | | | |
|---|---|---|---|---|
| 1 | WRGAAGTAA | 42 | 3.1000 | 31.63 |
| 2 | VVRFQEAAN | 54 | 2.0000 | 20.41 |
| 3 | LQGQWRGAA | 38 | 0.6000 | 6.12 |
| 4 | IRQAGVQYS | 75 | 0.3000 | 3.06 |
| 5 | MKTDAATLA | 3 | -0.1000 | 0 |
| 6 | FERISGDLK | 17 | -0.5000 | 0 |
| 7 | VRFQEAANK | 55 | -0.5000 | 0 |
| 8 | ISGDLKTQI | 20 | -0.9000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB1_1506 | Threshold for 3 % with score: 3.1 | Highest Score achievable by any peptide: 9.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VVRFQEAAN | 54 | 3.0000 | 30.61 |
| 2 | WRGAAGTAA | 42 | 2.1000 | 21.43 |
| 3 | LQGQWRGAA | 38 | 1.6000 | 16.33 |
| 4 | IRQAGVQYS | 75 | 1.3000 | 13.27 |
| 5 | MKTDAATLA | 3 | 0.9000 | 9.18 |
| 6 | VRFQEAANK | 55 | 0.5000 | 5.10 |
| 7 | ISGDLKTQI | 20 | 0.1000 | 1.02 |
| 8 | ISTNIRQAG | 71 | -0.6000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB5_0101 | Threshold for 3 % with score: 2.3 | Highest Score achievable by any peptide: 9.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VRFQEAANK | 55 | 4.0000 | 40.82 |
| 2 | FERISGDLK | 17 | 3.0000 | 30.61 |
| 3 | WRGAAGTAA | 42 | 2.4000 | 24.49 |
| 4 | FQEAANKQK | 57 | 2.3000 | 23.47 |
| 5 | IRQAGVQYS | 75 | 1.3000 | 13.27 |
| 6 | VESTAGSLQ | 31 | -0.2000 | 0 |
| 7 | VVRFQEAAN | 54 | -0.8000 | 0 |

| | | |
|---|---|---|
| ALLELE: DRB5_0105 | Threshold for 3 % with score: 2.3 | Highest Score achievable by any peptide: 9.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VRFQEAANK | 55 | 4.0000 | 40.82 |
| 2 | FERISGDLK | 17 | 3.0000 | 30.61 |
| 3 | WRGAAGTAA | 42 | 2.4000 | 24.49 |
| 4 | FQEAANKQK | 57 | 2.3000 | 23.47 |
| 5 | IRQAGVQYS | 75 | 1.3000 | 13.27 |
| 6 | VESTAGSLQ | 31 | -0.2000 | 0 |
| 7 | VVRFQEAAN | 54 | -0.8000 | 0 |