# 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 | Thu Mar 11 00:08:07 2010 |
| Length of input sequence | 586 amino acids |
| Number of nanomers from input sequence | 578 |
| Number of nanomers with obligatory P1 anchor residue | 180 |
| Threshold setting | 3 |
| Number of alleles in query | 51 |
| Number of top scorers to be displayed | 58 |

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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 | IVIEAARSV | 398 | 2.5900 | 43.17 |
| 2 | FVAFVGAAI | 537 | 2.5800 | 43.00 |
| 3 | FVTEDGAET | 66 | 1.2000 | 20.00 |
| 4 | YARARGLPV | 380 | 1.0000 | 16.67 |
| 5 | WVASDGCET | 338 | 0.9000 | 15.00 |
| 6 | VAALRSIGI | 206 | 0.6000 | 10.00 |
| 7 | IRGIEGKIG | 368 | 0.6000 | 10.00 |
| 8 | VFFLHVSLV | 180 | 0.5000 | 8.33 |

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|---|---|---|---|---|
| 9 | LGLCLGLQC | 389 | 0.5000 | 8.33 |
| 10 | IAYARARGL | 378 | 0.3900 | 6.50 |
| 11 | LLTARGLHV | 33 | 0.3000 | 5.00 |
| 12 | VLIPGGFGI | 360 | 0.3000 | 5.00 |
| 13 | YLNVDPGTM | 49 | 0.2300 | 3.83 |
| 14 | FVSGGVASS | 12 | 0.2000 | 3.33 |
| 15 | MQKLDPYLN | 43 | 0.2000 | 3.33 |
| 16 | VRRLNLPFR | 272 | -0.1300 | 0 |
| 17 | MRLGSYPAV | 445 | -0.1300 | 0 |
| 18 | LFVSGGVAS | 11 | -0.3000 | 0 |
| 19 | FQHGEVFVT | 60 | -0.3000 | 0 |
| 20 | FFLHVSLVP | 181 | -0.3000 | 0 |
| 21 | IEAARSVGL | 400 | -0.3000 | 0 |
| 22 | VRIALVGKY | 301 | -0.4000 | 0 |
| 23 | YVELSDAYL | 309 | -0.4000 | 0 |
| 24 | VELSDAYLS | 310 | -0.4000 | 0 |
| 25 | VGLTNANSA | 406 | -0.4000 | 0 |
| 26 | LVPYLAPSG | 187 | -0.4300 | 0 |
| 27 | LGREDVFFL | 175 | -0.5000 | 0 |
| 28 | IALMCDVDI | 235 | -0.5000 | 0 |
| 29 | LSVAEALRA | 317 | -0.5000 | 0 |
| 30 | LGDVHGVLI | 354 | -0.7500 | 0 |
| 31 | YEVNNAYRD | 477 | -0.7600 | 0 |
| 32 | VVAQAYQTT | 459 | -0.8000 | 0 |
| 33 | LLPVEIPEI | 552 | -0.8800 | 0 |
| 34 | ILAMAQPDA | 132 | -0.9300 | 0 |
| 35 | LHVSLVPYL | 183 | -0.9300 | 0 |
| 36 | FVVGTQAHP | 516 | -1.0000 | 0 |
| 37 | YKAGELLPV | 547 | -1.0000 | 0 |
| 38 | FLHVSLVPY | 182 | -1.0500 | 0 |
| 39 | LKNKIALMC | 231 | -1.2000 | 0 |
| 40 | YERFLDRNL | 81 | -1.2300 | 0 |
| 41 | YLGDTVQVI | 113 | -1.4000 | 0 |
| 42 | VITEIGGTV | 148 | -1.4000 | 0 |

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|---|---|---|---|---|
| 43 | FKHRAKVEI | 328 | -1.4000 | 0 |
| 44 | MRKHPQTAT | 0 | -1.4100 | 0 |
| 45 | VSGGVASSL | 13 | -1.5000 | 0 |
| 46 | VASSLGKGL | 17 | -1.5000 | 0 |
| 47 | VVRRLNLPF | 271 | -1.5000 | 0 |
| 48 | LTNANSAEF | 408 | -1.5000 | 0 |
| 49 | VVGTQAHPE | 517 | -1.5000 | 0 |
| 50 | YSTVIAKER | 101 | -1.5500 | 0 |
| 51 | LGQLLTARG | 30 | -1.6000 | 0 |
| 52 | VVITEIGGT | 147 | -1.6000 | 0 |
| 53 | LQCIVIEAA | 395 | -1.8000 | 0 |
| 54 | VRHYLGRED | 171 | -1.8100 | 0 |
| 55 | LRSIGITPD | 209 | -1.8100 | 0 |
| 56 | LFVAFVGAA | 536 | -1.9000 | 0 |
| 57 | IGITPDALI | 212 | -2.0000 | 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 |
|---|---|---|---|---|
| 1 | IVIEAARSV | 398 | 3.5900 | 59.83 |
| 2 | FVAFVGAAI | 537 | 2.5800 | 43.00 |
| 3 | VAALRSIGI | 206 | 1.6000 | 26.67 |
| 4 | IRGIEGKIG | 368 | 1.6000 | 26.67 |
| 5 | VFFLHVSLV | 180 | 1.5000 | 25.00 |
| 6 | LGLCLGLQC | 389 | 1.5000 | 25.00 |
| 7 | IAYARARGL | 378 | 1.3900 | 23.17 |
| 8 | LLTARGLHV | 33 | 1.3000 | 21.67 |
| 9 | VLIPGGFGI | 360 | 1.3000 | 21.67 |
| 10 | MQKLDPYLN | 43 | 1.2000 | 20.00 |
| 11 | FVTEDGAET | 66 | 1.2000 | 20.00 |
| 12 | VRRLNLPFR | 272 | 0.8700 | 14.50 |
| 13 | MRLGSYPAV | 445 | 0.8700 | 14.50 |
| 14 | LFVSGGVAS | 11 | 0.7000 | 11.67 |

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|---|---|---|---|---|
| 15 | IEAARSVGL | 400 | 0.7000 | 11.67 |
| 16 | VRIALVGKY | 301 | 0.6000 | 10.00 |
| 17 | VELSDAYLS | 310 | 0.6000 | 10.00 |
| 18 | VGLTNANSA | 406 | 0.6000 | 10.00 |
| 19 | LVPYLAPSG | 187 | 0.5700 | 9.50 |
| 20 | LGREDVFFL | 175 | 0.5000 | 8.33 |
| 21 | IALMCDVDI | 235 | 0.5000 | 8.33 |
| 22 | LSVAEALRA | 317 | 0.5000 | 8.33 |
| 23 | LGDVHGVLI | 354 | 0.2500 | 4.17 |
| 24 | FVSGGVASS | 12 | 0.2000 | 3.33 |
| 25 | VVAQAYQTT | 459 | 0.2000 | 3.33 |
| 26 | LLPVEIPEI | 552 | 0.1200 | 2.00 |
| 27 | ILAMAQPDA | 132 | 0.0700 | 1.17 |
| 28 | LHVSLVPYL | 183 | 0.0700 | 1.17 |
| 29 | WVASDGCET | 338 | -0.1000 | 0 |
| 30 | LKNKIALMC | 231 | -0.2000 | 0 |
| 31 | FQHGEVFVT | 60 | -0.3000 | 0 |
| 32 | FFLHVSLVP | 181 | -0.3000 | 0 |
| 33 | VITEIGGTV | 148 | -0.4000 | 0 |
| 34 | MRKHPQTAT | 0 | -0.4100 | 0 |
| 35 | VSGGVASSL | 13 | -0.5000 | 0 |
| 36 | VASSLGKGL | 17 | -0.5000 | 0 |
| 37 | VVRRLNLPF | 271 | -0.5000 | 0 |
| 38 | LTNANSAEF | 408 | -0.5000 | 0 |
| 39 | VVGTQAHPE | 517 | -0.5000 | 0 |
| 40 | LGQLLTARG | 30 | -0.6000 | 0 |
| 41 | VVITEIGGT | 147 | -0.6000 | 0 |
| 42 | YLNVDPGTM | 49 | -0.7700 | 0 |
| 43 | LQCIVIEAA | 395 | -0.8000 | 0 |
| 44 | VRHYLGRED | 171 | -0.8100 | 0 |
| 45 | LRSIGITPD | 209 | -0.8100 | 0 |
| 46 | LFVAFVGAA | 536 | -0.9000 | 0 |
| 47 | IGITPDALI | 212 | -1.0000 | 0 |
| 48 | IGAIAYARA | 375 | -1.0000 | 0 |

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|---|---|---|---|---|
| 49 | LRFSGTSPD | 492 | -1.0000 | 0 |
| 50 | FVVGTQAHP | 516 | -1.0000 | 0 |
| 51 | VGTQAHPEL | 518 | -1.0300 | 0 |
| 52 | FLHVSLVPY | 182 | -1.0500 | 0 |
| 53 | VGDIESQPF | 156 | -1.1000 | 0 |
| 54 | VPYLAPSGE | 188 | -1.1000 | 0 |
| 55 | VAFVGAAID | 538 | -1.1500 | 0 |
| 56 | LCLGLQCIV | 391 | -1.2000 | 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 | VRIALVGKY | 301 | 5.3000 | 55.79 |
| 2 | VRRLNLPFR | 272 | 4.3000 | 45.26 |
| 3 | YLGDTVQVI | 113 | 4.2000 | 44.21 |
| 4 | FVSGGVASS | 12 | 4.1000 | 43.16 |
| 5 | LRFSGTSPD | 492 | 3.9700 | 41.79 |
| 6 | LEPDSVVAQ | 454 | 3.9000 | 41.05 |
| 7 | LHVSLVPYL | 183 | 3.8600 | 40.63 |
| 8 | ITPDALILR | 214 | 3.7000 | 38.95 |
| 9 | VDIDGVIST | 241 | 3.6000 | 37.89 |
| 10 | LVGKYVELS | 305 | 3.4000 | 35.79 |
| 11 | MRLGSYPAV | 445 | 3.3000 | 34.74 |
| 12 | LLPVEIPEI | 552 | 3.3000 | 34.74 |
| 13 | VFFLHVSLV | 180 | 3.1700 | 33.37 |
| 14 | LGKGLTASS | 21 | 2.9000 | 30.53 |
| 15 | VVITEIGGT | 147 | 2.9000 | 30.53 |
| 16 | LRSIGITPD | 209 | 2.9000 | 30.53 |
| 17 | VELSDAYLS | 310 | 2.8500 | 30.00 |
| 18 | VHGVLIPGG | 357 | 2.8000 | 29.47 |
| 19 | LFVSGGVAS | 11 | 2.6000 | 27.37 |
| 20 | LFVAFVGAA | 536 | 2.6000 | 27.37 |
| 21 | LVPYLAPSG | 187 | 2.5000 | 26.32 |

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|---|---|---|---|---|
| 22 | IVAGEADLG | 434 | 2.4000 | 25.26 |
| 23 | VVRRLNLPF | 271 | 2.3000 | 24.21 |
| 24 | VNNAYRDKI | 479 | 2.3000 | 24.21 |
| 25 | YLNVDPGTM | 49 | 2.2000 | 23.16 |
| 26 | LNVDPGTMN | 50 | 2.2000 | 23.16 |
| 27 | VIPHITDEI | 120 | 2.2000 | 23.16 |
| 28 | VEICWVASD | 334 | 2.2000 | 23.16 |
| 29 | LQCIVIEAA | 395 | 2.2000 | 23.16 |
| 30 | FQHGEVFVT | 60 | 2.1000 | 22.11 |
| 31 | LGLQCIVIE | 393 | 2.1000 | 22.11 |
| 32 | LRCDRDVPE | 221 | 2.0000 | 21.05 |
| 33 | IVIEAARSV | 398 | 2.0000 | 21.05 |
| 34 | LGGTMRLGS | 441 | 2.0000 | 21.05 |
| 35 | YPPDRHPFV | 509 | 2.0000 | 21.05 |
| 36 | IALVGKYVE | 303 | 1.9500 | 20.53 |
| 37 | VQVIPHITD | 118 | 1.9000 | 20.00 |
| 38 | LKTKPTQHS | 197 | 1.9000 | 20.00 |
| 39 | LRRVHEPHE | 291 | 1.9000 | 20.00 |
| 40 | VLIPGGFGI | 360 | 1.9000 | 20.00 |
| 41 | LGREDVFFL | 175 | 1.8600 | 19.58 |
| 42 | ILRCDRDVP | 220 | 1.8000 | 18.95 |
| 43 | LMCDVDIDG | 237 | 1.8000 | 18.95 |
| 44 | VASDGCETT | 339 | 1.8000 | 18.95 |
| 45 | LGQLLTARG | 30 | 1.7000 | 17.89 |
| 46 | IRGIEGKIG | 368 | 1.7000 | 17.89 |
| 47 | LCLGLQCIV | 391 | 1.5000 | 15.79 |
| 48 | FVVGTQAHP | 516 | 1.5000 | 15.79 |
| 49 | VEIPEIPEH | 555 | 1.5000 | 15.79 |
| 50 | ILAMAQPDA | 132 | 1.4000 | 14.74 |
| 51 | FKHRAKVEI | 328 | 1.4000 | 14.74 |
| 52 | VIEAARSVG | 399 | 1.3700 | 14.42 |
| 53 | MRKHPQTAT | 0 | 1.3000 | 13.68 |
| 54 | VTMQKLDPY | 41 | 1.3000 | 13.68 |
| 55 | VLGLCLGLQ | 388 | 1.3000 | 13.68 |

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|---|---|---|---|---|
| 56 | LTNANSAEF | 408 | 1.3000 | 13.68 |
| 57 | YKAGELLPV | 547 | 1.3000 | 13.68 |
| 58 | FVGAAIDYK | 540 | 1.2000 | 12.63 |

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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 | FVSGGVASS | 12 | 4.7000 | 51.65 |
| 2 | YLGDTVQVI | 113 | 4.3000 | 47.25 |
| 3 | LEPDSVVAQ | 454 | 3.6000 | 39.56 |
| 4 | VRIALVGKY | 301 | 3.0000 | 32.97 |
| 5 | FQHGEVFVT | 60 | 2.4000 | 26.37 |
| 6 | FVGAAIDYK | 540 | 2.1000 | 23.08 |
| 7 | LVGKYVELS | 305 | 2.0000 | 21.98 |
| 8 | YPPDRHPFV | 509 | 2.0000 | 21.98 |
| 9 | LHVSLVPYL | 183 | 1.9000 | 20.88 |
| 10 | VDIDGVIST | 241 | 1.9000 | 20.88 |
| 11 | LRFSGTSPD | 492 | 1.8700 | 20.55 |
| 12 | VRRLNLPFR | 272 | 1.8000 | 19.78 |
| 13 | YLNVDPGTM | 49 | 1.7000 | 18.68 |
| 14 | LFVAFVGAA | 536 | 1.6000 | 17.58 |
| 15 | LGKGLTASS | 21 | 1.5000 | 16.48 |
| 16 | FKHRAKVEI | 328 | 1.5000 | 16.48 |
| 17 | FVVGTQAHP | 516 | 1.5000 | 16.48 |
| 18 | VELSDAYLS | 310 | 1.4500 | 15.93 |
| 19 | LLPVEIPEI | 552 | 1.4000 | 15.38 |
| 20 | MRLGSYPAV | 445 | 1.3000 | 14.29 |
| 21 | YKAGELLPV | 547 | 1.3000 | 14.29 |
| 22 | LFVSGGVAS | 11 | 1.2000 | 13.19 |
| 23 | VVITEIGGT | 147 | 1.2000 | 13.19 |
| 24 | ITPDALILR | 214 | 1.2000 | 13.19 |
| 25 | FGIRGIEGK | 366 | 1.2000 | 13.19 |
| 26 | LQCIVIEAA | 395 | 1.2000 | 13.19 |

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|---|---|---|---|---|
| 27 | VFFLHVSLV | 180 | 1.1700 | 12.86 |
| 28 | VEIPEIPEH | 555 | 1.0800 | 11.87 |
| 29 | VLGLCLGLQ | 388 | 1.0000 | 10.99 |
| 30 | WVASDGCET | 338 | 0.9000 | 9.89 |
| 31 | LRSIGITPD | 209 | 0.8000 | 8.79 |
| 32 | IYDIPKVLH | 255 | 0.6800 | 7.47 |
| 33 | FFLHVSLVP | 181 | 0.6000 | 6.59 |
| 34 | FLHVSLVPY | 182 | 0.6000 | 6.59 |
| 35 | LGGTMRLGS | 441 | 0.6000 | 6.59 |
| 36 | LKTKPTQHS | 197 | 0.5000 | 5.49 |
| 37 | FDPDTPDPV | 416 | 0.5000 | 5.49 |
| 38 | YQTTQVSER | 464 | 0.4700 | 5.16 |
| 39 | FVVRRLNLP | 270 | 0.4100 | 4.51 |
| 40 | LNVDPGTMN | 50 | 0.4000 | 4.40 |
| 41 | ILAMAQPDA | 132 | 0.4000 | 4.40 |
| 42 | VHGVLIPGG | 357 | 0.4000 | 4.40 |
| 43 | VNNAYRDKI | 479 | 0.4000 | 4.40 |
| 44 | FLDRNLPGS | 84 | 0.3000 | 3.30 |
| 45 | VIPHITDEI | 120 | 0.3000 | 3.30 |
| 46 | LVPYLAPSG | 187 | 0.1000 | 1.10 |
| 47 | VEICWVASD | 334 | 0.1000 | 1.10 |
| 48 | VASDGCETT | 339 | 0.1000 | 1.10 |
| 49 | FVAFVGAAI | 537 | 0.1000 | 1.10 |
| 50 | LGREDVFFL | 175 | -0.1000 | 0 |
| 51 | FVEYPPDRH | 506 | -0.1200 | 0 |
| 52 | VQVIPHITD | 118 | -0.2000 | 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 | LEPDSVVAQ | 454 | 4.4800 | 50.91 |
| 2 | FVSGGVASS | 12 | 3.7000 | 42.05 |
| 3 | YLGDTVQVI | 113 | 3.4000 | 38.64 |

| | | | | |
|---|---|---|---|---|
| 4 | LVGKYVELS | 305 | 3.4000 | 38.64 |
| 5 | VRIALVGKY | 301 | 2.6000 | 29.55 |
| 6 | LQCIVIEAA | 395 | 2.6000 | 29.55 |
| 7 | LRFSGTSPD | 492 | 2.6000 | 29.55 |
| 8 | VDIDGVIST | 241 | 2.5800 | 29.32 |
| 9 | LGKGLTASS | 21 | 2.5000 | 28.41 |
| 10 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 11 | LFVSGGVAS | 11 | 2.0800 | 23.64 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 21.59 |
| 13 | ITPDALILR | 214 | 1.8800 | 21.36 |
| 14 | LRSIGITPD | 209 | 1.8000 | 20.45 |
| 15 | VNNAYRDKI | 479 | 1.7000 | 19.32 |
| 16 | VIPHITDEI | 120 | 1.6000 | 18.18 |
| 17 | LKTKPTQHS | 197 | 1.6000 | 18.18 |
| 18 | IYDIPKVLH | 255 | 1.5600 | 17.73 |
| 19 | LHVSLVPYL | 183 | 1.5000 | 17.05 |
| 20 | VASDGCETT | 339 | 1.5000 | 17.05 |
| 21 | LGLCLGLQC | 389 | 1.5000 | 17.05 |
| 22 | LNVDPGTMN | 50 | 1.4000 | 15.91 |
| 23 | VRRLNLPFR | 272 | 1.4000 | 15.91 |
| 24 | FVGAAIDYK | 540 | 1.4000 | 15.91 |
| 25 | LKNKIALMC | 231 | 1.3000 | 14.77 |
| 26 | VELSDAYLS | 310 | 1.3000 | 14.77 |
| 27 | IVAGEADLG | 434 | 1.3000 | 14.77 |
| 28 | LFVAFVGAA | 536 | 1.2000 | 13.64 |
| 29 | ILRCDRDVP | 220 | 1.1000 | 12.50 |
| 30 | VEICWVASD | 334 | 1.1000 | 12.50 |
| 31 | VGLTNANSA | 406 | 1.1000 | 12.50 |
| 32 | IKRRILAMA | 128 | 1.0000 | 11.36 |
| 33 | LLPVEIPEI | 552 | 1.0000 | 11.36 |
| 34 | VVRRLNLPF | 271 | 0.9000 | 10.23 |
| 35 | LSVAEALRA | 317 | 0.9000 | 10.23 |
| 36 | IRGIEGKIG | 368 | 0.9000 | 10.23 |
| 37 | MRLGSYPAV | 445 | 0.9000 | 10.23 |

| | | | | |
|---|---|---|---|---|
| 38 | LLRRVHEPH | 290 | 0.8800 | 10.00 |
| 39 | VVITEIGGT | 147 | 0.8000 | 9.09 |
| 40 | YKAGELLPV | 547 | 0.8000 | 9.09 |
| 41 | IVIEAARSV | 398 | 0.7000 | 7.95 |
| 42 | VEIPEIPEH | 555 | 0.6800 | 7.73 |
| 43 | MRKHPQTAT | 0 | 0.6000 | 6.82 |
| 44 | FGIRGIEGK | 366 | 0.6000 | 6.82 |
| 45 | VLGLCLGLQ | 388 | 0.6000 | 6.82 |
| 46 | LGLQCIVIE | 393 | 0.5800 | 6.59 |
| 47 | LCLGLQCIV | 391 | 0.5000 | 5.68 |
| 48 | FVVGTQAHP | 516 | 0.5000 | 5.68 |
| 49 | VQVIPHITD | 118 | 0.4800 | 5.45 |
| 50 | LRCDRDVPE | 221 | 0.4800 | 5.45 |
| 51 | FKHRAKVEI | 328 | 0.3800 | 4.32 |
| 52 | LGQLLTARG | 30 | 0.3000 | 3.41 |
| 53 | LLTARGLHV | 33 | 0.3000 | 3.41 |
| 54 | VTMQKLDPY | 41 | 0.3000 | 3.41 |
| 55 | VGQPLPEPA | 574 | 0.2000 | 2.27 |
| 56 | FFLHVSLVP | 181 | 0.1000 | 1.14 |
| 57 | FVVRRLNLP | 270 | 0.1000 | 1.14 |
| 58 | VAQAYQTTQ | 460 | 0.1000 | 1.14 |

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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 | LEPDSVVAQ | 454 | 4.4800 | 50.91 |
| 2 | FVSGGVASS | 12 | 3.7000 | 42.05 |
| 3 | YLGDTVQVI | 113 | 3.4000 | 38.64 |
| 4 | LVGKYVELS | 305 | 3.4000 | 38.64 |
| 5 | VRIALVGKY | 301 | 2.6000 | 29.55 |
| 6 | LQCIVIEAA | 395 | 2.6000 | 29.55 |
| 7 | LRFSGTSPD | 492 | 2.6000 | 29.55 |
| 8 | VDIDGVIST | 241 | 2.5800 | 29.32 |

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|---|---|---|---|---|
| 9 | LGKGLTASS | 21 | 2.5000 | 28.41 |
| 10 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 11 | LFVSGGVAS | 11 | 2.0800 | 23.64 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 21.59 |
| 13 | ITPDALILR | 214 | 1.8800 | 21.36 |
| 14 | LRSIGITPD | 209 | 1.8000 | 20.45 |
| 15 | VNNAYRDKI | 479 | 1.7000 | 19.32 |
| 16 | VIPHITDEI | 120 | 1.6000 | 18.18 |
| 17 | LKTKPTQHS | 197 | 1.6000 | 18.18 |
| 18 | IYDIPKVLH | 255 | 1.5600 | 17.73 |
| 19 | LHVSLVPYL | 183 | 1.5000 | 17.05 |
| 20 | VASDGCETT | 339 | 1.5000 | 17.05 |
| 21 | LGLCLGLQC | 389 | 1.5000 | 17.05 |
| 22 | LNVDPGTMN | 50 | 1.4000 | 15.91 |
| 23 | VRRLNLPFR | 272 | 1.4000 | 15.91 |
| 24 | FVGAAIDYK | 540 | 1.4000 | 15.91 |
| 25 | LKNKIALMC | 231 | 1.3000 | 14.77 |
| 26 | VELSDAYLS | 310 | 1.3000 | 14.77 |
| 27 | IVAGEADLG | 434 | 1.3000 | 14.77 |
| 28 | LFVAFVGAA | 536 | 1.2000 | 13.64 |
| 29 | ILRCDRDVP | 220 | 1.1000 | 12.50 |
| 30 | VEICWVASD | 334 | 1.1000 | 12.50 |
| 31 | VGLTNANSA | 406 | 1.1000 | 12.50 |
| 32 | IKRRILAMA | 128 | 1.0000 | 11.36 |
| 33 | LLPVEIPEI | 552 | 1.0000 | 11.36 |
| 34 | VVRRLNLPF | 271 | 0.9000 | 10.23 |
| 35 | LSVAEALRA | 317 | 0.9000 | 10.23 |
| 36 | IRGIEGKIG | 368 | 0.9000 | 10.23 |
| 37 | MRLGSYPAV | 445 | 0.9000 | 10.23 |
| 38 | LLRRVHEPH | 290 | 0.8800 | 10.00 |
| 39 | VVITEIGGT | 147 | 0.8000 | 9.09 |
| 40 | YKAGELLPV | 547 | 0.8000 | 9.09 |
| 41 | IVIEAARSV | 398 | 0.7000 | 7.95 |
| 42 | VEIPEIPEH | 555 | 0.6800 | 7.73 |

|  |  |  |  |  |
|---|---|---|---|---|
| 43 | MRKHPQTAT | 0 | 0.6000 | 6.82 |
| 44 | FGIRGIEGK | 366 | 0.6000 | 6.82 |
| 45 | VLGLCLGLQ | 388 | 0.6000 | 6.82 |
| 46 | LGLQCIVIE | 393 | 0.5800 | 6.59 |
| 47 | LCLGLQCIV | 391 | 0.5000 | 5.68 |
| 48 | FVVGTQAHP | 516 | 0.5000 | 5.68 |
| 49 | VQVIPHITD | 118 | 0.4800 | 5.45 |
| 50 | LRCDRDVPE | 221 | 0.4800 | 5.45 |
| 51 | FKHRAKVEI | 328 | 0.3800 | 4.32 |
| 52 | LGQLLTARG | 30 | 0.3000 | 3.41 |
| 53 | LLTARGLHV | 33 | 0.3000 | 3.41 |
| 54 | VTMQKLDPY | 41 | 0.3000 | 3.41 |
| 55 | VGQPLPEPA | 574 | 0.2000 | 2.27 |
| 56 | FFLHVSLVP | 181 | 0.1000 | 1.14 |
| 57 | FVVRRLNLP | 270 | 0.1000 | 1.14 |
| 58 | VAQAYQTTQ | 460 | 0.1000 | 1.14 |

|  |  |  |
|---|---|---|
| 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 | LEPDSVVAQ | 454 | 4.4800 | 50.91 |
| 2 | FVSGGVASS | 12 | 3.7000 | 42.05 |
| 3 | YLGDTVQVI | 113 | 3.4000 | 38.64 |
| 4 | LVGKYVELS | 305 | 3.4000 | 38.64 |
| 5 | VRIALVGKY | 301 | 2.6000 | 29.55 |
| 6 | LQCIVIEAA | 395 | 2.6000 | 29.55 |
| 7 | LRFSGTSPD | 492 | 2.6000 | 29.55 |
| 8 | VDIDGVIST | 241 | 2.5800 | 29.32 |
| 9 | LGKGLTASS | 21 | 2.5000 | 28.41 |
| 10 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 11 | LFVSGGVAS | 11 | 2.0800 | 23.64 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 21.59 |
| 13 | ITPDALILR | 214 | 1.8800 | 21.36 |

| | | | | |
|---|---|---|---|---|
| 14 | LRSIGITPD | 209 | 1.8000 | 20.45 |
| 15 | VNNAYRDKI | 479 | 1.7000 | 19.32 |
| 16 | VIPHITDEI | 120 | 1.6000 | 18.18 |
| 17 | LKTKPTQHS | 197 | 1.6000 | 18.18 |
| 18 | IYDIPKVLH | 255 | 1.5600 | 17.73 |
| 19 | LHVSLVPYL | 183 | 1.5000 | 17.05 |
| 20 | VASDGCETT | 339 | 1.5000 | 17.05 |
| 21 | LGLCLGLQC | 389 | 1.5000 | 17.05 |
| 22 | LNVDPGTMN | 50 | 1.4000 | 15.91 |
| 23 | VRRLNLPFR | 272 | 1.4000 | 15.91 |
| 24 | FVGAAIDYK | 540 | 1.4000 | 15.91 |
| 25 | LKNKIALMC | 231 | 1.3000 | 14.77 |
| 26 | VELSDAYLS | 310 | 1.3000 | 14.77 |
| 27 | IVAGEADLG | 434 | 1.3000 | 14.77 |
| 28 | LFVAFVGAA | 536 | 1.2000 | 13.64 |
| 29 | ILRCDRDVP | 220 | 1.1000 | 12.50 |
| 30 | VEICWVASD | 334 | 1.1000 | 12.50 |
| 31 | VGLTNANSA | 406 | 1.1000 | 12.50 |
| 32 | IKRRILAMA | 128 | 1.0000 | 11.36 |
| 33 | LLPVEIPEI | 552 | 1.0000 | 11.36 |
| 34 | VVRRLNLPF | 271 | 0.9000 | 10.23 |
| 35 | LSVAEALRA | 317 | 0.9000 | 10.23 |
| 36 | IRGIEGKIG | 368 | 0.9000 | 10.23 |
| 37 | MRLGSYPAV | 445 | 0.9000 | 10.23 |
| 38 | LLRRVHEPH | 290 | 0.8800 | 10.00 |
| 39 | VVITEIGGT | 147 | 0.8000 | 9.09 |
| 40 | YKAGELLPV | 547 | 0.8000 | 9.09 |
| 41 | IVIEAARSV | 398 | 0.7000 | 7.95 |
| 42 | VEIPEIPEH | 555 | 0.6800 | 7.73 |
| 43 | MRKHPQTAT | 0 | 0.6000 | 6.82 |
| 44 | FGIRGIEGK | 366 | 0.6000 | 6.82 |
| 45 | VLGLCLGLQ | 388 | 0.6000 | 6.82 |
| 46 | LGLQCIVIE | 393 | 0.5800 | 6.59 |
| 47 | LCLGLQCIV | 391 | 0.5000 | 5.68 |

