# 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 | Wed Feb 24 13:32:19 2010 |
| Length of input sequence | 314 amino acids |
| Number of nanomers from input sequence | 306 |
| Number of nanomers with obligatory P1 anchor residue | 91 |
| Threshold setting | 3 |
| Number of alleles in query | 51 |
| Number of top scorers to be displayed | 31 |

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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 | FRHLYGLDC | 159 | 3.3000 | 55.00 |
| 2 | VVAIFAQAL | 188 | 2.3000 | 38.33 |
| 3 | VVFHLAAQI | 72 | 1.9000 | 31.67 |
| 4 | LYGLDCSHI | 162 | 1.5000 | 25.00 |
| 5 | VVGLDNFAT | 26 | 1.2000 | 20.00 |
| 6 | FHLAAQIDV | 74 | 0.9000 | 15.00 |
| 7 | FNIGTGKET | 237 | 0.9000 | 15.00 |
| 8 | VNVIGTVRL | 95 | 0.8000 | 13.33 |

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|---|---|---|---|---|
| 9 | VRLAEAARQ | 101 | 0.6000 | 10.00 |
| 10 | LHSAVAAAV | 250 | 0.3000 | 5.00 |
| 11 | LRFNIGTGK | 235 | 0.1300 | 2.17 |
| 12 | FVRVSADVG | 224 | -0.0500 | 0 |
| 13 | IVTADLHAI | 56 | -0.1000 | 0 |
| 14 | FATGRATNL | 32 | -0.1100 | 0 |
| 15 | VRALVTGAA | 0 | -0.2000 | 0 |
| 16 | FVEADIVTA | 51 | -0.3000 | 0 |
| 17 | LLSGKPTRV | 196 | -0.3100 | 0 |
| 18 | IELADGVRR | 294 | -0.5000 | 0 |
| 19 | IYLNTFRHL | 154 | -0.5700 | 0 |
| 20 | VRKIVHTSS | 112 | -0.7100 | 0 |
| 21 | VAIFAQALL | 189 | -0.7200 | 0 |
| 22 | VFHLAAQID | 73 | -0.8000 | 0 |
| 23 | YVFVDDVVD | 214 | -1.0500 | 0 |
| 24 | YGLDCSHIA | 163 | -1.4000 | 0 |
| 25 | IGLAERVLG | 281 | -1.4000 | 0 |
| 26 | WRPQIELAD | 290 | -1.4000 | 0 |
| 27 | VVDAFVRVS | 220 | -1.5100 | 0 |
| 28 | VTGAAGFIG | 4 | -1.6000 | 0 |
| 29 | VHTSSGGSI | 116 | -1.6000 | 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 |
|---|---|---|---|---|
| 1 | FRHLYGLDC | 159 | 3.3000 | 55.00 |
| 2 | VVAIFAQAL | 188 | 3.3000 | 55.00 |
| 3 | VVFHLAAQI | 72 | 2.9000 | 48.33 |
| 4 | LYGLDCSHI | 162 | 2.5000 | 41.67 |
| 5 | VVGLDNFAT | 26 | 2.2000 | 36.67 |
| 6 | VNVIGTVRL | 95 | 1.8000 | 30.00 |
| 7 | VRLAEAARQ | 101 | 1.6000 | 26.67 |
| 8 | LHSAVAAAV | 250 | 1.3000 | 21.67 |

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|---|---|---|---|---|
| 9 | LRFNIGTGK | 235 | 1.1300 | 18.83 |
| 10 | LVTGAAGFI | 3 | 1.0000 | 16.67 |
| 11 | IVTADLHAI | 56 | 0.9000 | 15.00 |
| 12 | FHLAAQIDV | 74 | 0.9000 | 15.00 |
| 13 | FNIGTGKET | 237 | 0.9000 | 15.00 |
| 14 | VRALVTGAA | 0 | 0.8000 | 13.33 |
| 15 | LLSGKPTRV | 196 | 0.6900 | 11.50 |
| 16 | IELADGVRR | 294 | 0.5000 | 8.33 |
| 17 | IYLNTFRHL | 154 | 0.4300 | 7.17 |
| 18 | VRKIVHTSS | 112 | 0.2900 | 4.83 |
| 19 | VAIFAQALL | 189 | 0.2800 | 4.67 |
| 20 | VFHLAAQID | 73 | 0.2000 | 3.33 |
| 21 | FVRVSADVG | 224 | -0.0500 | 0 |
| 22 | FATGRATNL | 32 | -0.1100 | 0 |
| 23 | FVEADIVTA | 51 | -0.3000 | 0 |
| 24 | IGLAERVLG | 281 | -0.4000 | 0 |
| 25 | VVDAFVRVS | 220 | -0.5100 | 0 |
| 26 | VTGAAGFIG | 4 | -0.6000 | 0 |
| 27 | VHTSSGGSI | 116 | -0.6000 | 0 |
| 28 | IVHTSSGGS | 115 | -0.7000 | 0 |
| 29 | VRVSADVGG | 225 | -0.8000 | 0 |
| 30 | VGGGLRFNI | 231 | -0.8000 | 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 | VFVDDVVDA | 215 | 5.0000 | 52.63 |
| 2 | VFGDGTNTR | 204 | 4.5100 | 47.47 |
| 3 | VRKIVHTSS | 112 | 3.6000 | 37.89 |
| 4 | FVDDVVDAF | 216 | 3.6000 | 37.89 |
| 5 | LLADGHSVV | 19 | 3.5700 | 37.58 |
| 6 | VVFHLAAQI | 72 | 3.5000 | 36.84 |
| 7 | LVTGAAGFI | 3 | 3.3000 | 34.74 |

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|---|---|---|---|---|
| 8 | VGGGLRFNI | 231 | 3.3000 | 34.74 |
| 9 | VRALVTGAA | 0 | 3.1000 | 32.63 |
| 10 | IGLAERVLG | 281 | 3.1000 | 32.63 |
| 11 | VRLAEAARQ | 101 | 3.0000 | 31.58 |
| 12 | VEADIVTAD | 52 | 2.9000 | 30.53 |
| 13 | VGLDNFATG | 27 | 2.8000 | 29.47 |
| 14 | VRRSVADPQ | 82 | 2.8000 | 29.47 |
| 15 | VNVIGTVRL | 95 | 2.7600 | 29.05 |
| 16 | LKRSCLDIG | 274 | 2.5000 | 26.32 |
| 17 | VVAIFAQAL | 188 | 2.4600 | 25.89 |
| 18 | IVHTSSGGS | 115 | 2.4000 | 25.26 |
| 19 | LLSGKPTRV | 196 | 2.4000 | 25.26 |
| 20 | VVDAFVRVS | 220 | 2.2000 | 23.16 |
| 21 | LRFNIGTGK | 235 | 2.2000 | 23.16 |
| 22 | VTADLHAIL | 57 | 2.1600 | 22.74 |
| 23 | IVTADLHAI | 56 | 2.1000 | 22.11 |
| 24 | FIGSTLVDR | 10 | 1.9000 | 20.00 |
| 25 | YGLDCSHIA | 163 | 1.9000 | 20.00 |
| 26 | ILEQHRPEV | 64 | 1.8000 | 18.95 |
| 27 | LYGLDCSHI | 162 | 1.7700 | 18.63 |
| 28 | VVGLDNFAT | 26 | 1.7000 | 17.89 |
| 29 | IFAQALLSG | 191 | 1.6000 | 16.84 |
| 30 | FVRVSADVG | 224 | 1.6000 | 16.84 |
| 31 | VRVSADVGG | 225 | 1.6000 | 16.84 |

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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 | VFVDDVVDA | 215 | 4.0000 | 43.96 |
| 2 | YGLDCSHIA | 163 | 2.9000 | 31.87 |
| 3 | VRLAEAARQ | 101 | 2.7000 | 29.67 |
| 4 | FVDDVVDAF | 216 | 2.7000 | 29.67 |
| 5 | VRRSVADPQ | 82 | 2.5000 | 27.47 |

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|---|---|---|---|---|
| 6 | VRKIVHTSS | 112 | 2.2000 | 24.18 |
| 7 | VRALVTGAA | 0 | 2.1000 | 23.08 |
| 8 | VFGDGTNTR | 204 | 2.0100 | 22.09 |
| 9 | FRHLYGLDC | 159 | 1.9000 | 20.88 |
| 10 | FVEADIVTA | 51 | 1.8000 | 19.78 |
| 11 | VVFHLAAQI | 72 | 1.6000 | 17.58 |
| 12 | LLADGHSVV | 19 | 1.5700 | 17.25 |
| 13 | LVTGAAGFI | 3 | 1.4000 | 15.38 |
| 14 | FIGSTLVDR | 10 | 1.4000 | 15.38 |
| 15 | VGGGLRFNI | 231 | 1.4000 | 15.38 |
| 16 | FHLAAQIDV | 74 | 1.2000 | 13.19 |
| 17 | FVRVSADVG | 224 | 1.2000 | 13.19 |
| 18 | LRFNIGTGK | 235 | 1.1000 | 12.09 |
| 19 | IVHTSSGGS | 115 | 1.0000 | 10.99 |
| 20 | VEADIVTAD | 52 | 0.8000 | 8.79 |
| 21 | VNVIGTVRL | 95 | 0.8000 | 8.79 |
| 22 | VVDAFVRVS | 220 | 0.8000 | 8.79 |
| 23 | IGLAERVLG | 281 | 0.7000 | 7.69 |
| 24 | VVAIFAQAL | 188 | 0.5000 | 5.49 |
| 25 | VGLDNFATG | 27 | 0.4000 | 4.40 |
| 26 | LLSGKPTRV | 196 | 0.4000 | 4.40 |
| 27 | IVTADLHAI | 56 | 0.2000 | 2.20 |
| 28 | VTADLHAIL | 57 | 0.2000 | 2.20 |
| 29 | LKRSCLDIG | 274 | 0.1000 | 1.10 |

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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 | VFVDDVVDA | 215 | 4.8800 | 55.45 |
| 2 | VRRSVADPQ | 82 | 3.8000 | 43.18 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 42.05 |
| 4 | VFGDGTNTR | 204 | 3.7000 | 42.05 |
| 5 | VRKIVHTSS | 112 | 3.2000 | 36.36 |

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|---|---|---|---|---|
| 6 | YGLDCSHIA | 163 | 2.7000 | 30.68 |
| 7 | VVFHLAAQI | 72 | 2.6000 | 29.55 |
| 8 | LLADGHSVV | 19 | 2.3000 | 26.14 |
| 9 | LRFNIGTGK | 235 | 2.1000 | 23.86 |
| 10 | IVTADLHAI | 56 | 2.0000 | 22.73 |
| 11 | FVDDVVDAF | 216 | 2.0000 | 22.73 |
| 12 | VEADIVTAD | 52 | 1.8000 | 20.45 |
| 13 | VRALVTGAA | 0 | 1.7000 | 19.32 |
| 14 | VNVIGTVRL | 95 | 1.6800 | 19.09 |
| 15 | VVAIFAQAL | 188 | 1.6000 | 18.18 |
| 16 | IGLAERVLG | 281 | 1.5800 | 17.95 |
| 17 | VVDAFVRVS | 220 | 1.5000 | 17.05 |
| 18 | VGLDNFATG | 27 | 1.4000 | 15.91 |
| 19 | FRHLYGLDC | 159 | 1.4000 | 15.91 |
| 20 | LLSGKPTRV | 196 | 1.4000 | 15.91 |
| 21 | LKRSCLDIG | 274 | 1.4000 | 15.91 |
| 22 | VTADLHAIL | 57 | 1.2000 | 13.64 |
| 23 | LVTGAAGFI | 3 | 1.0000 | 11.36 |
| 24 | VGGGLRFNI | 231 | 0.9000 | 10.23 |
| 25 | IGTVRLAEA | 98 | 0.7000 | 7.95 |
| 26 | IFAQALLSG | 191 | 0.7000 | 7.95 |
| 27 | FVEADIVTA | 51 | 0.6800 | 7.73 |
| 28 | IVHTSSGGS | 115 | 0.6000 | 6.82 |
| 29 | LYGLDCSHI | 162 | 0.6000 | 6.82 |
| 30 | FVRVSADVG | 224 | 0.5000 | 5.68 |
| 31 | VIGTVRLAE | 97 | 0.3000 | 3.41 |

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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 | VFVDDVVDA | 215 | 4.8800 | 55.45 |
| 2 | VRRSVADPQ | 82 | 3.8000 | 43.18 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 42.05 |

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|---|---|---|---|---|
| 4 | VFGDGTNTR | 204 | 3.7000 | 42.05 |
| 5 | VRKIVHTSS | 112 | 3.2000 | 36.36 |
| 6 | YGLDCSHIA | 163 | 2.7000 | 30.68 |
| 7 | VVFHLAAQI | 72 | 2.6000 | 29.55 |
| 8 | LLADGHSVV | 19 | 2.3000 | 26.14 |
| 9 | LRFNIGTGK | 235 | 2.1000 | 23.86 |
| 10 | IVTADLHAI | 56 | 2.0000 | 22.73 |
| 11 | FVDDVVDAF | 216 | 2.0000 | 22.73 |
| 12 | VEADIVTAD | 52 | 1.8000 | 20.45 |
| 13 | VRALVTGAA | 0 | 1.7000 | 19.32 |
| 14 | VNVIGTVRL | 95 | 1.6800 | 19.09 |
| 15 | VVAIFAQAL | 188 | 1.6000 | 18.18 |
| 16 | IGLAERVLG | 281 | 1.5800 | 17.95 |
| 17 | VVDAFVRVS | 220 | 1.5000 | 17.05 |
| 18 | VGLDNFATG | 27 | 1.4000 | 15.91 |
| 19 | FRHLYGLDC | 159 | 1.4000 | 15.91 |
| 20 | LLSGKPTRV | 196 | 1.4000 | 15.91 |
| 21 | LKRSCLDIG | 274 | 1.4000 | 15.91 |
| 22 | VTADLHAIL | 57 | 1.2000 | 13.64 |
| 23 | LVTGAAGFI | 3 | 1.0000 | 11.36 |
| 24 | VGGGLRFNI | 231 | 0.9000 | 10.23 |
| 25 | IGTVRLAEA | 98 | 0.7000 | 7.95 |
| 26 | IFAQALLSG | 191 | 0.7000 | 7.95 |
| 27 | FVEADIVTA | 51 | 0.6800 | 7.73 |
| 28 | IVHTSSGGS | 115 | 0.6000 | 6.82 |
| 29 | LYGLDCSHI | 162 | 0.6000 | 6.82 |
| 30 | FVRVSADVG | 224 | 0.5000 | 5.68 |
| 31 | VIGTVRLAE | 97 | 0.3000 | 3.41 |

