

## MHC Class-II Binding Peptide Prediction Results

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### INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Apr 21 00:31:10 2010
Length of input sequence	510 amino acids
Number of nanomers from input sequence	502
Number of nanomers with <a href="#">obligatory P1 anchor residue</a>	145
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	51

ALLELE: DRB1_0101	Threshold for 3 % with score: 0.14	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLVKASNA	480	1.8500	30.83
2	FLALPGARA	46	1.6000	26.67
3	VVVG TGRSI	422	1.3900	23.17
4	VVLNVGTAH	208	0.8300	13.83
5	VLAARPVGV	71	0.8000	13.33
6	LRPGDVVLV	475	0.7000	11.67
7	YLILEMAAR	182	0.6000	10.00
8	WTVLRATRR	171	0.4900	8.17

9	IVGGAVADI	11	0.2000	3.33
10	MAKLTAARV	255	0.2000	3.33
11	VKASNAAGL	483	-0.1000	0
12	VLAALAKLA	108	-0.2000	0
13	VLNVGTAHL	209	-0.2500	0
14	VSRLVVVGT	418	-0.3000	0
15	LILEMAARH	183	-0.4000	0
16	VALECGASV	319	-0.4000	0
17	VRLDVSRLV	414	-0.4100	0
18	VVLAARPVG	70	-0.4300	0
19	VAAGAAVVL	64	-0.5000	0
20	LATAVAAQL	115	-0.5000	0
21	IIGITGSSG	130	-0.5000	0
22	VTNALCAAA	310	-0.5000	0
23	MIELTVAQI	0	-0.6000	0
24	WIAHQPEAT	377	-0.6000	0
25	IGVVLVNVT	206	-0.6500	0
26	IELTVAQIA	1	-0.7000	0
27	FNNELGHPW	163	-0.7000	0
28	VRLGVCGDH	300	-0.7000	0
29	LALLRAELR	468	-0.7000	0
30	VPHSGAVVL	237	-0.8000	0
31	LVKASNAAG	482	-0.8000	0
32	LVAGGLTII	123	-0.8100	0
33	VPPVAAPNV	84	-0.8800	0
34	LVVVGTGRS	421	-1.0500	0
35	LVNVGTAHLG	210	-1.1000	0
36	LTAARVVRV	258	-1.1000	0
37	LTIIGITGS	128	-1.1100	0
38	LAEIAPPSI	198	-1.1300	0
39	VEQVAAALT	327	-1.1500	0
40	VGTGRSISA	424	-1.2000	0
41	LAKLATAVA	112	-1.3000	0
42	VIAQTKAEL	225	-1.3000	0

43	MRAGLQALA	368	-1.3000	0
44	LMAAVLAPL	145	-1.4000	0
45	ILEMAARHH	184	-1.4100	0
46	LFLALPGAR	45	-1.5000	0
47	LAPLGEVVA	150	-1.5000	0
48	LTAAPPVSR	334	-1.5000	0
49	VLGEMAELG	391	-1.6000	0
50	LTVAQIAEI	3	-1.7000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLVKASNA	480	2.8500	47.50
2	VVVG TGRSI	422	2.3900	39.83
3	VVLNVGTAH	208	1.8300	30.50
4	VLAARPVG V	71	1.8000	30.00
5	LRPGDVVLV	475	1.7000	28.33
6	FLALPGARA	46	1.6000	26.67
7	IVGGAVADI	11	1.2000	20.00
8	MAKLTAARV	255	1.2000	20.00
9	VKASNAAGL	483	0.9000	15.00
10	VLAALAKLA	108	0.8000	13.33
11	VLNVGTAHL	209	0.7500	12.50
12	VSRLVVVGT	418	0.7000	11.67
13	LILEMAARH	183	0.6000	10.00
14	VALECGASV	319	0.6000	10.00
15	VRLDVSR LV	414	0.5900	9.83
16	VVLAARPVG	70	0.5700	9.50
17	VAAGAAVVL	64	0.5000	8.33
18	LATAVAAQL	115	0.5000	8.33
19	IIGITGSSG	130	0.5000	8.33
20	VTNALCAAA	310	0.5000	8.33
21	MIELTVAQI	0	0.4000	6.67

22	IGVVLNVGT	206	0.3500	5.83
23	IELTVAQIA	1	0.3000	5.00
24	VRLGVCGDH	300	0.3000	5.00
25	LALLRAELR	468	0.3000	5.00
26	VPHSGAVVL	237	0.2000	3.33
27	LVKASNAAG	482	0.2000	3.33
28	LVAGGLTII	123	0.1900	3.17
29	VPPVAAPNV	84	0.1200	2.00
30	LVVVG TGRS	421	-0.0500	0
31	LNVGTAHLG	210	-0.1000	0
32	LTAARVVRV	258	-0.1000	0
33	LTIIGITGS	128	-0.1100	0
34	LAEIAPPSI	198	-0.1300	0
35	VEQVAAALT	327	-0.1500	0
36	VGTGRSISA	424	-0.2000	0
37	LAKLATAVA	112	-0.3000	0
38	VIAQTKAEL	225	-0.3000	0
39	MRAGLQALA	368	-0.3000	0
40	LMAAVLAPL	145	-0.4000	0
41	YLILEMAAR	182	-0.4000	0
42	ILEMAARHH	184	-0.4100	0
43	LFLALPGAR	45	-0.5000	0
44	LAPLGEVVA	150	-0.5000	0
45	LTAAPPVSR	334	-0.5000	0
46	WTVLRATTR	171	-0.5100	0
47	VLGEMAELG	391	-0.6000	0
48	LTVAQIAEI	3	-0.7000	0
49	VVPPVAAPN	83	-0.7000	0
50	FNNELGHPW	163	-0.7000	0

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
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1	LVADDTCGS	498	6.3000	66.32
2	VVLAARPVG	70	5.2000	54.74
3	VRLDVSRLV	414	4.8000	50.53
4	LRPGDVVLV	475	4.7000	49.47
5	IVGGAVADI	11	4.6000	48.42
6	VEFDSRAIG	33	4.6000	48.42
7	LVVVG TGRS	421	4.6000	48.42
8	VSRDNTGDV	266	3.9000	41.05
9	LTIIGITGS	128	3.7000	38.95
10	LNADDPAVA	245	3.6000	37.89
11	VVGTGRSIS	423	3.4700	36.53
12	LVAGGLTII	123	3.3000	34.74
13	VRLGVCGDH	300	3.3000	34.74
14	MHHGAVLEG	433	3.3000	34.74
15	VVLVKASNA	480	3.1700	33.37
16	LFLALPGAR	45	2.9000	30.53
17	VSLDELARP	279	2.9000	30.53
18	VVRVSRDNT	263	2.7000	28.42
19	IVVPPVAAP	82	2.5000	26.32
20	LRATRRTDY	174	2.4000	25.26
21	MRAGLQALA	368	2.4000	25.26
22	VIAQTKAEL	225	2.3600	24.84
23	VAGGLTIIG	124	2.3000	24.21
24	LRAELRPGD	471	2.3000	24.21
25	VLNVGTAHL	209	2.2600	23.79
26	VPAIVVPPV	79	2.2000	23.16
27	MQVTTRGDG	345	2.2000	23.16
28	LEMAARHHG	185	2.1000	22.11
29	VVVG TGRSI	422	2.1000	22.11
30	IGPGGLFLA	40	2.0000	21.05
31	VLAARPVGV	71	2.0000	21.05
32	VVLNVGTAH	208	2.0000	21.05
33	LVKASNAAG	482	1.9000	20.00
34	LTVAQIAEI	3	1.8000	18.95