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|---|---|---|---|---|
| 48 | FVVGTQAHP | 516 | 0.5000 | 5.68 |
| 49 | VQVIPHITD | 118 | 0.4800 | 5.45 |
| 50 | LRCDRDVPE | 221 | 0.4800 | 5.45 |
| 51 | FKHRAKVEI | 328 | 0.3800 | 4.32 |
| 52 | LGQLLTARG | 30 | 0.3000 | 3.41 |
| 53 | LLTARGLHV | 33 | 0.3000 | 3.41 |
| 54 | VTMQKLDPY | 41 | 0.3000 | 3.41 |
| 55 | VGQPLPEPA | 574 | 0.2000 | 2.27 |
| 56 | FFLHVSLVP | 181 | 0.1000 | 1.14 |
| 57 | FVVRRLNLP | 270 | 0.1000 | 1.14 |
| 58 | VAQAYQTTQ | 460 | 0.1000 | 1.14 |

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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 | YLGDTVQVI | 113 | 5.2000 | 54.74 |
| 2 | FVSGGVASS | 12 | 5.1000 | 53.68 |
| 3 | VRIALVGKY | 301 | 4.3000 | 45.26 |
| 4 | VRRLNLPFR | 272 | 3.3000 | 34.74 |
| 5 | YLNVDPGTM | 49 | 3.2000 | 33.68 |
| 6 | FQHGEVFVT | 60 | 3.1000 | 32.63 |
| 7 | YPPDRHPFV | 509 | 3.0000 | 31.58 |
| 8 | LRFSGTSPD | 492 | 2.9700 | 31.26 |
| 9 | LEPDSVVAQ | 454 | 2.9000 | 30.53 |
| 10 | LHVSLVPYL | 183 | 2.8600 | 30.11 |
| 11 | ITPDALILR | 214 | 2.7000 | 28.42 |
| 12 | VDIDGVIST | 241 | 2.6000 | 27.37 |
| 13 | FVVGTQAHP | 516 | 2.5000 | 26.32 |
| 14 | LVGKYVELS | 305 | 2.4000 | 25.26 |
| 15 | FKHRAKVEI | 328 | 2.4000 | 25.26 |
| 16 | MRLGSYPAV | 445 | 2.3000 | 24.21 |
| 17 | YKAGELLPV | 547 | 2.3000 | 24.21 |
| 18 | LLPVEIPEI | 552 | 2.3000 | 24.21 |

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|---|---|---|---|---|
| 19 | FVGAAIDYK | 540 | 2.2000 | 23.16 |
| 20 | VFFLHVSLV | 180 | 2.1700 | 22.84 |
| 21 | YQTTQVSER | 464 | 1.9700 | 20.74 |
| 22 | LGKGLTASS | 21 | 1.9000 | 20.00 |
| 23 | VVITEIGGT | 147 | 1.9000 | 20.00 |
| 24 | FLHVSLVPY | 182 | 1.9000 | 20.00 |
| 25 | LRSIGITPD | 209 | 1.9000 | 20.00 |
| 26 | VELSDAYLS | 310 | 1.8500 | 19.47 |
| 27 | VHGVLIPGG | 357 | 1.8000 | 18.95 |
| 28 | LFVSGGVAS | 11 | 1.6000 | 16.84 |
| 29 | FFLHVSLVP | 181 | 1.6000 | 16.84 |
| 30 | WVASDGCET | 338 | 1.6000 | 16.84 |
| 31 | LFVAFVGAA | 536 | 1.6000 | 16.84 |
| 32 | LVPYLAPSG | 187 | 1.5000 | 15.79 |
| 33 | FDPDTPDPV | 416 | 1.5000 | 15.79 |
| 34 | FVVRRLNLP | 270 | 1.4100 | 14.84 |
| 35 | IVAGEADLG | 434 | 1.4000 | 14.74 |
| 36 | VVRRLNLPF | 271 | 1.3000 | 13.68 |
| 37 | FGIRGIEGK | 366 | 1.3000 | 13.68 |
| 38 | VNNAYRDKI | 479 | 1.3000 | 13.68 |
| 39 | LNVDPGTMN | 50 | 1.2000 | 12.63 |
| 40 | VIPHITDEI | 120 | 1.2000 | 12.63 |
| 41 | FLEAARQVR | 164 | 1.2000 | 12.63 |
| 42 | VEICWVASD | 334 | 1.2000 | 12.63 |
| 43 | LQCIVIEAA | 395 | 1.2000 | 12.63 |
| 44 | YDIPKVLHR | 256 | 1.1000 | 11.58 |
| 45 | LGLQCIVIE | 393 | 1.1000 | 11.58 |
| 46 | LRCDRDVPE | 221 | 1.0000 | 10.53 |
| 47 | IVIEAARSV | 398 | 1.0000 | 10.53 |
| 48 | LGGTMRLGS | 441 | 1.0000 | 10.53 |
| 49 | FVAFVGAAI | 537 | 1.0000 | 10.53 |
| 50 | IALVGKYVE | 303 | 0.9500 | 10.00 |
| 51 | VQVIPHITD | 118 | 0.9000 | 9.47 |
| 52 | LKTKPTQHS | 197 | 0.9000 | 9.47 |

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|---|---|---|---|---|
| 53 | LRRVHEPHE | 291 | 0.9000 | 9.47 |
| 54 | VLIPGGFGI | 360 | 0.9000 | 9.47 |
| 55 | LGREDVFFL | 175 | 0.8600 | 9.05 |
| 56 | ILRCDRDVP | 220 | 0.8000 | 8.42 |
| 57 | LMCDVDIDG | 237 | 0.8000 | 8.42 |
| 58 | VASDGCETT | 339 | 0.8000 | 8.42 |

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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 | LEPDSVVAQ | 454 | 4.4800 | 50.91 |
| 2 | FVSGGVASS | 12 | 3.7000 | 42.05 |
| 3 | YLGDTVQVI | 113 | 3.4000 | 38.64 |
| 4 | LVGKYVELS | 305 | 3.4000 | 38.64 |
| 5 | VRIALVGKY | 301 | 2.6000 | 29.55 |
| 6 | LQCIVIEAA | 395 | 2.6000 | 29.55 |
| 7 | LRFSGTSPD | 492 | 2.6000 | 29.55 |
| 8 | VDIDGVIST | 241 | 2.5800 | 29.32 |
| 9 | LGKGLTASS | 21 | 2.5000 | 28.41 |
| 10 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 11 | LFVSGGVAS | 11 | 2.0800 | 23.64 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 21.59 |
| 13 | ITPDALILR | 214 | 1.8800 | 21.36 |
| 14 | LRSIGITPD | 209 | 1.8000 | 20.45 |
| 15 | VNNAYRDKI | 479 | 1.7000 | 19.32 |
| 16 | VIPHITDEI | 120 | 1.6000 | 18.18 |
| 17 | LKTKPTQHS | 197 | 1.6000 | 18.18 |
| 18 | IYDIPKVLH | 255 | 1.5600 | 17.73 |
| 19 | LHVSLVPYL | 183 | 1.5000 | 17.05 |
| 20 | VASDGCETT | 339 | 1.5000 | 17.05 |
| 21 | LGLCLGLQC | 389 | 1.5000 | 17.05 |
| 22 | LNVDPGTMN | 50 | 1.4000 | 15.91 |
| 23 | VRRLNLPFR | 272 | 1.4000 | 15.91 |

| | | | | |
|---|---|---|---|---|
| 24 | FVGAAIDYK | 540 | 1.4000 | 15.91 |
| 25 | LKNKIALMC | 231 | 1.3000 | 14.77 |
| 26 | VELSDAYLS | 310 | 1.3000 | 14.77 |
| 27 | IVAGEADLG | 434 | 1.3000 | 14.77 |
| 28 | LFVAFVGAA | 536 | 1.2000 | 13.64 |
| 29 | ILRCDRDVP | 220 | 1.1000 | 12.50 |
| 30 | VEICWVASD | 334 | 1.1000 | 12.50 |
| 31 | VGLTNANSA | 406 | 1.1000 | 12.50 |
| 32 | IKRRILAMA | 128 | 1.0000 | 11.36 |
| 33 | LLPVEIPEI | 552 | 1.0000 | 11.36 |
| 34 | VVRRLNLPF | 271 | 0.9000 | 10.23 |
| 35 | LSVAEALRA | 317 | 0.9000 | 10.23 |
| 36 | IRGIEGKIG | 368 | 0.9000 | 10.23 |
| 37 | MRLGSYPAV | 445 | 0.9000 | 10.23 |
| 38 | LLRRVHEPH | 290 | 0.8800 | 10.00 |
| 39 | VVITEIGGT | 147 | 0.8000 | 9.09 |
| 40 | YKAGELLPV | 547 | 0.8000 | 9.09 |
| 41 | IVIEAARSV | 398 | 0.7000 | 7.95 |
| 42 | VEIPEIPEH | 555 | 0.6800 | 7.73 |
| 43 | MRKHPQTAT | 0 | 0.6000 | 6.82 |
| 44 | FGIRGIEGK | 366 | 0.6000 | 6.82 |
| 45 | VLGLCLGLQ | 388 | 0.6000 | 6.82 |
| 46 | LGLQCIVIE | 393 | 0.5800 | 6.59 |
| 47 | LCLGLQCIV | 391 | 0.5000 | 5.68 |
| 48 | FVVGTQAHP | 516 | 0.5000 | 5.68 |
| 49 | VQVIPHITD | 118 | 0.4800 | 5.45 |
| 50 | LRCDRDVPE | 221 | 0.4800 | 5.45 |
| 51 | FKHRAKVEI | 328 | 0.3800 | 4.32 |
| 52 | LGQLLTARG | 30 | 0.3000 | 3.41 |
| 53 | LLTARGLHV | 33 | 0.3000 | 3.41 |
| 54 | VTMQKLDPY | 41 | 0.3000 | 3.41 |
| 55 | VGQPLPEPA | 574 | 0.2000 | 2.27 |
| 56 | FFLHVSLVP | 181 | 0.1000 | 1.14 |
| 57 | FVVRRLNLP | 270 | 0.1000 | 1.14 |

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|---|---|---|---|---|
| 58 | VAQAYQTTQ | 460 | 0.1000 | 1.14 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | FFLHVSLVP | 181 | 3.3000 | 38.37 |
| 2 | YLGDTVQVI | 113 | 3.2000 | 37.21 |
| 3 | VIPHITDEI | 120 | 2.8000 | 32.56 |
| 4 | LRFSGTSPD | 492 | 2.8000 | 32.56 |
| 5 | FVSGGVASS | 12 | 2.3000 | 26.74 |
| 6 | LEPDSVVAQ | 454 | 2.2800 | 26.51 |
| 7 | IVIEAARSV | 398 | 2.2000 | 25.58 |
| 8 | VGLTNANSA | 406 | 1.8000 | 20.93 |
| 9 | YQTTQVSER | 464 | 1.6000 | 18.60 |
| 10 | FVGAAIDYK | 540 | 1.6000 | 18.60 |
| 11 | VFFLHVSLV | 180 | 1.4000 | 16.28 |
| 12 | LVGKYVELS | 305 | 1.4000 | 16.28 |
| 13 | VRIALVGKY | 301 | 1.3000 | 15.12 |
| 14 | LGQLLTARG | 30 | 1.2000 | 13.95 |
| 15 | LQCIVIEAA | 395 | 1.1000 | 12.79 |
| 16 | LKTKPTQHS | 197 | 1.0000 | 11.63 |
| 17 | FVTEDGAET | 66 | 0.9000 | 10.47 |
| 18 | VVRRLNLPF | 271 | 0.9000 | 10.47 |
| 19 | VVITEIGGT | 147 | 0.7000 | 8.14 |
| 20 | LGREDVFFL | 175 | 0.6000 | 6.98 |
| 21 | VISTPDAPS | 246 | 0.6000 | 6.98 |
| 22 | VAALRSIGI | 206 | 0.5800 | 6.74 |
| 23 | LGKGLTASS | 21 | 0.5000 | 5.81 |
| 24 | VELSDAYLS | 310 | 0.4000 | 4.65 |
| 25 | LFVSGGVAS | 11 | 0.3800 | 4.42 |
| 26 | VDIDGVIST | 241 | 0.3800 | 4.42 |
| 27 | FSGTSPDGH | 494 | 0.3800 | 4.42 |
| 28 | LHVSLVPYL | 183 | 0.3000 | 3.49 |

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|---|---|---|---|---|
| 29 | LRSIGITPD | 209 | 0.3000 | 3.49 |
| 30 | IGITPDALI | 212 | 0.3000 | 3.49 |
| 31 | VVGTQAHPE | 517 | 0.3000 | 3.49 |
| 32 | WVASDGCET | 338 | 0.2000 | 2.33 |
| 33 | VRRLNLPFR | 272 | -0.1000 | 0 |
| 34 | LSVAEALRA | 317 | -0.1000 | 0 |
| 35 | FGIRGIEGK | 366 | -0.1000 | 0 |
| 36 | LFVAFVGAA | 536 | -0.1000 | 0 |
| 37 | LRCDRDVPE | 221 | -0.1200 | 0 |
| 38 | VEICWVASD | 334 | -0.2000 | 0 |
| 39 | IESQPFLEA | 159 | -0.3000 | 0 |
| 40 | LGLCLGLQC | 389 | -0.3000 | 0 |
| 41 | IPEHTPNGS | 560 | -0.3000 | 0 |
| 42 | LPGSANVTT | 89 | -0.3200 | 0 |
| 43 | LKNKIALMC | 231 | -0.4000 | 0 |
| 44 | LHREELDAF | 262 | -0.4000 | 0 |
| 45 | YVELSDAYL | 309 | -0.4000 | 0 |
| 46 | VASDGCETT | 339 | -0.4000 | 0 |
| 47 | IALMCDVDI | 235 | -0.4200 | 0 |
| 48 | LGLQCIVIE | 393 | -0.4200 | 0 |
| 49 | MRKHPQTAT | 0 | -0.5000 | 0 |
| 50 | LTNANSAEF | 408 | -0.5000 | 0 |
| 51 | LMCDVDIDG | 237 | -0.5200 | 0 |
| 52 | IRGIEGKIG | 368 | -0.6000 | 0 |
| 53 | FDPDTPDPV | 416 | -0.6000 | 0 |
| 54 | LGGTMRLGS | 441 | -0.6000 | 0 |
| 55 | FVAFVGAAI | 537 | -0.6000 | 0 |
| 56 | LPVEIPEIP | 553 | -0.6000 | 0 |
| 57 | VAGEADLGG | 435 | -0.7000 | 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 | LKSRPTRPH | 526 | 5.9800 | 62.29 |
| 2 | VVRRLNLPF | 271 | 5.1000 | 53.12 |
| 3 | LKTKPTQHS | 197 | 4.9000 | 51.04 |
| 4 | LILRCDRDV | 219 | 3.0000 | 31.25 |
| 5 | LVGKYVELS | 305 | 2.8000 | 29.17 |
| 6 | FFLHVSLVP | 181 | 2.7000 | 28.13 |
| 7 | LKNKIALMC | 231 | 2.7000 | 28.13 |
| 8 | LGKGLTASS | 21 | 2.4000 | 25.00 |
| 9 | IVIEAARSV | 398 | 2.3000 | 23.96 |
| 10 | FVSGGVASS | 12 | 2.2000 | 22.92 |
| 11 | VIPHITDEI | 120 | 2.1000 | 21.88 |
| 12 | LRFSGTSPD | 492 | 1.8000 | 18.75 |
| 13 | IKRRILAMA | 128 | 1.7000 | 17.71 |
| 14 | VELSDAYLS | 310 | 1.7000 | 17.71 |
| 15 | VGLTNANSA | 406 | 1.6000 | 16.67 |
| 16 | VRIALVGKY | 301 | 1.5000 | 15.62 |
| 17 | IAYARARGL | 378 | 1.5000 | 15.62 |
| 18 | LSVAEALRA | 317 | 1.2000 | 12.50 |
| 19 | LGLCLGLQC | 389 | 1.0000 | 10.42 |
| 20 | MRKHPQTAT | 0 | 0.8000 | 8.33 |
| 21 | LGQLLTARG | 30 | 0.8000 | 8.33 |
| 22 | VFFLHVSLV | 180 | 0.8000 | 8.33 |
| 23 | VLHREELDA | 261 | 0.8000 | 8.33 |
| 24 | FVVRRLNLP | 270 | 0.8000 | 8.33 |
| 25 | VEICWVASD | 334 | 0.8000 | 8.33 |
| 26 | IPEHTPNGS | 560 | 0.8000 | 8.33 |
| 27 | LRSIGITPD | 209 | 0.7800 | 8.12 |
| 28 | VAALRSIGI | 206 | 0.6000 | 6.25 |
| 29 | LDAFVVRRL | 267 | 0.6000 | 6.25 |
| 30 | VVGTQAHPE | 517 | 0.6000 | 6.25 |
| 31 | VRHYLGRED | 171 | 0.5000 | 5.21 |
| 32 | LTNANSAEF | 408 | 0.5000 | 5.21 |
| 33 | IALMCDVDI | 235 | 0.4000 | 4.17 |
| 34 | VISTPDAPS | 246 | 0.4000 | 4.17 |

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|---|---|---|---|---|
| 35 | FGIRGIEGK | 366 | 0.4000 | 4.17 |
| 36 | VGDIESQPF | 156 | 0.3800 | 3.96 |
| 37 | IEAARSVGL | 400 | 0.3000 | 3.12 |
| 38 | VGAAIDYKA | 541 | 0.3000 | 3.12 |
| 39 | LLRRVHEPH | 290 | 0.1800 | 1.88 |
| 40 | MQKLDPYLN | 43 | 0.1000 | 1.04 |
| 41 | IGITPDALI | 212 | 0.1000 | 1.04 |
| 42 | VVAQAYQTT | 459 | 0.1000 | 1.04 |
| 43 | LFVAFVGAA | 536 | 0.1000 | 1.04 |
| 44 | IRGIEGKIG | 368 | -0.0200 | 0 |
| 45 | LQCIVIEAA | 395 | -0.0200 | 0 |
| 46 | FQHGEVFVT | 60 | -0.1000 | 0 |
| 47 | VTTGQVYST | 95 | -0.1000 | 0 |
| 48 | VLIPGGFGI | 360 | -0.1000 | 0 |
| 49 | LLTARGLHV | 33 | -0.2000 | 0 |
| 50 | IESQPFLEA | 159 | -0.2000 | 0 |
| 51 | LFVSGGVAS | 11 | -0.3000 | 0 |
| 52 | YERFLDRNL | 81 | -0.3000 | 0 |
| 53 | VVITEIGGT | 147 | -0.3000 | 0 |
| 54 | VLEPDSVVA | 453 | -0.3000 | 0 |
| 55 | LEPDSVVAQ | 454 | -0.3000 | 0 |
| 56 | YLGDTVQVI | 113 | -0.4000 | 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 | VFFLHVSLV | 180 | 3.3000 | 37.50 |
| 2 | LRFSGTSPD | 492 | 3.0000 | 34.09 |
| 3 | LGQLLTARG | 30 | 2.4000 | 27.27 |
| 4 | VRIALVGKY | 301 | 2.4000 | 27.27 |
| 5 | LRSIGITPD | 209 | 2.1000 | 23.86 |
| 6 | LKTKPTQHS | 197 | 2.0000 | 22.73 |
| 7 | VAALRSIGI | 206 | 1.7800 | 20.23 |

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|---|---|---|---|---|
| 8 | LVGKYVELS | 305 | 1.7000 | 19.32 |
| 9 | LQCIVIEAA | 395 | 1.5000 | 17.05 |
| 10 | IALMCDVDI | 235 | 1.3000 | 14.77 |
| 11 | VGLTNANSA | 406 | 1.3000 | 14.77 |
| 12 | VVRRLNLPF | 271 | 1.0000 | 11.36 |
| 13 | LFVAFVGAA | 536 | 1.0000 | 11.36 |
| 14 | VELSDAYLS | 310 | 0.9000 | 10.23 |
| 15 | IVIEAARSV | 398 | 0.9000 | 10.23 |
| 16 | VIPHITDEI | 120 | 0.8000 | 9.09 |
| 17 | VRRLNLPFR | 272 | 0.8000 | 9.09 |
| 18 | VEICWVASD | 334 | 0.8000 | 9.09 |
| 19 | LGKGLTASS | 21 | 0.7000 | 7.95 |
| 20 | MQKLDPYLN | 43 | 0.6000 | 6.82 |
| 21 | LEPDSVVAQ | 454 | 0.6000 | 6.82 |
| 22 | FVSGGVASS | 12 | 0.5000 | 5.68 |
| 23 | LSVAEALRA | 317 | 0.5000 | 5.68 |
| 24 | LTNANSAEF | 408 | 0.5000 | 5.68 |
| 25 | LKNKIALMC | 231 | 0.4000 | 4.55 |
| 26 | VLGLCLGLQ | 388 | 0.4000 | 4.55 |
| 27 | LLPVEIPEI | 552 | 0.4000 | 4.55 |
| 28 | ILAMAQPDA | 132 | 0.3000 | 3.41 |
| 29 | ICWVASDGC | 336 | 0.3000 | 3.41 |
| 30 | LGLCLGLQC | 389 | 0.3000 | 3.41 |
| 31 | FVAFVGAAI | 537 | 0.3000 | 3.41 |
| 32 | VVITEIGGT | 147 | 0.2000 | 2.27 |
| 33 | VGDIESQPF | 156 | 0.1000 | 1.14 |
| 34 | VPYLAPSGE | 188 | 0.1000 | 1.14 |
| 35 | IGAIAYARA | 375 | 0.1000 | 1.14 |
| 36 | LKSRPTRPH | 526 | -0.0200 | 0 |
| 37 | LGREDVFFL | 175 | -0.0500 | 0 |
| 38 | FFLHVSLVP | 181 | -0.2000 | 0 |
| 39 | VQVIPHITD | 118 | -0.2200 | 0 |
| 40 | LFVSGGVAS | 11 | -0.3000 | 0 |
| 41 | IGITPDALI | 212 | -0.3000 | 0 |

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|---|---|---|---|---|
| 42 | IRGIEGKIG | 368 | -0.3000 | 0 |
| 43 | YQTTQVSER | 464 | -0.3000 | 0 |
| 44 | FVGAAIDYK | 540 | -0.3000 | 0 |
| 45 | LGLQCIVIE | 393 | -0.4000 | 0 |
| 46 | VAFVGAAID | 538 | -0.4000 | 0 |
| 47 | YLGDTVQVI | 113 | -0.5000 | 0 |
| 48 | IESQPFLEA | 159 | -0.5000 | 0 |
| 49 | LHVSLVPYL | 183 | -0.5000 | 0 |
| 50 | YLNVDPGTM | 49 | -0.6000 | 0 |
| 51 | VHGVLIPGG | 357 | -0.6000 | 0 |
| 52 | VLEPDSVVA | 453 | -0.6000 | 0 |
| 53 | VAQAYQTTQ | 460 | -0.6000 | 0 |
| 54 | VLIPGGFGI | 360 | -0.6500 | 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 | LRFSGTSPD | 492 | 4.7000 | 50.00 |
| 2 | LRSIGITPD | 209 | 3.8000 | 40.43 |
| 3 | LGQLLTARG | 30 | 2.7000 | 28.72 |
| 4 | VFFLHVSLV | 180 | 2.6000 | 27.66 |
| 5 | VRIALVGKY | 301 | 2.5000 | 26.60 |
| 6 | VEICWVASD | 334 | 2.5000 | 26.60 |
| 7 | VPYLAPSGE | 188 | 2.1000 | 22.34 |
| 8 | MQKLDPYLN | 43 | 1.6000 | 17.02 |
| 9 | LGLQCIVIE | 393 | 1.6000 | 17.02 |
| 10 | FVSGGVASS | 12 | 1.5000 | 15.96 |
| 11 | YLNVDPGTM | 49 | 1.5000 | 15.96 |
| 12 | FVAFVGAAI | 537 | 1.5000 | 15.96 |
| 13 | VQVIPHITD | 118 | 1.4800 | 15.74 |
| 14 | VVGTQAHPE | 517 | 1.3000 | 13.83 |
| 15 | VAFVGAAID | 538 | 1.3000 | 13.83 |
| 16 | FFLHVSLVP | 181 | 1.2000 | 12.77 |

| | | | | |
|---|---|---|---|---|
| 17 | LKTKPTQHS | 197 | 1.0000 | 10.64 |
| 18 | VAALRSIGI | 206 | 0.9800 | 10.43 |
| 19 | VVRRLNLPF | 271 | 0.9000 | 9.57 |
| 20 | IDGVISTPD | 243 | 0.8000 | 8.51 |
| 21 | YVELSDAYL | 309 | 0.8000 | 8.51 |
| 22 | IATMPDQEE | 425 | 0.8000 | 8.51 |
| 23 | YLGDTVQVI | 113 | 0.7000 | 7.45 |
| 24 | FRDVDWTEW | 279 | 0.7000 | 7.45 |
| 25 | LVGKYVELS | 305 | 0.7000 | 7.45 |
| 26 | YQTTQVSER | 464 | 0.7000 | 7.45 |
| 27 | YEVNNAYRD | 477 | 0.7000 | 7.45 |
| 28 | FLHVSLVPY | 182 | 0.6000 | 6.38 |
| 29 | FVEYPPDRH | 506 | 0.6000 | 6.38 |
| 30 | IALMCDVDI | 235 | 0.5000 | 5.32 |
| 31 | LQCIVIEAA | 395 | 0.5000 | 5.32 |
| 32 | LGSYPAVLE | 447 | 0.5000 | 5.32 |
| 33 | VYSTVIAKE | 100 | 0.4000 | 4.26 |
| 34 | LTNANSAEF | 408 | 0.4000 | 4.26 |
| 35 | LEPDSVVAQ | 454 | 0.4000 | 4.26 |
| 36 | LVPYLAPSG | 187 | 0.3000 | 3.19 |
| 37 | LRRVHEPHE | 291 | 0.3000 | 3.19 |
| 38 | VGLTNANSA | 406 | 0.3000 | 3.19 |
| 39 | LAMAQPDAD | 133 | 0.2000 | 2.13 |
| 40 | LRCDRDVPE | 221 | 0.2000 | 2.13 |
| 41 | VLGLCLGLQ | 388 | 0.2000 | 2.13 |
| 42 | IVIEAARSV | 398 | 0.2000 | 2.13 |
| 43 | LKSRPTRPH | 526 | 0.2000 | 2.13 |
| 44 | VVITEIGGT | 147 | 0.1000 | 1.06 |
| 45 | LGREDVFFL | 175 | -0.0500 | 0 |
| 46 | VELSDAYLS | 310 | -0.1000 | 0 |
| 47 | YERFLDRNL | 81 | -0.2000 | 0 |
| 48 | VRRLNLPFR | 272 | -0.2000 | 0 |
| 49 | LGKGLTASS | 21 | -0.3000 | 0 |
| 50 | VHGVLIPGG | 357 | -0.3000 | 0 |