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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 | VFVDDVVDA | 215 | 4.8800 | 55.45 |

| | | | | |
|---|---|---|---|---|
| 2 | VRRSVADPQ | 82 | 3.8000 | 43.18 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 42.05 |
| 4 | VFGDGTNTR | 204 | 3.7000 | 42.05 |
| 5 | VRKIVHTSS | 112 | 3.2000 | 36.36 |
| 6 | YGLDCSHIA | 163 | 2.7000 | 30.68 |
| 7 | VVFHLAAQI | 72 | 2.6000 | 29.55 |
| 8 | LLADGHSVV | 19 | 2.3000 | 26.14 |
| 9 | LRFNIGTGK | 235 | 2.1000 | 23.86 |
| 10 | IVTADLHAI | 56 | 2.0000 | 22.73 |
| 11 | FVDDVVDAF | 216 | 2.0000 | 22.73 |
| 12 | VEADIVTAD | 52 | 1.8000 | 20.45 |
| 13 | VRALVTGAA | 0 | 1.7000 | 19.32 |
| 14 | VNVIGTVRL | 95 | 1.6800 | 19.09 |
| 15 | VVAIFAQAL | 188 | 1.6000 | 18.18 |
| 16 | IGLAERVLG | 281 | 1.5800 | 17.95 |
| 17 | VVDAFVRVS | 220 | 1.5000 | 17.05 |
| 18 | VGLDNFATG | 27 | 1.4000 | 15.91 |
| 19 | FRHLYGLDC | 159 | 1.4000 | 15.91 |
| 20 | LLSGKPTRV | 196 | 1.4000 | 15.91 |
| 21 | LKRSCLDIG | 274 | 1.4000 | 15.91 |
| 22 | VTADLHAIL | 57 | 1.2000 | 13.64 |
| 23 | LVTGAAGFI | 3 | 1.0000 | 11.36 |
| 24 | VGGGLRFNI | 231 | 0.9000 | 10.23 |
| 25 | IGTVRLAEA | 98 | 0.7000 | 7.95 |
| 26 | IFAQALLSG | 191 | 0.7000 | 7.95 |
| 27 | FVEADIVTA | 51 | 0.6800 | 7.73 |
| 28 | IVHTSSGGS | 115 | 0.6000 | 6.82 |
| 29 | LYGLDCSHI | 162 | 0.6000 | 6.82 |
| 30 | FVRVSADVG | 224 | 0.5000 | 5.68 |
| 31 | VIGTVRLAE | 97 | 0.3000 | 3.41 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | FVDDVVDAF | 216 | 4.6000 | 48.42 |
| 2 | VFVDDVVDA | 215 | 4.0000 | 42.11 |
| 3 | VFGDGTNTR | 204 | 3.5100 | 36.95 |
| 4 | FIGSTLVDR | 10 | 2.9000 | 30.53 |
| 5 | YGLDCSHIA | 163 | 2.9000 | 30.53 |
| 6 | VRKIVHTSS | 112 | 2.6000 | 27.37 |
| 7 | FVRVSADVG | 224 | 2.6000 | 27.37 |
| 8 | LLADGHSVV | 19 | 2.5700 | 27.05 |
| 9 | VVFHLAAQI | 72 | 2.5000 | 26.32 |
| 10 | LVTGAAGFI | 3 | 2.3000 | 24.21 |
| 11 | VGGGLRFNI | 231 | 2.3000 | 24.21 |
| 12 | FHLAAQIDV | 74 | 2.2000 | 23.16 |
| 13 | VRALVTGAA | 0 | 2.1000 | 22.11 |
| 14 | IGLAERVLG | 281 | 2.1000 | 22.11 |
| 15 | VRLAEAARQ | 101 | 2.0000 | 21.05 |
| 16 | VEADIVTAD | 52 | 1.9000 | 20.00 |
| 17 | FRHLYGLDC | 159 | 1.9000 | 20.00 |
| 18 | VGLDNFATG | 27 | 1.8000 | 18.95 |
| 19 | FVEADIVTA | 51 | 1.8000 | 18.95 |
| 20 | VRRSVADPQ | 82 | 1.8000 | 18.95 |
| 21 | VNVIGTVRL | 95 | 1.7600 | 18.53 |
| 22 | LKRSCLDIG | 274 | 1.5000 | 15.79 |
| 23 | VVAIFAQAL | 188 | 1.4600 | 15.37 |
| 24 | IVHTSSGGS | 115 | 1.4000 | 14.74 |
| 25 | YAAGKVAGE | 145 | 1.4000 | 14.74 |
| 26 | LLSGKPTRV | 196 | 1.4000 | 14.74 |
| 27 | VVDAFVRVS | 220 | 1.2000 | 12.63 |
| 28 | LRFNIGTGK | 235 | 1.2000 | 12.63 |
| 29 | VTADLHAIL | 57 | 1.1600 | 12.21 |
| 30 | IVTADLHAI | 56 | 1.1000 | 11.58 |
| 31 | YLNTFRHLY | 155 | 1.0000 | 10.53 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VFVDDVVDA | 215 | 4.8800 | 55.45 |
| 2 | VRRSVADPQ | 82 | 3.8000 | 43.18 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 42.05 |
| 4 | VFGDGTNTR | 204 | 3.7000 | 42.05 |
| 5 | VRKIVHTSS | 112 | 3.2000 | 36.36 |
| 6 | YGLDCSHIA | 163 | 2.7000 | 30.68 |
| 7 | VVFHLAAQI | 72 | 2.6000 | 29.55 |
| 8 | LLADGHSVV | 19 | 2.3000 | 26.14 |
| 9 | LRFNIGTGK | 235 | 2.1000 | 23.86 |
| 10 | IVTADLHAI | 56 | 2.0000 | 22.73 |
| 11 | FVDDVVDAF | 216 | 2.0000 | 22.73 |
| 12 | VEADIVTAD | 52 | 1.8000 | 20.45 |
| 13 | VRALVTGAA | 0 | 1.7000 | 19.32 |
| 14 | VNVIGTVRL | 95 | 1.6800 | 19.09 |
| 15 | VVAIFAQAL | 188 | 1.6000 | 18.18 |
| 16 | IGLAERVLG | 281 | 1.5800 | 17.95 |
| 17 | VVDAFVRVS | 220 | 1.5000 | 17.05 |
| 18 | VGLDNFATG | 27 | 1.4000 | 15.91 |
| 19 | FRHLYGLDC | 159 | 1.4000 | 15.91 |
| 20 | LLSGKPTRV | 196 | 1.4000 | 15.91 |
| 21 | LKRSCLDIG | 274 | 1.4000 | 15.91 |
| 22 | VTADLHAIL | 57 | 1.2000 | 13.64 |
| 23 | LVTGAAGFI | 3 | 1.0000 | 11.36 |
| 24 | VGGGLRFNI | 231 | 0.9000 | 10.23 |
| 25 | IGTVRLAEA | 98 | 0.7000 | 7.95 |
| 26 | IFAQALLSG | 191 | 0.7000 | 7.95 |
| 27 | FVEADIVTA | 51 | 0.6800 | 7.73 |
| 28 | IVHTSSGGS | 115 | 0.6000 | 6.82 |
| 29 | LYGLDCSHI | 162 | 0.6000 | 6.82 |
| 30 | FVRVSADVG | 224 | 0.5000 | 5.68 |
| 31 | VIGTVRLAE | 97 | 0.3000 | 3.41 |

| ALLELE: DRB1_0401 | Threshold for 3 % with score: 1.48 | Highest Score achievable by any peptide: 8.6 |
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| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | YGLDCSHIA | 163 | 3.9000 | 45.35 |
| 2 | VRRSVADPQ | 82 | 2.9000 | 33.72 |
| 3 | VFGDGTNTR | 204 | 2.9000 | 33.72 |
| 4 | VVFHLAAQI | 72 | 2.7000 | 31.40 |
| 5 | VRLAEAARQ | 101 | 2.7000 | 31.40 |
| 6 | VFVDDVVDA | 215 | 2.6800 | 31.16 |
| 7 | VRALVTGAA | 0 | 2.6000 | 30.23 |
| 8 | IVHTSSGGS | 115 | 2.4000 | 27.91 |
| 9 | FRHLYGLDC | 159 | 2.4000 | 27.91 |
| 10 | VNVIGTVRL | 95 | 2.0800 | 24.19 |
| 11 | FVDDVVDAF | 216 | 1.8000 | 20.93 |
| 12 | VVGLDNFAT | 26 | 1.2000 | 13.95 |
| 13 | VRKIVHTSS | 112 | 1.2000 | 13.95 |
| 14 | LRFNIGTGK | 235 | 1.0000 | 11.63 |
| 15 | VVAIFAQAL | 188 | 0.9000 | 10.47 |
| 16 | FVEADIVTA | 51 | 0.8800 | 10.23 |
| 17 | FVRVSADVG | 224 | 0.6000 | 6.98 |
| 18 | VRVSADVGG | 225 | 0.4800 | 5.58 |
| 19 | LYGLDCSHI | 162 | 0.4000 | 4.65 |
| 20 | VVDAFVRVS | 220 | 0.2000 | 2.33 |
| 21 | FIGSTLVDR | 10 | 0.0800 | 0.93 |
| 22 | WRPQIELAD | 290 | -0.1000 | 0 |
| 23 | VGLDNFATG | 27 | -0.2000 | 0 |
| 24 | IVTADLHAI | 56 | -0.3000 | 0 |
| 25 | LEQHRPEVV | 65 | -0.3000 | 0 |
| 26 | IYGTPPEYP | 124 | -0.3000 | 0 |
| 27 | FHLAAQIDV | 74 | -0.3200 | 0 |
| 28 | LEHLADNSA | 40 | -0.4000 | 0 |
| 29 | VEADIVTAD | 52 | -0.4000 | 0 |

| ALLELE: DRB1_0402 | Threshold for 3 % with score: 1.8 | Highest Score achievable by any peptide: 9.6 |
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| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VVDAFVRVS | 220 | 4.1000 | 42.71 |
| 2 | VVFHLAAQI | 72 | 3.8000 | 39.58 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 38.54 |
| 4 | LSGKPTRVF | 197 | 2.6000 | 27.08 |
| 5 | VNVIGTVRL | 95 | 2.4800 | 25.83 |
| 6 | VVGLDNFAT | 26 | 2.3000 | 23.96 |
| 7 | VVAIFAQAL | 188 | 2.2800 | 23.75 |
| 8 | VLGWRPQIE | 287 | 2.2000 | 22.92 |
| 9 | VRKIVHTSS | 112 | 1.6800 | 17.50 |
| 10 | VRALVTGAA | 0 | 1.4000 | 14.58 |
| 11 | IVHTSSGGS | 115 | 1.4000 | 14.58 |
| 12 | IVTADLHAI | 56 | 1.2000 | 12.50 |
| 13 | IYLNTFRHL | 154 | 1.1000 | 11.46 |
| 14 | LRFNIGTGK | 235 | 0.9000 | 9.38 |
| 15 | IAPANVYGP | 170 | 0.8000 | 8.33 |
| 16 | VRRSVADPQ | 82 | 0.3000 | 3.12 |
| 17 | FRHLYGLDC | 159 | 0.3000 | 3.12 |
| 18 | LHSAVAAAV | 250 | 0.3000 | 3.12 |
| 19 | VFGDGTNTR | 204 | 0.2000 | 2.08 |
| 20 | VFVDDVVDA | 215 | 0.1000 | 1.04 |
| 21 | LLSGKPTRV | 196 | -0.1000 | 0 |
| 22 | VRRTVEYFR | 300 | -0.1000 | 0 |
| 23 | VFHLAAQID | 73 | -0.2000 | 0 |
| 24 | LYGLDCSHI | 162 | -0.2000 | 0 |
| 25 | VRVSADVGG | 225 | -0.2000 | 0 |
| 26 | LVDRLLADG | 15 | -0.3000 | 0 |
| 27 | IDVRRSVAD | 80 | -0.3000 | 0 |
| 28 | LNTFRHLYG | 156 | -0.3000 | 0 |
| 29 | YGLDCSHIA | 163 | -0.3000 | 0 |

| 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 | VRALVTGAA | 0 | 3.9000 | 44.32 |
| 2 | VRLAEAARQ | 101 | 3.7000 | 42.05 |
| 3 | VVGLDNFAT | 26 | 3.3500 | 38.07 |
| 4 | VNVIGTVRL | 95 | 3.2000 | 36.36 |
| 5 | VRKIVHTSS | 112 | 3.0000 | 34.09 |
| 6 | LYGLDCSHI | 162 | 2.3000 | 26.14 |
| 7 | VVAIFAQAL | 188 | 2.0000 | 22.73 |
| 8 | IVHTSSGGS | 115 | 1.9000 | 21.59 |
| 9 | VVFHLAAQI | 72 | 1.6000 | 18.18 |
| 10 | VRRSVADPQ | 82 | 1.5000 | 17.05 |
| 11 | VFGDGTNTR | 204 | 1.5000 | 17.05 |
| 12 | VVDAFVRVS | 220 | 1.5000 | 17.05 |
| 13 | FRHLYGLDC | 159 | 1.2000 | 13.64 |
| 14 | VFVDDVVDA | 215 | 1.0000 | 11.36 |
| 15 | LDNFATGRA | 29 | 0.9000 | 10.23 |
| 16 | LEHLADNSA | 40 | 0.9000 | 10.23 |
| 17 | LRFNIGTGK | 235 | 0.9000 | 10.23 |
| 18 | IVTADLHAI | 56 | 0.3000 | 3.41 |
| 19 | LHSAVAAAV | 250 | 0.3000 | 3.41 |
| 20 | VFHLAAQID | 73 | 0.1000 | 1.14 |
| 21 | FVRVSADVG | 224 | 0.1000 | 1.14 |
| 22 | IGTVRLAEA | 98 | -0.1000 | 0 |
| 23 | VRVSADVGG | 225 | -0.2000 | 0 |
| 24 | FVEADIVTA | 51 | -0.3000 | 0 |
| 25 | LNTFRHLYG | 156 | -0.3000 | 0 |
| 26 | IAPANVYGP | 170 | -0.3000 | 0 |
| 27 | YVFVDDVVD | 214 | -0.5000 | 0 |
| 28 | VDRLLADGH | 16 | -0.7200 | 0 |

| 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 | VRLAEAARQ | 101 | 3.5000 | 37.23 |
| 2 | VVGLDNFAT | 26 | 3.2500 | 34.57 |
| 3 | VNVIGTVRL | 95 | 3.2000 | 34.04 |
| 4 | YVFVDDVVD | 214 | 3.2000 | 34.04 |
| 5 | VRALVTGAA | 0 | 2.9000 | 30.85 |
| 6 | FVRVSADVG | 224 | 2.4000 | 25.53 |
| 7 | FRHLYGLDC | 159 | 2.2000 | 23.40 |
| 8 | VRKIVHTSS | 112 | 2.0000 | 21.28 |
| 9 | VVAIFAQAL | 188 | 2.0000 | 21.28 |
| 10 | VFHLAAQID | 73 | 1.8000 | 19.15 |
| 11 | LYGLDCSHI | 162 | 1.5000 | 15.96 |
| 12 | WRPQIELAD | 290 | 1.4000 | 14.89 |
| 13 | VRRSVADPQ | 82 | 1.3000 | 13.83 |
| 14 | VLGWRPQIE | 287 | 1.2500 | 13.30 |
| 15 | YGLDCSHIA | 163 | 1.0000 | 10.64 |
| 16 | IVHTSSGGS | 115 | 0.9000 | 9.57 |
| 17 | VVFHLAAQI | 72 | 0.8000 | 8.51 |
| 18 | FVEADIVTA | 51 | 0.7000 | 7.45 |
| 19 | VFGDGTNTR | 204 | 0.5000 | 5.32 |
| 20 | VVDAFVRVS | 220 | 0.5000 | 5.32 |
| 21 | VEADIVTAD | 52 | 0.3000 | 3.19 |
| 22 | FDAAVNVIG | 91 | 0.2000 | 2.13 |
| 23 | VRVSADVGG | 225 | 0.1000 | 1.06 |
| 24 | FHLAAQIDV | 74 | -0.0200 | 0 |
| 25 | LDNFATGRA | 29 | -0.1000 | 0 |
| 26 | LEHLADNSA | 40 | -0.1000 | 0 |
| 27 | YPTPETAPT | 131 | -0.2000 | 0 |