35	VCGDHQVTN	304	1.8000	18.95
36	LGEDAIAEH	398	1.8000	18.95
37	VKASNAAGL	483	1.7600	18.53
38	MIELTVAQI	0	1.7000	17.89
39	VGTAHLGEF	212	1.7000	17.89
40	LTAARVVRV	258	1.7000	17.89
41	VAAQLVAGG	119	1.6000	16.84
42	IIGITGSSG	130	1.5700	16.53
43	VAAMAKLTA	252	1.5000	15.79
44	LNVGTAHLG	210	1.4000	14.74
45	LLRAELRPG	470	1.4000	14.74
46	VADDTCGSV	499	1.4000	14.74
47	VRVSRDNTG	264	1.3100	13.79
48	VSRLVVVGT	418	1.3000	13.68
49	VGTEGRSISA	424	1.3000	13.68
50	LALLRAELR	468	1.3000	13.68
51	LMAAVLAPL	145	1.2600	13.26

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	LVADDTCGS	498	4.9000	53.85
2	LVVVGTGRS	421	3.2000	35.16
3	VRLGVCGDH	300	2.8800	31.65
4	VVLAARPVG	70	2.8000	30.77
5	VRLDVSRLV	414	2.8000	30.77
6	IVGGAVADI	11	2.7000	29.67
7	LRPGDVVLV	475	2.7000	29.67
8	LNADDPAVA	245	2.6000	28.57
9	LTIIIGTGS	128	2.3000	25.27
10	VEFDSRAIG	33	2.2000	24.18
11	VVLVKASNA	480	2.1700	23.85
12	VVGTGRSIS	423	2.0700	22.75

13	VSRDNTGDV	266	1.9000	20.88
14	FGSREVIAQ	220	1.8000	19.78
15	VVLNVGTAH	208	1.5800	17.36
16	LVAGGLTII	123	1.4000	15.38
17	MRAGLQALA	368	1.4000	15.38
18	LGEDAIAEH	398	1.3800	15.16
19	IGPGGLFLA	40	1.0000	10.99
20	VVRVSRDNT	263	1.0000	10.99
21	VSLDELARP	279	0.9000	9.89
22	MHHGAVLEG	433	0.9000	9.89
23	FTLHAHDAQ	289	0.8000	8.79
24	YLILEMAAR	182	0.6000	6.59
25	IVVPPVAAP	82	0.5000	5.49
26	VAAMAKLTA	252	0.5000	5.49
27	LFLALPGAR	45	0.4000	4.40
28	VIAQTKAEL	225	0.4000	4.40
29	FLALPGARA	46	0.3000	3.30
30	VLNVGTAHL	209	0.3000	3.30
31	VGTGRSISA	424	0.3000	3.30
32	VPAIVVPPV	79	0.2000	2.20
33	LECGASVEQ	321	0.2000	2.20
34	WIAHQPEAT	377	0.2000	2.20
35	VVVGTRRSI	422	0.2000	2.20
36	LRAELRPGD	471	0.2000	2.20
37	LILEMAARH	183	0.1800	1.98
38	LRATRRTDY	174	0.1000	1.10
39	LTVAQIAEI	3	-0.1000	0
40	VAGGLTIIG	124	-0.1000	0
41	MIELTVAQI	0	-0.2000	0
42	VGGAVADIS	12	-0.2000	0
43	LAKLATAVA	112	-0.2000	0
44	MQVTTRGDG	345	-0.2000	0
45	VKASNAAGL	483	-0.2000	0
46	LEMAARHHG	185	-0.3000	0

47	LTAARVVRV	258	-0.3000	0
48	IGITGSSGK	131	-0.3300	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVADDTCGS	498	5.9000	67.05
2	IVGGAVADI	11	3.7000	42.05
3	LNADDPAVA	245	3.6000	40.91
4	LRPGDVVLV	475	3.5800	40.68
5	VRLDVSRLV	414	3.5000	39.77
6	LTIIGITGS	128	3.3000	37.50
7	VEFDSRAIG	33	3.2000	36.36
8	VVLVKASNA	480	2.9000	32.95
9	LVVVGTGRS	421	2.8000	31.82
10	VVGTGRSIS	423	2.8000	31.82
11	VVLNVGTAH	208	2.5800	29.32
12	VRLGVCGDH	300	2.4800	28.18
13	VVLAARPVG	70	2.4000	27.27
14	LVAGGLTII	123	2.4000	27.27
15	MRAGLQALA	368	2.4000	27.27
16	MHHGAVLEG	433	2.4000	27.27
17	LGEDAIAEH	398	2.3800	27.05
18	VVRVSRDNT	263	2.3000	26.14
19	VAAMAKLTA	252	2.0000	22.73
20	VSLDELARP	279	1.9000	21.59
21	IVVPPVAAP	82	1.5000	17.05
22	LEMAARHHG	185	1.5000	17.05
23	VSRDNTGDV	266	1.5000	17.05
24	VIAQTKAEL	225	1.4000	15.91
25	VLNVGTAHL	209	1.3000	14.77
26	LILEMAARH	183	1.1800	13.41
27	VGGAVADIS	12	1.1000	12.50



28	LRATRRTDY	174	1.1000	12.50
29	LECGASVEQ	321	1.0800	12.27
30	VLVKASNAA	481	1.0000	11.36
31	VGTGRSISA	424	0.9800	11.14
32	LTVAQIAEI	3	0.9000	10.23
33	VVVGTRSI	422	0.9000	10.23
34	VLAARVGV	71	0.8800	10.00
35	VCGDHQVTN	304	0.8800	10.00
36	MIELTVAQI	0	0.8000	9.09
37	LAALAKLAT	109	0.8000	9.09
38	LAKLATAVA	112	0.8000	9.09
39	LNVTGHTLG	210	0.8000	9.09
40	VKASNAAGL	483	0.8000	9.09
41	VLAALAKLA	108	0.7000	7.95
42	ITGSSGKTS	133	0.6000	6.82
43	VVLNADDPA	243	0.6000	6.82
44	VRVSRDNTG	264	0.6000	6.82
45	VAGGLTIIG	124	0.5800	6.59
46	LTAARVVRV	258	0.5800	6.59
47	IGPGGLFLA	40	0.5000	5.68
48	VTNALCAAA	310	0.5000	5.68
49	LVKASNAAG	482	0.5000	5.68
50	FGSREVIAQ	220	0.4800	5.45
51	VSRLVVVGT	418	0.4800	5.45

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVADDTCGS	498	5.9000	67.05
2	IVGGAVADI	11	3.7000	42.05
3	LNADDPVA	245	3.6000	40.91
4	LRPGDVVLV	475	3.5800	40.68
5	VRLDVSRLV	414	3.5000	39.77