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|---|---|---|---|---|
| 51 | VRHYLGRED | 171 | -0.4000 | 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 | VFFLHVSLV | 180 | 2.3000 | 26.14 |
| 2 | LRFSGTSPD | 492 | 2.0000 | 22.73 |
| 3 | FVSGGVASS | 12 | 1.5000 | 17.05 |
| 4 | LGQLLTARG | 30 | 1.4000 | 15.91 |
| 5 | VRIALVGKY | 301 | 1.4000 | 15.91 |
| 6 | FVAFVGAAI | 537 | 1.3000 | 14.77 |
| 7 | LRSIGITPD | 209 | 1.1000 | 12.50 |
| 8 | LKTKPTQHS | 197 | 1.0000 | 11.36 |
| 9 | FFLHVSLVP | 181 | 0.8000 | 9.09 |
| 10 | VAALRSIGI | 206 | 0.7800 | 8.86 |
| 11 | LVGKYVELS | 305 | 0.7000 | 7.95 |
| 12 | YQTTQVSER | 464 | 0.7000 | 7.95 |
| 13 | FVGAAIDYK | 540 | 0.7000 | 7.95 |
| 14 | YLGDTVQVI | 113 | 0.5000 | 5.68 |
| 15 | LQCIVIEAA | 395 | 0.5000 | 5.68 |
| 16 | YLNVDPGTM | 49 | 0.4000 | 4.55 |
| 17 | IALMCDVDI | 235 | 0.3000 | 3.41 |
| 18 | VGLTNANSA | 406 | 0.3000 | 3.41 |
| 19 | VELSDAYLS | 310 | -0.1000 | 0 |
| 20 | IVIEAARSV | 398 | -0.1000 | 0 |
| 21 | VIPHITDEI | 120 | -0.2000 | 0 |
| 22 | VRRLNLPFR | 272 | -0.2000 | 0 |
| 23 | FRDVDWTEW | 279 | -0.2000 | 0 |
| 24 | YVELSDAYL | 309 | -0.2000 | 0 |
| 25 | VEICWVASD | 334 | -0.2000 | 0 |
| 26 | LGKGLTASS | 21 | -0.3000 | 0 |
| 27 | MQKLDPYLN | 43 | -0.4000 | 0 |
| 28 | LEPDSVVAQ | 454 | -0.4000 | 0 |

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|---|---|---|---|---|
| 29 | FLHVSLVPY | 182 | -0.5000 | 0 |
| 30 | LSVAEALRA | 317 | -0.5000 | 0 |
| 31 | LTNANSAEF | 408 | -0.5000 | 0 |
| 32 | LKNKIALMC | 231 | -0.6000 | 0 |
| 33 | VLGLCLGLQ | 388 | -0.6000 | 0 |
| 34 | LLPVEIPEI | 552 | -0.6000 | 0 |
| 35 | FVEYPPDRH | 506 | -0.6200 | 0 |
| 36 | ILAMAQPDA | 132 | -0.7000 | 0 |
| 37 | ICWVASDGC | 336 | -0.7000 | 0 |
| 38 | LGLCLGLQC | 389 | -0.7000 | 0 |
| 39 | VVITEIGGT | 147 | -0.8000 | 0 |
| 40 | VGDIESQPF | 156 | -0.9000 | 0 |
| 41 | VPYLAPSGE | 188 | -0.9000 | 0 |
| 42 | YDIPKVLHR | 256 | -0.9000 | 0 |
| 43 | IGAIAYARA | 375 | -0.9000 | 0 |
| 44 | LVPYLAPSG | 187 | -1.0000 | 0 |
| 45 | VISTPDAPS | 246 | -1.0000 | 0 |
| 46 | IEAARSVGL | 400 | -1.0000 | 0 |
| 47 | LKSRPTRPH | 526 | -1.0200 | 0 |
| 48 | LGREDVFFL | 175 | -1.0500 | 0 |
| 49 | YERFLDRNL | 81 | -1.2000 | 0 |
| 50 | YARARGLPV | 380 | -1.2000 | 0 |
| 51 | VQVIPHITD | 118 | -1.2200 | 0 |
| 52 | LFVSGGVAS | 11 | -1.3000 | 0 |
| 53 | IGITPDALI | 212 | -1.3000 | 0 |
| 54 | WVASDGCET | 338 | -1.3000 | 0 |
| 55 | IRGIEGKIG | 368 | -1.3000 | 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 | LRFSGTSPD | 492 | 5.7000 | 60.64 |
| 2 | LRSIGITPD | 209 | 4.8000 | 51.06 |

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|---|---|---|---|---|
| 3 | LGQLLTARG | 30 | 3.7000 | 39.36 |
| 4 | VFFLHVSLV | 180 | 3.6000 | 38.30 |
| 5 | VRIALVGKY | 301 | 3.5000 | 37.23 |
| 6 | VEICWVASD | 334 | 3.5000 | 37.23 |
| 7 | VPYLAPSGE | 188 | 3.1000 | 32.98 |
| 8 | MQKLDPYLN | 43 | 2.6000 | 27.66 |
| 9 | LGLQCIVIE | 393 | 2.6000 | 27.66 |
| 10 | VQVIPHITD | 118 | 2.4800 | 26.38 |
| 11 | VVGTQAHPE | 517 | 2.3000 | 24.47 |
| 12 | VAFVGAAID | 538 | 2.3000 | 24.47 |
| 13 | LKTKPTQHS | 197 | 2.0000 | 21.28 |
| 14 | VAALRSIGI | 206 | 1.9800 | 21.06 |
| 15 | VVRRLNLPF | 271 | 1.9000 | 20.21 |
| 16 | IDGVISTPD | 243 | 1.8000 | 19.15 |
| 17 | IATMPDQEE | 425 | 1.8000 | 19.15 |
| 18 | LVGKYVELS | 305 | 1.7000 | 18.09 |
| 19 | IALMCDVDI | 235 | 1.5000 | 15.96 |
| 20 | LQCIVIEAA | 395 | 1.5000 | 15.96 |
| 21 | LGSYPAVLE | 447 | 1.5000 | 15.96 |
| 22 | VYSTVIAKE | 100 | 1.4000 | 14.89 |
| 23 | LTNANSAEF | 408 | 1.4000 | 14.89 |
| 24 | LEPDSVVAQ | 454 | 1.4000 | 14.89 |
| 25 | LVPYLAPSG | 187 | 1.3000 | 13.83 |
| 26 | LRRVHEPHE | 291 | 1.3000 | 13.83 |
| 27 | VGLTNANSA | 406 | 1.3000 | 13.83 |
| 28 | LAMAQPDAD | 133 | 1.2000 | 12.77 |
| 29 | LRCDRDVPE | 221 | 1.2000 | 12.77 |
| 30 | VLGLCLGLQ | 388 | 1.2000 | 12.77 |
| 31 | IVIEAARSV | 398 | 1.2000 | 12.77 |
| 32 | LKSRPTRPH | 526 | 1.2000 | 12.77 |
| 33 | VVITEIGGT | 147 | 1.1000 | 11.70 |
| 34 | VIPHITDEI | 120 | 1.0000 | 10.64 |
| 35 | VGDIESQPF | 156 | 1.0000 | 10.64 |
| 36 | IRGIEGKIG | 368 | 1.0000 | 10.64 |

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|---|---|---|---|---|
| 37 | IEAARSVGL | 400 | 1.0000 | 10.64 |
| 38 | LFVAFVGAA | 536 | 1.0000 | 10.64 |
| 39 | LGREDVFFL | 175 | 0.9500 | 10.11 |
| 40 | VELSDAYLS | 310 | 0.9000 | 9.57 |
| 41 | VRRLNLPFR | 272 | 0.8000 | 8.51 |
| 42 | LGKGLTASS | 21 | 0.7000 | 7.45 |
| 43 | VHGVLIPGG | 357 | 0.7000 | 7.45 |
| 44 | VRHYLGRED | 171 | 0.6000 | 6.38 |
| 45 | LLPVEIPEI | 552 | 0.6000 | 6.38 |
| 46 | FVSGGVASS | 12 | 0.5000 | 5.32 |
| 47 | YLNVDPGTM | 49 | 0.5000 | 5.32 |
| 48 | LHVSLVPYL | 183 | 0.5000 | 5.32 |
| 49 | LSVAEALRA | 317 | 0.5000 | 5.32 |
| 50 | FVAFVGAAI | 537 | 0.5000 | 5.32 |
| 51 | VEIPEIPEH | 555 | 0.5000 | 5.32 |
| 52 | LKNKIALMC | 231 | 0.4000 | 4.26 |
| 53 | ILAMAQPDA | 132 | 0.3000 | 3.19 |
| 54 | ICWVASDGC | 336 | 0.3000 | 3.19 |
| 55 | LGLCLGLQC | 389 | 0.3000 | 3.19 |
| 56 | VIATMPDQE | 424 | 0.3000 | 3.19 |
| 57 | FFLHVSLVP | 181 | 0.2000 | 2.13 |
| 58 | IALVGKYVE | 303 | 0.2000 | 2.13 |

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|---|---|---|
| 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 | FFLHVSLVP | 181 | 4.3000 | 47.78 |
| 2 | YLGDTVQVI | 113 | 4.1000 | 45.56 |
| 3 | LRFSGTSPD | 492 | 3.9000 | 43.33 |
| 4 | VIPHITDEI | 120 | 3.7000 | 41.11 |
| 5 | IVIEAARSV | 398 | 3.2000 | 35.56 |
| 6 | YQTTQVSER | 464 | 3.1000 | 34.44 |
| 7 | VVRRLNLPF | 271 | 2.8000 | 31.11 |

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|---|---|---|---|---|
| 8 | FVSGGVASS | 12 | 2.7000 | 30.00 |
| 9 | LGQLLTARG | 30 | 2.6000 | 28.89 |
| 10 | VRIALVGKY | 301 | 2.6000 | 28.89 |
| 11 | VFFLHVSLV | 180 | 2.4000 | 26.67 |
| 12 | LVGKYVELS | 305 | 1.8000 | 20.00 |
| 13 | VGLTNANSA | 406 | 1.8000 | 20.00 |
| 14 | VVGTQAHPE | 517 | 1.7000 | 18.89 |
| 15 | FVGAAIDYK | 540 | 1.7000 | 18.89 |
| 16 | FVTEDGAET | 66 | 1.6000 | 17.78 |
| 17 | LEPDSVVAQ | 454 | 1.5800 | 17.56 |
| 18 | LGREDVFFL | 175 | 1.5600 | 17.33 |
| 19 | LHREELDAF | 262 | 1.5000 | 16.67 |
| 20 | VAALRSIGI | 206 | 1.4800 | 16.44 |
| 21 | VVITEIGGT | 147 | 1.4000 | 15.56 |
| 22 | LKTKPTQHS | 197 | 1.4000 | 15.56 |
| 23 | LRSIGITPD | 209 | 1.4000 | 15.56 |
| 24 | VRRLNLPFR | 272 | 1.4000 | 15.56 |
| 25 | LTNANSAEF | 408 | 1.4000 | 15.56 |
| 26 | LRCDRDVPE | 221 | 1.2800 | 14.22 |
| 27 | LHVSLVPYL | 183 | 1.2600 | 14.00 |
| 28 | IGITPDALI | 212 | 1.2000 | 13.33 |
| 29 | LQCIVIEAA | 395 | 1.1000 | 12.22 |
| 30 | VDIDGVIST | 241 | 1.0800 | 12.00 |
| 31 | VISTPDAPS | 246 | 1.0000 | 11.11 |
| 32 | LGLQCIVIE | 393 | 0.9800 | 10.89 |
| 33 | LGKGLTASS | 21 | 0.9000 | 10.00 |
| 34 | VGDIESQPF | 156 | 0.9000 | 10.00 |
| 35 | VEICWVASD | 334 | 0.9000 | 10.00 |
| 36 | WVASDGCET | 338 | 0.9000 | 10.00 |
| 37 | LMCDVDIDG | 237 | 0.8800 | 9.78 |
| 38 | VELSDAYLS | 310 | 0.8000 | 8.89 |
| 39 | IRGIEGKIG | 368 | 0.8000 | 8.89 |
| 40 | LFVSGGVAS | 11 | 0.7800 | 8.67 |
| 41 | YDIPKVLHR | 256 | 0.7000 | 7.78 |

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|---|---|---|---|---|
| 42 | VAGEADLGG | 435 | 0.7000 | 7.78 |
| 43 | YVELSDAYL | 309 | 0.5600 | 6.22 |
| 44 | IALMCDVDI | 235 | 0.4800 | 5.33 |
| 45 | YLNVDPGTM | 49 | 0.4000 | 4.44 |
| 46 | VYSTVIAKE | 100 | 0.4000 | 4.44 |
| 47 | FDPDTPDPV | 416 | 0.4000 | 4.44 |
| 48 | LPVEIPEIP | 553 | 0.4000 | 4.44 |
| 49 | LPGSANVTT | 89 | 0.3800 | 4.22 |
| 50 | VASDGCETT | 339 | 0.3000 | 3.33 |
| 51 | FVAFVGAAI | 537 | 0.3000 | 3.33 |
| 52 | MRKHPQTAT | 0 | 0.2000 | 2.22 |
| 53 | YARARGLPV | 380 | 0.2000 | 2.22 |
| 54 | VIATMPDQE | 424 | 0.2000 | 2.22 |
| 55 | ITPDALILR | 214 | 0.1800 | 2.00 |
| 56 | IEAARSVGL | 400 | 0.1400 | 1.56 |
| 57 | VTMQKLDPY | 41 | 0.1000 | 1.11 |
| 58 | IPEHTPNGS | 560 | 0.1000 | 1.11 |

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|---|---|---|
| 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 | VFFLHVSLV | 180 | 3.3000 | 37.50 |
| 2 | LRFSGTSPD | 492 | 3.0000 | 34.09 |
| 3 | LGQLLTARG | 30 | 2.4000 | 27.27 |
| 4 | VRIALVGKY | 301 | 2.4000 | 27.27 |
| 5 | LRSIGITPD | 209 | 2.1000 | 23.86 |
| 6 | LKTKPTQHS | 197 | 2.0000 | 22.73 |
| 7 | VAALRSIGI | 206 | 1.7800 | 20.23 |
| 8 | LVGKYVELS | 305 | 1.7000 | 19.32 |
| 9 | LQCIVIEAA | 395 | 1.5000 | 17.05 |
| 10 | IALMCDVDI | 235 | 1.3000 | 14.77 |
| 11 | VGLTNANSA | 406 | 1.3000 | 14.77 |
| 12 | VVRRLNLPF | 271 | 1.0000 | 11.36 |

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|---|---|---|---|---|
| 13 | LFVAFVGAA | 536 | 1.0000 | 11.36 |
| 14 | VELSDAYLS | 310 | 0.9000 | 10.23 |
| 15 | IVIEAARSV | 398 | 0.9000 | 10.23 |
| 16 | VIPHITDEI | 120 | 0.8000 | 9.09 |
| 17 | VRRLNLPFR | 272 | 0.8000 | 9.09 |
| 18 | VEICWVASD | 334 | 0.8000 | 9.09 |
| 19 | LGKGLTASS | 21 | 0.7000 | 7.95 |
| 20 | MQKLDPYLN | 43 | 0.6000 | 6.82 |
| 21 | LEPDSVVAQ | 454 | 0.6000 | 6.82 |
| 22 | FVSGGVASS | 12 | 0.5000 | 5.68 |
| 23 | LSVAEALRA | 317 | 0.5000 | 5.68 |
| 24 | LTNANSAEF | 408 | 0.5000 | 5.68 |
| 25 | LKNKIALMC | 231 | 0.4000 | 4.55 |
| 26 | VLGLCLGLQ | 388 | 0.4000 | 4.55 |
| 27 | LLPVEIPEI | 552 | 0.4000 | 4.55 |
| 28 | ILAMAQPDA | 132 | 0.3000 | 3.41 |
| 29 | ICWVASDGC | 336 | 0.3000 | 3.41 |
| 30 | LGLCLGLQC | 389 | 0.3000 | 3.41 |
| 31 | FVAFVGAAI | 537 | 0.3000 | 3.41 |
| 32 | VVITEIGGT | 147 | 0.2000 | 2.27 |
| 33 | VGDIESQPF | 156 | 0.1000 | 1.14 |
| 34 | VPYLAPSGE | 188 | 0.1000 | 1.14 |
| 35 | IGAIAYARA | 375 | 0.1000 | 1.14 |
| 36 | LKSRPTRPH | 526 | -0.0200 | 0 |
| 37 | LGREDVFFL | 175 | -0.0500 | 0 |
| 38 | FFLHVSLVP | 181 | -0.2000 | 0 |
| 39 | VQVIPHITD | 118 | -0.2200 | 0 |
| 40 | LFVSGGVAS | 11 | -0.3000 | 0 |
| 41 | IGITPDALI | 212 | -0.3000 | 0 |
| 42 | IRGIEGKIG | 368 | -0.3000 | 0 |
| 43 | YQTTQVSER | 464 | -0.3000 | 0 |
| 44 | FVGAAIDYK | 540 | -0.3000 | 0 |
| 45 | LGLQCIVIE | 393 | -0.4000 | 0 |
| 46 | VAFVGAAID | 538 | -0.4000 | 0 |

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|---|---|---|---|---|
| 47 | YLGDTVQVI | 113 | -0.5000 | 0 |
| 48 | IESQPFLEA | 159 | -0.5000 | 0 |
| 49 | LHVSLVPYL | 183 | -0.5000 | 0 |
| 50 | YLNVDPGTM | 49 | -0.6000 | 0 |
| 51 | VHGVLIPGG | 357 | -0.6000 | 0 |
| 52 | VLEPDSVVA | 453 | -0.6000 | 0 |
| 53 | VAQAYQTTQ | 460 | -0.6000 | 0 |
| 54 | VLIPGGFGI | 360 | -0.6500 | 0 |

| ALLELE: DRB1_0426 | Threshold for 3 % with score: 1.6 | Highest Score achievable by any peptide: 8.6 |
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| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | FFLHVSLVP | 181 | 3.3000 | 38.37 |
| 2 | YLGDTVQVI | 113 | 3.2000 | 37.21 |
| 3 | VIPHITDEI | 120 | 2.8000 | 32.56 |
| 4 | LRFSGTSPD | 492 | 2.8000 | 32.56 |
| 5 | FVSGGVASS | 12 | 2.3000 | 26.74 |
| 6 | LEPDSVVAQ | 454 | 2.2800 | 26.51 |
| 7 | IVIEAARSV | 398 | 2.2000 | 25.58 |
| 8 | VGLTNANSA | 406 | 1.8000 | 20.93 |
| 9 | YQTTQVSER | 464 | 1.6000 | 18.60 |
| 10 | FVGAAIDYK | 540 | 1.6000 | 18.60 |
| 11 | VFFLHVSLV | 180 | 1.4000 | 16.28 |
| 12 | LVGKYVELS | 305 | 1.4000 | 16.28 |
| 13 | VRIALVGKY | 301 | 1.3000 | 15.12 |
| 14 | LGQLLTARG | 30 | 1.2000 | 13.95 |
| 15 | LQCIVIEAA | 395 | 1.1000 | 12.79 |
| 16 | LKTKPTQHS | 197 | 1.0000 | 11.63 |
| 17 | FVTEDGAET | 66 | 0.9000 | 10.47 |
| 18 | VVRRLNLPF | 271 | 0.9000 | 10.47 |
| 19 | VVITEIGGT | 147 | 0.7000 | 8.14 |
| 20 | LGREDVFFL | 175 | 0.6000 | 6.98 |
| 21 | VISTPDAPS | 246 | 0.6000 | 6.98 |

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|---|---|---|---|---|
| 22 | VAALRSIGI | 206 | 0.5800 | 6.74 |
| 23 | LGKGLTASS | 21 | 0.5000 | 5.81 |
| 24 | VELSDAYLS | 310 | 0.4000 | 4.65 |
| 25 | LFVSGGVAS | 11 | 0.3800 | 4.42 |
| 26 | VDIDGVIST | 241 | 0.3800 | 4.42 |
| 27 | FSGTSPDGH | 494 | 0.3800 | 4.42 |
| 28 | LHVSLVPYL | 183 | 0.3000 | 3.49 |
| 29 | LRSIGITPD | 209 | 0.3000 | 3.49 |
| 30 | IGITPDALI | 212 | 0.3000 | 3.49 |
| 31 | VVGTQAHPE | 517 | 0.3000 | 3.49 |
| 32 | WVASDGCET | 338 | 0.2000 | 2.33 |
| 33 | VRRLNLPFR | 272 | -0.1000 | 0 |
| 34 | LSVAEALRA | 317 | -0.1000 | 0 |
| 35 | FGIRGIEGK | 366 | -0.1000 | 0 |
| 36 | LFVAFVGAA | 536 | -0.1000 | 0 |
| 37 | LRCDRDVPE | 221 | -0.1200 | 0 |
| 38 | VEICWVASD | 334 | -0.2000 | 0 |
| 39 | IESQPFLEA | 159 | -0.3000 | 0 |
| 40 | LGLCLGLQC | 389 | -0.3000 | 0 |
| 41 | IPEHTPNGS | 560 | -0.3000 | 0 |
| 42 | LPGSANVTT | 89 | -0.3200 | 0 |
| 43 | LKNKIALMC | 231 | -0.4000 | 0 |
| 44 | LHREELDAF | 262 | -0.4000 | 0 |
| 45 | YVELSDAYL | 309 | -0.4000 | 0 |
| 46 | VASDGCETT | 339 | -0.4000 | 0 |
| 47 | IALMCDVDI | 235 | -0.4200 | 0 |
| 48 | LGLQCIVIE | 393 | -0.4200 | 0 |
| 49 | MRKHPQTAT | 0 | -0.5000 | 0 |
| 50 | LTNANSAEF | 408 | -0.5000 | 0 |
| 51 | LMCDVDIDG | 237 | -0.5200 | 0 |
| 52 | IRGIEGKIG | 368 | -0.6000 | 0 |
| 53 | FDPDTPDPV | 416 | -0.6000 | 0 |
| 54 | LGGTMRLGS | 441 | -0.6000 | 0 |
| 55 | FVAFVGAAI | 537 | -0.6000 | 0 |

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|---|---|---|---|---|
| 56 | LPVEIPEIP | 553 | -0.6000 | 0 |
| 57 | VAGEADLGG | 435 | -0.7000 | 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 | VLIPGGFGI | 360 | 5.2000 | 44.83 |
| 2 | LHVSLVPYL | 183 | 5.1000 | 43.97 |
| 3 | FVAFVGAAI | 537 | 5.1000 | 43.97 |
| 4 | IEAARSVGL | 400 | 4.7000 | 40.52 |
| 5 | VAALRSIGI | 206 | 4.6000 | 39.66 |
| 6 | LGREDVFFL | 175 | 4.4000 | 37.93 |
| 7 | VVRRLNLPF | 271 | 4.4000 | 37.93 |
| 8 | YARARGLPV | 380 | 4.3000 | 37.07 |
| 9 | YLGDTVQVI | 113 | 4.2000 | 36.21 |
| 10 | FFLHVSLVP | 181 | 4.1000 | 35.34 |
| 11 | FKHRAKVEI | 328 | 4.1000 | 35.34 |
| 12 | VASSLGKGL | 17 | 4.0000 | 34.48 |
| 13 | YLNVDPGTM | 49 | 3.9000 | 33.62 |
| 14 | VVITEIGGT | 147 | 3.9000 | 33.62 |
| 15 | FLHVSLVPY | 182 | 3.9000 | 33.62 |
| 16 | VRIALVGKY | 301 | 3.9000 | 33.62 |
| 17 | IAYARARGL | 378 | 3.9000 | 33.62 |
| 18 | IVIEAARSV | 398 | 3.9000 | 33.62 |
| 19 | LLPVEIPEI | 552 | 3.9000 | 33.62 |
| 20 | LLTARGLHV | 33 | 3.6000 | 31.03 |
| 21 | LGDVHGVLI | 354 | 3.5000 | 30.17 |
| 22 | WVASDGCET | 338 | 3.4000 | 29.31 |
| 23 | IGITPDALI | 212 | 3.3000 | 28.45 |
| 24 | VGLTNANSA | 406 | 3.3000 | 28.45 |
| 25 | VVGTQAHPE | 517 | 3.3000 | 28.45 |
| 26 | YKAGELLPV | 547 | 3.3000 | 28.45 |
| 27 | VGDIESQPF | 156 | 3.1000 | 26.72 |

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|---|---|---|---|---|
| 28 | LTASSLGQL | 25 | 3.0000 | 25.86 |
| 29 | VELSDAYLS | 310 | 3.0000 | 25.86 |
| 30 | FQHGEVFVT | 60 | 2.9000 | 25.00 |
| 31 | LRFSGTSPD | 492 | 2.6200 | 22.59 |
| 32 | YERFLDRNL | 81 | 2.6000 | 22.41 |
| 33 | FRDVDWTEW | 279 | 2.6000 | 22.41 |
| 34 | VIPHITDEI | 120 | 2.5200 | 21.72 |
| 35 | LFVSGGVAS | 11 | 2.5000 | 21.55 |
| 36 | VFFLHVSLV | 180 | 2.3000 | 19.83 |
| 37 | YQTTQVSER | 464 | 2.3000 | 19.83 |
| 38 | VQVIPHITD | 118 | 2.2000 | 18.97 |
| 39 | LTNANSAEF | 408 | 2.2000 | 18.97 |
| 40 | IALMCDVDI | 235 | 2.1000 | 18.10 |
| 41 | LDAFVVRRL | 267 | 2.1000 | 18.10 |
| 42 | LGLCLGLQC | 389 | 2.1000 | 18.10 |
| 43 | LGGTMRLGS | 441 | 1.9000 | 16.38 |
| 44 | MRLGSYPAV | 445 | 1.9000 | 16.38 |
| 45 | IRGIEGKIG | 368 | 1.8000 | 15.52 |
| 46 | LRSIGITPD | 209 | 1.7000 | 14.66 |
| 47 | LQCIVIEAA | 395 | 1.7000 | 14.66 |
| 48 | VSGGVASSL | 13 | 1.6000 | 13.79 |
| 49 | LPGSANVTT | 89 | 1.6000 | 13.79 |
| 50 | MRKHPQTAT | 0 | 1.5000 | 12.93 |
| 51 | MNPFQHGEV | 57 | 1.5000 | 12.93 |
| 52 | LKNKIALMC | 231 | 1.5000 | 12.93 |
| 53 | FVVRRLNLP | 270 | 1.4000 | 12.07 |
| 54 | LSVAEALRA | 317 | 1.4000 | 12.07 |
| 55 | YLGREDVFF | 174 | 1.3000 | 11.21 |
| 56 | VNNAYRDKI | 479 | 1.3000 | 11.21 |
| 57 | VSLVPYLAP | 185 | 1.2000 | 10.34 |
| 58 | IALVGKYVE | 303 | 1.2000 | 10.34 |