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

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|---|---|---|
|  | 1.2 | 8.8 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VRALVTGAA | 0 | 2.9000 | 32.95 |
| 2 | VRLAEAARQ | 101 | 2.7000 | 30.68 |
| 3 | VVGLDNFAT | 26 | 2.3500 | 26.70 |
| 4 | VNVIGTVRL | 95 | 2.2000 | 25.00 |
| 5 | FRHLYGLDC | 159 | 2.2000 | 25.00 |
| 6 | VRKIVHTSS | 112 | 2.0000 | 22.73 |
| 7 | LYGLDCSHI | 162 | 1.3000 | 14.77 |
| 8 | FVRVSADVG | 224 | 1.1000 | 12.50 |
| 9 | YGLDCSHIA | 163 | 1.0000 | 11.36 |
| 10 | VVAIFAQAL | 188 | 1.0000 | 11.36 |
| 11 | IVHTSSGGS | 115 | 0.9000 | 10.23 |
| 12 | FVEADIVTA | 51 | 0.7000 | 7.95 |
| 13 | VVFHLAAQI | 72 | 0.6000 | 6.82 |
| 14 | VRRSVADPQ | 82 | 0.5000 | 5.68 |
| 15 | VFGDGTNTR | 204 | 0.5000 | 5.68 |
| 16 | YVFVDDVVD | 214 | 0.5000 | 5.68 |
| 17 | VVDAFVRVS | 220 | 0.5000 | 5.68 |
| 18 | LDNFATGRA | 29 | -0.1000 | 0 |
| 19 | LEHLADNSA | 40 | -0.1000 | 0 |
| 20 | LRFNIGTGK | 235 | -0.1000 | 0 |
| 21 | FHLAAQIDV | 74 | -0.3200 | 0 |
| 22 | IVTADLHAI | 56 | -0.7000 | 0 |
| 23 | LHSAVAAAV | 250 | -0.7000 | 0 |
| 24 | VFHLAAQID | 73 | -0.9000 | 0 |
| 25 | FAQALLSGK | 192 | -0.9000 | 0 |
| 26 | VAIFAQALL | 189 | -1.0000 | 0 |
| 27 | FDAAVNVIG | 91 | -1.1000 | 0 |
| 28 | IGTVRLAEA | 98 | -1.1000 | 0 |
| 29 | YPTPETAPT | 131 | -1.1000 | 0 |

| 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 | VRLAEAARQ | 101 | 4.5000 | 47.87 |
| 2 | VVGLDNFAT | 26 | 4.2500 | 45.21 |
| 3 | VNVIGTVRL | 95 | 4.2000 | 44.68 |
| 4 | VRALVTGAA | 0 | 3.9000 | 41.49 |
| 5 | VRKIVHTSS | 112 | 3.0000 | 31.91 |
| 6 | VVAIFAQAL | 188 | 3.0000 | 31.91 |
| 7 | VFHLAAQID | 73 | 2.8000 | 29.79 |
| 8 | LYGLDCSHI | 162 | 2.5000 | 26.60 |
| 9 | VRRSVADPQ | 82 | 2.3000 | 24.47 |
| 10 | VLGWRPQIE | 287 | 2.2500 | 23.94 |
| 11 | YVFVDDVVD | 214 | 2.2000 | 23.40 |
| 12 | IVHTSSGGS | 115 | 1.9000 | 20.21 |
| 13 | VVFHLAAQI | 72 | 1.8000 | 19.15 |
| 14 | VFGDGTNTR | 204 | 1.5000 | 15.96 |
| 15 | VVDAFVRVS | 220 | 1.5000 | 15.96 |
| 16 | FVRVSADVG | 224 | 1.4000 | 14.89 |
| 17 | VEADIVTAD | 52 | 1.3000 | 13.83 |
| 18 | FRHLYGLDC | 159 | 1.2000 | 12.77 |
| 19 | VRVSADVGG | 225 | 1.1000 | 11.70 |
| 20 | LNTFRHLYG | 156 | 1.0000 | 10.64 |
| 21 | VAIFAQALL | 189 | 1.0000 | 10.64 |
| 22 | VFVDDVVDA | 215 | 1.0000 | 10.64 |
| 23 | LDNFATGRA | 29 | 0.9000 | 9.57 |
| 24 | LEHLADNSA | 40 | 0.9000 | 9.57 |
| 25 | LHSAVAAAV | 250 | 0.6000 | 6.38 |
| 26 | VDRLLADGH | 16 | 0.5000 | 5.32 |
| 27 | IVTADLHAI | 56 | 0.5000 | 5.32 |
| 28 | WRPQIELAD | 290 | 0.4000 | 4.26 |
| 29 | IFAQALLSG | 191 | 0.3000 | 3.19 |
| 30 | LRFNIGTGK | 235 | 0.2000 | 2.13 |
| 31 | IAPANVYGP | 170 | 0.1000 | 1.06 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VFGDGTNTR | 204 | 4.4000 | 48.89 |
| 2 | YGLDCSHIA | 163 | 3.9000 | 43.33 |
| 3 | FVDDVVDAF | 216 | 3.7000 | 41.11 |
| 4 | VVFHLAAQI | 72 | 3.6000 | 40.00 |
| 5 | VNVIGTVRL | 95 | 3.0400 | 33.78 |
| 6 | IVHTSSGGS | 115 | 2.8000 | 31.11 |
| 7 | VFVDDVVDA | 215 | 2.6800 | 29.78 |
| 8 | VRALVTGAA | 0 | 2.6000 | 28.89 |
| 9 | FRHLYGLDC | 159 | 2.4000 | 26.67 |
| 10 | VRRSVADPQ | 82 | 2.2000 | 24.44 |
| 11 | VRLAEAARQ | 101 | 2.0000 | 22.22 |
| 12 | FVRVSADVG | 224 | 2.0000 | 22.22 |
| 13 | VVGLDNFAT | 26 | 1.9000 | 21.11 |
| 14 | VRVSADVGG | 225 | 1.8800 | 20.89 |
| 15 | VVAIFAQAL | 188 | 1.8600 | 20.67 |
| 16 | VRKIVHTSS | 112 | 1.6000 | 17.78 |
| 17 | FIGSTLVDR | 10 | 1.5800 | 17.56 |
| 18 | LYGLDCSHI | 162 | 1.3000 | 14.44 |
| 19 | VGLDNFATG | 27 | 1.2000 | 13.33 |
| 20 | LRFNIGTGK | 235 | 1.1000 | 12.22 |
| 21 | WRPQIELAD | 290 | 1.0000 | 11.11 |
| 22 | IGSTLVDRL | 11 | 0.9600 | 10.67 |
| 23 | FVEADIVTA | 51 | 0.8800 | 9.78 |
| 24 | VEADIVTAD | 52 | 0.7000 | 7.78 |
| 25 | LEQHRPEVV | 65 | 0.7000 | 7.78 |
| 26 | IYGTPPEYP | 124 | 0.7000 | 7.78 |
| 27 | FHLAAQIDV | 74 | 0.6800 | 7.56 |
| 28 | IVTADLHAI | 56 | 0.6000 | 6.67 |
| 29 | IFAQALLSG | 191 | 0.6000 | 6.67 |

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|---|---|---|---|---|
| 30 | VVDAFVRVS | 220 | 0.6000 | 6.67 |
| 31 | LKRSCLDIG | 274 | 0.6000 | 6.67 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VRALVTGAA | 0 | 3.9000 | 44.32 |
| 2 | VRLAEAARQ | 101 | 3.7000 | 42.05 |
| 3 | VVGLDNFAT | 26 | 3.3500 | 38.07 |
| 4 | VNVIGTVRL | 95 | 3.2000 | 36.36 |
| 5 | VRKIVHTSS | 112 | 3.0000 | 34.09 |
| 6 | LYGLDCSHI | 162 | 2.3000 | 26.14 |
| 7 | VVAIFAQAL | 188 | 2.0000 | 22.73 |
| 8 | IVHTSSGGS | 115 | 1.9000 | 21.59 |
| 9 | VVFHLAAQI | 72 | 1.6000 | 18.18 |
| 10 | VRRSVADPQ | 82 | 1.5000 | 17.05 |
| 11 | VFGDGTNTR | 204 | 1.5000 | 17.05 |
| 12 | VVDAFVRVS | 220 | 1.5000 | 17.05 |
| 13 | FRHLYGLDC | 159 | 1.2000 | 13.64 |
| 14 | VFVDDVVDA | 215 | 1.0000 | 11.36 |
| 15 | LDNFATGRA | 29 | 0.9000 | 10.23 |
| 16 | LEHLADNSA | 40 | 0.9000 | 10.23 |
| 17 | LRFNIGTGK | 235 | 0.9000 | 10.23 |
| 18 | IVTADLHAI | 56 | 0.3000 | 3.41 |
| 19 | LHSAVAAAV | 250 | 0.3000 | 3.41 |
| 20 | VFHLAAQID | 73 | 0.1000 | 1.14 |
| 21 | FVRVSADVG | 224 | 0.1000 | 1.14 |
| 22 | IGTVRLAEA | 98 | -0.1000 | 0 |
| 23 | VRVSADVGG | 225 | -0.2000 | 0 |
| 24 | FVEADIVTA | 51 | -0.3000 | 0 |
| 25 | LNTFRHLYG | 156 | -0.3000 | 0 |
| 26 | IAPANVYGP | 170 | -0.3000 | 0 |
| 27 | YVFVDDVVD | 214 | -0.5000 | 0 |

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|---|---|---|---|---|
| 28 | VDRLLADGH | 16 | -0.7200 | 0 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | YGLDCSHIA | 163 | 3.9000 | 45.35 |
| 2 | VRRSVADPQ | 82 | 2.9000 | 33.72 |
| 3 | VFGDGTNTR | 204 | 2.9000 | 33.72 |
| 4 | VVFHLAAQI | 72 | 2.7000 | 31.40 |
| 5 | VRLAEAARQ | 101 | 2.7000 | 31.40 |
| 6 | VFVDDVVDA | 215 | 2.6800 | 31.16 |
| 7 | VRALVTGAA | 0 | 2.6000 | 30.23 |
| 8 | IVHTSSGGS | 115 | 2.4000 | 27.91 |
| 9 | FRHLYGLDC | 159 | 2.4000 | 27.91 |
| 10 | VNVIGTVRL | 95 | 2.0800 | 24.19 |
| 11 | FVDDVVDAF | 216 | 1.8000 | 20.93 |
| 12 | VVGLDNFAT | 26 | 1.2000 | 13.95 |
| 13 | VRKIVHTSS | 112 | 1.2000 | 13.95 |
| 14 | LRFNIGTGK | 235 | 1.0000 | 11.63 |
| 15 | VVAIFAQAL | 188 | 0.9000 | 10.47 |
| 16 | FVEADIVTA | 51 | 0.8800 | 10.23 |
| 17 | FVRVSADVG | 224 | 0.6000 | 6.98 |
| 18 | VRVSADVGG | 225 | 0.4800 | 5.58 |
| 19 | LYGLDCSHI | 162 | 0.4000 | 4.65 |
| 20 | VVDAFVRVS | 220 | 0.2000 | 2.33 |
| 21 | FIGSTLVDR | 10 | 0.0800 | 0.93 |
| 22 | WRPQIELAD | 290 | -0.1000 | 0 |
| 23 | VGLDNFATG | 27 | -0.2000 | 0 |
| 24 | IVTADLHAI | 56 | -0.3000 | 0 |
| 25 | LEQHRPEVV | 65 | -0.3000 | 0 |
| 26 | IYGTPPEYP | 124 | -0.3000 | 0 |
| 27 | FHLAAQIDV | 74 | -0.3200 | 0 |
| 28 | LEHLADNSA | 40 | -0.4000 | 0 |

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|---|---|---|---|---|
| 29 | VEADIVTAD | 52 | -0.4000 | 0 |

| 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 | VVAIFAQAL | 188 | 6.7000 | 57.76 |
| 2 | VNVIGTVRL | 95 | 6.3200 | 54.48 |
| 3 | VVFHLAAQI | 72 | 5.4000 | 46.55 |
| 4 | FHLAAQIDV | 74 | 5.1000 | 43.97 |
| 5 | IVTADLHAI | 56 | 4.5000 | 38.79 |
| 6 | VHTSSGGSI | 116 | 4.1000 | 35.34 |
| 7 | YLNTFRHLY | 155 | 3.8000 | 32.76 |
| 8 | LVTGAAGFI | 3 | 3.4000 | 29.31 |
| 9 | IGSTLVDRL | 11 | 3.3000 | 28.45 |
| 10 | FATGRATNL | 32 | 3.2000 | 27.59 |
| 11 | FRHLYGLDC | 159 | 3.2000 | 27.59 |
| 12 | IYLNTFRHL | 154 | 3.1000 | 26.72 |
| 13 | LYGLDCSHI | 162 | 3.1000 | 26.72 |
| 14 | LGWRPQIEL | 288 | 3.1000 | 26.72 |
| 15 | IVHTSSGGS | 115 | 3.0000 | 25.86 |
| 16 | VAIFAQALL | 189 | 3.0000 | 25.86 |
| 17 | VGGGLRFNI | 231 | 3.0000 | 25.86 |
| 18 | FIGSTLVDR | 10 | 2.7000 | 23.28 |
| 19 | VIGTVRLAE | 97 | 2.5000 | 21.55 |
| 20 | VVGLDNFAT | 26 | 2.4000 | 20.69 |
| 21 | FHPPRLGDL | 266 | 2.4000 | 20.69 |
| 22 | VRKIVHTSS | 112 | 2.1000 | 18.10 |
| 23 | FVEADIVTA | 51 | 2.0000 | 17.24 |
| 24 | LHSAVAAAV | 250 | 2.0000 | 17.24 |
| 25 | FVRVSADVG | 224 | 1.8000 | 15.52 |
| 26 | YVFVDDVVD | 214 | 1.7000 | 14.66 |
| 27 | VRVSADVGG | 225 | 1.7000 | 14.66 |
| 28 | VRRTVEYFR | 300 | 1.7000 | 14.66 |

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|---|---|---|---|---|
| 29 | LEQHRPEVV | 65 | 1.6000 | 13.79 |
| 30 | LLSGKPTRV | 196 | 1.5000 | 12.93 |
| 31 | FNIGTGKET | 237 | 1.5000 | 12.93 |