6	LTIIGITGS	128	3.3000	37.50
7	VEFDSRAIG	33	3.2000	36.36
8	VVLVKASNA	480	2.9000	32.95
9	LVVVGTGRS	421	2.8000	31.82
10	VVGTGRSIS	423	2.8000	31.82
11	VVLNVGTAH	208	2.5800	29.32
12	VRLGVCGDH	300	2.4800	28.18
13	VVLAARPVG	70	2.4000	27.27
14	LVAGGLTII	123	2.4000	27.27
15	MRAGLQALA	368	2.4000	27.27
16	MHHGAVLEG	433	2.4000	27.27
17	LGEDAIAEH	398	2.3800	27.05
18	VVRVSRDNT	263	2.3000	26.14
19	VAAMAKLTA	252	2.0000	22.73
20	VSLDELARP	279	1.9000	21.59
21	IVVPPVAAP	82	1.5000	17.05
22	LEMAARHHG	185	1.5000	17.05
23	VSRDNTGDV	266	1.5000	17.05
24	VIAQTKAEL	225	1.4000	15.91
25	VLNVGTAHL	209	1.3000	14.77
26	LILEMAARH	183	1.1800	13.41
27	VGGAVADIS	12	1.1000	12.50
28	LRATRRTDY	174	1.1000	12.50
29	LECGASVEQ	321	1.0800	12.27
30	VLVKASNAA	481	1.0000	11.36
31	VGTGRSISA	424	0.9800	11.14
32	LTVAQIAEI	3	0.9000	10.23
33	VVVGTGRSI	422	0.9000	10.23
34	VLAARPVGV	71	0.8800	10.00
35	VCGDHQVTN	304	0.8800	10.00
36	MIELTVAQI	0	0.8000	9.09
37	LAALAKLAT	109	0.8000	9.09
38	LAKLATAVA	112	0.8000	9.09
39	LNVGTAHLG	210	0.8000	9.09

40	VKASNAAGL	483	0.8000	9.09
41	VLAALAKLA	108	0.7000	7.95
42	ITGSSGKTS	133	0.6000	6.82
43	VVLNADDDPA	243	0.6000	6.82
44	VRVSRDNTG	264	0.6000	6.82
45	VAGGLTIIG	124	0.5800	6.59
46	LTAARVVRV	258	0.5800	6.59
47	IGPGGLFLA	40	0.5000	5.68
48	VTNALCAAA	310	0.5000	5.68
49	LVKASNAAG	482	0.5000	5.68
50	FGSREVIAQ	220	0.4800	5.45
51	VSRLVVVGT	418	0.4800	5.45

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVADDTCGS	498	5.9000	67.05
2	IVGGAVADI	11	3.7000	42.05
3	LNADDDPAVA	245	3.6000	40.91
4	LRPGDVVLV	475	3.5800	40.68
5	VRLDVSRLV	414	3.5000	39.77
6	LTIIGITGS	128	3.3000	37.50
7	VEFDSRAIG	33	3.2000	36.36
8	VVLVKASNA	480	2.9000	32.95
9	LVVVGTGRS	421	2.8000	31.82
10	VVGTGRSIS	423	2.8000	31.82
11	VVLNVGTAH	208	2.5800	29.32
12	VRLGVCGDH	300	2.4800	28.18
13	VVLAARPVG	70	2.4000	27.27
14	LVAGGLTII	123	2.4000	27.27
15	MRAGLQALA	368	2.4000	27.27
16	MHHGAVLEG	433	2.4000	27.27
17	LGEDAIAEH	398	2.3800	27.05

18	VVRVSRDNT	263	2.3000	26.14
19	VAAMAKLTA	252	2.0000	22.73
20	VSLDELARP	279	1.9000	21.59
21	IVVPPVAAP	82	1.5000	17.05
22	LEMAARHHG	185	1.5000	17.05
23	VSRDNTGDV	266	1.5000	17.05
24	VIAQTKAEL	225	1.4000	15.91
25	VLNVGTAHL	209	1.3000	14.77
26	LILEMAARH	183	1.1800	13.41
27	VGGAVADIS	12	1.1000	12.50
28	LRATRRTDY	174	1.1000	12.50
29	LECGASVEQ	321	1.0800	12.27
30	VLVKASNAA	481	1.0000	11.36
31	VGTGRSISA	424	0.9800	11.14
32	LTVAQIAEI	3	0.9000	10.23
33	VVVG TGRSI	422	0.9000	10.23
34	VLAARPVGV	71	0.8800	10.00
35	VCGDHQVTN	304	0.8800	10.00
36	MIELTVAQI	0	0.8000	9.09
37	LAALAKLAT	109	0.8000	9.09
38	LAKLATAVA	112	0.8000	9.09
39	LNVGTAHLG	210	0.8000	9.09
40	VKASNAAGL	483	0.8000	9.09
41	VLAALAKLA	108	0.7000	7.95
42	ITGSSGKTS	133	0.6000	6.82
43	VVLNADDPA	243	0.6000	6.82
44	VRVSRDNTG	264	0.6000	6.82
45	VAGGLTIIG	124	0.5800	6.59
46	LTAARVVRV	258	0.5800	6.59
47	IGPGGLFLA	40	0.5000	5.68
48	VTNALCAAA	310	0.5000	5.68
49	LVKASNAAG	482	0.5000	5.68
50	FGSREVIAQ	220	0.4800	5.45
51	VSRLVVVGT	418	0.4800	5.45

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVADDTCGS	498	5.3000	55.79
2	VVLAARPVG	70	4.2000	44.21
3	VRLDVSRLV	414	3.8000	40.00
4	LRPGDVVLV	475	3.7000	38.95
5	IVGGAVADI	11	3.6000	37.89
6	VEFDSRAIG	33	3.6000	37.89
7	LVVVG TGRS	421	3.6000	37.89
8	VSRDNTGDV	266	2.9000	30.53
9	LTIIGITGS	128	2.7000	28.42
10	LNADDPAVA	245	2.6000	27.37
11	VVGTGRSIS	423	2.4700	26.00
12	LVAGGLTII	123	2.3000	24.21
13	VRLGVCGDH	300	2.3000	24.21
14	MHHGAVLEG	433	2.3000	24.21
15	VVLVKASNA	480	2.1700	22.84
16	YLILEMAAR	182	2.1000	22.11
17	LFLALPGAR	45	1.9000	20.00
18	VSLDELARP	279	1.9000	20.00
19	VVRVSRDNT	263	1.7000	17.89
20	IVVPPVAAP	82	1.5000	15.79
21	LRATRRTDY	174	1.4000	14.74
22	MRAGLQALA	368	1.4000	14.74
23	VIAQTKAEL	225	1.3600	14.32
24	VAGGLTIIG	124	1.3000	13.68
25	LRAELRPGD	471	1.3000	13.68
26	VLNVGTAHL	209	1.2600	13.26
27	VPAIVVPPV	79	1.2000	12.63
28	MQVTTRGDG	345	1.2000	12.63
29	LEMAARHHG	185	1.1000	11.58
30	FGSREVIAQ	220	1.1000	11.58

31	VVVGTRSI	422	1.1000	11.58
32	IGPGGLFLA	40	1.0000	10.53
33	VLAARVGV	71	1.0000	10.53
34	VVLNVGTAH	208	1.0000	10.53
35	WTVLRATRR	171	0.9000	9.47
36	WIAHQPEAT	377	0.9000	9.47
37	LVKASNAAG	482	0.9000	9.47
38	LTVAQIAEI	3	0.8000	8.42
39	VCGDHQVTN	304	0.8000	8.42
40	LGEDAIAEH	398	0.8000	8.42
41	VKASNAAGL	483	0.7600	8.00
42	MIELTVAQI	0	0.7000	7.37
43	VGTAHLGEF	212	0.7000	7.37
44	LTAARVVRV	258	0.7000	7.37
45	VAAQLVAGG	119	0.6000	6.32
46	IIGITGSSG	130	0.5700	6.00
47	VAAMAKLTA	252	0.5000	5.26
48	WGSGEATAD	443	0.5000	5.26
49	LNVGTAHLG	210	0.4000	4.21
50	LLRAELRPG	470	0.4000	4.21
51	VADDTCGSV	499	0.4000	4.21