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

| | | |
|---|---|---|
| | 4.0 | 11.6 |

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | VLIPGGFGI | 360 | 5.2000 | 44.83 |
| 2 | LHVSLVPYL | 183 | 5.1000 | 43.97 |
| 3 | FVAFVGAAI | 537 | 5.1000 | 43.97 |
| 4 | IEAARSVGL | 400 | 4.7000 | 40.52 |
| 5 | VAALRSIGI | 206 | 4.6000 | 39.66 |
| 6 | LGREDVFFL | 175 | 4.4000 | 37.93 |
| 7 | VVRRLNLPF | 271 | 4.4000 | 37.93 |
| 8 | YARARGLPV | 380 | 4.3000 | 37.07 |
| 9 | YLGDTVQVI | 113 | 4.2000 | 36.21 |
| 10 | FFLHVSLVP | 181 | 4.1000 | 35.34 |
| 11 | FKHRAKVEI | 328 | 4.1000 | 35.34 |
| 12 | VASSLGKGL | 17 | 4.0000 | 34.48 |
| 13 | YLNVDPGTM | 49 | 3.9000 | 33.62 |
| 14 | VVITEIGGT | 147 | 3.9000 | 33.62 |
| 15 | FLHVSLVPY | 182 | 3.9000 | 33.62 |
| 16 | VRIALVGKY | 301 | 3.9000 | 33.62 |
| 17 | IAYARARGL | 378 | 3.9000 | 33.62 |
| 18 | IVIEAARSV | 398 | 3.9000 | 33.62 |
| 19 | LLPVEIPEI | 552 | 3.9000 | 33.62 |
| 20 | LLTARGLHV | 33 | 3.6000 | 31.03 |
| 21 | LGDVHGVLI | 354 | 3.5000 | 30.17 |
| 22 | WVASDGCET | 338 | 3.4000 | 29.31 |
| 23 | IGITPDALI | 212 | 3.3000 | 28.45 |
| 24 | VGLTNANSA | 406 | 3.3000 | 28.45 |
| 25 | VVGTQAHPE | 517 | 3.3000 | 28.45 |
| 26 | YKAGELLPV | 547 | 3.3000 | 28.45 |
| 27 | VGDIESQPF | 156 | 3.1000 | 26.72 |
| 28 | LTASSLGQL | 25 | 3.0000 | 25.86 |
| 29 | VELSDAYLS | 310 | 3.0000 | 25.86 |
| 30 | FQHGEVFVT | 60 | 2.9000 | 25.00 |
| 31 | LRFSGTSPD | 492 | 2.6200 | 22.59 |
| 32 | YERFLDRNL | 81 | 2.6000 | 22.41 |

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|---|---|---|---|---|
| 33 | FRDVDWTEW | 279 | 2.6000 | 22.41 |
| 34 | VIPHITDEI | 120 | 2.5200 | 21.72 |
| 35 | LFVSGGVAS | 11 | 2.5000 | 21.55 |
| 36 | VFFLHVSLV | 180 | 2.3000 | 19.83 |
| 37 | YQTTQVSER | 464 | 2.3000 | 19.83 |
| 38 | VQVIPHITD | 118 | 2.2000 | 18.97 |
| 39 | LTNANSAEF | 408 | 2.2000 | 18.97 |
| 40 | IALMCDVDI | 235 | 2.1000 | 18.10 |
| 41 | LDAFVVRRL | 267 | 2.1000 | 18.10 |
| 42 | LGLCLGLQC | 389 | 2.1000 | 18.10 |
| 43 | LGGTMRLGS | 441 | 1.9000 | 16.38 |
| 44 | MRLGSYPAV | 445 | 1.9000 | 16.38 |
| 45 | IRGIEGKIG | 368 | 1.8000 | 15.52 |
| 46 | LRSIGITPD | 209 | 1.7000 | 14.66 |
| 47 | LQCIVIEAA | 395 | 1.7000 | 14.66 |
| 48 | VSGGVASSL | 13 | 1.6000 | 13.79 |
| 49 | LPGSANVTT | 89 | 1.6000 | 13.79 |
| 50 | MRKHPQTAT | 0 | 1.5000 | 12.93 |
| 51 | MNPFQHGEV | 57 | 1.5000 | 12.93 |
| 52 | LKNKIALMC | 231 | 1.5000 | 12.93 |
| 53 | FVVRRLNLP | 270 | 1.4000 | 12.07 |
| 54 | LSVAEALRA | 317 | 1.4000 | 12.07 |
| 55 | YLGREDVFF | 174 | 1.3000 | 11.21 |
| 56 | VNNAYRDKI | 479 | 1.3000 | 11.21 |
| 57 | VSLVPYLAP | 185 | 1.2000 | 10.34 |
| 58 | IALVGKYVE | 303 | 1.2000 | 10.34 |

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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 | VIAKERRGE | 104 | 4.1000 | 47.67 |
| 2 | LKSRPTRPH | 526 | 4.1000 | 47.67 |
| 3 | FKHRAKVEI | 328 | 3.7000 | 43.02 |

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|---|---|---|---|---|
| 4 | VRIALVGKY | 301 | 3.5000 | 40.70 |
| 5 | IKRRILAMA | 128 | 3.3000 | 38.37 |
| 6 | VRHYLGRED | 171 | 3.3000 | 38.37 |
| 7 | FVSGGVASS | 12 | 3.2000 | 37.21 |
| 8 | VVRRLNLPF | 271 | 3.1000 | 36.05 |
| 9 | LVGKYVELS | 305 | 3.1000 | 36.05 |
| 10 | VGHYERFLD | 78 | 3.0000 | 34.88 |
| 11 | FVVRRLNLP | 270 | 2.9000 | 33.72 |
| 12 | VEICWVASD | 334 | 2.8000 | 32.56 |
| 13 | LVPYLAPSG | 187 | 2.7000 | 31.40 |
| 14 | LKTKPTQHS | 197 | 2.7000 | 31.40 |
| 15 | LKNKIALMC | 231 | 2.6000 | 30.23 |
| 16 | YLNVDPGTM | 49 | 2.5000 | 29.07 |
| 17 | FVEYPPDRH | 506 | 2.5000 | 29.07 |
| 18 | LGSYPAVLE | 447 | 2.1000 | 24.42 |
| 19 | VLGLCLGLQ | 388 | 1.9000 | 22.09 |
| 20 | LLRRVHEPH | 290 | 1.8000 | 20.93 |
| 21 | IALVGKYVE | 303 | 1.8000 | 20.93 |
| 22 | FVAFVGAAI | 537 | 1.8000 | 20.93 |
| 23 | FLDRNLPGS | 84 | 1.7000 | 19.77 |
| 24 | FGIRGIEGK | 366 | 1.6000 | 18.60 |
| 25 | VVITEIGGT | 147 | 1.5000 | 17.44 |
| 26 | LRFSGTSPD | 492 | 1.5000 | 17.44 |
| 27 | LGQLLTARG | 30 | 1.3000 | 15.12 |
| 28 | VYSTVIAKE | 100 | 1.1000 | 12.79 |
| 29 | VQVIPHITD | 118 | 1.1000 | 12.79 |
| 30 | YRDKIAESG | 483 | 1.1000 | 12.79 |
| 31 | VAFVGAAID | 538 | 1.1000 | 12.79 |
| 32 | LRSIGITPD | 209 | 1.0000 | 11.63 |
| 33 | VGKYVELSD | 306 | 1.0000 | 11.63 |
| 34 | LFVAFVGAA | 536 | 1.0000 | 11.63 |
| 35 | MQKLDPYLN | 43 | 0.9000 | 10.47 |
| 36 | LRRVHEPHE | 291 | 0.9000 | 10.47 |
| 37 | IEGKIGAIA | 371 | 0.9000 | 10.47 |

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|---|---|---|---|---|
| 38 | VFFLHVSLV | 180 | 0.8000 | 9.30 |
| 39 | VLHREELDA | 261 | 0.8000 | 9.30 |
| 40 | FLHVSLVPY | 182 | 0.7000 | 8.14 |
| 41 | VVGTQAHPE | 517 | 0.7000 | 8.14 |
| 42 | VRRLNLPFR | 272 | 0.6000 | 6.98 |
| 43 | IVIEAARSV | 398 | 0.6000 | 6.98 |
| 44 | VPYLAPSGE | 188 | 0.5000 | 5.81 |
| 45 | IRGIEGKIG | 368 | 0.5000 | 5.81 |
| 46 | YEVNNAYRD | 477 | 0.5000 | 5.81 |
| 47 | FQHGEVFVT | 60 | 0.4000 | 4.65 |
| 48 | IYDIPKVLH | 255 | 0.4000 | 4.65 |
| 49 | LGLQCIVIE | 393 | 0.4000 | 4.65 |
| 50 | FVVGTQAHP | 516 | 0.4000 | 4.65 |
| 51 | VEIPEIPEH | 555 | 0.4000 | 4.65 |
| 52 | LTARGLHVT | 34 | 0.3000 | 3.49 |
| 53 | LPVLGLCLG | 386 | 0.2000 | 2.33 |
| 54 | FVTEDGAET | 66 | 0.1000 | 1.16 |
| 55 | YLGDTVQVI | 113 | 0.1000 | 1.16 |
| 56 | LPFRDVDWT | 277 | 0.1000 | 1.16 |
| 57 | WVASDGCET | 338 | 0.1000 | 1.16 |
| 58 | VHGVLIPGG | 357 | 0.1000 | 1.16 |

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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 | FKHRAKVEI | 328 | 3.5000 | 43.75 |
| 2 | IKRRILAMA | 128 | 3.3000 | 41.25 |
| 3 | FVSGGVASS | 12 | 3.2000 | 40.00 |
| 4 | LVGKYVELS | 305 | 3.1000 | 38.75 |
| 5 | LKSRPTRPH | 526 | 2.8800 | 36.00 |
| 6 | LKTKPTQHS | 197 | 2.7000 | 33.75 |
| 7 | LKNKIALMC | 231 | 2.6000 | 32.50 |
| 8 | FVVRRLNLP | 270 | 2.5000 | 31.25 |

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|---|---|---|---|---|
| 9 | VRIALVGKY | 301 | 2.4000 | 30.00 |
| 10 | FGIRGIEGK | 366 | 2.3000 | 28.75 |
| 11 | VVRRLNLPF | 271 | 2.2000 | 27.50 |
| 12 | FLDRNLPGS | 84 | 1.7000 | 21.25 |
| 13 | FVAFVGAAI | 537 | 1.6000 | 20.00 |
| 14 | YLNVDPGTM | 49 | 1.4000 | 17.50 |
| 15 | LVPYLAPSG | 187 | 1.4000 | 17.50 |
| 16 | FVEYPPDRH | 506 | 1.2800 | 16.00 |
| 17 | VIAKERRGE | 104 | 1.1000 | 13.75 |
| 18 | VLGLCLGLQ | 388 | 1.1000 | 13.75 |
| 19 | LFVAFVGAA | 536 | 1.0000 | 12.50 |
| 20 | IEGKIGAIA | 371 | 0.9000 | 11.25 |
| 21 | VLHREELDA | 261 | 0.8000 | 10.00 |
| 22 | VVITEIGGT | 147 | 0.6000 | 7.50 |
| 23 | VRHYLGRED | 171 | 0.6000 | 7.50 |
| 24 | VRRLNLPFR | 272 | 0.6000 | 7.50 |
| 25 | LLRRVHEPH | 290 | 0.5800 | 7.25 |
| 26 | VFFLHVSLV | 180 | 0.5000 | 6.25 |
| 27 | VGHYERFLD | 78 | 0.3000 | 3.75 |
| 28 | IVIEAARSV | 398 | 0.3000 | 3.75 |
| 29 | FVGAAIDYK | 540 | 0.3000 | 3.75 |
| 30 | VEICWVASD | 334 | 0.1000 | 1.25 |
| 31 | LGGTMRLGS | 441 | 0.1000 | 1.25 |
| 32 | YLGDTVQVI | 113 | -0.1000 | 0 |
| 33 | ILAMAQPDA | 132 | -0.1000 | 0 |
| 34 | YRDKIAESG | 483 | -0.2000 | 0 |
| 35 | LLPVEIPEI | 552 | -0.2000 | 0 |
| 36 | LILRCDRDV | 219 | -0.3000 | 0 |
| 37 | FLHVSLVPY | 182 | -0.4000 | 0 |
| 38 | FQHGEVFVT | 60 | -0.5000 | 0 |
| 39 | LGLCLGLQC | 389 | -0.5000 | 0 |
| 40 | LTARGLHVT | 34 | -0.6000 | 0 |
| 41 | MNPFQHGEV | 57 | -0.7000 | 0 |
| 42 | YKAGELLPV | 547 | -0.7000 | 0 |

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|---|---|---|---|---|
| 43 | FVTEDGAET | 66 | -0.8000 | 0 |
| 44 | LPFRDVDWT | 277 | -0.8000 | 0 |
| 45 | WVASDGCET | 338 | -0.8000 | 0 |
| 46 | IRGIEGKIG | 368 | -0.8000 | 0 |
| 47 | IYDIPKVLH | 255 | -0.8200 | 0 |
| 48 | VEIPEIPEH | 555 | -0.8200 | 0 |
| 49 | FFLHVSLVP | 181 | -0.9000 | 0 |
| 50 | YDIPKVLHR | 256 | -0.9000 | 0 |
| 51 | YLSVAEALR | 316 | -0.9000 | 0 |
| 52 | LGSYPAVLE | 447 | -0.9000 | 0 |
| 53 | YQTTQVSER | 464 | -0.9000 | 0 |
| 54 | YLGREDVFF | 174 | -1.0000 | 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 | IKRRILAMA | 128 | 4.3000 | 53.75 |
| 2 | LVGKYVELS | 305 | 4.1000 | 51.25 |
| 3 | LKSRPTRPH | 526 | 3.8800 | 48.50 |
| 4 | LKTKPTQHS | 197 | 3.7000 | 46.25 |
| 5 | LKNKIALMC | 231 | 3.6000 | 45.00 |
| 6 | VRIALVGKY | 301 | 3.4000 | 42.50 |
| 7 | VVRRLNLPF | 271 | 3.2000 | 40.00 |
| 8 | FKHRAKVEI | 328 | 2.5000 | 31.25 |
| 9 | LVPYLAPSG | 187 | 2.4000 | 30.00 |
| 10 | FVSGGVASS | 12 | 2.2000 | 27.50 |
| 11 | VIAKERRGE | 104 | 2.1000 | 26.25 |
| 12 | VLGLCLGLQ | 388 | 2.1000 | 26.25 |
| 13 | LFVAFVGAA | 536 | 2.0000 | 25.00 |
| 14 | IEGKIGAIA | 371 | 1.9000 | 23.75 |
| 15 | VLHREELDA | 261 | 1.8000 | 22.50 |
| 16 | VVITEIGGT | 147 | 1.6000 | 20.00 |
| 17 | VRHYLGRED | 171 | 1.6000 | 20.00 |

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|---|---|---|---|---|
| 18 | VRRLNLPFR | 272 | 1.6000 | 20.00 |
| 19 | LLRRVHEPH | 290 | 1.5800 | 19.75 |
| 20 | VFFLHVSLV | 180 | 1.5000 | 18.75 |
| 21 | FVVRRLNLP | 270 | 1.5000 | 18.75 |
| 22 | VGHYERFLD | 78 | 1.3000 | 16.25 |
| 23 | FGIRGIEGK | 366 | 1.3000 | 16.25 |
| 24 | IVIEAARSV | 398 | 1.3000 | 16.25 |
| 25 | VEICWVASD | 334 | 1.1000 | 13.75 |
| 26 | LGGTMRLGS | 441 | 1.1000 | 13.75 |
| 27 | LGKGLTASS | 21 | 1.0000 | 12.50 |
| 28 | LGQLLTARG | 30 | 1.0000 | 12.50 |
| 29 | ILAMAQPDA | 132 | 0.9000 | 11.25 |
| 30 | LLPVEIPEI | 552 | 0.8000 | 10.00 |
| 31 | FLDRNLPGS | 84 | 0.7000 | 8.75 |
| 32 | LILRCDRDV | 219 | 0.7000 | 8.75 |
| 33 | FVAFVGAAI | 537 | 0.6000 | 7.50 |
| 34 | LGLCLGLQC | 389 | 0.5000 | 6.25 |
| 35 | LTARGLHVT | 34 | 0.4000 | 5.00 |
| 36 | YLNVDPGTM | 49 | 0.4000 | 5.00 |
| 37 | MNPFQHGEV | 57 | 0.3000 | 3.75 |
| 38 | FVEYPPDRH | 506 | 0.2800 | 3.50 |
| 39 | LPFRDVDWT | 277 | 0.2000 | 2.50 |
| 40 | IRGIEGKIG | 368 | 0.2000 | 2.50 |
| 41 | IYDIPKVLH | 255 | 0.1800 | 2.25 |
| 42 | VEIPEIPEH | 555 | 0.1800 | 2.25 |
| 43 | LGSYPAVLE | 447 | 0.1000 | 1.25 |
| 44 | MQKLDPYLN | 43 | -0.1000 | 0 |
| 45 | LSVAEALRA | 317 | -0.1000 | 0 |
| 46 | LPVLGLCLG | 386 | -0.1000 | 0 |
| 47 | VSERHRHRY | 469 | -0.1000 | 0 |
| 48 | IALVGKYVE | 303 | -0.2000 | 0 |
| 49 | VHGVLIPGG | 357 | -0.2000 | 0 |
| 50 | LQCIVIEAA | 395 | -0.2000 | 0 |
| 51 | LRFSGTSPD | 492 | -0.2000 | 0 |

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|---|---|---|---|---|
| 52 | VELSDAYLS | 310 | -0.3000 | 0 |
| 53 | VLIPGGFGI | 360 | -0.4000 | 0 |
| 54 | VNNAYRDKI | 479 | -0.4000 | 0 |
| 55 | LGREDVFFL | 175 | -0.5000 | 0 |
| 56 | VAALRSIGI | 206 | -0.5000 | 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 | VIAKERRGE | 104 | 5.1000 | 59.30 |
| 2 | LKSRPTRPH | 526 | 5.1000 | 59.30 |
| 3 | VRIALVGKY | 301 | 4.5000 | 52.33 |
| 4 | IKRRILAMA | 128 | 4.3000 | 50.00 |
| 5 | VRHYLGRED | 171 | 4.3000 | 50.00 |
| 6 | VVRRLNLPF | 271 | 4.1000 | 47.67 |
| 7 | LVGKYVELS | 305 | 4.1000 | 47.67 |
| 8 | VGHYERFLD | 78 | 4.0000 | 46.51 |
| 9 | VEICWVASD | 334 | 3.8000 | 44.19 |
| 10 | LVPYLAPSG | 187 | 3.7000 | 43.02 |
| 11 | LKTKPTQHS | 197 | 3.7000 | 43.02 |
| 12 | LKNKIALMC | 231 | 3.6000 | 41.86 |
| 13 | LGSYPAVLE | 447 | 3.1000 | 36.05 |
| 14 | VLGLCLGLQ | 388 | 2.9000 | 33.72 |
| 15 | LLRRVHEPH | 290 | 2.8000 | 32.56 |
| 16 | IALVGKYVE | 303 | 2.8000 | 32.56 |
| 17 | FKHRAKVEI | 328 | 2.7000 | 31.40 |
| 18 | VVITEIGGT | 147 | 2.5000 | 29.07 |
| 19 | LRFSGTSPD | 492 | 2.5000 | 29.07 |
| 20 | LGQLLTARG | 30 | 2.3000 | 26.74 |
| 21 | FVSGGVASS | 12 | 2.2000 | 25.58 |
| 22 | VYSTVIAKE | 100 | 2.1000 | 24.42 |
| 23 | VQVIPHITD | 118 | 2.1000 | 24.42 |
| 24 | VAFVGAAID | 538 | 2.1000 | 24.42 |

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|---|---|---|---|---|
| 25 | LRSIGITPD | 209 | 2.0000 | 23.26 |
| 26 | VGKYVELSD | 306 | 2.0000 | 23.26 |
| 27 | LFVAFVGAA | 536 | 2.0000 | 23.26 |
| 28 | MQKLDPYLN | 43 | 1.9000 | 22.09 |
| 29 | FVVRRLNLP | 270 | 1.9000 | 22.09 |
| 30 | LRRVHEPHE | 291 | 1.9000 | 22.09 |
| 31 | IEGKIGAIA | 371 | 1.9000 | 22.09 |
| 32 | VFFLHVSLV | 180 | 1.8000 | 20.93 |
| 33 | VLHREELDA | 261 | 1.8000 | 20.93 |
| 34 | VVGTQAHPE | 517 | 1.7000 | 19.77 |
| 35 | VRRLNLPFR | 272 | 1.6000 | 18.60 |
| 36 | IVIEAARSV | 398 | 1.6000 | 18.60 |
| 37 | YLNVDPGTM | 49 | 1.5000 | 17.44 |
| 38 | VPYLAPSGE | 188 | 1.5000 | 17.44 |
| 39 | IRGIEGKIG | 368 | 1.5000 | 17.44 |
| 40 | FVEYPPDRH | 506 | 1.5000 | 17.44 |
| 41 | IYDIPKVLH | 255 | 1.4000 | 16.28 |
| 42 | LGLQCIVIE | 393 | 1.4000 | 16.28 |
| 43 | VEIPEIPEH | 555 | 1.4000 | 16.28 |
| 44 | LTARGLHVT | 34 | 1.3000 | 15.12 |
| 45 | LPVLGLCLG | 386 | 1.2000 | 13.95 |
| 46 | LPFRDVDWT | 277 | 1.1000 | 12.79 |
| 47 | VHGVLIPGG | 357 | 1.1000 | 12.79 |
| 48 | LGGTMRLGS | 441 | 1.1000 | 12.79 |
| 49 | LGKGLTASS | 21 | 1.0000 | 11.63 |
| 50 | LILRCDRDV | 219 | 1.0000 | 11.63 |
| 51 | VSERHRHRY | 469 | 1.0000 | 11.63 |
| 52 | LLPVEIPEI | 552 | 1.0000 | 11.63 |
| 53 | ILAMAQPDA | 132 | 0.9000 | 10.47 |
| 54 | LEPDSVVAQ | 454 | 0.8000 | 9.30 |
| 55 | FVAFVGAAI | 537 | 0.8000 | 9.30 |
| 56 | FLDRNLPGS | 84 | 0.7000 | 8.14 |
| 57 | MNPFQHGEV | 57 | 0.6000 | 6.98 |
| 58 | FGIRGIEGK | 366 | 0.6000 | 6.98 |

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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 | LVGKYVELS | 305 | 4.8000 | 55.17 |
| 2 | FVVRRLNLP | 270 | 4.5000 | 51.72 |
| 3 | FKHRAKVEI | 328 | 4.5000 | 51.72 |
| 4 | FGIRGIEGK | 366 | 4.0000 | 45.98 |
| 5 | LKTKPTQHS | 197 | 3.7000 | 42.53 |
| 6 | IKRRILAMA | 128 | 3.3000 | 37.93 |
| 7 | FVSGGVASS | 12 | 3.2000 | 36.78 |
| 8 | LKNKIALMC | 231 | 3.2000 | 36.78 |
| 9 | VVRRLNLPF | 271 | 2.8000 | 32.18 |
| 10 | LKSRPTRPH | 526 | 2.5800 | 29.66 |
| 11 | FVEYPPDRH | 506 | 2.4800 | 28.51 |
| 12 | VFFLHVSLV | 180 | 2.3000 | 26.44 |
| 13 | LLRRVHEPH | 290 | 2.2800 | 26.21 |
| 14 | FLDRNLPGS | 84 | 1.9000 | 21.84 |
| 15 | VRIALVGKY | 301 | 1.7000 | 19.54 |
| 16 | LVPYLAPSG | 187 | 1.6000 | 18.39 |
| 17 | FVAFVGAAI | 537 | 1.6000 | 18.39 |
| 18 | YRDKIAESG | 483 | 1.5000 | 17.24 |
| 19 | FVGAAIDYK | 540 | 1.5000 | 17.24 |
| 20 | VLHREELDA | 261 | 1.4000 | 16.09 |
| 21 | VGHYERFLD | 78 | 1.1500 | 13.22 |
| 22 | LRSIGITPD | 209 | 1.1000 | 12.64 |
| 23 | YLGDTVQVI | 113 | 0.9000 | 10.34 |
| 24 | IEGKIGAIA | 371 | 0.9000 | 10.34 |
| 25 | YQTTQVSER | 464 | 0.9000 | 10.34 |
| 26 | VIAKERRGE | 104 | 0.8000 | 9.20 |
| 27 | VRRLNLPFR | 272 | 0.8000 | 9.20 |
| 28 | YLNVDPGTM | 49 | 0.7000 | 8.05 |
| 29 | LGGTMRLGS | 441 | 0.7000 | 8.05 |
| 30 | FLHVSLVPY | 182 | 0.6000 | 6.90 |

|  |  |  |  |  |
|---|---|---|---|---|
| 31 | LRFSGTSPD | 492 | 0.6000 | 6.90 |
| 32 | LQCIVIEAA | 395 | 0.5000 | 5.75 |
| 33 | LPFRDVDWT | 277 | 0.4000 | 4.60 |
| 34 | VLGLCLGLQ | 388 | 0.4000 | 4.60 |
| 35 | FQHGEVFVT | 60 | 0.3500 | 4.02 |
| 36 | VRHYLGRED | 171 | 0.3000 | 3.45 |
| 37 | LFVAFVGAA | 536 | 0.3000 | 3.45 |
| 38 | VGLTNANSA | 406 | 0.2000 | 2.30 |
| 39 | IYDIPKVLH | 255 | 0.1800 | 2.07 |
| 40 | ILAMAQPDA | 132 | 0.1000 | 1.15 |
| 41 | VEICWVASD | 334 | 0.1000 | 1.15 |
| 42 | LGLCLGLQC | 389 | 0.1000 | 1.15 |
| 43 | LGSYPAVLE | 447 | 0.1000 | 1.15 |
| 44 | LTARGLHVT | 34 | -0.1000 | 0 |
| 45 | VVITEIGGT | 147 | -0.1000 | 0 |
| 46 | YKAGELLPV | 547 | -0.1000 | 0 |
| 47 | MQKLDPYLN | 43 | -0.2000 | 0 |
| 48 | VNNAYRDKI | 479 | -0.2000 | 0 |
| 49 | FFLHVSLVP | 181 | -0.3000 | 0 |
| 50 | YDIPKVLHR | 256 | -0.3000 | 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 | VVRRLNLPF | 271 | 4.9000 | 48.51 |
| 2 | LKNKIALMC | 231 | 4.4000 | 43.56 |
| 3 | VIAKERRGE | 104 | 4.3000 | 42.57 |
| 4 | LKSRPTRPH | 526 | 4.3000 | 42.57 |
| 5 | LVGKYVELS | 305 | 4.2000 | 41.58 |
| 6 | FKHRAKVEI | 328 | 4.2000 | 41.58 |
| 7 | LVPYLAPSG | 187 | 3.8500 | 38.12 |
| 8 | VRIALVGKY | 301 | 3.6000 | 35.64 |
| 9 | VGHYERFLD | 78 | 3.5000 | 34.65 |

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|---|---|---|---|---|
| 10 | VRHYLGRED | 171 | 3.5000 | 34.65 |
| 11 | IKRRILAMA | 128 | 3.3000 | 32.67 |
| 12 | FVSGGVASS | 12 | 3.2000 | 31.68 |
| 13 | FVVRRLNLP | 270 | 3.2000 | 31.68 |
| 14 | LLRRVHEPH | 290 | 2.9000 | 28.71 |
| 15 | FLDRNLPGS | 84 | 2.8500 | 28.22 |
| 16 | LKTKPTQHS | 197 | 2.8000 | 27.72 |
| 17 | VGKYVELSD | 306 | 2.8000 | 27.72 |
| 18 | VEICWVASD | 334 | 2.8000 | 27.72 |
| 19 | VQVIPHITD | 118 | 2.7000 | 26.73 |
| 20 | FGIRGIEGK | 366 | 2.7000 | 26.73 |
| 21 | YLNVDPGTM | 49 | 2.6000 | 25.74 |
| 22 | VLHREELDA | 261 | 2.6000 | 25.74 |
| 23 | LGSYPAVLE | 447 | 2.6000 | 25.74 |
| 24 | IALVGKYVE | 303 | 2.5000 | 24.75 |
| 25 | YRDKIAESG | 483 | 2.2000 | 21.78 |
| 26 | FVEYPPDRH | 506 | 2.2000 | 21.78 |
| 27 | LRSIGITPD | 209 | 2.1000 | 20.79 |
| 28 | LRRVHEPHE | 291 | 2.0500 | 20.30 |
| 29 | VLGLCLGLQ | 388 | 2.0000 | 19.80 |
| 30 | LGGTMRLGS | 441 | 1.9000 | 18.81 |
| 31 | FVAFVGAAI | 537 | 1.8000 | 17.82 |
| 32 | VRRLNLPFR | 272 | 1.7500 | 17.33 |
| 33 | MQKLDPYLN | 43 | 1.6000 | 15.84 |
| 34 | VVITEIGGT | 147 | 1.6000 | 15.84 |
| 35 | VEIPEIPEH | 555 | 1.5500 | 15.35 |
| 36 | LRFSGTSPD | 492 | 1.5000 | 14.85 |
| 37 | VVGTQAHPE | 517 | 1.4000 | 13.86 |
| 38 | YKAGELLPV | 547 | 1.4000 | 13.86 |
| 39 | LGQLLTARG | 30 | 1.3000 | 12.87 |
| 40 | FFLHVSLVP | 181 | 1.3000 | 12.87 |
| 41 | LGLCLGLQC | 389 | 1.3000 | 12.87 |
| 42 | VHGVLIPGG | 357 | 1.2500 | 12.38 |
| 43 | FLHVSLVPY | 182 | 1.2000 | 11.88 |