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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 | VVAIFAQAL | 188 | 6.7000 | 57.76 |
| 2 | VNVIGTVRL | 95 | 6.3200 | 54.48 |
| 3 | VVFHLAAQI | 72 | 5.4000 | 46.55 |
| 4 | FHLAAQIDV | 74 | 5.1000 | 43.97 |
| 5 | IVTADLHAI | 56 | 4.5000 | 38.79 |
| 6 | VHTSSGGSI | 116 | 4.1000 | 35.34 |
| 7 | YLNTFRHLY | 155 | 3.8000 | 32.76 |
| 8 | LVTGAAGFI | 3 | 3.4000 | 29.31 |
| 9 | IGSTLVDRL | 11 | 3.3000 | 28.45 |
| 10 | FATGRATNL | 32 | 3.2000 | 27.59 |
| 11 | FRHLYGLDC | 159 | 3.2000 | 27.59 |
| 12 | IYLNTFRHL | 154 | 3.1000 | 26.72 |
| 13 | LYGLDCSHI | 162 | 3.1000 | 26.72 |
| 14 | LGWRPQIEL | 288 | 3.1000 | 26.72 |
| 15 | IVHTSSGGS | 115 | 3.0000 | 25.86 |
| 16 | VAIFAQALL | 189 | 3.0000 | 25.86 |
| 17 | VGGGLRFNI | 231 | 3.0000 | 25.86 |
| 18 | FIGSTLVDR | 10 | 2.7000 | 23.28 |
| 19 | VIGTVRLAE | 97 | 2.5000 | 21.55 |
| 20 | VVGLDNFAT | 26 | 2.4000 | 20.69 |
| 21 | FHPPRLGDL | 266 | 2.4000 | 20.69 |
| 22 | VRKIVHTSS | 112 | 2.1000 | 18.10 |
| 23 | FVEADIVTA | 51 | 2.0000 | 17.24 |
| 24 | LHSAVAAAV | 250 | 2.0000 | 17.24 |
| 25 | FVRVSADVG | 224 | 1.8000 | 15.52 |
| 26 | YVFVDDVVD | 214 | 1.7000 | 14.66 |

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|---|---|---|---|---|
| 27 | VRVSADVGG | 225 | 1.7000 | 14.66 |
| 28 | VRRTVEYFR | 300 | 1.7000 | 14.66 |
| 29 | LEQHRPEVV | 65 | 1.6000 | 13.79 |
| 30 | LLSGKPTRV | 196 | 1.5000 | 12.93 |
| 31 | FNIGTGKET | 237 | 1.5000 | 12.93 |

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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 |
|---|---|---|---|---|
| 1 | VRLAEAARQ | 101 | 3.5000 | 40.70 |
| 2 | LVDRLLADG | 15 | 2.6000 | 30.23 |
| 3 | VRALVTGAA | 0 | 2.2000 | 25.58 |
| 4 | FRHLYGLDC | 159 | 2.1000 | 24.42 |
| 5 | YAAGKVAGE | 145 | 1.5000 | 17.44 |
| 6 | VIGTVRLAE | 97 | 1.3000 | 15.12 |
| 7 | LSGKPTRVF | 197 | 1.3000 | 15.12 |
| 8 | VVDAFVRVS | 220 | 1.1000 | 12.79 |
| 9 | FVRVSADVG | 224 | 1.0000 | 11.63 |
| 10 | VVFHLAAQI | 72 | 0.8000 | 9.30 |
| 11 | VLGWRPQIE | 287 | 0.8000 | 9.30 |
| 12 | WRPQIELAD | 290 | 0.8000 | 9.30 |
| 13 | YLNTFRHLY | 155 | 0.7000 | 8.14 |
| 14 | VAIFAQALL | 189 | 0.7000 | 8.14 |
| 15 | YVFVDDVVD | 214 | 0.7000 | 8.14 |
| 16 | IGLAERVLG | 281 | 0.7000 | 8.14 |
| 17 | LGWRPQIEL | 288 | 0.7000 | 8.14 |
| 18 | FVEADIVTA | 51 | 0.5000 | 5.81 |
| 19 | VFHLAAQID | 73 | 0.5000 | 5.81 |
| 20 | IVHTSSGGS | 115 | 0.4000 | 4.65 |
| 21 | IVTADLHAI | 56 | 0.3000 | 3.49 |
| 22 | FHLAAQIDV | 74 | 0.3000 | 3.49 |
| 23 | IDVRRSVAD | 80 | 0.3000 | 3.49 |
| 24 | VNVIGTVRL | 95 | 0.3000 | 3.49 |

|  |  |  |  |  |
|---|---|---|---|---|
| 25 | VVGLDNFAT | 26 | 0.2000 | 2.33 |
| 26 | LNTFRHLYG | 156 | 0.2000 | 2.33 |
| 27 | VVAIFAQAL | 188 | 0.2000 | 2.33 |
| 28 | VRRSVADPQ | 82 | -0.2000 | 0 |
| 29 | YGPRQDPHG | 176 | -0.2000 | 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 | VRLAEAARQ | 101 | 2.7000 | 33.75 |
| 2 | VRALVTGAA | 0 | 2.2000 | 27.50 |
| 3 | FRHLYGLDC | 159 | 2.1000 | 26.25 |
| 4 | LVDRLLADG | 15 | 1.3000 | 16.25 |
| 5 | VVDAFVRVS | 220 | 1.1000 | 13.75 |
| 6 | VVFHLAAQI | 72 | 0.6000 | 7.50 |
| 7 | FVEADIVTA | 51 | 0.5000 | 6.25 |
| 8 | IVHTSSGGS | 115 | 0.4000 | 5.00 |
| 9 | LSGKPTRVF | 197 | 0.4000 | 5.00 |
| 10 | IVTADLHAI | 56 | 0.1000 | 1.25 |
| 11 | VRKIVHTSS | 112 | -0.3000 | 0 |
| 12 | VAIFAQALL | 189 | -0.3000 | 0 |
| 13 | FVRVSADVG | 224 | -0.3000 | 0 |
| 14 | LGWRPQIEL | 288 | -0.3000 | 0 |
| 15 | YLNTFRHLY | 155 | -0.4000 | 0 |
| 16 | YGLDCSHIA | 163 | -0.5000 | 0 |
| 17 | VFVDDVVDA | 215 | -0.6000 | 0 |
| 18 | IGLAERVLG | 281 | -0.6000 | 0 |
| 19 | LVTGAAGFI | 3 | -0.7000 | 0 |
| 20 | VVGLDNFAT | 26 | -0.7000 | 0 |
| 21 | VNVIGTVRL | 95 | -0.7000 | 0 |
| 22 | LHSAVAAAV | 250 | -0.7000 | 0 |
| 23 | LYGLDCSHI | 162 | -0.8000 | 0 |
| 24 | VVAIFAQAL | 188 | -0.8000 | 0 |

| | | | | |
|---|---|---|---|---|
| 25 | LDNFATGRA | 29 | -1.0000 | 0 |
| 26 | VRRSVADPQ | 82 | -1.0000 | 0 |
| 27 | LNTFRHLYG | 156 | -1.1000 | 0 |
| 28 | FHPPRLGDL | 266 | -1.2000 | 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 | VRLAEAARQ | 101 | 3.7000 | 46.25 |
| 2 | VRALVTGAA | 0 | 3.2000 | 40.00 |
| 3 | LVDRLLADG | 15 | 2.3000 | 28.75 |
| 4 | VVDAFVRVS | 220 | 2.1000 | 26.25 |
| 5 | VVFHLAAQI | 72 | 1.6000 | 20.00 |
| 6 | IVHTSSGGS | 115 | 1.4000 | 17.50 |
| 7 | LSGKPTRVF | 197 | 1.4000 | 17.50 |
| 8 | IVTADLHAI | 56 | 1.1000 | 13.75 |
| 9 | FRHLYGLDC | 159 | 1.1000 | 13.75 |
| 10 | IGTVRLAEA | 98 | 1.0000 | 12.50 |
| 11 | VRKIVHTSS | 112 | 0.7000 | 8.75 |
| 12 | VAIFAQALL | 189 | 0.7000 | 8.75 |
| 13 | LGWRPQIEL | 288 | 0.7000 | 8.75 |
| 14 | VFVDDVVDA | 215 | 0.4000 | 5.00 |
| 15 | IGLAERVLG | 281 | 0.4000 | 5.00 |
| 16 | LVTGAAGFI | 3 | 0.3000 | 3.75 |
| 17 | VVGLDNFAT | 26 | 0.3000 | 3.75 |
| 18 | VNVIGTVRL | 95 | 0.3000 | 3.75 |
| 19 | LHSAVAAAV | 250 | 0.3000 | 3.75 |
| 20 | LYGLDCSHI | 162 | 0.2000 | 2.50 |
| 21 | VVAIFAQAL | 188 | 0.2000 | 2.50 |
| 22 | LNTFRHLYG | 156 | -0.1000 | 0 |
| 23 | LAERVLGWR | 283 | -0.2000 | 0 |
| 24 | LRFNIGTGK | 235 | -0.4000 | 0 |
| 25 | FVEADIVTA | 51 | -0.5000 | 0 |

|  |  |  |  |  |
|---|---|---|---|---|
| 26 | VGGGLRFNI | 231 | -0.5000 | 0 |
| 27 | VIGTVRLAE | 97 | -0.7000 | 0 |
| 28 | VEYFRHKHT | 304 | -0.7000 | 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 | VRLAEAARQ | 101 | 4.5000 | 52.33 |
| 2 | LVDRLLADG | 15 | 3.6000 | 41.86 |
| 3 | VRALVTGAA | 0 | 3.2000 | 37.21 |
| 4 | VIGTVRLAE | 97 | 2.3000 | 26.74 |
| 5 | LSGKPTRVF | 197 | 2.3000 | 26.74 |
| 6 | VVDAFVRVS | 220 | 2.1000 | 24.42 |
| 7 | VVFHLAAQI | 72 | 1.8000 | 20.93 |
| 8 | VLGWRPQIE | 287 | 1.8000 | 20.93 |
| 9 | VAIFAQALL | 189 | 1.7000 | 19.77 |
| 10 | IGLAERVLG | 281 | 1.7000 | 19.77 |
| 11 | LGWRPQIEL | 288 | 1.7000 | 19.77 |
| 12 | VFHLAAQID | 73 | 1.5000 | 17.44 |
| 13 | IVHTSSGGS | 115 | 1.4000 | 16.28 |
| 14 | IVTADLHAI | 56 | 1.3000 | 15.12 |
| 15 | IDVRRSVAD | 80 | 1.3000 | 15.12 |
| 16 | VNVIGTVRL | 95 | 1.3000 | 15.12 |
| 17 | VVGLDNFAT | 26 | 1.2000 | 13.95 |
| 18 | LNTFRHLYG | 156 | 1.2000 | 13.95 |
| 19 | VVAIFAQAL | 188 | 1.2000 | 13.95 |
| 20 | FRHLYGLDC | 159 | 1.1000 | 12.79 |
| 21 | IGTVRLAEA | 98 | 1.0000 | 11.63 |
| 22 | VRRSVADPQ | 82 | 0.8000 | 9.30 |
| 23 | VRKIVHTSS | 112 | 0.7000 | 8.14 |
| 24 | LHSAVAAAV | 250 | 0.6000 | 6.98 |
| 25 | LVTGAAGFI | 3 | 0.5000 | 5.81 |
| 26 | YAAGKVAGE | 145 | 0.5000 | 5.81 |

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|---|---|---|---|---|
| 27 | LYGLDCSHI | 162 | 0.4000 | 4.65 |
| 28 | VFVDDVVDA | 215 | 0.4000 | 4.65 |
| 29 | VEYFRHKHT | 304 | 0.2000 | 2.33 |

| 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 | VRLAEAARQ | 101 | 2.7000 | 31.03 |
| 2 | FRHLYGLDC | 159 | 2.7000 | 31.03 |
| 3 | VRKIVHTSS | 112 | 2.5000 | 28.74 |
| 4 | VRALVTGAA | 0 | 1.5000 | 17.24 |
| 5 | FVEADIVTA | 51 | 1.5000 | 17.24 |
| 6 | LRFNIGTGK | 235 | 1.4000 | 16.09 |
| 7 | LVDRLLADG | 15 | 1.3000 | 14.94 |
| 8 | LYGLDCSHI | 162 | 1.0000 | 11.49 |
| 9 | FVRVSADVG | 224 | 0.9000 | 10.34 |
| 10 | FHLAAQIDV | 74 | 0.8800 | 10.11 |
| 11 | VVDAFVRVS | 220 | 0.8000 | 9.20 |
| 12 | IVTADLHAI | 56 | 0.6000 | 6.90 |
| 13 | VVFHLAAQI | 72 | 0.6000 | 6.90 |
| 14 | LGWRPQIEL | 288 | 0.5800 | 6.67 |
| 15 | FAQALLSGK | 192 | 0.4000 | 4.60 |
| 16 | VFVDDVVDA | 215 | 0.4000 | 4.60 |
| 17 | IGLAERVLG | 281 | 0.4000 | 4.60 |
| 18 | VNVIGTVRL | 95 | 0.3000 | 3.45 |
| 19 | VRRSVADPQ | 82 | 0.2000 | 2.30 |
| 20 | VVAIFAQAL | 188 | 0.2000 | 2.30 |
| 21 | VVGLDNFAT | 26 | 0.1500 | 1.72 |
| 22 | YLNTFRHLY | 155 | 0.1000 | 1.15 |
| 23 | LSGKPTRVF | 197 | 0.1000 | 1.15 |
| 24 | IVHTSSGGS | 115 | -0.3000 | 0 |
| 25 | VAIFAQALL | 189 | -0.3000 | 0 |
| 26 | LNTFRHLYG | 156 | -0.5000 | 0 |

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|---|---|---|---|---|
| 27 | VFGDGTNTR | 204 | -0.5000 | 0 |
| 28 | FIGSTLVDR | 10 | -0.6000 | 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 | FRHLYGLDC | 159 | 3.9000 | 38.61 |
| 2 | VRLAEAARQ | 101 | 3.5000 | 34.65 |
| 3 | VIGTVRLAE | 97 | 3.1000 | 30.69 |
| 4 | LVDRLLADG | 15 | 2.6000 | 25.74 |
| 5 | WRPQIELAD | 290 | 2.6000 | 25.74 |
| 6 | VRALVTGAA | 0 | 2.3000 | 22.77 |
| 7 | LGWRPQIEL | 288 | 2.3000 | 22.77 |
| 8 | LNTFRHLYG | 156 | 2.0000 | 19.80 |
| 9 | FHLAAQIDV | 74 | 1.9000 | 18.81 |
| 10 | YAAGKVAGE | 145 | 1.5000 | 14.85 |
| 11 | LSGKPTRVF | 197 | 1.5000 | 14.85 |
| 12 | YLNTFRHLY | 155 | 1.4000 | 13.86 |
| 13 | VVDAFVRVS | 220 | 1.3000 | 12.87 |
| 14 | YVFVDDVVD | 214 | 1.2000 | 11.88 |
| 15 | IGLAERVLG | 281 | 1.2000 | 11.88 |
| 16 | FVEADIVTA | 51 | 1.0000 | 9.90 |
| 17 | IVTADLHAI | 56 | 1.0000 | 9.90 |
| 18 | YGPRQDPHG | 176 | 0.9500 | 9.41 |
| 19 | VLGWRPQIE | 287 | 0.9000 | 8.91 |
| 20 | VVFHLAAQI | 72 | 0.8000 | 7.92 |
| 21 | IDVRRSVAD | 80 | 0.8000 | 7.92 |
| 22 | VNVIGTVRL | 95 | 0.8000 | 7.92 |
| 23 | VRKIVHTSS | 112 | 0.8000 | 7.92 |
| 24 | IFAQALLSG | 191 | 0.8000 | 7.92 |
| 25 | VVGLDNFAT | 26 | 0.7000 | 6.93 |
| 26 | VAIFAQALL | 189 | 0.7000 | 6.93 |
| 27 | FVRVSADVG | 224 | 0.7000 | 6.93 |