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	LVADDTCGS	498	5.9000	67.05
2	IVGGAVADI	11	3.7000	42.05
3	LNADDPAVA	245	3.6000	40.91
4	LRPGDVVLV	475	3.5800	40.68
5	VRLDVSRLV	414	3.5000	39.77
6	LTIIGITGS	128	3.3000	37.50
7	VEFDSRAIG	33	3.2000	36.36
8	VVLVKASNA	480	2.9000	32.95

9	LVVVGTGRS	421	2.8000	31.82
10	VVGTGRSIS	423	2.8000	31.82
11	VVLNVGTAH	208	2.5800	29.32
12	VRLGVCGDH	300	2.4800	28.18
13	VVLAARPVG	70	2.4000	27.27
14	LVAGGLTII	123	2.4000	27.27
15	MRAGLQALA	368	2.4000	27.27
16	MHHGAVLEG	433	2.4000	27.27
17	LGEDAIAEH	398	2.3800	27.05
18	VVRVSRDNT	263	2.3000	26.14
19	VAAMAKLTA	252	2.0000	22.73
20	VSLDELARP	279	1.9000	21.59
21	IVVPPVAAP	82	1.5000	17.05
22	LEMAARHHG	185	1.5000	17.05
23	VSRDNTGDV	266	1.5000	17.05
24	VIAQTKAEL	225	1.4000	15.91
25	VLNVGTAHL	209	1.3000	14.77
26	LILEMAARH	183	1.1800	13.41
27	VGGAVADIS	12	1.1000	12.50
28	LRATRRTDY	174	1.1000	12.50
29	LECGASVEQ	321	1.0800	12.27
30	VLVKASNAA	481	1.0000	11.36
31	VGTGRSISA	424	0.9800	11.14
32	LTVAQIAEI	3	0.9000	10.23
33	VVVGTGRSI	422	0.9000	10.23
34	VLAARPVGV	71	0.8800	10.00
35	VCGDHQVTN	304	0.8800	10.00
36	MIELTVAQI	0	0.8000	9.09
37	LAALAKLAT	109	0.8000	9.09
38	LAKLATAVA	112	0.8000	9.09
39	LVNVGTAHLG	210	0.8000	9.09
40	VKASNAAGL	483	0.8000	9.09
41	VLAALAKLA	108	0.7000	7.95
42	ITGSSGKTS	133	0.6000	6.82

43	VVLNADDDPA	243	0.6000	6.82
44	VRVSRDNTG	264	0.6000	6.82
45	VAGGLTIIG	124	0.5800	6.59
46	LTAARVVRV	258	0.5800	6.59
47	IGPGGLFLA	40	0.5000	5.68
48	VTNALCAAA	310	0.5000	5.68
49	LVKASNAAG	482	0.5000	5.68
50	FGSREVIAQ	220	0.4800	5.45
51	VSRLVVVGT	418	0.4800	5.45

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	LVADDTCS	498	5.1000	59.30
2	VRLDVSRLV	414	2.7000	31.40
3	LILEMAARH	183	2.6800	31.16
4	IGITGSSGK	131	2.2000	25.58
5	LVVVGTGRS	421	2.0000	23.26
6	LTIGITGS	128	1.8000	20.93
7	LAKLATAVA	112	1.7000	19.77
8	VLEHDNDGS	96	1.6000	18.60
9	VVLNADDDPA	243	1.6000	18.60
10	VVLNVGTAH	208	1.4800	17.21
11	LVKASNAAG	482	1.4000	16.28
12	YLILEMAAR	182	1.2000	13.95
13	LNADDDPAVA	245	1.2000	13.95
14	WIAHQPEAT	377	1.2000	13.95
15	VRVSRDNTG	264	1.0000	11.63
16	VVLVKASNA	480	1.0000	11.63
17	FTLHAHDAQ	289	0.9000	10.47
18	VLGEMAELG	391	0.9000	10.47
19	IELTVAQIA	1	0.8000	9.30
20	VSRDNTGDV	266	0.7000	8.14



21	VLNVGTAHL	209	0.5000	5.81
22	VLVKASNAA	481	0.4000	4.65
23	MIELTVAQI	0	0.3000	3.49
24	IVGGAVADI	11	0.3000	3.49
25	FLALPGARA	46	0.3000	3.49
26	FNNELGHPW	163	0.3000	3.49
27	FGSREVIAQ	220	0.2800	3.26
28	WTVLRATRR	171	0.2000	2.33
29	LRPGDVVLV	475	0.1800	2.09
30	LQALAWIAH	372	0.1600	1.86
31	VGGAVADIS	12	0.1000	1.16
32	VVGTGRSIS	423	0.1000	1.16
33	VSRLVVVGT	418	-0.0200	0
34	VKASNAAGL	483	-0.1000	0
35	VLAALAKLA	108	-0.3000	0
36	VAAQLVAGG	119	-0.3000	0
37	LGEDAIAEH	398	-0.3200	0
38	IVVPPVAAP	82	-0.4000	0
39	VAAALTAAP	330	-0.4000	0
40	VTNALCAAA	310	-0.5000	0
41	YNANPDSMR	361	-0.6000	0
42	VLAARVGV	71	-0.6200	0
43	VRLGVCGDH	300	-0.6200	0
44	VALECGASV	319	-0.7000	0
45	IGVVLVNVT	206	-0.7200	0
46	LTAARVVRV	258	-0.7200	0
47	LHAHDAQAE	291	-0.8000	0
48	LTVAQIAEI	3	-0.9000	0
49	MAKLTAARV	255	-0.9000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6
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Rank	Sequence	At Position	Score	% of Highest Score
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1	VLVKASNAA	481	3.2000	33.33
2	VRLDVSRLV	414	2.9000	30.21
3	FGSREVIAQ	220	2.6000	27.08
4	LVVVGTGRS	421	2.4000	25.00
5	LVKASNAAG	482	2.4000	25.00
6	LVADDTCGS	498	2.4000	25.00
7	LTIIGITGS	128	2.2800	23.75
8	IVGGAVADI	11	2.2000	22.92
9	LRPGDVVLV	475	2.2000	22.92
10	ILEMAARHH	184	2.1800	22.71
11	VVLVKASNA	480	2.0000	20.83
12	IGITGSSGK	131	1.8000	18.75
13	VVVGTGRSI	422	1.8000	18.75
14	IELTVAQIA	1	1.7000	17.71
15	VLNVGTAHL	209	1.7000	17.71
16	LGEFGSREV	217	1.6000	16.67
17	IGRLAVRLD	409	1.5000	15.62
18	LHAHDAQAE	291	1.4000	14.58
19	VVLNVGTAH	208	1.3800	14.37
20	LAKLATAVA	112	1.3000	13.54
21	VGTGRSISA	424	1.3000	13.54
22	LLRAELRPG	470	1.3000	13.54
23	MHHGAVLEG	433	1.2000	12.50
24	LECGASVEQ	321	1.1000	11.46
25	VLAALAKLA	108	1.0000	10.42
26	IVVPPVAAP	82	0.9000	9.38
27	VLEHDNDGS	96	0.9000	9.38
28	VAGGLTIIG	124	0.9000	9.38
29	IGVVLVNVT	206	0.6000	6.25
30	VAAALTAAP	330	0.6000	6.25
31	VLAARPVGV	71	0.5000	5.21
32	LGHPWTVLR	167	0.5000	5.21
33	VTNALCAAA	310	0.5000	5.21
34	VRLGVCGDH	300	0.4800	5.00