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|---|---|---|---|---|
| 44 | YEVNNAYRD | 477 | 1.2000 | 11.88 |
| 45 | LLPVEIPEI | 552 | 1.1500 | 11.39 |
| 46 | VYSTVIAKE | 100 | 1.1000 | 10.89 |
| 47 | IRGIEGKIG | 368 | 1.1000 | 10.89 |
| 48 | YARARGLPV | 380 | 1.1000 | 10.89 |
| 49 | LFVAFVGAA | 536 | 1.1000 | 10.89 |
| 50 | VAFVGAAID | 538 | 1.1000 | 10.89 |
| 51 | ILAMAQPDA | 132 | 1.0500 | 10.40 |
| 52 | LTARGLHVT | 34 | 1.0000 | 9.90 |
| 53 | FQHGEVFVT | 60 | 0.9000 | 8.91 |
| 54 | IYDIPKVLH | 255 | 0.9000 | 8.91 |
| 55 | YDIPKVLHR | 256 | 0.9000 | 8.91 |
| 56 | IEGKIGAIA | 371 | 0.9000 | 8.91 |
| 57 | LGLQCIVIE | 393 | 0.9000 | 8.91 |
| 58 | VFFLHVSLV | 180 | 0.8000 | 7.92 |

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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 | FVSGGVASS | 12 | 2.5000 | 30.12 |
| 2 | VRIALVGKY | 301 | 2.5000 | 30.12 |
| 3 | LGGTMRLGS | 441 | 2.3000 | 27.71 |
| 4 | VRRLNLPFR | 272 | 2.1500 | 25.90 |
| 5 | YLNVDPGTM | 49 | 1.6000 | 19.28 |
| 6 | LKNKIALMC | 231 | 1.6000 | 19.28 |
| 7 | VLGLCLGLQ | 388 | 1.6000 | 19.28 |
| 8 | FVAFVGAAI | 537 | 1.5000 | 18.07 |
| 9 | LVGKYVELS | 305 | 1.4000 | 16.87 |
| 10 | FFLHVSLVP | 181 | 1.3000 | 15.66 |
| 11 | LGLCLGLQC | 389 | 1.3000 | 15.66 |
| 12 | VVITEIGGT | 147 | 1.1000 | 13.25 |
| 13 | LFVAFVGAA | 536 | 1.1000 | 13.25 |
| 14 | LLPVEIPEI | 552 | 1.0500 | 12.65 |

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|---|---|---|---|---|
| 15 | VVRRLNLPF | 271 | 1.0000 | 12.05 |
| 16 | FKHRAKVEI | 328 | 1.0000 | 12.05 |
| 17 | VFFLHVSLV | 180 | 0.9000 | 10.84 |
| 18 | YARARGLPV | 380 | 0.8000 | 9.64 |
| 19 | LSVAEALRA | 317 | 0.7000 | 8.43 |
| 20 | ILAMAQPDA | 132 | 0.6500 | 7.83 |
| 21 | VQVIPHITD | 118 | 0.6000 | 7.23 |
| 22 | VAALRSIGI | 206 | 0.5000 | 6.02 |
| 23 | LQCIVIEAA | 395 | 0.5000 | 6.02 |
| 24 | LGQLLTARG | 30 | 0.4000 | 4.82 |
| 25 | FGIRGIEGK | 366 | 0.4000 | 4.82 |
| 26 | IRGIEGKIG | 368 | 0.4000 | 4.82 |
| 27 | YKAGELLPV | 547 | 0.4000 | 4.82 |
| 28 | IKRRILAMA | 128 | 0.3000 | 3.61 |
| 29 | IYDIPKVLH | 255 | 0.2800 | 3.37 |
| 30 | FLHVSLVPY | 182 | 0.2000 | 2.41 |
| 31 | YDIPKVLHR | 256 | 0.2000 | 2.41 |
| 32 | LLTARGLHV | 33 | 0.1000 | 1.20 |
| 33 | VEICWVASD | 334 | 0.1000 | 1.20 |
| 34 | LKSRPTRPH | 526 | 0.0800 | 0.96 |
| 35 | VHGVLIPGG | 357 | 0.0500 | 0.60 |
| 36 | FLDRNLPGS | 84 | -0.1500 | 0 |
| 37 | FVVRRLNLP | 270 | -0.2000 | 0 |
| 38 | IVIEAARSV | 398 | -0.2000 | 0 |
| 39 | LHVSLVPYL | 183 | -0.2500 | 0 |
| 40 | VELSDAYLS | 310 | -0.3000 | 0 |
| 41 | LVPYLAPSG | 187 | -0.3500 | 0 |
| 42 | VEIPEIPEH | 555 | -0.3700 | 0 |
| 43 | VLHREELDA | 261 | -0.4000 | 0 |
| 44 | IALVGKYVE | 303 | -0.4000 | 0 |
| 45 | WVASDGCET | 338 | -0.5000 | 0 |
| 46 | YQTTQVSER | 464 | -0.5000 | 0 |
| 47 | LGKGLTASS | 21 | -0.7000 | 0 |
| 48 | MNPFQHGEV | 57 | -0.7000 | 0 |

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|---|---|---|---|---|
| 49 | FQHGEVFVT | 60 | -0.7000 | 0 |
| 50 | YLGDTVQVI | 113 | -0.7000 | 0 |
| 51 | LPVLGLCLG | 386 | -0.7000 | 0 |
| 52 | FVVGTQAHP | 516 | -0.7000 | 0 |
| 53 | YLSVAEALR | 316 | -0.8000 | 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 | LVGKYVELS | 305 | 4.0000 | 47.62 |
| 2 | LKSRPTRPH | 526 | 3.5800 | 42.62 |
| 3 | LKTKPTQHS | 197 | 3.0000 | 35.71 |
| 4 | IVIEAARSV | 398 | 3.0000 | 35.71 |
| 5 | LKNKIALMC | 231 | 2.8000 | 33.33 |
| 6 | VIAKERRGE | 104 | 2.4000 | 28.57 |
| 7 | VRIALVGKY | 301 | 2.4000 | 28.57 |
| 8 | IKRRILAMA | 128 | 2.2000 | 26.19 |
| 9 | VRRLNLPFR | 272 | 2.0000 | 23.81 |
| 10 | VIPHITDEI | 120 | 1.9000 | 22.62 |
| 11 | VVRRLNLPF | 271 | 1.8000 | 21.43 |
| 12 | FVSGGVASS | 12 | 1.7000 | 20.24 |
| 13 | LGGTMRLGS | 441 | 1.7000 | 20.24 |
| 14 | VRHYLGRED | 171 | 1.6000 | 19.05 |
| 15 | VFFLHVSLV | 180 | 1.6000 | 19.05 |
| 16 | FKHRAKVEI | 328 | 1.4000 | 16.67 |
| 17 | MRKHPQTAT | 0 | 1.3000 | 15.48 |
| 18 | FFLHVSLVP | 181 | 1.3000 | 15.48 |
| 19 | LVPYLAPSG | 187 | 1.3000 | 15.48 |
| 20 | LGLCLGLQC | 389 | 1.2000 | 14.29 |
| 21 | VEICWVASD | 334 | 1.1000 | 13.10 |
| 22 | IPEHTPNGS | 560 | 1.1000 | 13.10 |
| 23 | VGHYERFLD | 78 | 1.0000 | 11.90 |
| 24 | ILAMAQPDA | 132 | 1.0000 | 11.90 |

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|---|---|---|---|---|
| 25 | VELSDAYLS | 310 | 1.0000 | 11.90 |
| 26 | IAYARARGL | 378 | 1.0000 | 11.90 |
| 27 | LGLQCIVIE | 393 | 1.0000 | 11.90 |
| 28 | LFVAFVGAA | 536 | 1.0000 | 11.90 |
| 29 | LGREDVFFL | 175 | 0.9000 | 10.71 |
| 30 | LDAFVVRRL | 267 | 0.9000 | 10.71 |
| 31 | FVAFVGAAI | 537 | 0.9000 | 10.71 |
| 32 | LLRRVHEPH | 290 | 0.8800 | 10.48 |
| 33 | FVVRRLNLP | 270 | 0.8000 | 9.52 |
| 34 | VLGLCLGLQ | 388 | 0.8000 | 9.52 |
| 35 | LGQLLTARG | 30 | 0.7000 | 8.33 |
| 36 | LFVSGGVAS | 11 | 0.6000 | 7.14 |
| 37 | LSVAEALRA | 317 | 0.6000 | 7.14 |
| 38 | VLIPGGFGI | 360 | 0.6000 | 7.14 |
| 39 | FGIRGIEGK | 366 | 0.6000 | 7.14 |
| 40 | LEPDSVVAQ | 454 | 0.6000 | 7.14 |
| 41 | LRFSGTSPD | 492 | 0.6000 | 7.14 |
| 42 | LGKGLTASS | 21 | 0.5000 | 5.95 |
| 43 | MQKLDPYLN | 43 | 0.5000 | 5.95 |
| 44 | VVITEIGGT | 147 | 0.5000 | 5.95 |
| 45 | VGLTNANSA | 406 | 0.5000 | 5.95 |
| 46 | VNNAYRDKI | 479 | 0.5000 | 5.95 |
| 47 | LHVSLVPYL | 183 | 0.4000 | 4.76 |
| 48 | LILRCDRDV | 219 | 0.4000 | 4.76 |
| 49 | VLHREELDA | 261 | 0.4000 | 4.76 |
| 50 | IEGKIGAIA | 371 | 0.4000 | 4.76 |
| 51 | VEIPEIPEH | 555 | 0.3800 | 4.52 |
| 52 | LQCIVIEAA | 395 | 0.3000 | 3.57 |
| 53 | IAESGLRFS | 487 | 0.3000 | 3.57 |
| 54 | LLPVEIPEI | 552 | 0.3000 | 3.57 |
| 55 | IYDIPKVLH | 255 | 0.2800 | 3.33 |
| 56 | FVGAAIDYK | 540 | 0.2000 | 2.38 |
| 57 | IRGIEGKIG | 368 | 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 | VRIALVGKY | 301 | 3.5000 | 42.17 |
| 2 | LGGTMRLGS | 441 | 3.3000 | 39.76 |
| 3 | VRRLNLPFR | 272 | 3.1500 | 37.95 |
| 4 | LKNKIALMC | 231 | 2.6000 | 31.33 |
| 5 | VLGLCLGLQ | 388 | 2.6000 | 31.33 |
| 6 | LVGKYVELS | 305 | 2.4000 | 28.92 |
| 7 | LGLCLGLQC | 389 | 2.3000 | 27.71 |
| 8 | VVITEIGGT | 147 | 2.1000 | 25.30 |
| 9 | LFVAFVGAA | 536 | 2.1000 | 25.30 |
| 10 | LLPVEIPEI | 552 | 2.0500 | 24.70 |
| 11 | VVRRLNLPF | 271 | 2.0000 | 24.10 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 22.89 |
| 13 | LSVAEALRA | 317 | 1.7000 | 20.48 |
| 14 | ILAMAQPDA | 132 | 1.6500 | 19.88 |
| 15 | VQVIPHITD | 118 | 1.6000 | 19.28 |
| 16 | FVSGGVASS | 12 | 1.5000 | 18.07 |
| 17 | VAALRSIGI | 206 | 1.5000 | 18.07 |
| 18 | LQCIVIEAA | 395 | 1.5000 | 18.07 |
| 19 | LGQLLTARG | 30 | 1.4000 | 16.87 |
| 20 | IRGIEGKIG | 368 | 1.4000 | 16.87 |
| 21 | IKRRILAMA | 128 | 1.3000 | 15.66 |
| 22 | IYDIPKVLH | 255 | 1.2800 | 15.42 |
| 23 | LLTARGLHV | 33 | 1.1000 | 13.25 |
| 24 | VEICWVASD | 334 | 1.1000 | 13.25 |
| 25 | LKSRPTRPH | 526 | 1.0800 | 13.01 |
| 26 | VHGVLIPGG | 357 | 1.0500 | 12.65 |
| 27 | MQKLDPYLN | 43 | 1.0000 | 12.05 |
| 28 | LKTKPTQHS | 197 | 1.0000 | 12.05 |
| 29 | LRSIGITPD | 209 | 1.0000 | 12.05 |
| 30 | IVIEAARSV | 398 | 0.8000 | 9.64 |

| | | | | |
|---|---|---|---|---|
| 31 | LHVSLVPYL | 183 | 0.7500 | 9.04 |
| 32 | VELSDAYLS | 310 | 0.7000 | 8.43 |
| 33 | LVPYLAPSG | 187 | 0.6500 | 7.83 |
| 34 | VEIPEIPEH | 555 | 0.6300 | 7.59 |
| 35 | YLNVDPGTM | 49 | 0.6000 | 7.23 |
| 36 | VLHREELDA | 261 | 0.6000 | 7.23 |
| 37 | IALVGKYVE | 303 | 0.6000 | 7.23 |
| 38 | FVAFVGAAI | 537 | 0.5000 | 6.02 |
| 39 | LGKGLTASS | 21 | 0.3000 | 3.61 |
| 40 | MNPFQHGEV | 57 | 0.3000 | 3.61 |
| 41 | FFLHVSLVP | 181 | 0.3000 | 3.61 |
| 42 | LPVLGLCLG | 386 | 0.3000 | 3.61 |
| 43 | LRRVHEPHE | 291 | 0.1500 | 1.81 |
| 44 | LRFSGTSPD | 492 | 0.1000 | 1.20 |
| 45 | VSLVPYLAP | 185 | -0.1000 | 0 |
| 46 | VGLTNANSA | 406 | -0.1000 | 0 |
| 47 | YARARGLPV | 380 | -0.2000 | 0 |
| 48 | LEPDSVVAQ | 454 | -0.2000 | 0 |
| 49 | VVGTQAHPE | 517 | -0.2000 | 0 |
| 50 | LLRRVHEPH | 290 | -0.3200 | 0 |
| 51 | LDRNLPGSA | 85 | -0.5000 | 0 |
| 52 | VYSTVIAKE | 100 | -0.5000 | 0 |
| 53 | VIAKERRGE | 104 | -0.5000 | 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 | VRIALVGKY | 301 | 3.5000 | 42.17 |
| 2 | LGGTMRLGS | 441 | 3.3000 | 39.76 |
| 3 | VRRLNLPFR | 272 | 3.1500 | 37.95 |
| 4 | LKNKIALMC | 231 | 2.6000 | 31.33 |
| 5 | VLGLCLGLQ | 388 | 2.6000 | 31.33 |
| 6 | LVGKYVELS | 305 | 2.4000 | 28.92 |

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|---|---|---|---|---|
| 7 | LGLCLGLQC | 389 | 2.3000 | 27.71 |
| 8 | VVITEIGGT | 147 | 2.1000 | 25.30 |
| 9 | LFVAFVGAA | 536 | 2.1000 | 25.30 |
| 10 | LLPVEIPEI | 552 | 2.0500 | 24.70 |
| 11 | VVRRLNLPF | 271 | 2.0000 | 24.10 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 22.89 |
| 13 | LSVAEALRA | 317 | 1.7000 | 20.48 |
| 14 | ILAMAQPDA | 132 | 1.6500 | 19.88 |
| 15 | VQVIPHITD | 118 | 1.6000 | 19.28 |
| 16 | FVSGGVASS | 12 | 1.5000 | 18.07 |
| 17 | VAALRSIGI | 206 | 1.5000 | 18.07 |
| 18 | LQCIVIEAA | 395 | 1.5000 | 18.07 |
| 19 | LGQLLTARG | 30 | 1.4000 | 16.87 |
| 20 | IRGIEGKIG | 368 | 1.4000 | 16.87 |
| 21 | IKRRILAMA | 128 | 1.3000 | 15.66 |
| 22 | IYDIPKVLH | 255 | 1.2800 | 15.42 |
| 23 | LLTARGLHV | 33 | 1.1000 | 13.25 |
| 24 | VEICWVASD | 334 | 1.1000 | 13.25 |
| 25 | LKSRPTRPH | 526 | 1.0800 | 13.01 |
| 26 | VHGVLIPGG | 357 | 1.0500 | 12.65 |
| 27 | MQKLDPYLN | 43 | 1.0000 | 12.05 |
| 28 | LKTKPTQHS | 197 | 1.0000 | 12.05 |
| 29 | LRSIGITPD | 209 | 1.0000 | 12.05 |
| 30 | IVIEAARSV | 398 | 0.8000 | 9.64 |
| 31 | LHVSLVPYL | 183 | 0.7500 | 9.04 |
| 32 | VELSDAYLS | 310 | 0.7000 | 8.43 |
| 33 | LVPYLAPSG | 187 | 0.6500 | 7.83 |
| 34 | VEIPEIPEH | 555 | 0.6300 | 7.59 |
| 35 | YLNVDPGTM | 49 | 0.6000 | 7.23 |
| 36 | VLHREELDA | 261 | 0.6000 | 7.23 |
| 37 | IALVGKYVE | 303 | 0.6000 | 7.23 |
| 38 | FVAFVGAAI | 537 | 0.5000 | 6.02 |
| 39 | LGKGLTASS | 21 | 0.3000 | 3.61 |
| 40 | MNPFQHGEV | 57 | 0.3000 | 3.61 |

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|---|---|---|---|---|
| 41 | FFLHVSLVP | 181 | 0.3000 | 3.61 |
| 42 | LPVLGLCLG | 386 | 0.3000 | 3.61 |
| 43 | LRRVHEPHE | 291 | 0.1500 | 1.81 |
| 44 | LRFSGTSPD | 492 | 0.1000 | 1.20 |
| 45 | VSLVPYLAP | 185 | -0.1000 | 0 |
| 46 | VGLTNANSA | 406 | -0.1000 | 0 |
| 47 | YARARGLPV | 380 | -0.2000 | 0 |
| 48 | LEPDSVVAQ | 454 | -0.2000 | 0 |
| 49 | VVGTQAHPE | 517 | -0.2000 | 0 |
| 50 | LLRRVHEPH | 290 | -0.3200 | 0 |
| 51 | LDRNLPGSA | 85 | -0.5000 | 0 |
| 52 | VYSTVIAKE | 100 | -0.5000 | 0 |
| 53 | VIAKERRGE | 104 | -0.5000 | 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 | LEPDSVVAQ | 454 | 4.6000 | 50.55 |
| 2 | VRIALVGKY | 301 | 4.0000 | 43.96 |
| 3 | FVSGGVASS | 12 | 3.7000 | 40.66 |
| 4 | YLGDTVQVI | 113 | 3.3000 | 36.26 |
| 5 | LVGKYVELS | 305 | 3.0000 | 32.97 |
| 6 | LHVSLVPYL | 183 | 2.9000 | 31.87 |
| 7 | VDIDGVIST | 241 | 2.9000 | 31.87 |
| 8 | LRFSGTSPD | 492 | 2.8700 | 31.54 |
| 9 | VRRLNLPFR | 272 | 2.8000 | 30.77 |
| 10 | LFVAFVGAA | 536 | 2.6000 | 28.57 |
| 11 | LGKGLTASS | 21 | 2.5000 | 27.47 |
| 12 | VELSDAYLS | 310 | 2.4500 | 26.92 |
| 13 | LLPVEIPEI | 552 | 2.4000 | 26.37 |
| 14 | MRLGSYPAV | 445 | 2.3000 | 25.27 |
| 15 | LFVSGGVAS | 11 | 2.2000 | 24.18 |
| 16 | VVITEIGGT | 147 | 2.2000 | 24.18 |

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|---|---|---|---|---|
| 17 | ITPDALILR | 214 | 2.2000 | 24.18 |
| 18 | LQCIVIEAA | 395 | 2.2000 | 24.18 |
| 19 | VFFLHVSLV | 180 | 2.1700 | 23.85 |
| 20 | VEIPEIPEH | 555 | 2.0800 | 22.86 |
| 21 | VLGLCLGLQ | 388 | 2.0000 | 21.98 |
| 22 | LRSIGITPD | 209 | 1.8000 | 19.78 |
| 23 | IYDIPKVLH | 255 | 1.6800 | 18.46 |
| 24 | LGGTMRLGS | 441 | 1.6000 | 17.58 |
| 25 | LKTKPTQHS | 197 | 1.5000 | 16.48 |
| 26 | LNVDPGTMN | 50 | 1.4000 | 15.38 |
| 27 | FQHGEVFVT | 60 | 1.4000 | 15.38 |
| 28 | ILAMAQPDA | 132 | 1.4000 | 15.38 |
| 29 | VHGVLIPGG | 357 | 1.4000 | 15.38 |
| 30 | VNNAYRDKI | 479 | 1.4000 | 15.38 |
| 31 | VIPHITDEI | 120 | 1.3000 | 14.29 |
| 32 | LVPYLAPSG | 187 | 1.1000 | 12.09 |
| 33 | VEICWVASD | 334 | 1.1000 | 12.09 |
| 34 | VASDGCETT | 339 | 1.1000 | 12.09 |
| 35 | FVGAAIDYK | 540 | 1.1000 | 12.09 |
| 36 | IKRRILAMA | 128 | 1.0000 | 10.99 |
| 37 | VLIPGGFGI | 360 | 1.0000 | 10.99 |
| 38 | LGLCLGLQC | 389 | 1.0000 | 10.99 |
| 39 | IVIEAARSV | 398 | 1.0000 | 10.99 |
| 40 | IVAGEADLG | 434 | 1.0000 | 10.99 |
| 41 | YPPDRHPFV | 509 | 1.0000 | 10.99 |
| 42 | LGREDVFFL | 175 | 0.9000 | 9.89 |
| 43 | VQVIPHITD | 118 | 0.8000 | 8.79 |
| 44 | ILRCDRDVP | 220 | 0.8000 | 8.79 |
| 45 | LKNKIALMC | 231 | 0.8000 | 8.79 |
| 46 | YLNVDPGTM | 49 | 0.7000 | 7.69 |
| 47 | LGLQCIVIE | 393 | 0.7000 | 7.69 |
| 48 | MRKHPQTAT | 0 | 0.6000 | 6.59 |
| 49 | LRCDRDVPE | 221 | 0.6000 | 6.59 |
| 50 | IALVGKYVE | 303 | 0.5500 | 6.04 |

| | | | | |
|---|---|---|---|---|
| 51 | LRRVHEPHE | 291 | 0.5000 | 5.49 |
| 52 | FKHRAKVEI | 328 | 0.5000 | 5.49 |
| 53 | LCLGLQCIV | 391 | 0.5000 | 5.49 |
| 54 | FVVGTQAHP | 516 | 0.5000 | 5.49 |
| 55 | LLRRVHEPH | 290 | 0.4800 | 5.27 |
| 56 | VTTGQVYST | 95 | 0.4500 | 4.95 |
| 57 | VGLTNANSA | 406 | 0.4100 | 4.51 |
| 58 | LMCDVDIDG | 237 | 0.4000 | 4.40 |

| 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 | LVGKYVELS | 305 | 3.0000 | 35.71 |
| 2 | FVSGGVASS | 12 | 2.7000 | 32.14 |
| 3 | LKSRPTRPH | 526 | 2.5800 | 30.71 |
| 4 | FKHRAKVEI | 328 | 2.4000 | 28.57 |
| 5 | FFLHVSLVP | 181 | 2.3000 | 27.38 |
| 6 | LKTKPTQHS | 197 | 2.0000 | 23.81 |
| 7 | IVIEAARSV | 398 | 2.0000 | 23.81 |
| 8 | FVAFVGAAI | 537 | 1.9000 | 22.62 |
| 9 | LKNKIALMC | 231 | 1.8000 | 21.43 |
| 10 | FVVRRLNLP | 270 | 1.8000 | 21.43 |
| 11 | FGIRGIEGK | 366 | 1.6000 | 19.05 |
| 12 | VIAKERRGE | 104 | 1.4000 | 16.67 |
| 13 | VRIALVGKY | 301 | 1.4000 | 16.67 |
| 14 | IKRRILAMA | 128 | 1.2000 | 14.29 |
| 15 | FVGAAIDYK | 540 | 1.2000 | 14.29 |
| 16 | VRRLNLPFR | 272 | 1.0000 | 11.90 |
| 17 | VIPHITDEI | 120 | 0.9000 | 10.71 |
| 18 | VVRRLNLPF | 271 | 0.8000 | 9.52 |
| 19 | LGGTMRLGS | 441 | 0.7000 | 8.33 |
| 20 | VRHYLGRED | 171 | 0.6000 | 7.14 |
| 21 | VFFLHVSLV | 180 | 0.6000 | 7.14 |

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|---|---|---|---|---|
| 22 | FQHGEVFVT | 60 | 0.5000 | 5.95 |
| 23 | FVEYPPDRH | 506 | 0.3800 | 4.52 |
| 24 | MRKHPQTAT | 0 | 0.3000 | 3.57 |
| 25 | FLDRNLPGS | 84 | 0.3000 | 3.57 |
| 26 | YLGDTVQVI | 113 | 0.3000 | 3.57 |
| 27 | LVPYLAPSG | 187 | 0.3000 | 3.57 |
| 28 | LGLCLGLQC | 389 | 0.2000 | 2.38 |
| 29 | VEICWVASD | 334 | 0.1000 | 1.19 |
| 30 | IPEHTPNGS | 560 | 0.1000 | 1.19 |
| 31 | WDDLLRRVH | 287 | 0.0800 | 0.95 |
| 32 | LGREDVFFL | 175 | -0.1000 | 0 |
| 33 | LDAFVVRRL | 267 | -0.1000 | 0 |
| 34 | LLRRVHEPH | 290 | -0.1200 | 0 |
| 35 | VLGLCLGLQ | 388 | -0.2000 | 0 |
| 36 | LGQLLTARG | 30 | -0.3000 | 0 |
| 37 | YARARGLPV | 380 | -0.3000 | 0 |
| 38 | YRDKIAESG | 483 | -0.3000 | 0 |
| 39 | LFVSGGVAS | 11 | -0.4000 | 0 |
| 40 | LSVAEALRA | 317 | -0.4000 | 0 |
| 41 | WVASDGCET | 338 | -0.4000 | 0 |
| 42 | VLIPGGFGI | 360 | -0.4000 | 0 |
| 43 | LEPDSVVAQ | 454 | -0.4000 | 0 |
| 44 | LRFSGTSPD | 492 | -0.4000 | 0 |
| 45 | LGKGLTASS | 21 | -0.5000 | 0 |
| 46 | MQKLDPYLN | 43 | -0.5000 | 0 |
| 47 | VVITEIGGT | 147 | -0.5000 | 0 |
| 48 | VGLTNANSA | 406 | -0.5000 | 0 |
| 49 | VNNAYRDKI | 479 | -0.5000 | 0 |
| 50 | FVVGTQAHP | 516 | -0.5000 | 0 |
| 51 | YKAGELLPV | 547 | -0.5000 | 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 | LVGKYVELS | 305 | 3.4000 | 38.64 |
| 2 | FFLHVSLVP | 181 | 3.3000 | 37.50 |
| 3 | FKHRAKVEI | 328 | 3.3000 | 37.50 |
| 4 | FVSGGVASS | 12 | 3.1000 | 35.23 |
| 5 | IVIEAARSV | 398 | 3.0000 | 34.09 |
| 6 | VIAKERRGE | 104 | 2.8000 | 31.82 |
| 7 | FVVRRLNLP | 270 | 2.8000 | 31.82 |
| 8 | FVAFVGAAI | 537 | 2.8000 | 31.82 |
| 9 | VVRRLNLPF | 271 | 2.7000 | 30.68 |
| 10 | VRIALVGKY | 301 | 2.7000 | 30.68 |
| 11 | VRRLNLPFR | 272 | 2.5000 | 28.41 |
| 12 | LKTKPTQHS | 197 | 2.4000 | 27.27 |
| 13 | LKSRPTRPH | 526 | 2.0000 | 22.73 |
| 14 | VIPHITDEI | 120 | 1.8000 | 20.45 |
| 15 | LKNKIALMC | 231 | 1.8000 | 20.45 |
| 16 | VRHYLGRED | 171 | 1.7000 | 19.32 |
| 17 | LVPYLAPSG | 187 | 1.7000 | 19.32 |
| 18 | FGIRGIEGK | 366 | 1.7000 | 19.32 |
| 19 | VFFLHVSLV | 180 | 1.6000 | 18.18 |
| 20 | LGLQCIVIE | 393 | 1.4000 | 15.91 |
| 21 | FVGAAIDYK | 540 | 1.3000 | 14.77 |
| 22 | FQHGEVFVT | 60 | 1.2000 | 13.64 |
| 23 | YLGDTVQVI | 113 | 1.2000 | 13.64 |
| 24 | IKRRILAMA | 128 | 1.2000 | 13.64 |
| 25 | VEICWVASD | 334 | 1.2000 | 13.64 |
| 26 | LGQLLTARG | 30 | 1.1000 | 12.50 |
| 27 | VGHYERFLD | 78 | 1.1000 | 12.50 |
| 28 | LGGTMRLGS | 441 | 1.1000 | 12.50 |
| 29 | YRDKIAESG | 483 | 1.1000 | 12.50 |
| 30 | MRKHPQTAT | 0 | 1.0000 | 11.36 |
| 31 | IAYARARGL | 378 | 0.9600 | 10.91 |
| 32 | FLEAARQVR | 164 | 0.9000 | 10.23 |
| 33 | YQTTQVSER | 464 | 0.9000 | 10.23 |