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|---|---|---|---|---|
| 28 | VFHLAAQID | 73 | 0.6000 | 5.94 |
| 29 | IVHTSSGGS | 115 | 0.5000 | 4.95 |
| 30 | VVAIFAQAL | 188 | 0.3000 | 2.97 |
| 31 | YGLDCSHIA | 163 | 0.2000 | 1.98 |

| 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 | FRHLYGLDC | 159 | 4.3000 | 51.81 |
| 2 | VRALVTGAA | 0 | 2.7000 | 32.53 |
| 3 | VRLAEAARQ | 101 | 2.7000 | 32.53 |
| 4 | FHLAAQIDV | 74 | 1.6000 | 19.28 |
| 5 | VRKIVHTSS | 112 | 1.4000 | 16.87 |
| 6 | VVDAFVRVS | 220 | 1.3000 | 15.66 |
| 7 | FVEADIVTA | 51 | 1.0000 | 12.05 |
| 8 | VVFHLAAQI | 72 | 1.0000 | 12.05 |
| 9 | IVHTSSGGS | 115 | 0.9000 | 10.84 |
| 10 | IVTADLHAI | 56 | 0.8000 | 9.64 |
| 11 | YLNTFRHLY | 155 | 0.7000 | 8.43 |
| 12 | LNTFRHLYG | 156 | 0.6000 | 7.23 |
| 13 | VIGTVRLAE | 97 | 0.5000 | 6.02 |
| 14 | WRPQIELAD | 290 | 0.5000 | 6.02 |
| 15 | VNVIGTVRL | 95 | 0.4000 | 4.82 |
| 16 | VVGLDNFAT | 26 | 0.2000 | 2.41 |
| 17 | IGTVRLAEA | 98 | 0.1000 | 1.20 |
| 18 | IFAQALLSG | 191 | 0.1000 | 1.20 |
| 19 | VVAIFAQAL | 188 | -0.1000 | 0 |
| 20 | IGLAERVLG | 281 | -0.1000 | 0 |
| 21 | LRFNIGTGK | 235 | -0.3000 | 0 |
| 22 | LYGLDCSHI | 162 | -0.4000 | 0 |
| 23 | VAIFAQALL | 189 | -0.4000 | 0 |
| 24 | YGLDCSHIA | 163 | -0.5000 | 0 |
| 25 | FVRVSADVG | 224 | -0.5000 | 0 |

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|---|---|---|---|---|
| 26 | LHSAVAAAV | 250 | -0.7000 | 0 |
| 27 | FIGSTLVDR | 10 | -0.8000 | 0 |
| 28 | VFVDDVVDA | 215 | -0.8000 | 0 |
| 29 | LDNFATGRA | 29 | -1.0000 | 0 |
| 30 | VRRSVADPQ | 82 | -1.0000 | 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 | VVFHLAAQI | 72 | 4.1000 | 48.81 |
| 2 | VVDAFVRVS | 220 | 3.9000 | 46.43 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 44.05 |
| 4 | IVTADLHAI | 56 | 2.3000 | 27.38 |
| 5 | VRALVTGAA | 0 | 1.9000 | 22.62 |
| 6 | LSGKPTRVF | 197 | 1.7000 | 20.24 |
| 7 | VVGLDNFAT | 26 | 1.5000 | 17.86 |
| 8 | FRHLYGLDC | 159 | 1.5000 | 17.86 |
| 9 | IGLAERVLG | 281 | 1.4000 | 16.67 |
| 10 | VRRSVADPQ | 82 | 1.3000 | 15.48 |
| 11 | VRKIVHTSS | 112 | 1.3000 | 15.48 |
| 12 | LRFNIGTGK | 235 | 1.2000 | 14.29 |
| 13 | VAIFAQALL | 189 | 1.0000 | 11.90 |
| 14 | IFAQALLSG | 191 | 1.0000 | 11.90 |
| 15 | VFVDDVVDA | 215 | 1.0000 | 11.90 |
| 16 | LNTFRHLYG | 156 | 0.9000 | 10.71 |
| 17 | IYLNTFRHL | 154 | 0.8000 | 9.52 |
| 18 | FVEADIVTA | 51 | 0.5000 | 5.95 |
| 19 | VGGGLRFNI | 231 | 0.5000 | 5.95 |
| 20 | LEQHRPEVV | 65 | 0.4000 | 4.76 |
| 21 | VNVIGTVRL | 95 | 0.4000 | 4.76 |
| 22 | VDAFVRVSA | 221 | 0.4000 | 4.76 |
| 23 | VEYFRHKHT | 304 | 0.4000 | 4.76 |
| 24 | IVHTSSGGS | 115 | 0.3000 | 3.57 |

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|---|---|---|---|---|
| 25 | LYGLDCSHI | 162 | 0.3000 | 3.57 |
| 26 | LHSAVAAAV | 250 | 0.3000 | 3.57 |
| 27 | VLGWRPQIE | 287 | 0.3000 | 3.57 |
| 28 | LVDRLLADG | 15 | 0.2000 | 2.38 |
| 29 | ILEQHRPEV | 64 | 0.2000 | 2.38 |
| 30 | VVAIFAQAL | 188 | 0.1000 | 1.19 |

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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 | VRALVTGAA | 0 | 3.7000 | 44.58 |
| 2 | VRLAEAARQ | 101 | 3.7000 | 44.58 |
| 3 | FRHLYGLDC | 159 | 3.3000 | 39.76 |
| 4 | VRKIVHTSS | 112 | 2.4000 | 28.92 |
| 5 | VVDAFVRVS | 220 | 2.3000 | 27.71 |
| 6 | VVFHLAAQI | 72 | 2.0000 | 24.10 |
| 7 | IVHTSSGGS | 115 | 1.9000 | 22.89 |
| 8 | IVTADLHAI | 56 | 1.8000 | 21.69 |
| 9 | LNTFRHLYG | 156 | 1.6000 | 19.28 |
| 10 | VIGTVRLAE | 97 | 1.5000 | 18.07 |
| 11 | VNVIGTVRL | 95 | 1.4000 | 16.87 |
| 12 | VVGLDNFAT | 26 | 1.2000 | 14.46 |
| 13 | IGTVRLAEA | 98 | 1.1000 | 13.25 |
| 14 | IFAQALLSG | 191 | 1.1000 | 13.25 |
| 15 | VVAIFAQAL | 188 | 0.9000 | 10.84 |
| 16 | IGLAERVLG | 281 | 0.9000 | 10.84 |
| 17 | LRFNIGTGK | 235 | 0.7000 | 8.43 |
| 18 | FHLAAQIDV | 74 | 0.6000 | 7.23 |
| 19 | LYGLDCSHI | 162 | 0.6000 | 7.23 |
| 20 | VAIFAQALL | 189 | 0.6000 | 7.23 |
| 21 | LHSAVAAAV | 250 | 0.3000 | 3.61 |
| 22 | VFVDDVVDA | 215 | 0.2000 | 2.41 |
| 23 | IAPANVYGP | 170 | -0.2000 | 0 |

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|---|---|---|---|---|
| 24 | VEYFRHKHT | 304 | -0.2000 | 0 |
| 25 | LVTGAAGFI | 3 | -0.3000 | 0 |
| 26 | YLNTFRHLY | 155 | -0.3000 | 0 |
| 27 | ILEQHRPEV | 64 | -0.3500 | 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 | VRALVTGAA | 0 | 3.7000 | 44.58 |
| 2 | VRLAEAARQ | 101 | 3.7000 | 44.58 |
| 3 | FRHLYGLDC | 159 | 3.3000 | 39.76 |
| 4 | VRKIVHTSS | 112 | 2.4000 | 28.92 |
| 5 | VVDAFVRVS | 220 | 2.3000 | 27.71 |
| 6 | VVFHLAAQI | 72 | 2.0000 | 24.10 |
| 7 | IVHTSSGGS | 115 | 1.9000 | 22.89 |
| 8 | IVTADLHAI | 56 | 1.8000 | 21.69 |
| 9 | LNTFRHLYG | 156 | 1.6000 | 19.28 |
| 10 | VIGTVRLAE | 97 | 1.5000 | 18.07 |
| 11 | VNVIGTVRL | 95 | 1.4000 | 16.87 |
| 12 | VVGLDNFAT | 26 | 1.2000 | 14.46 |
| 13 | IGTVRLAEA | 98 | 1.1000 | 13.25 |
| 14 | IFAQALLSG | 191 | 1.1000 | 13.25 |
| 15 | VVAIFAQAL | 188 | 0.9000 | 10.84 |
| 16 | IGLAERVLG | 281 | 0.9000 | 10.84 |
| 17 | LRFNIGTGK | 235 | 0.7000 | 8.43 |
| 18 | FHLAAQIDV | 74 | 0.6000 | 7.23 |
| 19 | LYGLDCSHI | 162 | 0.6000 | 7.23 |
| 20 | VAIFAQALL | 189 | 0.6000 | 7.23 |
| 21 | LHSAVAAAV | 250 | 0.3000 | 3.61 |
| 22 | VFVDDVVDA | 215 | 0.2000 | 2.41 |
| 23 | IAPANVYGP | 170 | -0.2000 | 0 |
| 24 | VEYFRHKHT | 304 | -0.2000 | 0 |
| 25 | LVTGAAGFI | 3 | -0.3000 | 0 |

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|---|---|---|---|---|
| 26 | YLNTFRHLY | 155 | -0.3000 | 0 |
| 27 | ILEQHRPEV | 64 | -0.3500 | 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 | VFVDDVVDA | 215 | 5.0000 | 54.95 |
| 2 | VRLAEAARQ | 101 | 3.7000 | 40.66 |
| 3 | VRRSVADPQ | 82 | 3.5000 | 38.46 |
| 4 | VRKIVHTSS | 112 | 3.2000 | 35.16 |
| 5 | VRALVTGAA | 0 | 3.1000 | 34.07 |
| 6 | VFGDGTNTR | 204 | 3.0100 | 33.08 |
| 7 | VVFHLAAQI | 72 | 2.6000 | 28.57 |
| 8 | LLADGHSVV | 19 | 2.5700 | 28.24 |
| 9 | LVTGAAGFI | 3 | 2.4000 | 26.37 |
| 10 | VGGGLRFNI | 231 | 2.4000 | 26.37 |
| 11 | LRFNIGTGK | 235 | 2.1000 | 23.08 |
| 12 | IVHTSSGGS | 115 | 2.0000 | 21.98 |
| 13 | YGLDCSHIA | 163 | 1.9000 | 20.88 |
| 14 | VEADIVTAD | 52 | 1.8000 | 19.78 |
| 15 | VNVIGTVRL | 95 | 1.8000 | 19.78 |
| 16 | VVDAFVRVS | 220 | 1.8000 | 19.78 |
| 17 | FVDDVVDAF | 216 | 1.7000 | 18.68 |
| 18 | IGLAERVLG | 281 | 1.7000 | 18.68 |
| 19 | VVAIFAQAL | 188 | 1.5000 | 16.48 |
| 20 | VGLDNFATG | 27 | 1.4000 | 15.38 |
| 21 | LLSGKPTRV | 196 | 1.4000 | 15.38 |
| 22 | IVTADLHAI | 56 | 1.2000 | 13.19 |
| 23 | VTADLHAIL | 57 | 1.2000 | 13.19 |
| 24 | LKRSCLDIG | 274 | 1.1000 | 12.09 |
| 25 | VVGLDNFAT | 26 | 1.0000 | 10.99 |
| 26 | FRHLYGLDC | 159 | 0.9000 | 9.89 |
| 27 | LYGLDCSHI | 162 | 0.8700 | 9.56 |

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|---|---|---|---|---|
| 28 | FVEADIVTA | 51 | 0.8000 | 8.79 |
| 29 | ILEQHRPEV | 64 | 0.8000 | 8.79 |
| 30 | IGTVRLAEA | 98 | 0.7000 | 7.69 |
| 31 | VHTSSGGSI | 116 | 0.6000 | 6.59 |

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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 | VVFHLAAQI | 72 | 3.1000 | 36.90 |
| 2 | VVDAFVRVS | 220 | 2.9000 | 34.52 |
| 3 | VRLAEAARQ | 101 | 2.7000 | 32.14 |
| 4 | FRHLYGLDC | 159 | 2.5000 | 29.76 |
| 5 | FVEADIVTA | 51 | 1.5000 | 17.86 |
| 6 | IVTADLHAI | 56 | 1.3000 | 15.48 |
| 7 | VRALVTGAA | 0 | 0.9000 | 10.71 |
| 8 | YLNTFRHLY | 155 | 0.7000 | 8.33 |
| 9 | LSGKPTRVF | 197 | 0.7000 | 8.33 |
| 10 | VVGLDNFAT | 26 | 0.5000 | 5.95 |
| 11 | IGLAERVLG | 281 | 0.4000 | 4.76 |
| 12 | WRPQIELAD | 290 | 0.4000 | 4.76 |
| 13 | FHLAAQIDV | 74 | 0.3000 | 3.57 |
| 14 | VRRSVADPQ | 82 | 0.3000 | 3.57 |
| 15 | VRKIVHTSS | 112 | 0.3000 | 3.57 |
| 16 | YGLDCSHIA | 163 | 0.3000 | 3.57 |
| 17 | LRFNIGTGK | 235 | 0.2000 | 2.38 |
| 18 | LNTFRHLYG | 156 | -0.1000 | 0 |
| 19 | FIGSTLVDR | 10 | -0.2000 | 0 |
| 20 | IYLNTFRHL | 154 | -0.2000 | 0 |
| 21 | VGGGLRFNI | 231 | -0.5000 | 0 |
| 22 | LEQHRPEVV | 65 | -0.6000 | 0 |
| 23 | VNVIGTVRL | 95 | -0.6000 | 0 |
| 24 | VDAFVRVSA | 221 | -0.6000 | 0 |
| 25 | FVRVSADVG | 224 | -0.6000 | 0 |