35	LTAARVVRV	258	0.4000	4.17
36	VSRHRMQVT	340	0.4000	4.17
37	VRVSRDNTG	264	0.2000	2.08
38	LQALAWIAH	372	0.1800	1.88
39	LTVAQIAEI	3	0.1000	1.04
40	LVAGGLTII	123	0.1000	1.04
41	LNVGTAHLG	210	0.1000	1.04
42	MIELTVAQI	0	-0.1000	0
43	VADISPQDA	16	-0.1200	0
44	LILEMAARH	183	-0.1200	0
45	LALPGARAD	47	-0.3000	0
46	VVPPVAAPN	83	-0.3000	0
47	LGVCGDHQV	302	-0.3000	0
48	VSRLVVVGT	418	-0.3000	0
49	VVGTGRSIS	423	-0.3000	0

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVGTGRS	421	4.5000	51.14
2	VVLVKASNA	480	4.1000	46.59
3	LTIIGITGS	128	3.6000	40.91
4	LVADDTCS	498	3.6000	40.91
5	LAKLATAVA	112	2.9000	32.95
6	VLNVGTAHL	209	2.9000	32.95
7	LVKASNAAG	482	2.4000	27.27
8	IGITGSSGK	131	2.3000	26.14
9	VLVKASNAA	481	1.7000	19.32
10	MIELTVAQI	0	1.5000	17.05
11	IGVVLVVGT	206	1.5000	17.05
12	VRLDVSRLV	414	1.5000	17.05
13	VVLNVGTAH	208	1.3800	15.68
14	LQALAWIAH	372	1.3600	15.45

15	LILEMAARH	183	1.0800	12.27
16	VSRLVVVGT	418	1.0000	11.36
17	IVVPPVAAP	82	0.9000	10.23
18	ILEMAARHH	184	0.7800	8.86
19	VRVSRDNTG	264	0.6000	6.82
20	VAAALTAAP	330	0.6000	6.82
21	IVGGAVADI	11	0.5000	5.68
22	VTNALCAAA	310	0.5000	5.68
23	IGRLAVRLD	409	0.5000	5.68
24	IIGITGSSG	130	0.4000	4.55
25	YLILEMAAR	182	0.4000	4.55
26	MAKLTAARV	255	0.3000	3.41
27	LALLRAELR	468	0.3000	3.41
28	VGGAVADIS	12	0.2000	2.27
29	VLAARPVG V	71	0.2000	2.27
30	LGHPWTVLR	167	0.2000	2.27
31	VVGTGRSIS	423	0.2000	2.27
32	LRPGDVVLV	475	0.2000	2.27
33	LTVAQIAEI	3	0.1000	1.14
34	VVLNADDDPA	243	0.1000	1.14
35	LTAARVVRV	258	0.1000	1.14
36	VAAQLVAGG	119	-0.1000	0
37	WTVLRATRR	171	-0.1000	0
38	VPAIVVPPV	79	-0.2000	0
39	VVPPVAAPN	83	-0.3000	0
40	VLAALAKLA	108	-0.3000	0
41	LGEFGSREV	217	-0.3000	0
42	LNADDDPAVA	245	-0.3000	0
43	VAAMAKLTA	252	-0.3000	0
44	VRLGVCGDH	300	-0.3200	0
45	VADISPQDA	16	-0.4000	0
46	LFLALPGAR	45	-0.4000	0
47	VLEHDNDGS	96	-0.4000	0
48	FLALPGARA	46	-0.5000	0

49	VEQVAAALT	327	-0.6000	0
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ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	3.5000	37.23
2	VVLVKASNA	480	3.1000	32.98
3	VLNVGT A HL	209	2.9000	30.85
4	LVKASNAAG	482	2.7000	28.72
5	LTIIGITGS	128	2.6000	27.66
6	LVADDT CGS	498	2.6000	27.66
7	IGRLAVRLD	409	2.2000	23.40
8	LAKLATAVA	112	1.9000	20.21
9	VVLNVGT AH	208	1.6000	17.02
10	LQALAWIAH	372	1.5800	16.81
11	WAGPVS LDE	275	1.5000	15.96
12	YLILEMAAR	182	1.4000	14.89
13	IGVVLNVGT	206	1.4000	14.89
14	LILEMAARH	183	1.3000	13.83
15	LCAA VALE	314	1.2000	12.77
16	WAVLGEMAE	389	1.1000	11.70
17	ILEMAARHH	184	1.0000	10.64
18	WTVLRATRR	171	0.9000	9.57
19	VRVSRDNTG	264	0.9000	9.57
20	VSRLVVVGT	418	0.9000	9.57
21	VRLDVSRLV	414	0.8000	8.51
22	MIELTVAQI	0	0.7000	7.45
23	VVPPVAAPN	83	0.7000	7.45
24	IIGITGSSG	130	0.7000	7.45
25	VLVKASNAA	481	0.7000	7.45
26	IGITGSSGK	131	0.6000	6.38
27	FGSREVIAQ	220	0.5800	6.17
28	FLALPGARA	46	0.5000	5.32

29	IVVPPVAAP	82	0.3000	3.19
30	VAAQLVAGG	119	0.2000	2.13
31	VTVIDDAYN	354	0.1000	1.06
32	LHAHDAQAE	291	-0.1000	0
33	VRLGVCGDH	300	-0.1000	0
34	LAWIAHQPE	375	-0.2000	0
35	IVGGAVADI	11	-0.3000	0
36	WGSGEATAD	443	-0.3000	0
37	MAKLTAARV	255	-0.4000	0
38	LEGAWGSGE	439	-0.4000	0
39	VADALVADD	494	-0.4000	0
40	VAPPGSFNN	157	-0.4500	0
41	VLAARPVGV	71	-0.5000	0
42	VTNALCAAA	310	-0.5000	0
43	LRPGDVVLV	475	-0.5000	0
44	VVAPPGSFN	156	-0.6000	0
45	LTAARVVRV	258	-0.6000	0
46	VKASNAAGL	483	-0.6000	0
47	LTVAQIAEI	3	-0.7000	0
48	VEQVAAALT	327	-0.7000	0
49	LGEMAELGE	392	-0.7000	0

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	LVVVG TGRS	421	3.5000	39.77
2	VVLV KASNA	480	3.1000	35.23
3	LTIIGITGS	128	2.6000	29.55
4	LVADDTCGS	498	2.6000	29.55
5	LAKLATAVA	112	1.9000	21.59
6	VLNVGTAHL	209	1.9000	21.59
7	YLILEMAAR	182	1.4000	15.91
8	LVKASNAAG	482	1.4000	15.91