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|---|---|---|---|---|
| 34 | LGREDVFFL | 175 | 0.8600 | 9.77 |
| 35 | LDAFVVRRL | 267 | 0.8600 | 9.77 |
| 36 | YDIPKVLHR | 256 | 0.8000 | 9.09 |
| 37 | YLNVDPGTM | 49 | 0.7000 | 7.95 |
| 38 | FLDRNLPGS | 84 | 0.7000 | 7.95 |
| 39 | FLHVSLVPY | 182 | 0.7000 | 7.95 |
| 40 | YARARGLPV | 380 | 0.7000 | 7.95 |
| 41 | LRFSGTSPD | 492 | 0.7000 | 7.95 |
| 42 | VLIPGGFGI | 360 | 0.5000 | 5.68 |
| 43 | IRGIEGKIG | 368 | 0.5000 | 5.68 |
| 44 | FVVGTQAHP | 516 | 0.5000 | 5.68 |
| 45 | YKAGELLPV | 547 | 0.5000 | 5.68 |
| 46 | IPEHTPNGS | 560 | 0.5000 | 5.68 |
| 47 | LILRCDRDV | 219 | 0.4000 | 4.55 |
| 48 | VELSDAYLS | 310 | 0.4000 | 4.55 |
| 49 | VNNAYRDKI | 479 | 0.4000 | 4.55 |
| 50 | YERFLDRNL | 81 | 0.3600 | 4.09 |
| 51 | LHVSLVPYL | 183 | 0.3600 | 4.09 |
| 52 | MQKLDPYLN | 43 | 0.3000 | 3.41 |
| 53 | WVASDGCET | 338 | 0.3000 | 3.41 |
| 54 | LTNANSAEF | 408 | 0.3000 | 3.41 |
| 55 | VVITEIGGT | 147 | 0.2000 | 2.27 |
| 56 | LGLCLGLQC | 389 | 0.2000 | 2.27 |
| 57 | VVGTQAHPE | 517 | 0.2000 | 2.27 |
| 58 | LLPVEIPEI | 552 | 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 | LVGKYVELS | 305 | 4.0000 | 47.62 |
| 2 | LKSRPTRPH | 526 | 3.5800 | 42.62 |
| 3 | LKTKPTQHS | 197 | 3.0000 | 35.71 |
| 4 | IVIEAARSV | 398 | 3.0000 | 35.71 |

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|---|---|---|---|---|
| 5 | LKNKIALMC | 231 | 2.8000 | 33.33 |
| 6 | VIAKERRGE | 104 | 2.4000 | 28.57 |
| 7 | VRIALVGKY | 301 | 2.4000 | 28.57 |
| 8 | IKRRILAMA | 128 | 2.2000 | 26.19 |
| 9 | VRRLNLPFR | 272 | 2.0000 | 23.81 |
| 10 | VIPHITDEI | 120 | 1.9000 | 22.62 |
| 11 | VVRRLNLPF | 271 | 1.8000 | 21.43 |
| 12 | FVSGGVASS | 12 | 1.7000 | 20.24 |
| 13 | LGGTMRLGS | 441 | 1.7000 | 20.24 |
| 14 | VRHYLGRED | 171 | 1.6000 | 19.05 |
| 15 | VFFLHVSLV | 180 | 1.6000 | 19.05 |
| 16 | FKHRAKVEI | 328 | 1.4000 | 16.67 |
| 17 | MRKHPQTAT | 0 | 1.3000 | 15.48 |
| 18 | FFLHVSLVP | 181 | 1.3000 | 15.48 |
| 19 | LVPYLAPSG | 187 | 1.3000 | 15.48 |
| 20 | LGLCLGLQC | 389 | 1.2000 | 14.29 |
| 21 | VEICWVASD | 334 | 1.1000 | 13.10 |
| 22 | IPEHTPNGS | 560 | 1.1000 | 13.10 |
| 23 | VGHYERFLD | 78 | 1.0000 | 11.90 |
| 24 | ILAMAQPDA | 132 | 1.0000 | 11.90 |
| 25 | VELSDAYLS | 310 | 1.0000 | 11.90 |
| 26 | IAYARARGL | 378 | 1.0000 | 11.90 |
| 27 | LGLQCIVIE | 393 | 1.0000 | 11.90 |
| 28 | LFVAFVGAA | 536 | 1.0000 | 11.90 |
| 29 | LGREDVFFL | 175 | 0.9000 | 10.71 |
| 30 | LDAFVVRRL | 267 | 0.9000 | 10.71 |
| 31 | FVAFVGAAI | 537 | 0.9000 | 10.71 |
| 32 | LLRRVHEPH | 290 | 0.8800 | 10.48 |
| 33 | FVVRRLNLP | 270 | 0.8000 | 9.52 |
| 34 | VLGLCLGLQ | 388 | 0.8000 | 9.52 |
| 35 | LGQLLTARG | 30 | 0.7000 | 8.33 |
| 36 | LFVSGGVAS | 11 | 0.6000 | 7.14 |
| 37 | LSVAEALRA | 317 | 0.6000 | 7.14 |
| 38 | VLIPGGFGI | 360 | 0.6000 | 7.14 |

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|---|---|---|---|---|
| 39 | FGIRGIEGK | 366 | 0.6000 | 7.14 |
| 40 | LEPDSVVAQ | 454 | 0.6000 | 7.14 |
| 41 | LRFSGTSPD | 492 | 0.6000 | 7.14 |
| 42 | LGKGLTASS | 21 | 0.5000 | 5.95 |
| 43 | MQKLDPYLN | 43 | 0.5000 | 5.95 |
| 44 | VVITEIGGT | 147 | 0.5000 | 5.95 |
| 45 | VGLTNANSA | 406 | 0.5000 | 5.95 |
| 46 | VNNAYRDKI | 479 | 0.5000 | 5.95 |
| 47 | LHVSLVPYL | 183 | 0.4000 | 4.76 |
| 48 | LILRCDRDV | 219 | 0.4000 | 4.76 |
| 49 | VLHREELDA | 261 | 0.4000 | 4.76 |
| 50 | IEGKIGAIA | 371 | 0.4000 | 4.76 |
| 51 | VEIPEIPEH | 555 | 0.3800 | 4.52 |
| 52 | LQCIVIEAA | 395 | 0.3000 | 3.57 |
| 53 | IAESGLRFS | 487 | 0.3000 | 3.57 |
| 54 | LLPVEIPEI | 552 | 0.3000 | 3.57 |
| 55 | IYDIPKVLH | 255 | 0.2800 | 3.33 |
| 56 | FVGAAIDYK | 540 | 0.2000 | 2.38 |
| 57 | IRGIEGKIG | 368 | 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 | VRIALVGKY | 301 | 3.8000 | 43.68 |
| 2 | VRRLNLPFR | 272 | 3.6500 | 41.95 |
| 3 | YLNVDPGTM | 49 | 3.1000 | 35.63 |
| 4 | FVSGGVASS | 12 | 2.9000 | 33.33 |
| 5 | VVRRLNLPF | 271 | 2.9000 | 33.33 |
| 6 | LGGTMRLGS | 441 | 2.7000 | 31.03 |
| 7 | FVAFVGAAI | 537 | 2.4000 | 27.59 |
| 8 | FFLHVSLVP | 181 | 2.3000 | 26.44 |
| 9 | LLPVEIPEI | 552 | 1.9500 | 22.41 |
| 10 | VFFLHVSLV | 180 | 1.9000 | 21.84 |

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|---|---|---|---|---|
| 11 | FKHRAKVEI | 328 | 1.9000 | 21.84 |
| 12 | LGQLLTARG | 30 | 1.8000 | 20.69 |
| 13 | VVITEIGGT | 147 | 1.8000 | 20.69 |
| 14 | LVGKYVELS | 305 | 1.8000 | 20.69 |
| 15 | IRGIEGKIG | 368 | 1.8000 | 20.69 |
| 16 | YARARGLPV | 380 | 1.8000 | 20.69 |
| 17 | VQVIPHITD | 118 | 1.7000 | 19.54 |
| 18 | YDIPKVLHR | 256 | 1.7000 | 19.54 |
| 19 | LKNKIALMC | 231 | 1.6000 | 18.39 |
| 20 | FLHVSLVPY | 182 | 1.5000 | 17.24 |
| 21 | VHGVLIPGG | 357 | 1.4500 | 16.67 |
| 22 | VAALRSIGI | 206 | 1.4000 | 16.09 |
| 23 | YKAGELLPV | 547 | 1.4000 | 16.09 |
| 24 | LGLCLGLQC | 389 | 1.3000 | 14.94 |
| 25 | VEICWVASD | 334 | 1.2000 | 13.79 |
| 26 | LLTARGLHV | 33 | 1.1000 | 12.64 |
| 27 | LRSIGITPD | 209 | 1.1000 | 12.64 |
| 28 | LFVAFVGAA | 536 | 1.1000 | 12.64 |
| 29 | LVPYLAPSG | 187 | 1.0500 | 12.07 |
| 30 | IALVGKYVE | 303 | 1.0000 | 11.49 |
| 31 | YQTTQVSER | 464 | 1.0000 | 11.49 |
| 32 | VLGLCLGLQ | 388 | 0.9000 | 10.34 |
| 33 | MQKLDPYLN | 43 | 0.8000 | 9.20 |
| 34 | FVVRRLNLP | 270 | 0.8000 | 9.20 |
| 35 | IVIEAARSV | 398 | 0.8000 | 9.20 |
| 36 | LHVSLVPYL | 183 | 0.7100 | 8.16 |
| 37 | YLSVAEALR | 316 | 0.7000 | 8.05 |
| 38 | LSVAEALRA | 317 | 0.7000 | 8.05 |
| 39 | LPVLGLCLG | 386 | 0.7000 | 8.05 |
| 40 | ILAMAQPDA | 132 | 0.6500 | 7.47 |
| 41 | LRRVHEPHE | 291 | 0.5500 | 6.32 |
| 42 | FGIRGIEGK | 366 | 0.5000 | 5.75 |
| 43 | LQCIVIEAA | 395 | 0.5000 | 5.75 |
| 44 | YSTVIAKER | 101 | 0.4000 | 4.60 |

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|---|---|---|---|---|
| 45 | LKTKPTQHS | 197 | 0.4000 | 4.60 |
| 46 | MNPFQHGEV | 57 | 0.3000 | 3.45 |
| 47 | IKRRILAMA | 128 | 0.3000 | 3.45 |
| 48 | LTNANSAEF | 408 | 0.3000 | 3.45 |
| 49 | FVVGTQAHP | 516 | 0.3000 | 3.45 |
| 50 | FLDRNLPGS | 84 | 0.2500 | 2.87 |
| 51 | YLGDTVQVI | 113 | 0.2000 | 2.30 |
| 52 | FLEAARQVR | 164 | 0.2000 | 2.30 |
| 53 | WVASDGCET | 338 | 0.2000 | 2.30 |
| 54 | LRFSGTSPD | 492 | 0.2000 | 2.30 |
| 55 | VVGTQAHPE | 517 | 0.2000 | 2.30 |
| 56 | VELSDAYLS | 310 | 0.1000 | 1.15 |
| 57 | FVGAAIDYK | 540 | 0.1000 | 1.15 |

| ALLELE: DRB1_1301 | Threshold for 3 % with score: 2.6 | Highest Score achievable by any peptide: 8.8 |
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| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | LVGKYVELS | 305 | 4.4000 | 50.00 |
| 2 | IVIEAARSV | 398 | 4.0000 | 45.45 |
| 3 | VIAKERRGE | 104 | 3.8000 | 43.18 |
| 4 | VVRRLNLPF | 271 | 3.7000 | 42.05 |
| 5 | VRIALVGKY | 301 | 3.7000 | 42.05 |
| 6 | VRRLNLPFR | 272 | 3.5000 | 39.77 |
| 7 | LKTKPTQHS | 197 | 3.4000 | 38.64 |
| 8 | LKSRPTRPH | 526 | 3.0000 | 34.09 |
| 9 | VIPHITDEI | 120 | 2.8000 | 31.82 |
| 10 | LKNKIALMC | 231 | 2.8000 | 31.82 |
| 11 | VRHYLGRED | 171 | 2.7000 | 30.68 |
| 12 | LVPYLAPSG | 187 | 2.7000 | 30.68 |
| 13 | VFFLHVSLV | 180 | 2.6000 | 29.55 |
| 14 | LGLQCIVIE | 393 | 2.4000 | 27.27 |
| 15 | FFLHVSLVP | 181 | 2.3000 | 26.14 |
| 16 | FKHRAKVEI | 328 | 2.3000 | 26.14 |

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|---|---|---|---|---|
| 17 | IKRRILAMA | 128 | 2.2000 | 25.00 |
| 18 | VEICWVASD | 334 | 2.2000 | 25.00 |
| 19 | FVSGGVASS | 12 | 2.1000 | 23.86 |
| 20 | LGQLLTARG | 30 | 2.1000 | 23.86 |
| 21 | VGHYERFLD | 78 | 2.1000 | 23.86 |
| 22 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 23 | MRKHPQTAT | 0 | 2.0000 | 22.73 |
| 24 | IAYARARGL | 378 | 1.9600 | 22.27 |
| 25 | LGREDVFFL | 175 | 1.8600 | 21.14 |
| 26 | LDAFVVRRL | 267 | 1.8600 | 21.14 |
| 27 | FVVRRLNLP | 270 | 1.8000 | 20.45 |
| 28 | FVAFVGAAI | 537 | 1.8000 | 20.45 |
| 29 | LRFSGTSPD | 492 | 1.7000 | 19.32 |
| 30 | VLIPGGFGI | 360 | 1.5000 | 17.05 |
| 31 | IRGIEGKIG | 368 | 1.5000 | 17.05 |
| 32 | IPEHTPNGS | 560 | 1.5000 | 17.05 |
| 33 | LILRCDRDV | 219 | 1.4000 | 15.91 |
| 34 | VELSDAYLS | 310 | 1.4000 | 15.91 |
| 35 | VNNAYRDKI | 479 | 1.4000 | 15.91 |
| 36 | LHVSLVPYL | 183 | 1.3600 | 15.45 |
| 37 | MQKLDPYLN | 43 | 1.3000 | 14.77 |
| 38 | LTNANSAEF | 408 | 1.3000 | 14.77 |
| 39 | VVITEIGGT | 147 | 1.2000 | 13.64 |
| 40 | LGLCLGLQC | 389 | 1.2000 | 13.64 |
| 41 | VVGTQAHPE | 517 | 1.2000 | 13.64 |
| 42 | LLPVEIPEI | 552 | 1.2000 | 13.64 |
| 43 | LFVSGGVAS | 11 | 1.0000 | 11.36 |
| 44 | LLTARGLHV | 33 | 1.0000 | 11.36 |
| 45 | VTMQKLDPY | 41 | 1.0000 | 11.36 |
| 46 | ILAMAQPDA | 132 | 1.0000 | 11.36 |
| 47 | LRSIGITPD | 209 | 1.0000 | 11.36 |
| 48 | LPVLGLCLG | 386 | 1.0000 | 11.36 |
| 49 | LFVAFVGAA | 536 | 1.0000 | 11.36 |
| 50 | LGKGLTASS | 21 | 0.9000 | 10.23 |

| | | | | |
|---|---|---|---|---|
| 51 | ILRCDRDVP | 220 | 0.9000 | 10.23 |
| 52 | IALVGKYVE | 303 | 0.9000 | 10.23 |
| 53 | ITDEIKRRI | 124 | 0.7000 | 7.95 |
| 54 | VHGVLIPGG | 357 | 0.7000 | 7.95 |
| 55 | FGIRGIEGK | 366 | 0.7000 | 7.95 |
| 56 | LGSYPAVLE | 447 | 0.7000 | 7.95 |
| 57 | IAESGLRFS | 487 | 0.7000 | 7.95 |
| 58 | MNPFQHGEV | 57 | 0.6000 | 6.82 |

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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 | LVGKYVELS | 305 | 3.4000 | 38.64 |
| 2 | FFLHVSLVP | 181 | 3.3000 | 37.50 |
| 3 | FKHRAKVEI | 328 | 3.3000 | 37.50 |
| 4 | FVSGGVASS | 12 | 3.1000 | 35.23 |
| 5 | IVIEAARSV | 398 | 3.0000 | 34.09 |
| 6 | VIAKERRGE | 104 | 2.8000 | 31.82 |
| 7 | FVVRRLNLP | 270 | 2.8000 | 31.82 |
| 8 | FVAFVGAAI | 537 | 2.8000 | 31.82 |
| 9 | VVRRLNLPF | 271 | 2.7000 | 30.68 |
| 10 | VRIALVGKY | 301 | 2.7000 | 30.68 |
| 11 | VRRLNLPFR | 272 | 2.5000 | 28.41 |
| 12 | LKTKPTQHS | 197 | 2.4000 | 27.27 |
| 13 | LKSRPTRPH | 526 | 2.0000 | 22.73 |
| 14 | VIPHITDEI | 120 | 1.8000 | 20.45 |
| 15 | LKNKIALMC | 231 | 1.8000 | 20.45 |
| 16 | VRHYLGRED | 171 | 1.7000 | 19.32 |
| 17 | LVPYLAPSG | 187 | 1.7000 | 19.32 |
| 18 | FGIRGIEGK | 366 | 1.7000 | 19.32 |
| 19 | VFFLHVSLV | 180 | 1.6000 | 18.18 |
| 20 | LGLQCIVIE | 393 | 1.4000 | 15.91 |
| 21 | FVGAAIDYK | 540 | 1.3000 | 14.77 |

| | | | | |
|---|---|---|---|---|
| 22 | FQHGEVFVT | 60 | 1.2000 | 13.64 |
| 23 | YLGDTVQVI | 113 | 1.2000 | 13.64 |
| 24 | IKRRILAMA | 128 | 1.2000 | 13.64 |
| 25 | VEICWVASD | 334 | 1.2000 | 13.64 |
| 26 | LGQLLTARG | 30 | 1.1000 | 12.50 |
| 27 | VGHYERFLD | 78 | 1.1000 | 12.50 |
| 28 | LGGTMRLGS | 441 | 1.1000 | 12.50 |
| 29 | YRDKIAESG | 483 | 1.1000 | 12.50 |
| 30 | MRKHPQTAT | 0 | 1.0000 | 11.36 |
| 31 | IAYARARGL | 378 | 0.9600 | 10.91 |
| 32 | FLEAARQVR | 164 | 0.9000 | 10.23 |
| 33 | YQTTQVSER | 464 | 0.9000 | 10.23 |
| 34 | LGREDVFFL | 175 | 0.8600 | 9.77 |
| 35 | LDAFVVRRL | 267 | 0.8600 | 9.77 |
| 36 | YDIPKVLHR | 256 | 0.8000 | 9.09 |
| 37 | YLNVDPGTM | 49 | 0.7000 | 7.95 |
| 38 | FLDRNLPGS | 84 | 0.7000 | 7.95 |
| 39 | FLHVSLVPY | 182 | 0.7000 | 7.95 |
| 40 | YARARGLPV | 380 | 0.7000 | 7.95 |
| 41 | LRFSGTSPD | 492 | 0.7000 | 7.95 |
| 42 | VLIPGGFGI | 360 | 0.5000 | 5.68 |
| 43 | IRGIEGKIG | 368 | 0.5000 | 5.68 |
| 44 | FVVGTQAHP | 516 | 0.5000 | 5.68 |
| 45 | YKAGELLPV | 547 | 0.5000 | 5.68 |
| 46 | IPEHTPNGS | 560 | 0.5000 | 5.68 |
| 47 | LILRCDRDV | 219 | 0.4000 | 4.55 |
| 48 | VELSDAYLS | 310 | 0.4000 | 4.55 |
| 49 | VNNAYRDKI | 479 | 0.4000 | 4.55 |
| 50 | YERFLDRNL | 81 | 0.3600 | 4.09 |
| 51 | LHVSLVPYL | 183 | 0.3600 | 4.09 |
| 52 | MQKLDPYLN | 43 | 0.3000 | 3.41 |
| 53 | WVASDGCET | 338 | 0.3000 | 3.41 |
| 54 | LTNANSAEF | 408 | 0.3000 | 3.41 |
| 55 | VVITEIGGT | 147 | 0.2000 | 2.27 |

| | | | | |
|---|---|---|---|---|
| 56 | LGLCLGLQC | 389 | 0.2000 | 2.27 |
| 57 | VVGTQAHPE | 517 | 0.2000 | 2.27 |
| 58 | LLPVEIPEI | 552 | 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 | VIAKERRGE | 104 | 5.4000 | 60.00 |
| 2 | LKSRPTRPH | 526 | 4.8000 | 53.33 |
| 3 | VRHYLGRED | 171 | 4.3000 | 47.78 |
| 4 | LVGKYVELS | 305 | 4.0000 | 44.44 |
| 5 | LGLQCIVIE | 393 | 4.0000 | 44.44 |
| 6 | VEICWVASD | 334 | 3.8000 | 42.22 |
| 7 | VGHYERFLD | 78 | 3.7000 | 41.11 |
| 8 | VRIALVGKY | 301 | 3.5000 | 38.89 |
| 9 | IVIEAARSV | 398 | 3.3000 | 36.67 |
| 10 | LRFSGTSPD | 492 | 3.3000 | 36.67 |
| 11 | LKTKPTQHS | 197 | 3.0000 | 33.33 |
| 12 | LKNKIALMC | 231 | 2.8000 | 31.11 |
| 13 | VVGTQAHPE | 517 | 2.8000 | 31.11 |
| 14 | VVRRLNLPF | 271 | 2.7000 | 30.00 |
| 15 | LVPYLAPSG | 187 | 2.6000 | 28.89 |
| 16 | LRSIGITPD | 209 | 2.6000 | 28.89 |
| 17 | MQKLDPYLN | 43 | 2.5000 | 27.78 |
| 18 | IALVGKYVE | 303 | 2.5000 | 27.78 |
| 19 | LGSYPAVLE | 447 | 2.3000 | 25.56 |
| 20 | MRKHPQTAT | 0 | 2.2000 | 24.44 |
| 21 | IKRRILAMA | 128 | 2.2000 | 24.44 |
| 22 | VIPHITDEI | 120 | 2.1000 | 23.33 |
| 23 | LLRRVHEPH | 290 | 2.1000 | 23.33 |
| 24 | LGQLLTARG | 30 | 2.0000 | 22.22 |
| 25 | VYSTVIAKE | 100 | 2.0000 | 22.22 |
| 26 | VRRLNLPFR | 272 | 2.0000 | 22.22 |

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|---|---|---|---|---|
| 27 | IAYARARGL | 378 | 2.0000 | 22.22 |
| 28 | LGREDVFFL | 175 | 1.9000 | 21.11 |
| 29 | VFFLHVSLV | 180 | 1.9000 | 21.11 |
| 30 | LDAFVVRRL | 267 | 1.9000 | 21.11 |
| 31 | FVSGGVASS | 12 | 1.7000 | 18.89 |
| 32 | FFLHVSLVP | 181 | 1.7000 | 18.89 |
| 33 | LGGTMRLGS | 441 | 1.7000 | 18.89 |
| 34 | VPYLAPSGE | 188 | 1.6000 | 17.78 |
| 35 | FKHRAKVEI | 328 | 1.6000 | 17.78 |
| 36 | VLGLCLGLQ | 388 | 1.6000 | 17.78 |
| 37 | VEIPEIPEH | 555 | 1.6000 | 17.78 |
| 38 | VQVIPHITD | 118 | 1.5000 | 16.67 |
| 39 | IYDIPKVLH | 255 | 1.5000 | 16.67 |
| 40 | LAMAQPDAD | 133 | 1.4000 | 15.56 |
| 41 | VVITEIGGT | 147 | 1.4000 | 15.56 |
| 42 | LHVSLVPYL | 183 | 1.4000 | 15.56 |
| 43 | LRRVHEPHE | 291 | 1.4000 | 15.56 |
| 44 | IRGIEGKIG | 368 | 1.4000 | 15.56 |
| 45 | LEPDSVVAQ | 454 | 1.4000 | 15.56 |
| 46 | FVVRRLNLP | 270 | 1.2000 | 13.33 |
| 47 | LGLCLGLQC | 389 | 1.2000 | 13.33 |
| 48 | FVAFVGAAI | 537 | 1.1000 | 12.22 |
| 49 | IPEHTPNGS | 560 | 1.1000 | 12.22 |
| 50 | ILAMAQPDA | 132 | 1.0000 | 11.11 |
| 51 | LEAARQVRH | 165 | 1.0000 | 11.11 |
| 52 | IPKVLHREE | 258 | 1.0000 | 11.11 |
| 53 | VELSDAYLS | 310 | 1.0000 | 11.11 |
| 54 | LFVAFVGAA | 536 | 1.0000 | 11.11 |
| 55 | LHVTMQKLD | 39 | 0.9000 | 10.00 |
| 56 | VGKYVELSD | 306 | 0.9000 | 10.00 |
| 57 | LPVLGLCLG | 386 | 0.9000 | 10.00 |
| 58 | VAFVGAAID | 538 | 0.9000 | 10.00 |

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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 | VRIALVGKY | 301 | 3.8000 | 43.68 |
| 2 | VRRLNLPFR | 272 | 3.6500 | 41.95 |
| 3 | YLNVDPGTM | 49 | 3.1000 | 35.63 |
| 4 | FVSGGVASS | 12 | 2.9000 | 33.33 |
| 5 | VVRRLNLPF | 271 | 2.9000 | 33.33 |
| 6 | LGGTMRLGS | 441 | 2.7000 | 31.03 |
| 7 | FVAFVGAAI | 537 | 2.4000 | 27.59 |
| 8 | FFLHVSLVP | 181 | 2.3000 | 26.44 |
| 9 | LLPVEIPEI | 552 | 1.9500 | 22.41 |
| 10 | VFFLHVSLV | 180 | 1.9000 | 21.84 |
| 11 | FKHRAKVEI | 328 | 1.9000 | 21.84 |
| 12 | LGQLLTARG | 30 | 1.8000 | 20.69 |
| 13 | VVITEIGGT | 147 | 1.8000 | 20.69 |
| 14 | LVGKYVELS | 305 | 1.8000 | 20.69 |
| 15 | IRGIEGKIG | 368 | 1.8000 | 20.69 |
| 16 | YARARGLPV | 380 | 1.8000 | 20.69 |
| 17 | VQVIPHITD | 118 | 1.7000 | 19.54 |
| 18 | YDIPKVLHR | 256 | 1.7000 | 19.54 |
| 19 | LKNKIALMC | 231 | 1.6000 | 18.39 |
| 20 | FLHVSLVPY | 182 | 1.5000 | 17.24 |
| 21 | VHGVLIPGG | 357 | 1.4500 | 16.67 |
| 22 | VAALRSIGI | 206 | 1.4000 | 16.09 |
| 23 | YKAGELLPV | 547 | 1.4000 | 16.09 |
| 24 | LGLCLGLQC | 389 | 1.3000 | 14.94 |
| 25 | VEICWVASD | 334 | 1.2000 | 13.79 |
| 26 | LLTARGLHV | 33 | 1.1000 | 12.64 |
| 27 | LRSIGITPD | 209 | 1.1000 | 12.64 |
| 28 | LFVAFVGAA | 536 | 1.1000 | 12.64 |
| 29 | LVPYLAPSG | 187 | 1.0500 | 12.07 |
| 30 | IALVGKYVE | 303 | 1.0000 | 11.49 |
| 31 | YQTTQVSER | 464 | 1.0000 | 11.49 |