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|---|---|---|---|---|
| 26 | VEYFRHKHT | 304 | -0.6000 | 0 |
| 27 | IVHTSSGGS | 115 | -0.7000 | 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 | VVFHLAAQI | 72 | 4.0000 | 45.45 |
| 2 | VVDAFVRVS | 220 | 3.3000 | 37.50 |
| 3 | LSGKPTRVF | 197 | 2.6000 | 29.55 |
| 4 | FRHLYGLDC | 159 | 2.5000 | 28.41 |
| 5 | IVTADLHAI | 56 | 2.2000 | 25.00 |
| 6 | VRLAEAARQ | 101 | 2.0000 | 22.73 |
| 7 | YLNTFRHLY | 155 | 2.0000 | 22.73 |
| 8 | IGLAERVLG | 281 | 1.8000 | 20.45 |
| 9 | FVEADIVTA | 51 | 1.5000 | 17.05 |
| 10 | WRPQIELAD | 290 | 1.5000 | 17.05 |
| 11 | IFAQALLSG | 191 | 1.4000 | 15.91 |
| 12 | FIGSTLVDR | 10 | 1.3000 | 14.77 |
| 13 | FHLAAQIDV | 74 | 1.3000 | 14.77 |
| 14 | LNTFRHLYG | 156 | 1.3000 | 14.77 |
| 15 | VVGLDNFAT | 26 | 1.2000 | 13.64 |
| 16 | VAIFAQALL | 189 | 0.9600 | 10.91 |
| 17 | VRALVTGAA | 0 | 0.9000 | 10.23 |
| 18 | FVRVSADVG | 224 | 0.8000 | 9.09 |
| 19 | IYLNTFRHL | 154 | 0.7600 | 8.64 |
| 20 | VRKIVHTSS | 112 | 0.7000 | 7.95 |
| 21 | VLGWRPQIE | 287 | 0.7000 | 7.95 |
| 22 | LVDRLLADG | 15 | 0.6000 | 6.82 |
| 23 | LEQHRPEVV | 65 | 0.4000 | 4.55 |
| 24 | VGGGLRFNI | 231 | 0.4000 | 4.55 |
| 25 | VNVIGTVRL | 95 | 0.3600 | 4.09 |
| 26 | VIGTVRLAE | 97 | 0.3000 | 3.41 |
| 27 | YGLDCSHIA | 163 | 0.3000 | 3.41 |

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|---|---|---|---|---|
| 28 | LRFNIGTGK | 235 | 0.3000 | 3.41 |
| 29 | LHSAVAAAV | 250 | 0.3000 | 3.41 |
| 30 | ILEQHRPEV | 64 | 0.2000 | 2.27 |
| 31 | LYGLDCSHI | 162 | 0.2000 | 2.27 |

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|---|---|---|
| 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 | VVFHLAAQI | 72 | 4.1000 | 48.81 |
| 2 | VVDAFVRVS | 220 | 3.9000 | 46.43 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 44.05 |
| 4 | IVTADLHAI | 56 | 2.3000 | 27.38 |
| 5 | VRALVTGAA | 0 | 1.9000 | 22.62 |
| 6 | LSGKPTRVF | 197 | 1.7000 | 20.24 |
| 7 | VVGLDNFAT | 26 | 1.5000 | 17.86 |
| 8 | FRHLYGLDC | 159 | 1.5000 | 17.86 |
| 9 | IGLAERVLG | 281 | 1.4000 | 16.67 |
| 10 | VRRSVADPQ | 82 | 1.3000 | 15.48 |
| 11 | VRKIVHTSS | 112 | 1.3000 | 15.48 |
| 12 | LRFNIGTGK | 235 | 1.2000 | 14.29 |
| 13 | VAIFAQALL | 189 | 1.0000 | 11.90 |
| 14 | IFAQALLSG | 191 | 1.0000 | 11.90 |
| 15 | VFVDDVVDA | 215 | 1.0000 | 11.90 |
| 16 | LNTFRHLYG | 156 | 0.9000 | 10.71 |
| 17 | IYLNTFRHL | 154 | 0.8000 | 9.52 |
| 18 | FVEADIVTA | 51 | 0.5000 | 5.95 |
| 19 | VGGGLRFNI | 231 | 0.5000 | 5.95 |
| 20 | LEQHRPEVV | 65 | 0.4000 | 4.76 |
| 21 | VNVIGTVRL | 95 | 0.4000 | 4.76 |
| 22 | VDAFVRVSA | 221 | 0.4000 | 4.76 |
| 23 | VEYFRHKHT | 304 | 0.4000 | 4.76 |
| 24 | IVHTSSGGS | 115 | 0.3000 | 3.57 |
| 25 | LYGLDCSHI | 162 | 0.3000 | 3.57 |

|  |  |  |  |  |
|---|---|---|---|---|
| 26 | LHSAVAAAV | 250 | 0.3000 | 3.57 |
| 27 | VLGWRPQIE | 287 | 0.3000 | 3.57 |
| 28 | LVDRLLADG | 15 | 0.2000 | 2.38 |
| 29 | ILEQHRPEV | 64 | 0.2000 | 2.38 |
| 30 | VVAIFAQAL | 188 | 0.1000 | 1.19 |

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|---|---|---|
| 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 | FRHLYGLDC | 159 | 4.3000 | 49.43 |
| 2 | VRALVTGAA | 0 | 2.7000 | 31.03 |
| 3 | FHLAAQIDV | 74 | 2.6000 | 29.89 |
| 4 | VRLAEAARQ | 101 | 2.0000 | 22.99 |
| 5 | YLNTFRHLY | 155 | 2.0000 | 22.99 |
| 6 | LNTFRHLYG | 156 | 2.0000 | 22.99 |
| 7 | VVFHLAAQI | 72 | 1.9000 | 21.84 |
| 8 | VIGTVRLAE | 97 | 1.9000 | 21.84 |
| 9 | VRKIVHTSS | 112 | 1.8000 | 20.69 |
| 10 | IVTADLHAI | 56 | 1.7000 | 19.54 |
| 11 | VVDAFVRVS | 220 | 1.7000 | 19.54 |
| 12 | WRPQIELAD | 290 | 1.6000 | 18.39 |
| 13 | IFAQALLSG | 191 | 1.5000 | 17.24 |
| 14 | VNVIGTVRL | 95 | 1.3600 | 15.63 |
| 15 | IVHTSSGGS | 115 | 1.3000 | 14.94 |
| 16 | IGLAERVLG | 281 | 1.3000 | 14.94 |
| 17 | FVEADIVTA | 51 | 1.0000 | 11.49 |
| 18 | VVGLDNFAT | 26 | 0.9000 | 10.34 |
| 19 | FVRVSADVG | 224 | 0.9000 | 10.34 |
| 20 | VVAIFAQAL | 188 | 0.8600 | 9.89 |
| 21 | FIGSTLVDR | 10 | 0.7000 | 8.05 |
| 22 | VAIFAQALL | 189 | 0.5600 | 6.44 |
| 23 | LYGLDCSHI | 162 | 0.5000 | 5.75 |
| 24 | LHSAVAAAV | 250 | 0.3000 | 3.45 |

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|---|---|---|---|---|
| 25 | IGTVRLAEA | 98 | 0.1000 | 1.15 |
| 26 | IAPANVYGP | 170 | -0.2000 | 0 |
| 27 | LRFNIGTGK | 235 | -0.2000 | 0 |
| 28 | LVDRLLADG | 15 | -0.3000 | 0 |
| 29 | LSGKPTRVF | 197 | -0.3000 | 0 |

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|---|---|---|
| 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 | VVFHLAAQI | 72 | 5.0000 | 56.82 |
| 2 | VVDAFVRVS | 220 | 4.3000 | 48.86 |
| 3 | LSGKPTRVF | 197 | 3.6000 | 40.91 |
| 4 | IVTADLHAI | 56 | 3.2000 | 36.36 |
| 5 | VRLAEAARQ | 101 | 3.0000 | 34.09 |
| 6 | IGLAERVLG | 281 | 2.8000 | 31.82 |
| 7 | IFAQALLSG | 191 | 2.4000 | 27.27 |
| 8 | LNTFRHLYG | 156 | 2.3000 | 26.14 |
| 9 | VVGLDNFAT | 26 | 2.2000 | 25.00 |
| 10 | VAIFAQALL | 189 | 1.9600 | 22.27 |
| 11 | VRALVTGAA | 0 | 1.9000 | 21.59 |
| 12 | IYLNTFRHL | 154 | 1.7600 | 20.00 |
| 13 | VRKIVHTSS | 112 | 1.7000 | 19.32 |
| 14 | VLGWRPQIE | 287 | 1.7000 | 19.32 |
| 15 | LVDRLLADG | 15 | 1.6000 | 18.18 |
| 16 | FRHLYGLDC | 159 | 1.5000 | 17.05 |
| 17 | LEQHRPEVV | 65 | 1.4000 | 15.91 |
| 18 | VGGGLRFNI | 231 | 1.4000 | 15.91 |
| 19 | VNVIGTVRL | 95 | 1.3600 | 15.45 |
| 20 | VIGTVRLAE | 97 | 1.3000 | 14.77 |
| 21 | LRFNIGTGK | 235 | 1.3000 | 14.77 |
| 22 | LHSAVAAAV | 250 | 1.3000 | 14.77 |
| 23 | ILEQHRPEV | 64 | 1.2000 | 13.64 |
| 24 | LYGLDCSHI | 162 | 1.2000 | 13.64 |

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|---|---|---|---|---|
| 25 | VEYFRHKHT | 304 | 1.1000 | 12.50 |
| 26 | VVAIFAQAL | 188 | 1.0600 | 12.05 |
| 27 | YLNTFRHLY | 155 | 1.0000 | 11.36 |
| 28 | IAPANVYGP | 170 | 1.0000 | 11.36 |
| 29 | VFGDGTNTR | 204 | 1.0000 | 11.36 |
| 30 | VFVDDVVDA | 215 | 1.0000 | 11.36 |
| 31 | IELADGVRR | 294 | 0.8000 | 9.09 |

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|---|---|---|
| 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 | VVFHLAAQI | 72 | 4.0000 | 45.45 |
| 2 | VVDAFVRVS | 220 | 3.3000 | 37.50 |
| 3 | LSGKPTRVF | 197 | 2.6000 | 29.55 |
| 4 | FRHLYGLDC | 159 | 2.5000 | 28.41 |
| 5 | IVTADLHAI | 56 | 2.2000 | 25.00 |
| 6 | VRLAEAARQ | 101 | 2.0000 | 22.73 |
| 7 | YLNTFRHLY | 155 | 2.0000 | 22.73 |
| 8 | IGLAERVLG | 281 | 1.8000 | 20.45 |
| 9 | FVEADIVTA | 51 | 1.5000 | 17.05 |
| 10 | WRPQIELAD | 290 | 1.5000 | 17.05 |
| 11 | IFAQALLSG | 191 | 1.4000 | 15.91 |
| 12 | FIGSTLVDR | 10 | 1.3000 | 14.77 |
| 13 | FHLAAQIDV | 74 | 1.3000 | 14.77 |
| 14 | LNTFRHLYG | 156 | 1.3000 | 14.77 |
| 15 | VVGLDNFAT | 26 | 1.2000 | 13.64 |
| 16 | VAIFAQALL | 189 | 0.9600 | 10.91 |
| 17 | VRALVTGAA | 0 | 0.9000 | 10.23 |
| 18 | FVRVSADVG | 224 | 0.8000 | 9.09 |
| 19 | IYLNTFRHL | 154 | 0.7600 | 8.64 |
| 20 | VRKIVHTSS | 112 | 0.7000 | 7.95 |
| 21 | VLGWRPQIE | 287 | 0.7000 | 7.95 |
| 22 | LVDRLLADG | 15 | 0.6000 | 6.82 |

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|---|---|---|---|---|
| 23 | LEQHRPEVV | 65 | 0.4000 | 4.55 |
| 24 | VGGGLRFNI | 231 | 0.4000 | 4.55 |
| 25 | VNVIGTVRL | 95 | 0.3600 | 4.09 |
| 26 | VIGTVRLAE | 97 | 0.3000 | 3.41 |
| 27 | YGLDCSHIA | 163 | 0.3000 | 3.41 |
| 28 | LRFNIGTGK | 235 | 0.3000 | 3.41 |
| 29 | LHSAVAAAV | 250 | 0.3000 | 3.41 |
| 30 | ILEQHRPEV | 64 | 0.2000 | 2.27 |
| 31 | LYGLDCSHI | 162 | 0.2000 | 2.27 |

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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 | VRLAEAARQ | 101 | 4.5000 | 50.00 |
| 2 | VVFHLAAQI | 72 | 4.3000 | 47.78 |
| 3 | VVDAFVRVS | 220 | 3.9000 | 43.33 |
| 4 | VLGWRPQIE | 287 | 3.3000 | 36.67 |
| 5 | VIGTVRLAE | 97 | 2.9000 | 32.22 |
| 6 | IGLAERVLG | 281 | 2.7000 | 30.00 |
| 7 | LSGKPTRVF | 197 | 2.6000 | 28.89 |
| 8 | IVTADLHAI | 56 | 2.5000 | 27.78 |
| 9 | VVGLDNFAT | 26 | 2.4000 | 26.67 |
| 10 | IFAQALLSG | 191 | 2.3000 | 25.56 |
| 11 | LNTFRHLYG | 156 | 2.2000 | 24.44 |
| 12 | VRRSVADPQ | 82 | 2.1000 | 23.33 |
| 13 | WRPQIELAD | 290 | 2.1000 | 23.33 |
| 14 | VFHLAAQID | 73 | 2.0000 | 22.22 |
| 15 | VAIFAQALL | 189 | 2.0000 | 22.22 |
| 16 | VRALVTGAA | 0 | 1.9000 | 21.11 |
| 17 | IYLNTFRHL | 154 | 1.8000 | 20.00 |
| 18 | LVDRLLADG | 15 | 1.5000 | 16.67 |
| 19 | FRHLYGLDC | 159 | 1.5000 | 16.67 |
| 20 | VNVIGTVRL | 95 | 1.4000 | 15.56 |

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|---|---|---|---|---|
| 21 | VRKIVHTSS | 112 | 1.3000 | 14.44 |
| 22 | VEYFRHKHT | 304 | 1.3000 | 14.44 |
| 23 | VVAIFAQAL | 188 | 1.1000 | 12.22 |
| 24 | VFVDDVVDA | 215 | 1.0000 | 11.11 |
| 25 | YLNTFRHLY | 155 | 0.8000 | 8.89 |
| 26 | LEQHRPEVV | 65 | 0.7000 | 7.78 |
| 27 | VGGGLRFNI | 231 | 0.7000 | 7.78 |
| 28 | LHSAVAAAV | 250 | 0.6000 | 6.67 |
| 29 | FVEADIVTA | 51 | 0.5000 | 5.56 |
| 30 | ILEQHRPEV | 64 | 0.5000 | 5.56 |
| 31 | LYGLDCSHI | 162 | 0.5000 | 5.56 |

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|---|---|---|
| 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 | FRHLYGLDC | 159 | 4.3000 | 49.43 |
| 2 | VRALVTGAA | 0 | 2.7000 | 31.03 |
| 3 | FHLAAQIDV | 74 | 2.6000 | 29.89 |
| 4 | VRLAEAARQ | 101 | 2.0000 | 22.99 |
| 5 | YLNTFRHLY | 155 | 2.0000 | 22.99 |
| 6 | LNTFRHLYG | 156 | 2.0000 | 22.99 |
| 7 | VVFHLAAQI | 72 | 1.9000 | 21.84 |
| 8 | VIGTVRLAE | 97 | 1.9000 | 21.84 |
| 9 | VRKIVHTSS | 112 | 1.8000 | 20.69 |
| 10 | IVTADLHAI | 56 | 1.7000 | 19.54 |
| 11 | VVDAFVRVS | 220 | 1.7000 | 19.54 |
| 12 | WRPQIELAD | 290 | 1.6000 | 18.39 |
| 13 | IFAQALLSG | 191 | 1.5000 | 17.24 |
| 14 | VNVIGTVRL | 95 | 1.3600 | 15.63 |
| 15 | IVHTSSGGS | 115 | 1.3000 | 14.94 |
| 16 | IGLAERVLG | 281 | 1.3000 | 14.94 |
| 17 | FVEADIVTA | 51 | 1.0000 | 11.49 |
| 18 | VVGLDNFAT | 26 | 0.9000 | 10.34 |