9	IGITGSSGK	131	1.3000	14.77
10	WTVLRATRR	171	0.9000	10.23
11	VLVKASNAA	481	0.7000	7.95
12	MIELTVAQI	0	0.5000	5.68
13	FLALPGARA	46	0.5000	5.68
14	IGVVLNVGT	206	0.5000	5.68
15	VRLDVSRLV	414	0.5000	5.68
16	VVLNVGTAH	208	0.3800	4.32
17	LQALAWIAH	372	0.3600	4.09
18	LILEMAARH	183	0.0800	0.91
19	IVVPPVAAP	82	-0.1000	0
20	ILEMAARHH	184	-0.2200	0
21	FGSREVIAQ	220	-0.2200	0
22	VRVSRDNTG	264	-0.4000	0
23	VAAALTAAP	330	-0.4000	0
24	IVGGAVADI	11	-0.5000	0
25	VTNALCAAA	310	-0.5000	0
26	IGRLAVRLD	409	-0.5000	0
27	IIGITGSSG	130	-0.6000	0
28	MAKLTAARV	255	-0.7000	0
29	LALLRAELR	468	-0.7000	0
30	VGGAVADIS	12	-0.8000	0
31	VLAARPVGV	71	-0.8000	0
32	LGHPWTVLR	167	-0.8000	0
33	VVGTGRSIS	423	-0.8000	0
34	LRPGDVVLV	475	-0.8000	0
35	LTVAQIAEI	3	-0.9000	0
36	VVLNADDPA	243	-0.9000	0
37	LTAARVVRV	258	-0.9000	0
38	IELTVAQIA	1	-1.0000	0
39	VAAQLVAGG	119	-1.1000	0
40	VPAIVVPPV	79	-1.2000	0
41	VVPPVAAPN	83	-1.3000	0
42	VLAALAKLA	108	-1.3000	0

43	LGEFGSREV	217	-1.3000	0
44	LNADDPAVA	245	-1.3000	0
45	VAAMAKLTA	252	-1.3000	0
46	VRLGVCGDH	300	-1.3200	0
47	VADISPQDA	16	-1.4000	0
48	LFLALPGAR	45	-1.4000	0
49	VLEHDNDGS	96	-1.4000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	4.5000	47.87
2	VVLVKASNA	480	4.1000	43.62
3	VLNVGT A HL	209	3.9000	41.49
4	LVKASNAAG	482	3.7000	39.36
5	LTIIGITGS	128	3.6000	38.30
6	LVADDT CGS	498	3.6000	38.30
7	IGRLAVRLD	409	3.2000	34.04
8	LAKLATAVA	112	2.9000	30.85
9	VVLNVGT AH	208	2.6000	27.66
10	LQALAWIAH	372	2.5800	27.45
11	IGVV LNVGT	206	2.4000	25.53
12	LILEMAARH	183	2.3000	24.47
13	LCAA VALE	314	2.2000	23.40
14	ILEMAARHH	184	2.0000	21.28
15	VRVSRDNTG	264	1.9000	20.21
16	VSRLV VVGT	418	1.9000	20.21
17	VRLDV SRLV	414	1.8000	19.15
18	MIELTVAQI	0	1.7000	18.09
19	VVPPVAAPN	83	1.7000	18.09
20	IIGITGSSG	130	1.7000	18.09
21	VLVKASNAA	481	1.7000	18.09
22	IGITGSSGK	131	1.6000	17.02



23	IVVPPVAAP	82	1.3000	13.83
24	VAAQLVAGG	119	1.2000	12.77
25	VTVIDDAYN	354	1.1000	11.70
26	VAAALTAAP	330	1.0000	10.64
27	LHAHDAQAE	291	0.9000	9.57
28	VRLGVCGDH	300	0.9000	9.57
29	LAWIAHQPE	375	0.8000	8.51
30	IVGGAVADI	11	0.7000	7.45
31	MAKLTAARV	255	0.6000	6.38
32	LEGAWGSGE	439	0.6000	6.38
33	VADALVADD	494	0.6000	6.38
34	VAPPGSFNN	157	0.5500	5.85
35	VLAARPVGV	71	0.5000	5.32
36	WAGPVSLE	275	0.5000	5.32
37	VTNALCAA	310	0.5000	5.32
38	LRPGDVVLV	475	0.5000	5.32
39	VVAPPGSFN	156	0.4000	4.26
40	YLILEMAAR	182	0.4000	4.26
41	LTAARVVRV	258	0.4000	4.26
42	VKASNAAGL	483	0.4000	4.26
43	LTVAQIAEI	3	0.3000	3.19
44	VEQVAAALT	327	0.3000	3.19
45	LGEMAEELGE	392	0.3000	3.19
46	LALLRAELR	468	0.3000	3.19
47	VGGAVADIS	12	0.2000	2.13
48	VAAPNVLAG	87	0.2000	2.13
49	LGHPWTVLR	167	0.2000	2.13
50	VVGTGRSIS	423	0.2000	2.13
51	VPAIVVPPV	79	0.1000	1.06

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9		
Rank	Sequence	At Position	Score	% of Highest Score

1	LVADDTCGS	498	5.5000	61.11
2	VRLDVSRLV	414	3.7000	41.11
3	LVKASNAAG	482	2.8000	31.11
4	YLILEMAAR	182	2.7000	30.00
5	VRVSRDNTG	264	2.4000	26.67
6	LVVVGTGRS	421	2.4000	26.67
7	IGITGSSGK	131	2.3000	25.56
8	VLGEMAELG	391	2.3000	25.56
9	LTIIGITGS	128	2.2000	24.44
10	LILEMAARH	183	2.1000	23.33
11	VLEHDNDGS	96	2.0000	22.22
12	WIAHQPEAT	377	1.9000	21.11
13	LAKLATAVA	112	1.7000	18.89
14	WTVLRATRR	171	1.7000	18.89
15	VSRDNTGDV	266	1.7000	18.89
16	VVLNADDPA	243	1.6000	17.78
17	LALLRAELR	468	1.5000	16.67
18	VLNVGTAHL	209	1.4600	16.22
19	MIELTVAQI	0	1.2000	13.33
20	IVGGAVADI	11	1.2000	13.33
21	LNADDPAVA	245	1.2000	13.33
22	LRPGDVVLV	475	1.1800	13.11
23	VAAQLVAGG	119	1.1000	12.22
24	VVLVKASNA	480	1.0000	11.11
25	VVLNVGTAH	208	0.9000	10.00
26	YNANPDSMR	361	0.9000	10.00
27	VKASNAAGL	483	0.8600	9.56
28	IELTVAQIA	1	0.8000	8.89
29	VSRLVVVGT	418	0.6800	7.56
30	IVVPPVAAP	82	0.6000	6.67
31	LHAHDAQAE	291	0.6000	6.67
32	VAAALTAAP	330	0.6000	6.67
33	LGHPWTVLR	167	0.5800	6.44
34	VGGAVADIS	12	0.5000	5.56

35	VVGTGRSIS	423	0.5000	5.56
36	MHHGAVLEG	433	0.4000	4.44
37	VLVKASNAA	481	0.4000	4.44
38	VLAARPVGV	71	0.3800	4.22
39	ISPQDAAHR	19	0.3000	3.33
40	FLALPGARA	46	0.3000	3.33
41	FNNELGHPW	163	0.3000	3.33
42	VALECGASV	319	0.3000	3.33
43	LTAARVVRV	258	0.2800	3.11
44	FTLHAHDAQ	289	0.2000	2.22
45	MAKLTAARV	255	0.1000	1.11
46	IGRLAVRLD	409	0.1000	1.11
47	VAGGLTIIG	124	-0.0200	0

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	LVVVGTGRS	421	4.5000	51.14
2	VVLVKASNA	480	4.1000	46.59
3	LTIIGITGS	128	3.6000	40.91
4	LVADDTCGS	498	3.6000	40.91
5	LAKLATAVA	112	2.9000	32.95
6	VLNVGTAHL	209	2.9000	32.95
7	LVKASNAAG	482	2.4000	27.27
8	IGITGSSGK	131	2.3000	26.14
9	VLVKASNAA	481	1.7000	19.32
10	MIELTVAQI	0	1.5000	17.05
11	IGVVLVNVT	206	1.5000	17.05
12	VRLDVSRLV	414	1.5000	17.05
13	VVLNVGTAH	208	1.3800	15.68
14	LQALAWIAH	372	1.3600	15.45
15	LILEMAARH	183	1.0800	12.27
16	VSRLVVVGT	418	1.0000	11.36