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|---|---|---|---|---|
| 32 | VLGLCLGLQ | 388 | 0.9000 | 10.34 |
| 33 | MQKLDPYLN | 43 | 0.8000 | 9.20 |
| 34 | FVVRRLNLP | 270 | 0.8000 | 9.20 |
| 35 | IVIEAARSV | 398 | 0.8000 | 9.20 |
| 36 | LHVSLVPYL | 183 | 0.7100 | 8.16 |
| 37 | YLSVAEALR | 316 | 0.7000 | 8.05 |
| 38 | LSVAEALRA | 317 | 0.7000 | 8.05 |
| 39 | LPVLGLCLG | 386 | 0.7000 | 8.05 |
| 40 | ILAMAQPDA | 132 | 0.6500 | 7.47 |
| 41 | LRRVHEPHE | 291 | 0.5500 | 6.32 |
| 42 | FGIRGIEGK | 366 | 0.5000 | 5.75 |
| 43 | LQCIVIEAA | 395 | 0.5000 | 5.75 |
| 44 | YSTVIAKER | 101 | 0.4000 | 4.60 |
| 45 | LKTKPTQHS | 197 | 0.4000 | 4.60 |
| 46 | MNPFQHGEV | 57 | 0.3000 | 3.45 |
| 47 | IKRRILAMA | 128 | 0.3000 | 3.45 |
| 48 | LTNANSAEF | 408 | 0.3000 | 3.45 |
| 49 | FVVGTQAHP | 516 | 0.3000 | 3.45 |
| 50 | FLDRNLPGS | 84 | 0.2500 | 2.87 |
| 51 | YLGDTVQVI | 113 | 0.2000 | 2.30 |
| 52 | FLEAARQVR | 164 | 0.2000 | 2.30 |
| 53 | WVASDGCET | 338 | 0.2000 | 2.30 |
| 54 | LRFSGTSPD | 492 | 0.2000 | 2.30 |
| 55 | VVGTQAHPE | 517 | 0.2000 | 2.30 |
| 56 | VELSDAYLS | 310 | 0.1000 | 1.15 |
| 57 | FVGAAIDYK | 540 | 0.1000 | 1.15 |

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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 | FVSGGVASS | 12 | 2.5000 | 36.76 |
| 2 | VRIALVGKY | 301 | 2.4000 | 35.29 |
| 3 | YLNVDPGTM | 49 | 1.5000 | 22.06 |

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|---|---|---|---|---|
| 4 | VLGLCLGLQ | 388 | 1.5000 | 22.06 |
| 5 | FVAFVGAAI | 537 | 1.5000 | 22.06 |
| 6 | VVITEIGGT | 147 | 1.0000 | 14.71 |
| 7 | VRRLNLPFR | 272 | 1.0000 | 14.71 |
| 8 | LFVAFVGAA | 536 | 1.0000 | 14.71 |
| 9 | VFFLHVSLV | 180 | 0.9000 | 13.24 |
| 10 | FKHRAKVEI | 328 | 0.5000 | 7.35 |
| 11 | LGGTMRLGS | 441 | 0.5000 | 7.35 |
| 12 | LGQLLTARG | 30 | 0.4000 | 5.88 |
| 13 | IKRRILAMA | 128 | 0.3000 | 4.41 |
| 14 | LVGKYVELS | 305 | 0.3000 | 4.41 |
| 15 | FVGAAIDYK | 540 | 0.3000 | 4.41 |
| 16 | VEICWVASD | 334 | 0.1000 | 1.47 |
| 17 | LKTKPTQHS | 197 | -0.1000 | 0 |
| 18 | LLPVEIPEI | 552 | -0.1000 | 0 |
| 19 | LKSRPTRPH | 526 | -0.1200 | 0 |
| 20 | LKNKIALMC | 231 | -0.2000 | 0 |
| 21 | IRGIEGKIG | 368 | -0.2000 | 0 |
| 22 | IYDIPKVLH | 255 | -0.2200 | 0 |
| 23 | FLHVSLVPY | 182 | -0.3000 | 0 |
| 24 | IVIEAARSV | 398 | -0.4000 | 0 |
| 25 | ILAMAQPDA | 132 | -0.5000 | 0 |
| 26 | FFLHVSLVP | 181 | -0.5000 | 0 |
| 27 | FVVRRLNLP | 270 | -0.5000 | 0 |
| 28 | WVASDGCET | 338 | -0.5000 | 0 |
| 29 | LGLCLGLQC | 389 | -0.5000 | 0 |
| 30 | YQTTQVSER | 464 | -0.5000 | 0 |
| 31 | LQCIVIEAA | 395 | -0.6000 | 0 |
| 32 | LGKGLTASS | 21 | -0.7000 | 0 |
| 33 | MQKLDPYLN | 43 | -0.7000 | 0 |
| 34 | FGIRGIEGK | 366 | -0.7000 | 0 |
| 35 | LPVLGLCLG | 386 | -0.7000 | 0 |
| 36 | FVVGTQAHP | 516 | -0.7000 | 0 |
| 37 | MNPFQHGEV | 57 | -0.8000 | 0 |

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|---|---|---|---|---|
| 38 | YLGDTVQVI | 113 | -0.8000 | 0 |
| 39 | VVRRLNLPF | 271 | -0.8000 | 0 |
| 40 | YLSVAEALR | 316 | -0.8000 | 0 |
| 41 | LRFSGTSPD | 492 | -0.9000 | 0 |
| 42 | VQVIPHITD | 118 | -1.0000 | 0 |
| 43 | VELSDAYLS | 310 | -1.0000 | 0 |
| 44 | IGAIAYARA | 375 | -1.0000 | 0 |
| 45 | YARARGLPV | 380 | -1.0000 | 0 |
| 46 | WDDLLRRVH | 287 | -1.0200 | 0 |
| 47 | VAALRSIGI | 206 | -1.1000 | 0 |
| 48 | LRSIGITPD | 209 | -1.1000 | 0 |
| 49 | IALVGKYVE | 303 | -1.1000 | 0 |
| 50 | LSVAEALRA | 317 | -1.1000 | 0 |
| 51 | VHGVLIPGG | 357 | -1.1000 | 0 |
| 52 | FQHGEVFVT | 60 | -1.2000 | 0 |
| 53 | FLDRNLPGS | 84 | -1.3000 | 0 |
| 54 | FLEAARQVR | 164 | -1.4000 | 0 |
| 55 | LHVSLVPYL | 183 | -1.4000 | 0 |
| 56 | YVELSDAYL | 309 | -1.4000 | 0 |
| 57 | VGLTNANSA | 406 | -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 | VRIALVGKY | 301 | 3.5000 | 42.17 |
| 2 | LGGTMRLGS | 441 | 3.3000 | 39.76 |
| 3 | VRRLNLPFR | 272 | 3.1500 | 37.95 |
| 4 | LKNKIALMC | 231 | 2.6000 | 31.33 |
| 5 | VLGLCLGLQ | 388 | 2.6000 | 31.33 |
| 6 | LVGKYVELS | 305 | 2.4000 | 28.92 |
| 7 | LGLCLGLQC | 389 | 2.3000 | 27.71 |
| 8 | VVITEIGGT | 147 | 2.1000 | 25.30 |
| 9 | LFVAFVGAA | 536 | 2.1000 | 25.30 |

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|---|---|---|---|---|
| 10 | LLPVEIPEI | 552 | 2.0500 | 24.70 |
| 11 | VVRRLNLPF | 271 | 2.0000 | 24.10 |
| 12 | VFFLHVSLV | 180 | 1.9000 | 22.89 |
| 13 | LSVAEALRA | 317 | 1.7000 | 20.48 |
| 14 | ILAMAQPDA | 132 | 1.6500 | 19.88 |
| 15 | VQVIPHITD | 118 | 1.6000 | 19.28 |
| 16 | FVSGGVASS | 12 | 1.5000 | 18.07 |
| 17 | VAALRSIGI | 206 | 1.5000 | 18.07 |
| 18 | LQCIVIEAA | 395 | 1.5000 | 18.07 |
| 19 | LGQLLTARG | 30 | 1.4000 | 16.87 |
| 20 | IRGIEGKIG | 368 | 1.4000 | 16.87 |
| 21 | IKRRILAMA | 128 | 1.3000 | 15.66 |
| 22 | IYDIPKVLH | 255 | 1.2800 | 15.42 |
| 23 | LLTARGLHV | 33 | 1.1000 | 13.25 |
| 24 | VEICWVASD | 334 | 1.1000 | 13.25 |
| 25 | LKSRPTRPH | 526 | 1.0800 | 13.01 |
| 26 | VHGVLIPGG | 357 | 1.0500 | 12.65 |
| 27 | MQKLDPYLN | 43 | 1.0000 | 12.05 |
| 28 | LKTKPTQHS | 197 | 1.0000 | 12.05 |
| 29 | LRSIGITPD | 209 | 1.0000 | 12.05 |
| 30 | IVIEAARSV | 398 | 0.8000 | 9.64 |
| 31 | LHVSLVPYL | 183 | 0.7500 | 9.04 |
| 32 | VELSDAYLS | 310 | 0.7000 | 8.43 |
| 33 | LVPYLAPSG | 187 | 0.6500 | 7.83 |
| 34 | VEIPEIPEH | 555 | 0.6300 | 7.59 |
| 35 | YLNVDPGTM | 49 | 0.6000 | 7.23 |
| 36 | VLHREELDA | 261 | 0.6000 | 7.23 |
| 37 | IALVGKYVE | 303 | 0.6000 | 7.23 |
| 38 | FVAFVGAAI | 537 | 0.5000 | 6.02 |
| 39 | LGKGLTASS | 21 | 0.3000 | 3.61 |
| 40 | MNPFQHGEV | 57 | 0.3000 | 3.61 |
| 41 | FFLHVSLVP | 181 | 0.3000 | 3.61 |
| 42 | LPVLGLCLG | 386 | 0.3000 | 3.61 |
| 43 | LRRVHEPHE | 291 | 0.1500 | 1.81 |

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|---|---|---|---|---|
| 44 | LRFSGTSPD | 492 | 0.1000 | 1.20 |
| 45 | VSLVPYLAP | 185 | -0.1000 | 0 |
| 46 | VGLTNANSA | 406 | -0.1000 | 0 |
| 47 | YARARGLPV | 380 | -0.2000 | 0 |
| 48 | LEPDSVVAQ | 454 | -0.2000 | 0 |
| 49 | VVGTQAHPE | 517 | -0.2000 | 0 |
| 50 | LLRRVHEPH | 290 | -0.3200 | 0 |
| 51 | LDRNLPGSA | 85 | -0.5000 | 0 |
| 52 | VYSTVIAKE | 100 | -0.5000 | 0 |
| 53 | VIAKERRGE | 104 | -0.5000 | 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 | VRIALVGKY | 301 | 3.6000 | 40.45 |
| 2 | VQVIPHITD | 118 | 3.3000 | 37.08 |
| 3 | VEICWVASD | 334 | 2.8000 | 31.46 |
| 4 | YLNVDPGTM | 49 | 2.7000 | 30.34 |
| 5 | LRSIGITPD | 209 | 2.7000 | 30.34 |
| 6 | IALVGKYVE | 303 | 2.6000 | 29.21 |
| 7 | FVSGGVASS | 12 | 2.5000 | 28.09 |
| 8 | VLGLCLGLQ | 388 | 2.4000 | 26.97 |
| 9 | LGGTMRLGS | 441 | 2.3000 | 25.84 |
| 10 | VRRLNLPFR | 272 | 2.1500 | 24.16 |
| 11 | LRRVHEPHE | 291 | 2.1500 | 24.16 |
| 12 | MQKLDPYLN | 43 | 2.0000 | 22.47 |
| 13 | VVITEIGGT | 147 | 2.0000 | 22.47 |
| 14 | VVRRLNLPF | 271 | 1.9000 | 21.35 |
| 15 | LRFSGTSPD | 492 | 1.8000 | 20.22 |
| 16 | VVGTQAHPE | 517 | 1.8000 | 20.22 |
| 17 | LGQLLTARG | 30 | 1.7000 | 19.10 |
| 18 | FFLHVSLVP | 181 | 1.7000 | 19.10 |
| 19 | IRGIEGKIG | 368 | 1.7000 | 19.10 |

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|---|---|---|---|---|
| 20 | FVAFVGAAI | 537 | 1.7000 | 19.10 |
| 21 | LKNKIALMC | 231 | 1.6000 | 17.98 |
| 22 | VYSTVIAKE | 100 | 1.5000 | 16.85 |
| 23 | VIAKERRGE | 104 | 1.5000 | 16.85 |
| 24 | IYDIPKVLH | 255 | 1.5000 | 16.85 |
| 25 | LGLQCIVIE | 393 | 1.5000 | 16.85 |
| 26 | LVGKYVELS | 305 | 1.4000 | 15.73 |
| 27 | VHGVLIPGG | 357 | 1.3500 | 15.17 |
| 28 | FLHVSLVPY | 182 | 1.3000 | 14.61 |
| 29 | LGLCLGLQC | 389 | 1.3000 | 14.61 |
| 30 | LKSRPTRPH | 526 | 1.3000 | 14.61 |
| 31 | LLPVEIPEI | 552 | 1.2500 | 14.04 |
| 32 | VFFLHVSLV | 180 | 1.2000 | 13.48 |
| 33 | FKHRAKVEI | 328 | 1.2000 | 13.48 |
| 34 | YEVNNAYRD | 477 | 1.2000 | 13.48 |
| 35 | VAFVGAAID | 538 | 1.2000 | 13.48 |
| 36 | YARARGLPV | 380 | 1.1000 | 12.36 |
| 37 | LFVAFVGAA | 536 | 1.1000 | 12.36 |
| 38 | LVPYLAPSG | 187 | 0.9500 | 10.67 |
| 39 | VPYLAPSGE | 188 | 0.9000 | 10.11 |
| 40 | VEIPEIPEH | 555 | 0.8500 | 9.55 |
| 41 | LHVSLVPYL | 183 | 0.7500 | 8.43 |
| 42 | VAALRSIGI | 206 | 0.7000 | 7.87 |
| 43 | LSVAEALRA | 317 | 0.7000 | 7.87 |
| 44 | YKAGELLPV | 547 | 0.7000 | 7.87 |
| 45 | ILAMAQPDA | 132 | 0.6500 | 7.30 |
| 46 | VGHYERFLD | 78 | 0.6000 | 6.74 |
| 47 | VRHYLGRED | 171 | 0.6000 | 6.74 |
| 48 | LPVLGLCLG | 386 | 0.6000 | 6.74 |
| 49 | LQCIVIEAA | 395 | 0.5000 | 5.62 |
| 50 | LLTARGLHV | 33 | 0.4000 | 4.49 |
| 51 | WDDLLRRVH | 287 | 0.4000 | 4.49 |
| 52 | WVASDGCET | 338 | 0.4000 | 4.49 |
| 53 | IKRRILAMA | 128 | 0.3000 | 3.37 |

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|---|---|---|---|---|
| 54 | LHVTMQKLD | 39 | 0.2000 | 2.25 |
| 55 | FQHGEVFVT | 60 | 0.2000 | 2.25 |
| 56 | YDIPKVLHR | 256 | 0.2000 | 2.25 |
| 57 | FVVRRLNLP | 270 | 0.2000 | 2.25 |
| 58 | IVIEAARSV | 398 | 0.1000 | 1.12 |

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

| Rank | Sequence | At Position | Score | % of Highest Score |
|---|---|---|---|---|
| 1 | LVGKYVELS | 305 | 4.0000 | 47.62 |
| 2 | LKSRPTRPH | 526 | 3.5800 | 42.62 |
| 3 | LKTKPTQHS | 197 | 3.0000 | 35.71 |
| 4 | IVIEAARSV | 398 | 3.0000 | 35.71 |
| 5 | LKNKIALMC | 231 | 2.8000 | 33.33 |
| 6 | VIAKERRGE | 104 | 2.4000 | 28.57 |
| 7 | VRIALVGKY | 301 | 2.4000 | 28.57 |
| 8 | IKRRILAMA | 128 | 2.2000 | 26.19 |
| 9 | VRRLNLPFR | 272 | 2.0000 | 23.81 |
| 10 | VIPHITDEI | 120 | 1.9000 | 22.62 |
| 11 | VVRRLNLPF | 271 | 1.8000 | 21.43 |
| 12 | FVSGGVASS | 12 | 1.7000 | 20.24 |
| 13 | LGGTMRLGS | 441 | 1.7000 | 20.24 |
| 14 | VRHYLGRED | 171 | 1.6000 | 19.05 |
| 15 | VFFLHVSLV | 180 | 1.6000 | 19.05 |
| 16 | FKHRAKVEI | 328 | 1.4000 | 16.67 |
| 17 | MRKHPQTAT | 0 | 1.3000 | 15.48 |
| 18 | FFLHVSLVP | 181 | 1.3000 | 15.48 |
| 19 | LVPYLAPSG | 187 | 1.3000 | 15.48 |
| 20 | LGLCLGLQC | 389 | 1.2000 | 14.29 |
| 21 | VEICWVASD | 334 | 1.1000 | 13.10 |
| 22 | IPEHTPNGS | 560 | 1.1000 | 13.10 |
| 23 | VGHYERFLD | 78 | 1.0000 | 11.90 |
| 24 | ILAMAQPDA | 132 | 1.0000 | 11.90 |

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|---|---|---|---|---|
| 25 | VELSDAYLS | 310 | 1.0000 | 11.90 |
| 26 | IAYARARGL | 378 | 1.0000 | 11.90 |
| 27 | LGLQCIVIE | 393 | 1.0000 | 11.90 |
| 28 | LFVAFVGAA | 536 | 1.0000 | 11.90 |
| 29 | LGREDVFFL | 175 | 0.9000 | 10.71 |
| 30 | LDAFVVRRL | 267 | 0.9000 | 10.71 |
| 31 | FVAFVGAAI | 537 | 0.9000 | 10.71 |
| 32 | LLRRVHEPH | 290 | 0.8800 | 10.48 |
| 33 | FVVRRLNLP | 270 | 0.8000 | 9.52 |
| 34 | VLGLCLGLQ | 388 | 0.8000 | 9.52 |
| 35 | LGQLLTARG | 30 | 0.7000 | 8.33 |
| 36 | LFVSGGVAS | 11 | 0.6000 | 7.14 |
| 37 | LSVAEALRA | 317 | 0.6000 | 7.14 |
| 38 | VLIPGGFGI | 360 | 0.6000 | 7.14 |
| 39 | FGIRGIEGK | 366 | 0.6000 | 7.14 |
| 40 | LEPDSVVAQ | 454 | 0.6000 | 7.14 |
| 41 | LRFSGTSPD | 492 | 0.6000 | 7.14 |
| 42 | LGKGLTASS | 21 | 0.5000 | 5.95 |
| 43 | MQKLDPYLN | 43 | 0.5000 | 5.95 |
| 44 | VVITEIGGT | 147 | 0.5000 | 5.95 |
| 45 | VGLTNANSA | 406 | 0.5000 | 5.95 |
| 46 | VNNAYRDKI | 479 | 0.5000 | 5.95 |
| 47 | LHVSLVPYL | 183 | 0.4000 | 4.76 |
| 48 | LILRCDRDV | 219 | 0.4000 | 4.76 |
| 49 | VLHREELDA | 261 | 0.4000 | 4.76 |
| 50 | IEGKIGAIA | 371 | 0.4000 | 4.76 |
| 51 | VEIPEIPEH | 555 | 0.3800 | 4.52 |
| 52 | LQCIVIEAA | 395 | 0.3000 | 3.57 |
| 53 | IAESGLRFS | 487 | 0.3000 | 3.57 |
| 54 | LLPVEIPEI | 552 | 0.3000 | 3.57 |
| 55 | IYDIPKVLH | 255 | 0.2800 | 3.33 |
| 56 | FVGAAIDYK | 540 | 0.2000 | 2.38 |
| 57 | IRGIEGKIG | 368 | 0.1000 | 1.19 |

| 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 | LVGKYVELS | 305 | 3.0000 | 35.71 |
| 2 | FVSGGVASS | 12 | 2.7000 | 32.14 |
| 3 | LKSRPTRPH | 526 | 2.5800 | 30.71 |
| 4 | FKHRAKVEI | 328 | 2.4000 | 28.57 |
| 5 | FFLHVSLVP | 181 | 2.3000 | 27.38 |
| 6 | LKTKPTQHS | 197 | 2.0000 | 23.81 |
| 7 | IVIEAARSV | 398 | 2.0000 | 23.81 |
| 8 | FVAFVGAAI | 537 | 1.9000 | 22.62 |
| 9 | LKNKIALMC | 231 | 1.8000 | 21.43 |
| 10 | FVVRRLNLP | 270 | 1.8000 | 21.43 |
| 11 | FGIRGIEGK | 366 | 1.6000 | 19.05 |
| 12 | VIAKERRGE | 104 | 1.4000 | 16.67 |
| 13 | VRIALVGKY | 301 | 1.4000 | 16.67 |
| 14 | IKRRILAMA | 128 | 1.2000 | 14.29 |
| 15 | FVGAAIDYK | 540 | 1.2000 | 14.29 |
| 16 | VRRLNLPFR | 272 | 1.0000 | 11.90 |
| 17 | VIPHITDEI | 120 | 0.9000 | 10.71 |
| 18 | VVRRLNLPF | 271 | 0.8000 | 9.52 |
| 19 | LGGTMRLGS | 441 | 0.7000 | 8.33 |
| 20 | VRHYLGRED | 171 | 0.6000 | 7.14 |
| 21 | VFFLHVSLV | 180 | 0.6000 | 7.14 |
| 22 | FQHGEVFVT | 60 | 0.5000 | 5.95 |
| 23 | FVEYPPDRH | 506 | 0.3800 | 4.52 |
| 24 | MRKHPQTAT | 0 | 0.3000 | 3.57 |
| 25 | FLDRNLPGS | 84 | 0.3000 | 3.57 |
| 26 | YLGDTVQVI | 113 | 0.3000 | 3.57 |
| 27 | LVPYLAPSG | 187 | 0.3000 | 3.57 |
| 28 | LGLCLGLQC | 389 | 0.2000 | 2.38 |
| 29 | VEICWVASD | 334 | 0.1000 | 1.19 |
| 30 | IPEHTPNGS | 560 | 0.1000 | 1.19 |

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|---|---|---|---|---|
| 31 | WDDLLRRVH | 287 | 0.0800 | 0.95 |
| 32 | LGREDVFFL | 175 | -0.1000 | 0 |
| 33 | LDAFVVRRL | 267 | -0.1000 | 0 |
| 34 | LLRRVHEPH | 290 | -0.1200 | 0 |
| 35 | VLGLCLGLQ | 388 | -0.2000 | 0 |
| 36 | LGQLLTARG | 30 | -0.3000 | 0 |
| 37 | YARARGLPV | 380 | -0.3000 | 0 |
| 38 | YRDKIAESG | 483 | -0.3000 | 0 |
| 39 | LFVSGGVAS | 11 | -0.4000 | 0 |
| 40 | LSVAEALRA | 317 | -0.4000 | 0 |
| 41 | WVASDGCET | 338 | -0.4000 | 0 |
| 42 | VLIPGGFGI | 360 | -0.4000 | 0 |
| 43 | LEPDSVVAQ | 454 | -0.4000 | 0 |
| 44 | LRFSGTSPD | 492 | -0.4000 | 0 |
| 45 | LGKGLTASS | 21 | -0.5000 | 0 |
| 46 | MQKLDPYLN | 43 | -0.5000 | 0 |
| 47 | VVITEIGGT | 147 | -0.5000 | 0 |
| 48 | VGLTNANSA | 406 | -0.5000 | 0 |
| 49 | VNNAYRDKI | 479 | -0.5000 | 0 |
| 50 | FVVGTQAHP | 516 | -0.5000 | 0 |
| 51 | YKAGELLPV | 547 | -0.5000 | 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 | LVGKYVELS | 305 | 4.4000 | 50.00 |
| 2 | IVIEAARSV | 398 | 4.0000 | 45.45 |
| 3 | VIAKERRGE | 104 | 3.8000 | 43.18 |
| 4 | VVRRLNLPF | 271 | 3.7000 | 42.05 |
| 5 | VRIALVGKY | 301 | 3.7000 | 42.05 |
| 6 | VRRLNLPFR | 272 | 3.5000 | 39.77 |
| 7 | LKTKPTQHS | 197 | 3.4000 | 38.64 |
| 8 | LKSRPTRPH | 526 | 3.0000 | 34.09 |

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|---|---|---|---|---|
| 9 | VIPHITDEI | 120 | 2.8000 | 31.82 |
| 10 | LKNKIALMC | 231 | 2.8000 | 31.82 |
| 11 | VRHYLGRED | 171 | 2.7000 | 30.68 |
| 12 | LVPYLAPSG | 187 | 2.7000 | 30.68 |
| 13 | VFFLHVSLV | 180 | 2.6000 | 29.55 |
| 14 | LGLQCIVIE | 393 | 2.4000 | 27.27 |
| 15 | FFLHVSLVP | 181 | 2.3000 | 26.14 |
| 16 | FKHRAKVEI | 328 | 2.3000 | 26.14 |
| 17 | IKRRILAMA | 128 | 2.2000 | 25.00 |
| 18 | VEICWVASD | 334 | 2.2000 | 25.00 |
| 19 | FVSGGVASS | 12 | 2.1000 | 23.86 |
| 20 | LGQLLTARG | 30 | 2.1000 | 23.86 |
| 21 | VGHYERFLD | 78 | 2.1000 | 23.86 |
| 22 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 23 | MRKHPQTAT | 0 | 2.0000 | 22.73 |
| 24 | IAYARARGL | 378 | 1.9600 | 22.27 |
| 25 | LGREDVFFL | 175 | 1.8600 | 21.14 |
| 26 | LDAFVVRRL | 267 | 1.8600 | 21.14 |
| 27 | FVVRRLNLP | 270 | 1.8000 | 20.45 |
| 28 | FVAFVGAAI | 537 | 1.8000 | 20.45 |
| 29 | LRFSGTSPD | 492 | 1.7000 | 19.32 |
| 30 | VLIPGGFGI | 360 | 1.5000 | 17.05 |
| 31 | IRGIEGKIG | 368 | 1.5000 | 17.05 |
| 32 | IPEHTPNGS | 560 | 1.5000 | 17.05 |
| 33 | LILRCDRDV | 219 | 1.4000 | 15.91 |
| 34 | VELSDAYLS | 310 | 1.4000 | 15.91 |
| 35 | VNNAYRDKI | 479 | 1.4000 | 15.91 |
| 36 | LHVSLVPYL | 183 | 1.3600 | 15.45 |
| 37 | MQKLDPYLN | 43 | 1.3000 | 14.77 |
| 38 | LTNANSAEF | 408 | 1.3000 | 14.77 |
| 39 | VVITEIGGT | 147 | 1.2000 | 13.64 |
| 40 | LGLCLGLQC | 389 | 1.2000 | 13.64 |
| 41 | VVGTQAHPE | 517 | 1.2000 | 13.64 |
| 42 | LLPVEIPEI | 552 | 1.2000 | 13.64 |