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|---|---|---|---|---|
| 19 | FVRVSADVG | 224 | 0.9000 | 10.34 |
| 20 | VVAIFAQAL | 188 | 0.8600 | 9.89 |
| 21 | FIGSTLVDR | 10 | 0.7000 | 8.05 |
| 22 | VAIFAQALL | 189 | 0.5600 | 6.44 |
| 23 | LYGLDCSHI | 162 | 0.5000 | 5.75 |
| 24 | LHSAVAAAV | 250 | 0.3000 | 3.45 |
| 25 | IGTVRLAEA | 98 | 0.1000 | 1.15 |
| 26 | IAPANVYGP | 170 | -0.2000 | 0 |
| 27 | LRFNIGTGK | 235 | -0.2000 | 0 |
| 28 | LVDRLLADG | 15 | -0.3000 | 0 |
| 29 | LSGKPTRVF | 197 | -0.3000 | 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 | VRLAEAARQ | 101 | 2.7000 | 39.71 |
| 2 | VRALVTGAA | 0 | 2.6000 | 38.24 |
| 3 | FRHLYGLDC | 159 | 2.5000 | 36.76 |
| 4 | VVDAFVRVS | 220 | 1.1000 | 16.18 |
| 5 | VVFHLAAQI | 72 | 1.0000 | 14.71 |
| 6 | IVHTSSGGS | 115 | 0.8000 | 11.76 |
| 7 | FVEADIVTA | 51 | 0.5000 | 7.35 |
| 8 | VRKIVHTSS | 112 | 0.3000 | 4.41 |
| 9 | IVTADLHAI | 56 | 0.1000 | 1.47 |
| 10 | IGTVRLAEA | 98 | 0.1000 | 1.47 |
| 11 | VNVIGTVRL | 95 | -0.1000 | 0 |
| 12 | VVAIFAQAL | 188 | -0.2000 | 0 |
| 13 | FVRVSADVG | 224 | -0.2000 | 0 |
| 14 | VVGLDNFAT | 26 | -0.3000 | 0 |
| 15 | LYGLDCSHI | 162 | -0.4000 | 0 |
| 16 | VAIFAQALL | 189 | -0.4000 | 0 |
| 17 | IGLAERVLG | 281 | -0.6000 | 0 |
| 18 | VRRSVADPQ | 82 | -0.7000 | 0 |

| | | | | |
|---|---|---|---|---|
| 19 | LHSAVAAAV | 250 | -0.7000 | 0 |
| 20 | LDNFATGRA | 29 | -1.1000 | 0 |
| 21 | LNTFRHLYG | 156 | -1.2000 | 0 |
| 22 | YGLDCSHIA | 163 | -1.2000 | 0 |
| 23 | FIGSTLVDR | 10 | -1.3000 | 0 |
| 24 | VIGTVRLAE | 97 | -1.3000 | 0 |
| 25 | VFVDDVVDA | 215 | -1.3000 | 0 |
| 26 | WRPQIELAD | 290 | -1.3000 | 0 |
| 27 | LVTGAAGFI | 3 | -1.4000 | 0 |
| 28 | FAQALLSGK | 192 | -1.4000 | 0 |

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|---|---|---|
| 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 | VRALVTGAA | 0 | 3.7000 | 44.58 |
| 2 | VRLAEAARQ | 101 | 3.7000 | 44.58 |
| 3 | FRHLYGLDC | 159 | 3.3000 | 39.76 |
| 4 | VRKIVHTSS | 112 | 2.4000 | 28.92 |
| 5 | VVDAFVRVS | 220 | 2.3000 | 27.71 |
| 6 | VVFHLAAQI | 72 | 2.0000 | 24.10 |
| 7 | IVHTSSGGS | 115 | 1.9000 | 22.89 |
| 8 | IVTADLHAI | 56 | 1.8000 | 21.69 |
| 9 | LNTFRHLYG | 156 | 1.6000 | 19.28 |
| 10 | VIGTVRLAE | 97 | 1.5000 | 18.07 |
| 11 | VNVIGTVRL | 95 | 1.4000 | 16.87 |
| 12 | VVGLDNFAT | 26 | 1.2000 | 14.46 |
| 13 | IGTVRLAEA | 98 | 1.1000 | 13.25 |
| 14 | IFAQALLSG | 191 | 1.1000 | 13.25 |
| 15 | VVAIFAQAL | 188 | 0.9000 | 10.84 |
| 16 | IGLAERVLG | 281 | 0.9000 | 10.84 |
| 17 | LRFNIGTGK | 235 | 0.7000 | 8.43 |
| 18 | FHLAAQIDV | 74 | 0.6000 | 7.23 |
| 19 | LYGLDCSHI | 162 | 0.6000 | 7.23 |

| | | | | |
|---|---|---|---|---|
| 20 | VAIFAQALL | 189 | 0.6000 | 7.23 |
| 21 | LHSAVAAAV | 250 | 0.3000 | 3.61 |
| 22 | VFVDDVVDA | 215 | 0.2000 | 2.41 |
| 23 | IAPANVYGP | 170 | -0.2000 | 0 |
| 24 | VEYFRHKHT | 304 | -0.2000 | 0 |
| 25 | LVTGAAGFI | 3 | -0.3000 | 0 |
| 26 | YLNTFRHLY | 155 | -0.3000 | 0 |
| 27 | ILEQHRPEV | 64 | -0.3500 | 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 | FRHLYGLDC | 159 | 4.3000 | 48.31 |
| 2 | VIGTVRLAE | 97 | 3.5000 | 39.33 |
| 3 | VRLAEAARQ | 101 | 3.5000 | 39.33 |
| 4 | WRPQIELAD | 290 | 3.2000 | 35.96 |
| 5 | VRALVTGAA | 0 | 2.7000 | 30.34 |
| 6 | FHLAAQIDV | 74 | 1.9000 | 21.35 |
| 7 | LNTFRHLYG | 156 | 1.9000 | 21.35 |
| 8 | YLNTFRHLY | 155 | 1.8000 | 20.22 |
| 9 | VNVIGTVRL | 95 | 1.4000 | 15.73 |
| 10 | VRKIVHTSS | 112 | 1.4000 | 15.73 |
| 11 | IFAQALLSG | 191 | 1.4000 | 15.73 |
| 12 | YVFVDDVVD | 214 | 1.3000 | 14.61 |
| 13 | VVDAFVRVS | 220 | 1.3000 | 14.61 |
| 14 | VVFHLAAQI | 72 | 1.2000 | 13.48 |
| 15 | IGLAERVLG | 281 | 1.2000 | 13.48 |
| 16 | VVGLDNFAT | 26 | 1.1000 | 12.36 |
| 17 | FVEADIVTA | 51 | 1.0000 | 11.24 |
| 18 | IVTADLHAI | 56 | 1.0000 | 11.24 |
| 19 | VFHLAAQID | 73 | 1.0000 | 11.24 |
| 20 | IVHTSSGGS | 115 | 0.9000 | 10.11 |
| 21 | VVAIFAQAL | 188 | 0.9000 | 10.11 |

| | | | | |
|---|---|---|---|---|
| 22 | YAAGKVAGE | 145 | 0.8000 | 8.99 |
| 23 | FVRVSADVG | 224 | 0.8000 | 8.99 |
| 24 | VLGWRPQIE | 287 | 0.8000 | 8.99 |
| 25 | VAIFAQALL | 189 | 0.6000 | 6.74 |
| 26 | IGTVRLAEA | 98 | 0.1000 | 1.12 |
| 27 | VRRSVADPQ | 82 | -0.2000 | 0 |
| 28 | LYGLDCSHI | 162 | -0.2000 | 0 |
| 29 | VEYFRHKHT | 304 | -0.3000 | 0 |
| 30 | LVDRLLADG | 15 | -0.4000 | 0 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VVFHLAAQI | 72 | 4.1000 | 48.81 |
| 2 | VVDAFVRVS | 220 | 3.9000 | 46.43 |
| 3 | VRLAEAARQ | 101 | 3.7000 | 44.05 |
| 4 | IVTADLHAI | 56 | 2.3000 | 27.38 |
| 5 | VRALVTGAA | 0 | 1.9000 | 22.62 |
| 6 | LSGKPTRVF | 197 | 1.7000 | 20.24 |
| 7 | VVGLDNFAT | 26 | 1.5000 | 17.86 |
| 8 | FRHLYGLDC | 159 | 1.5000 | 17.86 |
| 9 | IGLAERVLG | 281 | 1.4000 | 16.67 |
| 10 | VRRSVADPQ | 82 | 1.3000 | 15.48 |
| 11 | VRKIVHTSS | 112 | 1.3000 | 15.48 |
| 12 | LRFNIGTGK | 235 | 1.2000 | 14.29 |
| 13 | VAIFAQALL | 189 | 1.0000 | 11.90 |
| 14 | IFAQALLSG | 191 | 1.0000 | 11.90 |
| 15 | VFVDDVVDA | 215 | 1.0000 | 11.90 |
| 16 | LNTFRHLYG | 156 | 0.9000 | 10.71 |
| 17 | IYLNTFRHL | 154 | 0.8000 | 9.52 |
| 18 | FVEADIVTA | 51 | 0.5000 | 5.95 |
| 19 | VGGGLRFNI | 231 | 0.5000 | 5.95 |
| 20 | LEQHRPEVV | 65 | 0.4000 | 4.76 |

| | | | | |
|---|---|---|---|---|
| 21 | VNVIGTVRL | 95 | 0.4000 | 4.76 |
| 22 | VDAFVRVSA | 221 | 0.4000 | 4.76 |
| 23 | VEYFRHKHT | 304 | 0.4000 | 4.76 |
| 24 | IVHTSSGGS | 115 | 0.3000 | 3.57 |
| 25 | LYGLDCSHI | 162 | 0.3000 | 3.57 |
| 26 | LHSAVAAAV | 250 | 0.3000 | 3.57 |
| 27 | VLGWRPQIE | 287 | 0.3000 | 3.57 |
| 28 | LVDRLLADG | 15 | 0.2000 | 2.38 |
| 29 | ILEQHRPEV | 64 | 0.2000 | 2.38 |
| 30 | VVAIFAQAL | 188 | 0.1000 | 1.19 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VVFHLAAQI | 72 | 3.1000 | 36.90 |
| 2 | VVDAFVRVS | 220 | 2.9000 | 34.52 |
| 3 | VRLAEAARQ | 101 | 2.7000 | 32.14 |
| 4 | FRHLYGLDC | 159 | 2.5000 | 29.76 |
| 5 | FVEADIVTA | 51 | 1.5000 | 17.86 |
| 6 | IVTADLHAI | 56 | 1.3000 | 15.48 |
| 7 | VRALVTGAA | 0 | 0.9000 | 10.71 |
| 8 | YLNTFRHLY | 155 | 0.7000 | 8.33 |
| 9 | LSGKPTRVF | 197 | 0.7000 | 8.33 |
| 10 | VVGLDNFAT | 26 | 0.5000 | 5.95 |
| 11 | IGLAERVLG | 281 | 0.4000 | 4.76 |
| 12 | WRPQIELAD | 290 | 0.4000 | 4.76 |
| 13 | FHLAAQIDV | 74 | 0.3000 | 3.57 |
| 14 | VRRSVADPQ | 82 | 0.3000 | 3.57 |
| 15 | VRKIVHTSS | 112 | 0.3000 | 3.57 |
| 16 | YGLDCSHIA | 163 | 0.3000 | 3.57 |
| 17 | LRFNIGTGK | 235 | 0.2000 | 2.38 |
| 18 | LNTFRHLYG | 156 | -0.1000 | 0 |
| 19 | FIGSTLVDR | 10 | -0.2000 | 0 |

| | | | | |
|---|---|---|---|---|
| 20 | IYLNTFRHL | 154 | -0.2000 | 0 |
| 21 | VGGGLRFNI | 231 | -0.5000 | 0 |
| 22 | LEQHRPEVV | 65 | -0.6000 | 0 |
| 23 | VNVIGTVRL | 95 | -0.6000 | 0 |
| 24 | VDAFVRVSA | 221 | -0.6000 | 0 |
| 25 | FVRVSADVG | 224 | -0.6000 | 0 |
| 26 | VEYFRHKHT | 304 | -0.6000 | 0 |
| 27 | IVHTSSGGS | 115 | -0.7000 | 0 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VVFHLAAQI | 72 | 5.0000 | 56.82 |
| 2 | VVDAFVRVS | 220 | 4.3000 | 48.86 |
| 3 | LSGKPTRVF | 197 | 3.6000 | 40.91 |
| 4 | IVTADLHAI | 56 | 3.2000 | 36.36 |
| 5 | VRLAEAARQ | 101 | 3.0000 | 34.09 |
| 6 | IGLAERVLG | 281 | 2.8000 | 31.82 |
| 7 | IFAQALLSG | 191 | 2.4000 | 27.27 |
| 8 | LNTFRHLYG | 156 | 2.3000 | 26.14 |
| 9 | VVGLDNFAT | 26 | 2.2000 | 25.00 |
| 10 | VAIFAQALL | 189 | 1.9600 | 22.27 |
| 11 | VRALVTGAA | 0 | 1.9000 | 21.59 |
| 12 | IYLNTFRHL | 154 | 1.7600 | 20.00 |
| 13 | VRKIVHTSS | 112 | 1.7000 | 19.32 |
| 14 | VLGWRPQIE | 287 | 1.7000 | 19.32 |
| 15 | LVDRLLADG | 15 | 1.6000 | 18.18 |
| 16 | FRHLYGLDC | 159 | 1.5000 | 17.05 |
| 17 | LEQHRPEVV | 65 | 1.4000 | 15.91 |
| 18 | VGGGLRFNI | 231 | 1.4000 | 15.91 |
| 19 | VNVIGTVRL | 95 | 1.3600 | 15.45 |
| 20 | VIGTVRLAE | 97 | 1.3000 | 14.77 |
| 21 | LRFNIGTGK | 235 | 1.3000 | 14.77 |

| | | | | |
|---|---|---|---|---|
| 22 | LHSAVAAAV | 250 | 1.3000 | 14.77 |
| 23 | ILEQHRPEV | 64 | 1.2000 | 13.64 |
| 24 | LYGLDCSHI | 162 | 1.2000 | 13.64 |
| 25 | VEYFRHKHT | 304 | 1.1000 | 12.50 |
| 26 | VVAIFAQAL | 188 | 1.0600 | 12.05 |
| 27 | YLNTFRHLY | 155 | 1.0000 | 11.36 |
| 28 | IAPANVYGP | 170 | 1.0000 | 11.36 |
| 29 | VFGDGTNTR | 204 | 1.0000 | 11.36 |
| 30 | VFVDDVVDA | 215 | 1.0000 | 11.36 |
| 31 | IELADGVRR | 294 | 0.8000 | 9.09 |