17	IVVPPVAAP	82	0.9000	10.23
18	ILEMAARHH	184	0.7800	8.86
19	VRVSRDNTG	264	0.6000	6.82
20	VAAALTAAP	330	0.6000	6.82
21	IVGGAVADI	11	0.5000	5.68
22	VTNALCAAA	310	0.5000	5.68
23	IGRLAVRLD	409	0.5000	5.68
24	IIGITGSSG	130	0.4000	4.55
25	YLILEMAAR	182	0.4000	4.55
26	MAKLTAARV	255	0.3000	3.41
27	LALLRAELR	468	0.3000	3.41
28	VGGAVADIS	12	0.2000	2.27
29	VLAARPVGV	71	0.2000	2.27
30	LGHPWTVLR	167	0.2000	2.27
31	VVGTGRSIS	423	0.2000	2.27
32	LRPGDVVLV	475	0.2000	2.27
33	LTVAQIAEI	3	0.1000	1.14
34	VVLNADDPA	243	0.1000	1.14
35	LTAARVVRV	258	0.1000	1.14
36	VAAQLVAGG	119	-0.1000	0
37	WTVLRATRR	171	-0.1000	0
38	VPAIVVPPV	79	-0.2000	0
39	VVPPVAAPN	83	-0.3000	0
40	VLAALAKLA	108	-0.3000	0
41	LGEFGSREV	217	-0.3000	0
42	LNADDPAVA	245	-0.3000	0
43	VAAMAKLTA	252	-0.3000	0
44	VRLGVCGDH	300	-0.3200	0
45	VADISPQDA	16	-0.4000	0
46	LFLALPGAR	45	-0.4000	0
47	VLEHDNDGS	96	-0.4000	0
48	FLALPGARA	46	-0.5000	0
49	VEQVAAALT	327	-0.6000	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	LVADDTCGS	498	5.1000	59.30
2	VRLDVSRLV	414	2.7000	31.40
3	LILEMAARH	183	2.6800	31.16
4	IGITGSSGK	131	2.2000	25.58
5	LVVVG TGRS	421	2.0000	23.26
6	LTIIGITGS	128	1.8000	20.93
7	LAKLATAVA	112	1.7000	19.77
8	VLEHDNDGS	96	1.6000	18.60
9	VVLNADDPA	243	1.6000	18.60
10	VVLNVGTAH	208	1.4800	17.21
11	LVKASNAAG	482	1.4000	16.28
12	YLILEMAAR	182	1.2000	13.95
13	LNADDPAVA	245	1.2000	13.95
14	WIAHQPEAT	377	1.2000	13.95
15	VRVSRDNTG	264	1.0000	11.63
16	VVLVKASNA	480	1.0000	11.63
17	FTLHAHDAQ	289	0.9000	10.47
18	VLGEMAELG	391	0.9000	10.47
19	IELTVAQIA	1	0.8000	9.30
20	VSRDNTGDV	266	0.7000	8.14
21	VLNVGTAHL	209	0.5000	5.81
22	VLVKASNAA	481	0.4000	4.65
23	MIELTVAQI	0	0.3000	3.49
24	IVGGAVADI	11	0.3000	3.49
25	FLALPGARA	46	0.3000	3.49
26	FNNELGHPW	163	0.3000	3.49
27	FGSREVIAQ	220	0.2800	3.26
28	WTVLRATRR	171	0.2000	2.33
29	LRPGDVVLV	475	0.1800	2.09
30	LQALAWIAH	372	0.1600	1.86

31	VGGAVADIS	12	0.1000	1.16
32	VVGTGRSIS	423	0.1000	1.16
33	VSRLVVVGT	418	-0.0200	0
34	VKASNAAGL	483	-0.1000	0
35	VLAALAKLA	108	-0.3000	0
36	VAAQLVAGG	119	-0.3000	0
37	LGEDAIAEH	398	-0.3200	0
38	IVVPPVAAP	82	-0.4000	0
39	VAAALTAAP	330	-0.4000	0
40	VTNALCAAA	310	-0.5000	0
41	YNANPDSMR	361	-0.6000	0
42	VLAARVGV	71	-0.6200	0
43	VRLGVCGDH	300	-0.6200	0
44	VALECGASV	319	-0.7000	0
45	IGVVLNVGT	206	-0.7200	0
46	LTAARVVRV	258	-0.7200	0
47	LHAHDAQAE	291	-0.8000	0
48	LTVAQIAEI	3	-0.9000	0
49	MAKLTAARV	255	-0.9000	0

ALLELE: DRB1_0701		Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6	
Rank	Sequence	At Position	Score	% of Highest Score
1	VPHSGAVVL	237	5.2000	44.83
2	VKASNAAGL	483	5.0000	43.10
3	VLNVGTAHL	209	4.7200	40.69
4	LRPGDVVLV	475	4.1000	35.34
5	VVGTGRSI	422	4.0000	34.48
6	VRLDVSRLV	414	3.9000	33.62
7	IVGGAVADI	11	3.7000	31.90
8	LRATRRTDY	174	3.5000	30.17
9	LVAGGLTII	123	3.4000	29.31
10	VVLVKASNA	480	3.4000	29.31

11	VLAARPVGV	71	3.1000	26.72
12	VAAGAAVVL	64	2.9000	25.00
13	LTAARVVRV	258	2.7000	23.28
14	IELTVAQIA	1	2.6000	22.41
15	LMAAVLAPL	145	2.6000	22.41
16	LTVAQIAEI	3	2.4000	20.69
17	LATAVAAQL	115	2.4000	20.69
18	LDVSRLVVV	416	2.4000	20.69
19	IGITGSSGK	131	2.3000	19.83
20	IGVVLNVGT	206	2.3000	19.83
21	LVVVGTGRS	421	2.1200	18.28
22	WIAHQPEAT	377	2.0000	17.24
23	LGEFGSREV	217	1.8000	15.52
24	LTIIGITGS	128	1.7000	14.66
25	VVGTGRSIS	423	1.7000	14.66
26	MIELTVAQI	0	1.6000	13.79
27	LAEIAPPSI	198	1.6000	13.79
28	VPAIVVPPV	79	1.5000	12.93
29	VPPVAAPNV	84	1.5000	12.93
30	VRVSRDNTG	264	1.5000	12.93
31	WAGPVSLDE	275	1.5000	12.93
32	VGTGRSISA	424	1.4000	12.07
33	FGSREVIAQ	220	1.2000	10.34
34	VLVKASNAA	481	1.2000	10.34
35	VLAPLGEVV	149	1.1000	9.48
36	VVLNVGTAH	208	1.1000	9.48
37	FNNELGHPW	163	1.0000	8.62
38	VIAQTKAEL	225	0.9000	7.76
39	VRLGVCGDH	300	0.9000	7.76
40	VGTAHLGEF	212	0.7000	6.03
41	IAQTKAELP	226	0.7000	6.03
42	VVRVSRDNT	263	0.7000	6.03
43	LHAHDAQAE	291	0.7000	6.03
44	LQALAWIAH	372	0.7000	6.03

45	VSRLVVVGT	418	0.7000	6.03
46	IIGITGSSG	130	0.6000	5.17
47	MHHGAVLEG	433	0.6000	5.17
48	VLAALAKLA	108	0.5000	4.31
49	MAARHHGNI	187	0.5000	4.31
50	LGVCGDHQV	302	0.4000	3.45
51	VEQVAAALT	327	0.4000	3.45