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|---|---|---|---|---|
| 43 | LFVSGGVAS | 11 | 1.0000 | 11.36 |
| 44 | LLTARGLHV | 33 | 1.0000 | 11.36 |
| 45 | VTMQKLDPY | 41 | 1.0000 | 11.36 |
| 46 | ILAMAQPDA | 132 | 1.0000 | 11.36 |
| 47 | LRSIGITPD | 209 | 1.0000 | 11.36 |
| 48 | LPVLGLCLG | 386 | 1.0000 | 11.36 |
| 49 | LFVAFVGAA | 536 | 1.0000 | 11.36 |
| 50 | LGKGLTASS | 21 | 0.9000 | 10.23 |
| 51 | ILRCDRDVP | 220 | 0.9000 | 10.23 |
| 52 | IALVGKYVE | 303 | 0.9000 | 10.23 |
| 53 | ITDEIKRRI | 124 | 0.7000 | 7.95 |
| 54 | VHGVLIPGG | 357 | 0.7000 | 7.95 |
| 55 | FGIRGIEGK | 366 | 0.7000 | 7.95 |
| 56 | LGSYPAVLE | 447 | 0.7000 | 7.95 |
| 57 | IAESGLRFS | 487 | 0.7000 | 7.95 |
| 58 | MNPFQHGEV | 57 | 0.6000 | 6.82 |

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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 | LVGKYVELS | 305 | 4.4000 | 50.00 |
| 2 | IVIEAARSV | 398 | 4.0000 | 45.45 |
| 3 | VIAKERRGE | 104 | 3.8000 | 43.18 |
| 4 | VVRRLNLPF | 271 | 3.7000 | 42.05 |
| 5 | VRIALVGKY | 301 | 3.7000 | 42.05 |
| 6 | VRRLNLPFR | 272 | 3.5000 | 39.77 |
| 7 | LKTKPTQHS | 197 | 3.4000 | 38.64 |
| 8 | LKSRPTRPH | 526 | 3.0000 | 34.09 |
| 9 | VIPHITDEI | 120 | 2.8000 | 31.82 |
| 10 | LKNKIALMC | 231 | 2.8000 | 31.82 |
| 11 | VRHYLGRED | 171 | 2.7000 | 30.68 |
| 12 | LVPYLAPSG | 187 | 2.7000 | 30.68 |
| 13 | VFFLHVSLV | 180 | 2.6000 | 29.55 |

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|---|---|---|---|---|
| 14 | LGLQCIVIE | 393 | 2.4000 | 27.27 |
| 15 | FFLHVSLVP | 181 | 2.3000 | 26.14 |
| 16 | FKHRAKVEI | 328 | 2.3000 | 26.14 |
| 17 | IKRRILAMA | 128 | 2.2000 | 25.00 |
| 18 | VEICWVASD | 334 | 2.2000 | 25.00 |
| 19 | FVSGGVASS | 12 | 2.1000 | 23.86 |
| 20 | LGQLLTARG | 30 | 2.1000 | 23.86 |
| 21 | VGHYERFLD | 78 | 2.1000 | 23.86 |
| 22 | LGGTMRLGS | 441 | 2.1000 | 23.86 |
| 23 | MRKHPQTAT | 0 | 2.0000 | 22.73 |
| 24 | IAYARARGL | 378 | 1.9600 | 22.27 |
| 25 | LGREDVFFL | 175 | 1.8600 | 21.14 |
| 26 | LDAFVVRRL | 267 | 1.8600 | 21.14 |
| 27 | FVVRRLNLP | 270 | 1.8000 | 20.45 |
| 28 | FVAFVGAAI | 537 | 1.8000 | 20.45 |
| 29 | LRFSGTSPD | 492 | 1.7000 | 19.32 |
| 30 | VLIPGGFGI | 360 | 1.5000 | 17.05 |
| 31 | IRGIEGKIG | 368 | 1.5000 | 17.05 |
| 32 | IPEHTPNGS | 560 | 1.5000 | 17.05 |
| 33 | LILRCDRDV | 219 | 1.4000 | 15.91 |
| 34 | VELSDAYLS | 310 | 1.4000 | 15.91 |
| 35 | VNNAYRDKI | 479 | 1.4000 | 15.91 |
| 36 | LHVSLVPYL | 183 | 1.3600 | 15.45 |
| 37 | MQKLDPYLN | 43 | 1.3000 | 14.77 |
| 38 | LTNANSAEF | 408 | 1.3000 | 14.77 |
| 39 | VVITEIGGT | 147 | 1.2000 | 13.64 |
| 40 | LGLCLGLQC | 389 | 1.2000 | 13.64 |
| 41 | VVGTQAHPE | 517 | 1.2000 | 13.64 |
| 42 | LLPVEIPEI | 552 | 1.2000 | 13.64 |
| 43 | LFVSGGVAS | 11 | 1.0000 | 11.36 |
| 44 | LLTARGLHV | 33 | 1.0000 | 11.36 |
| 45 | VTMQKLDPY | 41 | 1.0000 | 11.36 |
| 46 | ILAMAQPDA | 132 | 1.0000 | 11.36 |
| 47 | LRSIGITPD | 209 | 1.0000 | 11.36 |

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|---|---|---|---|---|
| 48 | LPVLGLCLG | 386 | 1.0000 | 11.36 |
| 49 | LFVAFVGAA | 536 | 1.0000 | 11.36 |
| 50 | LGKGLTASS | 21 | 0.9000 | 10.23 |
| 51 | ILRCDRDVP | 220 | 0.9000 | 10.23 |
| 52 | IALVGKYVE | 303 | 0.9000 | 10.23 |
| 53 | ITDEIKRRI | 124 | 0.7000 | 7.95 |
| 54 | VHGVLIPGG | 357 | 0.7000 | 7.95 |
| 55 | FGIRGIEGK | 366 | 0.7000 | 7.95 |
| 56 | LGSYPAVLE | 447 | 0.7000 | 7.95 |
| 57 | IAESGLRFS | 487 | 0.7000 | 7.95 |
| 58 | MNPFQHGEV | 57 | 0.6000 | 6.82 |

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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 | VVRRLNLPF | 271 | 5.2000 | 53.06 |
| 2 | VLIPGGFGI | 360 | 4.8000 | 48.98 |
| 3 | FVAFVGAAI | 537 | 4.7000 | 47.96 |
| 4 | LVPYLAPSG | 187 | 4.4000 | 44.90 |
| 5 | MRLGSYPAV | 445 | 4.2000 | 42.86 |
| 6 | LGLCLGLQC | 389 | 3.9000 | 39.80 |
| 7 | LLTARGLHV | 33 | 3.7000 | 37.76 |
| 8 | VGHYERFLD | 78 | 3.7000 | 37.76 |
| 9 | MNPFQHGEV | 57 | 3.3000 | 33.67 |
| 10 | FFLHVSLVP | 181 | 3.3000 | 33.67 |
| 11 | VAALRSIGI | 206 | 3.3000 | 33.67 |
| 12 | VVITEIGGT | 147 | 3.1500 | 32.14 |
| 13 | VRHYLGRED | 171 | 3.0000 | 30.61 |
| 14 | LGGTMRLGS | 441 | 3.0000 | 30.61 |
| 15 | VRRLNLPFR | 272 | 2.9000 | 29.59 |
| 16 | LKNKIALMC | 231 | 2.8000 | 28.57 |
| 17 | IVIEAARSV | 398 | 2.8000 | 28.57 |
| 18 | IALMCDVDI | 235 | 2.6000 | 26.53 |

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|---|---|---|---|---|
| 19 | LLPVEIPEI | 552 | 2.5500 | 26.02 |
| 20 | MRKHPQTAT | 0 | 2.5000 | 25.51 |
| 21 | VRIALVGKY | 301 | 2.5000 | 25.51 |
| 22 | YKAGELLPV | 547 | 2.5000 | 25.51 |
| 23 | VIPHITDEI | 120 | 2.4600 | 25.10 |
| 24 | VFFLHVSLV | 180 | 2.4000 | 24.49 |
| 25 | IRGIEGKIG | 368 | 2.4000 | 24.49 |
| 26 | YARARGLPV | 380 | 2.4000 | 24.49 |
| 27 | VLHREELDA | 261 | 2.3000 | 23.47 |
| 28 | VNNAYRDKI | 479 | 2.3000 | 23.47 |
| 29 | IKRRILAMA | 128 | 2.2000 | 22.45 |
| 30 | LGREDVFFL | 175 | 2.2000 | 22.45 |
| 31 | VSLVPYLAP | 185 | 2.1000 | 21.43 |
| 32 | LSVAEALRA | 317 | 2.1000 | 21.43 |
| 33 | IGITPDALI | 212 | 2.0000 | 20.41 |
| 34 | VGKYVELSD | 306 | 2.0000 | 20.41 |
| 35 | VGLTNANSA | 406 | 1.9000 | 19.39 |
| 36 | LVEFVEYPP | 503 | 1.9000 | 19.39 |
| 37 | YERFLDRNL | 81 | 1.8000 | 18.37 |
| 38 | LILRCDRDV | 219 | 1.7000 | 17.35 |
| 39 | FVVRRLNLP | 270 | 1.6000 | 16.33 |
| 40 | LGSYPAVLE | 447 | 1.6000 | 16.33 |
| 41 | LFVSGGVAS | 11 | 1.5000 | 15.31 |
| 42 | ILAMAQPDA | 132 | 1.5000 | 15.31 |
| 43 | LHVSLVPYL | 183 | 1.5000 | 15.31 |
| 44 | IGAIAYARA | 375 | 1.5000 | 15.31 |
| 45 | IEAARSVGL | 400 | 1.5000 | 15.31 |
| 46 | LDPYLNVDP | 46 | 1.4000 | 14.29 |
| 47 | VQVIPHITD | 118 | 1.4000 | 14.29 |
| 48 | LRSIGITPD | 209 | 1.3500 | 13.78 |
| 49 | FQHGEVFVT | 60 | 1.3000 | 13.27 |
| 50 | VITEIGGTV | 148 | 1.3000 | 13.27 |
| 51 | VELSDAYLS | 310 | 1.2000 | 12.24 |
| 52 | FKHRAKVEI | 328 | 1.2000 | 12.24 |

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|---|---|---|---|---|
| 53 | VVAQAYQTT | 459 | 1.2000 | 12.24 |
| 54 | LQCIVIEAA | 395 | 1.1500 | 11.73 |
| 55 | IESQPFLEA | 159 | 1.1000 | 11.22 |
| 56 | WVASDGCET | 338 | 1.1000 | 11.22 |
| 57 | LRFSGTSPD | 492 | 1.0600 | 10.82 |
| 58 | MQKLDPYLN | 43 | 1.0000 | 10.20 |

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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 | FVAFVGAAI | 537 | 5.7000 | 58.16 |
| 2 | FFLHVSLVP | 181 | 4.3000 | 43.88 |
| 3 | VVRRLNLPF | 271 | 4.2000 | 42.86 |
| 4 | VLIPGGFGI | 360 | 3.8000 | 38.78 |
| 5 | YKAGELLPV | 547 | 3.5000 | 35.71 |
| 6 | LVPYLAPSG | 187 | 3.4000 | 34.69 |
| 7 | YARARGLPV | 380 | 3.4000 | 34.69 |
| 8 | MRLGSYPAV | 445 | 3.2000 | 32.65 |
| 9 | LGLCLGLQC | 389 | 2.9000 | 29.59 |
| 10 | YERFLDRNL | 81 | 2.8000 | 28.57 |
| 11 | LLTARGLHV | 33 | 2.7000 | 27.55 |
| 12 | VGHYERFLD | 78 | 2.7000 | 27.55 |
| 13 | FVVRRLNLP | 270 | 2.6000 | 26.53 |
| 14 | MNPFQHGEV | 57 | 2.3000 | 23.47 |
| 15 | FQHGEVFVT | 60 | 2.3000 | 23.47 |
| 16 | VAALRSIGI | 206 | 2.3000 | 23.47 |
| 17 | FKHRAKVEI | 328 | 2.2000 | 22.45 |
| 18 | VVITEIGGT | 147 | 2.1500 | 21.94 |
| 19 | WVASDGCET | 338 | 2.1000 | 21.43 |
| 20 | VRHYLGRED | 171 | 2.0000 | 20.41 |
| 21 | LGGTMRLGS | 441 | 2.0000 | 20.41 |
| 22 | VRRLNLPFR | 272 | 1.9000 | 19.39 |
| 23 | FVTEDGAET | 66 | 1.8000 | 18.37 |

| | | | | |
|---|---|---|---|---|
| 24 | LKNKIALMC | 231 | 1.8000 | 18.37 |
| 25 | IVIEAARSV | 398 | 1.8000 | 18.37 |
| 26 | FVSGGVASS | 12 | 1.7000 | 17.35 |
| 27 | IALMCDVDI | 235 | 1.6000 | 16.33 |
| 28 | YLNVDPGTM | 49 | 1.5800 | 16.12 |
| 29 | LLPVEIPEI | 552 | 1.5500 | 15.82 |
| 30 | MRKHPQTAT | 0 | 1.5000 | 15.31 |
| 31 | VRIALVGKY | 301 | 1.5000 | 15.31 |
| 32 | YVELSDAYL | 309 | 1.5000 | 15.31 |
| 33 | VIPHITDEI | 120 | 1.4600 | 14.90 |
| 34 | VFFLHVSLV | 180 | 1.4000 | 14.29 |
| 35 | IRGIEGKIG | 368 | 1.4000 | 14.29 |
| 36 | FVEYPPDRH | 506 | 1.4000 | 14.29 |
| 37 | VLHREELDA | 261 | 1.3000 | 13.27 |
| 38 | VNNAYRDKI | 479 | 1.3000 | 13.27 |
| 39 | IKRRILAMA | 128 | 1.2000 | 12.24 |
| 40 | LGREDVFFL | 175 | 1.2000 | 12.24 |
| 41 | VSLVPYLAP | 185 | 1.1000 | 11.22 |
| 42 | LSVAEALRA | 317 | 1.1000 | 11.22 |
| 43 | FLHVSLVPY | 182 | 1.0000 | 10.20 |
| 44 | IGITPDALI | 212 | 1.0000 | 10.20 |
| 45 | VGKYVELSD | 306 | 1.0000 | 10.20 |
| 46 | YLGDTVQVI | 113 | 0.9000 | 9.18 |
| 47 | YLGREDVFF | 174 | 0.9000 | 9.18 |
| 48 | VGLTNANSA | 406 | 0.9000 | 9.18 |
| 49 | LVEFVEYPP | 503 | 0.9000 | 9.18 |
| 50 | LILRCDRDV | 219 | 0.7000 | 7.14 |
| 51 | FVVGTQAHP | 516 | 0.7000 | 7.14 |
| 52 | LGSYPAVLE | 447 | 0.6000 | 6.12 |
| 53 | LFVSGGVAS | 11 | 0.5000 | 5.10 |
| 54 | ILAMAQPDA | 132 | 0.5000 | 5.10 |
| 55 | LHVSLVPYL | 183 | 0.5000 | 5.10 |
| 56 | YDIPKVLHR | 256 | 0.5000 | 5.10 |
| 57 | IGAIAYARA | 375 | 0.5000 | 5.10 |

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| 58 | IEAARSVGL | 400 | 0.5000 | 5.10 |

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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 | VVRRLNLPF | 271 | 5.2000 | 53.06 |
| 2 | VLIPGGFGI | 360 | 4.8000 | 48.98 |
| 3 | FVAFVGAAI | 537 | 4.7000 | 47.96 |
| 4 | LVPYLAPSG | 187 | 4.4000 | 44.90 |
| 5 | MRLGSYPAV | 445 | 4.2000 | 42.86 |
| 6 | LGLCLGLQC | 389 | 3.9000 | 39.80 |
| 7 | LLTARGLHV | 33 | 3.7000 | 37.76 |
| 8 | VGHYERFLD | 78 | 3.7000 | 37.76 |
| 9 | MNPFQHGEV | 57 | 3.3000 | 33.67 |
| 10 | FFLHVSLVP | 181 | 3.3000 | 33.67 |
| 11 | VAALRSIGI | 206 | 3.3000 | 33.67 |
| 12 | VVITEIGGT | 147 | 3.1500 | 32.14 |
| 13 | VRHYLGRED | 171 | 3.0000 | 30.61 |
| 14 | LGGTMRLGS | 441 | 3.0000 | 30.61 |
| 15 | VRRLNLPFR | 272 | 2.9000 | 29.59 |
| 16 | LKNKIALMC | 231 | 2.8000 | 28.57 |
| 17 | IVIEAARSV | 398 | 2.8000 | 28.57 |
| 18 | IALMCDVDI | 235 | 2.6000 | 26.53 |
| 19 | LLPVEIPEI | 552 | 2.5500 | 26.02 |
| 20 | MRKHPQTAT | 0 | 2.5000 | 25.51 |
| 21 | VRIALVGKY | 301 | 2.5000 | 25.51 |
| 22 | YKAGELLPV | 547 | 2.5000 | 25.51 |
| 23 | VIPHITDEI | 120 | 2.4600 | 25.10 |
| 24 | VFFLHVSLV | 180 | 2.4000 | 24.49 |
| 25 | IRGIEGKIG | 368 | 2.4000 | 24.49 |
| 26 | YARARGLPV | 380 | 2.4000 | 24.49 |
| 27 | VLHREELDA | 261 | 2.3000 | 23.47 |
| 28 | VNNAYRDKI | 479 | 2.3000 | 23.47 |

| | | | | |
|---|---|---|---|---|
| 29 | IKRRILAMA | 128 | 2.2000 | 22.45 |
| 30 | LGREDVFFL | 175 | 2.2000 | 22.45 |
| 31 | VSLVPYLAP | 185 | 2.1000 | 21.43 |
| 32 | LSVAEALRA | 317 | 2.1000 | 21.43 |
| 33 | IGITPDALI | 212 | 2.0000 | 20.41 |
| 34 | VGKYVELSD | 306 | 2.0000 | 20.41 |
| 35 | VGLTNANSA | 406 | 1.9000 | 19.39 |
| 36 | LVEFVEYPP | 503 | 1.9000 | 19.39 |
| 37 | YERFLDRNL | 81 | 1.8000 | 18.37 |
| 38 | LILRCDRDV | 219 | 1.7000 | 17.35 |
| 39 | FVVRRLNLP | 270 | 1.6000 | 16.33 |
| 40 | LGSYPAVLE | 447 | 1.6000 | 16.33 |
| 41 | LFVSGGVAS | 11 | 1.5000 | 15.31 |
| 42 | ILAMAQPDA | 132 | 1.5000 | 15.31 |
| 43 | LHVSLVPYL | 183 | 1.5000 | 15.31 |
| 44 | IGAIAYARA | 375 | 1.5000 | 15.31 |
| 45 | IEAARSVGL | 400 | 1.5000 | 15.31 |
| 46 | LDPYLNVDP | 46 | 1.4000 | 14.29 |
| 47 | VQVIPHITD | 118 | 1.4000 | 14.29 |
| 48 | LRSIGITPD | 209 | 1.3500 | 13.78 |
| 49 | FQHGEVFVT | 60 | 1.3000 | 13.27 |
| 50 | VITEIGGTV | 148 | 1.3000 | 13.27 |
| 51 | VELSDAYLS | 310 | 1.2000 | 12.24 |
| 52 | FKHRAKVEI | 328 | 1.2000 | 12.24 |
| 53 | VVAQAYQTT | 459 | 1.2000 | 12.24 |
| 54 | LQCIVIEAA | 395 | 1.1500 | 11.73 |
| 55 | IESQPFLEA | 159 | 1.1000 | 11.22 |
| 56 | WVASDGCET | 338 | 1.1000 | 11.22 |
| 57 | LRFSGTSPD | 492 | 1.0600 | 10.82 |
| 58 | MQKLDPYLN | 43 | 1.0000 | 10.20 |

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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 | YSTVIAKER | 101 | 4.2000 | 42.86 |
| 2 | YLNVDPGTM | 49 | 3.9000 | 39.80 |
| 3 | IRGIEGKIG | 368 | 3.7000 | 37.76 |
| 4 | VRRLNLPFR | 272 | 3.4000 | 34.69 |
| 5 | VRIALVGKY | 301 | 3.3000 | 33.67 |
| 6 | YLSVAEALR | 316 | 2.8000 | 28.57 |
| 7 | YQTTQVSER | 464 | 2.5000 | 25.51 |
| 8 | VLIPGGFGI | 360 | 2.4000 | 24.49 |
| 9 | IAYARARGL | 378 | 2.4000 | 24.49 |
| 10 | IVIEAARSV | 398 | 2.4000 | 24.49 |
| 11 | FVAFVGAAI | 537 | 2.4000 | 24.49 |
| 12 | FLHVSLVPY | 182 | 2.3000 | 23.47 |
| 13 | MQKLDPYLN | 43 | 2.2000 | 22.45 |
| 14 | VVGTQAHPE | 517 | 2.2000 | 22.45 |
| 15 | FVGAAIDYK | 540 | 2.1000 | 21.43 |
| 16 | VVITEIGGT | 147 | 1.9000 | 19.39 |
| 17 | FLEAARQVR | 164 | 1.7000 | 17.35 |
| 18 | VAALRSIGI | 206 | 1.5000 | 15.31 |
| 19 | VELSDAYLS | 310 | 1.5000 | 15.31 |
| 20 | LRAGGFKHR | 323 | 1.3000 | 13.27 |
| 21 | VGLTNANSA | 406 | 1.3000 | 13.27 |
| 22 | WVASDGCET | 338 | 1.1000 | 11.22 |
| 23 | VLGLCLGLQ | 388 | 1.1000 | 11.22 |
| 24 | YLAPSGELK | 190 | 1.0000 | 10.20 |
| 25 | VGDIESQPF | 156 | 0.9000 | 9.18 |
| 26 | YERFLDRNL | 81 | 0.8000 | 8.16 |
| 27 | YVELSDAYL | 309 | 0.8000 | 8.16 |
| 28 | YARARGLPV | 380 | 0.8000 | 8.16 |
| 29 | LGLCLGLQC | 389 | 0.8000 | 8.16 |
| 30 | FGIRGIEGK | 366 | 0.7000 | 7.14 |
| 31 | VASSLGKGL | 17 | 0.6000 | 6.12 |
| 32 | LVPYLAPSG | 187 | 0.6000 | 6.12 |
| 33 | IALMCDVDI | 235 | 0.6000 | 6.12 |

| | | | | |
|---|---|---|---|---|
| 34 | VVRRLNLPF | 271 | 0.6000 | 6.12 |
| 35 | LLPVEIPEI | 552 | 0.6000 | 6.12 |
| 36 | VQVIPHITD | 118 | 0.5000 | 5.10 |
| 37 | IGITPDALI | 212 | 0.5000 | 5.10 |
| 38 | YDIPKVLHR | 256 | 0.5000 | 5.10 |
| 39 | LGREDVFFL | 175 | 0.4000 | 4.08 |
| 40 | FVTEDGAET | 66 | 0.3000 | 3.06 |
| 41 | VRHYLGRED | 171 | 0.3000 | 3.06 |
| 42 | IALVGKYVE | 303 | 0.2000 | 2.04 |
| 43 | LIPGGFGIR | 361 | 0.2000 | 2.04 |
| 44 | LTNANSAEF | 408 | 0.2000 | 2.04 |
| 45 | FVSGGVASS | 12 | 0.1000 | 1.02 |
| 46 | LLTARGLHV | 33 | 0.1000 | 1.02 |
| 47 | LRSIGITPD | 209 | 0.1000 | 1.02 |
| 48 | ITPDALILR | 214 | 0.1000 | 1.02 |
| 49 | LKSRPTRPH | 526 | 0.1000 | 1.02 |
| 50 | LFVSGGVAS | 11 | -0.1000 | 0 |
| 51 | YLGDTVQVI | 113 | -0.1000 | 0 |
| 52 | FRDVDWTEW | 279 | -0.1000 | 0 |
| 53 | LGDVHGVLI | 354 | -0.1000 | 0 |
| 54 | VVAQAYQTT | 459 | -0.1000 | 0 |
| 55 | FSGTSPDGH | 494 | -0.1000 | 0 |

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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 | YSTVIAKER | 101 | 4.2000 | 42.86 |
| 2 | YLNVDPGTM | 49 | 3.9000 | 39.80 |
| 3 | IRGIEGKIG | 368 | 3.7000 | 37.76 |
| 4 | VRRLNLPFR | 272 | 3.4000 | 34.69 |
| 5 | VRIALVGKY | 301 | 3.3000 | 33.67 |
| 6 | YLSVAEALR | 316 | 2.8000 | 28.57 |
| 7 | YQTTQVSER | 464 | 2.5000 | 25.51 |

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|---|---|---|---|---|
| 8 | VLIPGGFGI | 360 | 2.4000 | 24.49 |
| 9 | IAYARARGL | 378 | 2.4000 | 24.49 |
| 10 | IVIEAARSV | 398 | 2.4000 | 24.49 |
| 11 | FVAFVGAAI | 537 | 2.4000 | 24.49 |
| 12 | FLHVSLVPY | 182 | 2.3000 | 23.47 |
| 13 | MQKLDPYLN | 43 | 2.2000 | 22.45 |
| 14 | VVGTQAHPE | 517 | 2.2000 | 22.45 |
| 15 | FVGAAIDYK | 540 | 2.1000 | 21.43 |
| 16 | VVITEIGGT | 147 | 1.9000 | 19.39 |
| 17 | FLEAARQVR | 164 | 1.7000 | 17.35 |
| 18 | VAALRSIGI | 206 | 1.5000 | 15.31 |
| 19 | VELSDAYLS | 310 | 1.5000 | 15.31 |
| 20 | LRAGGFKHR | 323 | 1.3000 | 13.27 |
| 21 | VGLTNANSA | 406 | 1.3000 | 13.27 |
| 22 | WVASDGCET | 338 | 1.1000 | 11.22 |
| 23 | VLGLCLGLQ | 388 | 1.1000 | 11.22 |
| 24 | YLAPSGELK | 190 | 1.0000 | 10.20 |
| 25 | VGDIESQPF | 156 | 0.9000 | 9.18 |
| 26 | YERFLDRNL | 81 | 0.8000 | 8.16 |
| 27 | YVELSDAYL | 309 | 0.8000 | 8.16 |
| 28 | YARARGLPV | 380 | 0.8000 | 8.16 |
| 29 | LGLCLGLQC | 389 | 0.8000 | 8.16 |
| 30 | FGIRGIEGK | 366 | 0.7000 | 7.14 |
| 31 | VASSLGKGL | 17 | 0.6000 | 6.12 |
| 32 | LVPYLAPSG | 187 | 0.6000 | 6.12 |
| 33 | IALMCDVDI | 235 | 0.6000 | 6.12 |
| 34 | VVRRLNLPF | 271 | 0.6000 | 6.12 |
| 35 | LLPVEIPEI | 552 | 0.6000 | 6.12 |
| 36 | VQVIPHITD | 118 | 0.5000 | 5.10 |
| 37 | IGITPDALI | 212 | 0.5000 | 5.10 |
| 38 | YDIPKVLHR | 256 | 0.5000 | 5.10 |
| 39 | LGREDVFFL | 175 | 0.4000 | 4.08 |
| 40 | FVTEDGAET | 66 | 0.3000 | 3.06 |
| 41 | VRHYLGRED | 171 | 0.3000 | 3.06 |

| | | | | |
|---|---|---|---|---|
| 42 | IALVGKYVE | 303 | 0.2000 | 2.04 |
| 43 | LIPGGFGIR | 361 | 0.2000 | 2.04 |
| 44 | LTNANSAEF | 408 | 0.2000 | 2.04 |
| 45 | FVSGGVASS | 12 | 0.1000 | 1.02 |
| 46 | LLTARGLHV | 33 | 0.1000 | 1.02 |
| 47 | LRSIGITPD | 209 | 0.1000 | 1.02 |
| 48 | ITPDALILR | 214 | 0.1000 | 1.02 |
| 49 | LKSRPTRPH | 526 | 0.1000 | 1.02 |
| 50 | LFVSGGVAS | 11 | -0.1000 | 0 |
| 51 | YLGDTVQVI | 113 | -0.1000 | 0 |
| 52 | FRDVDWTEW | 279 | -0.1000 | 0 |
| 53 | LGDVHGVLI | 354 | -0.1000 | 0 |
| 54 | VVAQAYQTT | 459 | -0.1000 | 0 |
| 55 | FSGTSPDGH | 494 | -0.1000 | 0 |