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| 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 | VVFHLAAQI | 72 | 5.0000 | 56.82 |
| 2 | VVDAFVRVS | 220 | 4.3000 | 48.86 |
| 3 | LSGKPTRVF | 197 | 3.6000 | 40.91 |
| 4 | IVTADLHAI | 56 | 3.2000 | 36.36 |
| 5 | VRLAEAARQ | 101 | 3.0000 | 34.09 |
| 6 | IGLAERVLG | 281 | 2.8000 | 31.82 |
| 7 | IFAQALLSG | 191 | 2.4000 | 27.27 |
| 8 | LNTFRHLYG | 156 | 2.3000 | 26.14 |
| 9 | VVGLDNFAT | 26 | 2.2000 | 25.00 |
| 10 | VAIFAQALL | 189 | 1.9600 | 22.27 |
| 11 | VRALVTGAA | 0 | 1.9000 | 21.59 |
| 12 | IYLNTFRHL | 154 | 1.7600 | 20.00 |
| 13 | VRKIVHTSS | 112 | 1.7000 | 19.32 |
| 14 | VLGWRPQIE | 287 | 1.7000 | 19.32 |
| 15 | LVDRLLADG | 15 | 1.6000 | 18.18 |
| 16 | FRHLYGLDC | 159 | 1.5000 | 17.05 |
| 17 | LEQHRPEVV | 65 | 1.4000 | 15.91 |
| 18 | VGGGLRFNI | 231 | 1.4000 | 15.91 |
| 19 | VNVIGTVRL | 95 | 1.3600 | 15.45 |

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|---|---|---|---|---|
| 20 | VIGTVRLAE | 97 | 1.3000 | 14.77 |
| 21 | LRFNIGTGK | 235 | 1.3000 | 14.77 |
| 22 | LHSAVAAAV | 250 | 1.3000 | 14.77 |
| 23 | ILEQHRPEV | 64 | 1.2000 | 13.64 |
| 24 | LYGLDCSHI | 162 | 1.2000 | 13.64 |
| 25 | VEYFRHKHT | 304 | 1.1000 | 12.50 |
| 26 | VVAIFAQAL | 188 | 1.0600 | 12.05 |
| 27 | YLNTFRHLY | 155 | 1.0000 | 11.36 |
| 28 | IAPANVYGP | 170 | 1.0000 | 11.36 |
| 29 | VFGDGTNTR | 204 | 1.0000 | 11.36 |
| 30 | VFVDDVVDA | 215 | 1.0000 | 11.36 |
| 31 | IELADGVRR | 294 | 0.8000 | 9.09 |

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| 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 | VVGLDNFAT | 26 | 4.7000 | 47.96 |
| 2 | VVFHLAAQI | 72 | 4.7000 | 47.96 |
| 3 | FRHLYGLDC | 159 | 4.3000 | 43.88 |
| 4 | LNTFRHLYG | 156 | 3.8000 | 38.78 |
| 5 | VGGGLRFNI | 231 | 3.8000 | 38.78 |
| 6 | IVTADLHAI | 56 | 3.6000 | 36.73 |
| 7 | VAIFAQALL | 189 | 3.6000 | 36.73 |
| 8 | VVAIFAQAL | 188 | 2.9000 | 29.59 |
| 9 | LVTGAAGFI | 3 | 2.8000 | 28.57 |
| 10 | VRALVTGAA | 0 | 2.6600 | 27.14 |
| 11 | VNVIGTVRL | 95 | 2.6600 | 27.14 |
| 12 | LYGLDCSHI | 162 | 2.6000 | 26.53 |
| 13 | VDAFVRVSA | 221 | 2.4000 | 24.49 |
| 14 | IVHTSSGGS | 115 | 2.3000 | 23.47 |
| 15 | VEYFRHKHT | 304 | 2.3000 | 23.47 |
| 16 | VRKIVHTSS | 112 | 2.2000 | 22.45 |
| 17 | VIGTVRLAE | 97 | 2.0000 | 20.41 |

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|---|---|---|---|---|
| 18 | IGLAERVLG | 281 | 2.0000 | 20.41 |
| 19 | LGWRPQIEL | 288 | 1.9000 | 19.39 |
| 20 | FHLAAQIDV | 74 | 1.8000 | 18.37 |
| 21 | LRFNIGTGK | 235 | 1.8000 | 18.37 |
| 22 | VHTSSGGSI | 116 | 1.7000 | 17.35 |
| 23 | VAGEIYLNT | 150 | 1.7000 | 17.35 |
| 24 | VFVEADIVT | 50 | 1.6000 | 16.33 |
| 25 | VRLAEAARQ | 101 | 1.6000 | 16.33 |
| 26 | LDNFATGRA | 29 | 1.5600 | 15.92 |
| 27 | LLSGKPTRV | 196 | 1.5000 | 15.31 |
| 28 | VRVSADVGG | 225 | 1.5000 | 15.31 |
| 29 | LGDLKRSCL | 271 | 1.5000 | 15.31 |
| 30 | IYLNTFRHL | 154 | 1.4000 | 14.29 |
| 31 | VTGAAGFIG | 4 | 1.3000 | 13.27 |

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|---|---|---|
| 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 | FRHLYGLDC | 159 | 5.3000 | 54.08 |
| 2 | VVGLDNFAT | 26 | 3.7000 | 37.76 |
| 3 | VVFHLAAQI | 72 | 3.7000 | 37.76 |
| 4 | FHLAAQIDV | 74 | 2.8000 | 28.57 |
| 5 | LNTFRHLYG | 156 | 2.8000 | 28.57 |
| 6 | VGGGLRFNI | 231 | 2.8000 | 28.57 |
| 7 | IVTADLHAI | 56 | 2.6000 | 26.53 |
| 8 | VAIFAQALL | 189 | 2.6000 | 26.53 |
| 9 | YGLDCSHIA | 163 | 2.3000 | 23.47 |
| 10 | FNIGTGKET | 237 | 2.3000 | 23.47 |
| 11 | YLNTFRHLY | 155 | 1.9000 | 19.39 |
| 12 | VVAIFAQAL | 188 | 1.9000 | 19.39 |
| 13 | LVTGAAGFI | 3 | 1.8000 | 18.37 |
| 14 | VRALVTGAA | 0 | 1.6600 | 16.94 |
| 15 | VNVIGTVRL | 95 | 1.6600 | 16.94 |

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|---|---|---|---|---|
| 16 | LYGLDCSHI | 162 | 1.6000 | 16.33 |
| 17 | FVRVSADVG | 224 | 1.5000 | 15.31 |
| 18 | FHPPRLGDL | 266 | 1.5000 | 15.31 |
| 19 | VDAFVRVSA | 221 | 1.4000 | 14.29 |
| 20 | IVHTSSGGS | 115 | 1.3000 | 13.27 |
| 21 | VEYFRHKHT | 304 | 1.3000 | 13.27 |
| 22 | FVEADIVTA | 51 | 1.2500 | 12.76 |
| 23 | VRKIVHTSS | 112 | 1.2000 | 12.24 |
| 24 | YVFVDDVVD | 214 | 1.1000 | 11.22 |
| 25 | VIGTVRLAE | 97 | 1.0000 | 10.20 |
| 26 | IGLAERVLG | 281 | 1.0000 | 10.20 |
| 27 | LGWRPQIEL | 288 | 0.9000 | 9.18 |
| 28 | LRFNIGTGK | 235 | 0.8000 | 8.16 |
| 29 | FATGRATNL | 32 | 0.7000 | 7.14 |
| 30 | VHTSSGGSI | 116 | 0.7000 | 7.14 |
| 31 | VAGEIYLNT | 150 | 0.7000 | 7.14 |

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|---|---|---|
| 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 | VVGLDNFAT | 26 | 4.7000 | 47.96 |
| 2 | VVFHLAAQI | 72 | 4.7000 | 47.96 |
| 3 | FRHLYGLDC | 159 | 4.3000 | 43.88 |
| 4 | LNTFRHLYG | 156 | 3.8000 | 38.78 |
| 5 | VGGGLRFNI | 231 | 3.8000 | 38.78 |
| 6 | IVTADLHAI | 56 | 3.6000 | 36.73 |
| 7 | VAIFAQALL | 189 | 3.6000 | 36.73 |
| 8 | VVAIFAQAL | 188 | 2.9000 | 29.59 |
| 9 | LVTGAAGFI | 3 | 2.8000 | 28.57 |
| 10 | VRALVTGAA | 0 | 2.6600 | 27.14 |
| 11 | VNVIGTVRL | 95 | 2.6600 | 27.14 |
| 12 | LYGLDCSHI | 162 | 2.6000 | 26.53 |
| 13 | VDAFVRVSA | 221 | 2.4000 | 24.49 |

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| 14 | IVHTSSGGS | 115 | 2.3000 | 23.47 |
| 15 | VEYFRHKHT | 304 | 2.3000 | 23.47 |
| 16 | VRKIVHTSS | 112 | 2.2000 | 22.45 |
| 17 | VIGTVRLAE | 97 | 2.0000 | 20.41 |
| 18 | IGLAERVLG | 281 | 2.0000 | 20.41 |
| 19 | LGWRPQIEL | 288 | 1.9000 | 19.39 |
| 20 | FHLAAQIDV | 74 | 1.8000 | 18.37 |
| 21 | LRFNIGTGK | 235 | 1.8000 | 18.37 |
| 22 | VHTSSGGSI | 116 | 1.7000 | 17.35 |
| 23 | VAGEIYLNT | 150 | 1.7000 | 17.35 |
| 24 | VFVEADIVT | 50 | 1.6000 | 16.33 |
| 25 | VRLAEAARQ | 101 | 1.6000 | 16.33 |
| 26 | LDNFATGRA | 29 | 1.5600 | 15.92 |
| 27 | LLSGKPTRV | 196 | 1.5000 | 15.31 |
| 28 | VRVSADVGG | 225 | 1.5000 | 15.31 |
| 29 | LGDLKRSCL | 271 | 1.5000 | 15.31 |
| 30 | IYLNTFRHL | 154 | 1.4000 | 14.29 |
| 31 | VTGAAGFIG | 4 | 1.3000 | 13.27 |

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|---|---|---|
| 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 | VVAIFAQAL | 188 | 4.4000 | 44.90 |
| 2 | VRRTVEYFR | 300 | 3.9000 | 39.80 |
| 3 | FRHLYGLDC | 159 | 3.3000 | 33.67 |
| 4 | YLNTFRHLY | 155 | 3.0000 | 30.61 |
| 5 | LRFNIGTGK | 235 | 3.0000 | 30.61 |
| 6 | VRLAEAARQ | 101 | 2.9000 | 29.59 |
| 7 | FVRVSADVG | 224 | 2.8000 | 28.57 |
| 8 | IVTADLHAI | 56 | 2.5000 | 25.51 |
| 9 | IVHTSSGGS | 115 | 2.4000 | 24.49 |
| 10 | LHAILEQHR | 61 | 2.3000 | 23.47 |
| 11 | VRKIVHTSS | 112 | 2.3000 | 23.47 |

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| 12 | FIGSTLVDR | 10 | 2.0000 | 20.41 |
| 13 | IELADGVRR | 294 | 2.0000 | 20.41 |
| 14 | VVGLDNFAT | 26 | 1.9000 | 19.39 |
| 15 | VNVIGTVRL | 95 | 1.8000 | 18.37 |
| 16 | VVFHLAAQI | 72 | 1.7000 | 17.35 |
| 17 | LYGLDCSHI | 162 | 1.7000 | 17.35 |
| 18 | VRALVTGAA | 0 | 1.6000 | 16.33 |
| 19 | FAQALLSGK | 192 | 1.5000 | 15.31 |
| 20 | FHLAAQIDV | 74 | 1.4000 | 14.29 |
| 21 | LVTGAAGFI | 3 | 1.3000 | 13.27 |
| 22 | FNIGTGKET | 237 | 1.1000 | 11.22 |
| 23 | VTGAAGFIG | 4 | 0.8000 | 8.16 |
| 24 | VHTSSGGSI | 116 | 0.8000 | 8.16 |
| 25 | VRRSVADPQ | 82 | 0.6000 | 6.12 |
| 26 | VVDAFVRVS | 220 | 0.5000 | 5.10 |
| 27 | FHPPRLGDL | 266 | 0.5000 | 5.10 |
| 28 | YGLDCSHIA | 163 | 0.3000 | 3.06 |
| 29 | VFGDGTNTR | 204 | 0.3000 | 3.06 |
| 30 | YVFVDDVVD | 214 | 0.2000 | 2.04 |
| 31 | IYLNTFRHL | 154 | 0.1000 | 1.02 |

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|---|---|---|
| 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 | VVAIFAQAL | 188 | 4.4000 | 44.90 |
| 2 | VRRTVEYFR | 300 | 3.9000 | 39.80 |
| 3 | FRHLYGLDC | 159 | 3.3000 | 33.67 |
| 4 | YLNTFRHLY | 155 | 3.0000 | 30.61 |
| 5 | LRFNIGTGK | 235 | 3.0000 | 30.61 |
| 6 | VRLAEAARQ | 101 | 2.9000 | 29.59 |
| 7 | FVRVSADVG | 224 | 2.8000 | 28.57 |
| 8 | IVTADLHAI | 56 | 2.5000 | 25.51 |
| 9 | IVHTSSGGS | 115 | 2.4000 | 24.49 |

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|---|---|---|---|---|
| 10 | LHAILEQHR | 61 | 2.3000 | 23.47 |
| 11 | VRKIVHTSS | 112 | 2.3000 | 23.47 |
| 12 | FIGSTLVDR | 10 | 2.0000 | 20.41 |
| 13 | IELADGVRR | 294 | 2.0000 | 20.41 |
| 14 | VVGLDNFAT | 26 | 1.9000 | 19.39 |
| 15 | VNVIGTVRL | 95 | 1.8000 | 18.37 |
| 16 | VVFHLAAQI | 72 | 1.7000 | 17.35 |
| 17 | LYGLDCSHI | 162 | 1.7000 | 17.35 |
| 18 | VRALVTGAA | 0 | 1.6000 | 16.33 |
| 19 | FAQALLSGK | 192 | 1.5000 | 15.31 |
| 20 | FHLAAQIDV | 74 | 1.4000 | 14.29 |
| 21 | LVTGAAGFI | 3 | 1.3000 | 13.27 |
| 22 | FNIGTGKET | 237 | 1.1000 | 11.22 |
| 23 | VTGAAGFIG | 4 | 0.8000 | 8.16 |
| 24 | VHTSSGGSI | 116 | 0.8000 | 8.16 |
| 25 | VRRSVADPQ | 82 | 0.6000 | 6.12 |
| 26 | VVDAFVRVS | 220 | 0.5000 | 5.10 |
| 27 | FHPPRLGDL | 266 | 0.5000 | 5.10 |
| 28 | YGLDCSHIA | 163 | 0.3000 | 3.06 |
| 29 | VFGDGTNTR | 204 | 0.3000 | 3.06 |
| 30 | YVFVDDVVD | 214 | 0.2000 | 2.04 |
| 31 | IYLNTFRHL | 154 | 0.1000 | 1.02 |