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	VPHSGAVVL	237	5.2000	44.83
2	VKASNAAGL	483	5.0000	43.10
3	VLNVGTAHL	209	4.7200	40.69
4	LRPGDVVLV	475	4.1000	35.34
5	VVVG TGRSI	422	4.0000	34.48
6	VRLDVSRLV	414	3.9000	33.62
7	IVGGAVADI	11	3.7000	31.90
8	LRATRRTDY	174	3.5000	30.17
9	LVAGGLTII	123	3.4000	29.31
10	VVLVKASNA	480	3.4000	29.31
11	VLAARPVGV	71	3.1000	26.72
12	VAAGAAVVL	64	2.9000	25.00
13	LTAARVVRV	258	2.7000	23.28
14	IELTVAQIA	1	2.6000	22.41
15	LMAAVLAPL	145	2.6000	22.41
16	LTVAQIAEI	3	2.4000	20.69
17	LATAVAAQL	115	2.4000	20.69
18	LDVSRLVVV	416	2.4000	20.69
19	IGITGSSGK	131	2.3000	19.83
20	IGVVLNVGT	206	2.3000	19.83
21	LVVVG TGRS	421	2.1200	18.28
22	WIAHQPEAT	377	2.0000	17.24



23	LGEFGSREV	217	1.8000	15.52
24	LTIIGITGS	128	1.7000	14.66
25	VVGTGRSIS	423	1.7000	14.66
26	MIELTVAQI	0	1.6000	13.79
27	LAEIAPPSI	198	1.6000	13.79
28	VPAIVVPPV	79	1.5000	12.93
29	VPPVAAPNV	84	1.5000	12.93
30	VRVSRDNTG	264	1.5000	12.93
31	WAGPVSLE	275	1.5000	12.93
32	VGTGRSISA	424	1.4000	12.07
33	FGSREVIAQ	220	1.2000	10.34
34	VLVKASNAA	481	1.2000	10.34
35	VLAPLGEVV	149	1.1000	9.48
36	VVLNVGTAH	208	1.1000	9.48
37	FNNELGHPW	163	1.0000	8.62
38	VIAQTKAEL	225	0.9000	7.76
39	VRLGVCGDH	300	0.9000	7.76
40	VGTAHLGEF	212	0.7000	6.03
41	IAQTKAELP	226	0.7000	6.03
42	VVRVSRDNT	263	0.7000	6.03
43	LHAHDAQAE	291	0.7000	6.03
44	LQALAWIAH	372	0.7000	6.03
45	VSRLVVVGT	418	0.7000	6.03
46	IIGITGSSG	130	0.6000	5.17
47	MHHGAVLEG	433	0.6000	5.17
48	VLAALAKLA	108	0.5000	4.31
49	MAARHHGNI	187	0.5000	4.31
50	LGVCGDHQV	302	0.4000	3.45
51	VEQVAAALT	327	0.4000	3.45

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	FGSREVIAQ	220	4.7000	54.65
2	LVVVGTGRS	421	2.9000	33.72
3	IGRLAVRLD	409	2.5000	29.07
4	VVLAARPVG	70	2.2000	25.58
5	VLRATRRTD	173	2.1000	24.42
6	VRLGVCGDH	300	2.0000	23.26
7	FDSRAIGPG	35	1.7000	19.77
8	VLNVGTAHL	209	1.6000	18.60
9	LVADDTCS	498	1.6000	18.60
10	LCAAVALE	314	1.5000	17.44
11	IVGGAVADI	11	1.4000	16.28
12	LILEMAARH	183	1.4000	16.28
13	VAAMAKLTA	252	1.4000	16.28
14	VLVKASNAA	481	1.4000	16.28
15	YLILEMAAR	182	1.3000	15.12
16	LAARPVGVP	72	1.1000	12.79
17	VVLVKASNA	480	1.1000	12.79
18	FLALPGARA	46	1.0000	11.63
19	VVPPVAAPN	83	1.0000	11.63
20	LRAELRPGD	471	1.0000	11.63
21	IVVPPVAAP	82	0.9000	10.47
22	ILEMAARHH	184	0.9000	10.47
23	LEMAARHHG	185	0.9000	10.47
24	WAVLGEMAE	389	0.8000	9.30
25	LVKASNAAG	482	0.8000	9.30
26	MIELTVAQI	0	0.7000	8.14
27	VVGTGRSIS	423	0.7000	8.14
28	MAARHHGNI	187	0.6000	6.98
29	LLRAELRPG	470	0.6000	6.98
30	LAKLATAVA	112	0.5000	5.81
31	MQVTTRGDG	345	0.5000	5.81
32	LAALAKLAT	109	0.4000	4.65
33	VIAQTKAEL	225	0.4000	4.65
34	VVRVSRDNT	263	0.4000	4.65

35	LMAAVLAPL	145	0.3000	3.49
36	VVLNVGTAH	208	0.3000	3.49
37	VEFDSRAIG	33	0.2000	2.33
38	MHHGAVLEG	433	0.2000	2.33
39	LRPGDVVLV	475	0.2000	2.33
40	LTVAQIAEI	3	0.1000	1.16
41	WAGPVSLE	275	0.1000	1.16
42	VRLDVSRLV	414	0.1000	1.16
43	MRAGLQALA	368	-0.1000	0
44	VSRLVVVGT	418	-0.1000	0
45	VADALVADD	494	-0.1000	0
46	LFLALPGAR	45	-0.2000	0
47	LTIIGITGS	128	-0.2000	0
48	VAAQLVAGG	119	-0.5000	0
49	VTNALCAAA	310	-0.5000	0

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	FGSREVIAQ	220	3.9000	48.75
2	LVVVGTGRS	421	2.9000	36.25
3	LVADDTCS	498	1.6000	20.00
4	VAAMAKLTA	252	1.4000	17.50
5	VLVKASNAA	481	1.4000	17.50
6	YLILEMAAR	182	1.3000	16.25
7	IVGGAVADI	11	1.2000	15.00
8	VVLVKASNA	480	1.1000	13.75
9	FLALPGARA	46	1.0000	12.50
10	VVLAARPVG	70	0.9000	11.25
11	VRLGVCGDH	300	0.7800	9.75
12	LAARPVGVP	72	0.7000	8.75
13	VVGTGRSIS	423	0.7000	8.75
14	VLNVGTAHL	209	0.6000	7.50

15	MIELTVAQI	0	0.5000	6.25
16	IVVPPVAAP	82	0.5000	6.25
17	LAKLATAVA	112	0.5000	6.25
18	FDSRAIGPG	35	0.4000	5.00
19	MAARHHGNI	187	0.4000	5.00
20	LILEMAARH	183	0.1800	2.25
21	LTVAQIAEI	3	-0.1000	0
22	MRAGLQALA	368	-0.1000	0
23	LRPGDVVLV	475	-0.1000	0
24	LFLALPGAR	45	-0.2000	0
25	LTIIGITGS	128	-0.2000	0
26	IGRLAVRLD	409	-0.2000	0
27	VRLDVSRLV	414	-0.2000	0
28	ILEMAARHH	184	-0.3200	0
29	LEMAARHHG	185	-0.4000	0
30	LAALAKLAT	109	-0.5000	0
31	VVRVSRDNT	263	-0.5000	0
32	VTNALCAAA	310	-0.5000	0
33	LVKASNAAG	482	-0.5000	0
34	VLRATRRTD	173	-0.6000	0
35	VIAQTKAEL	225	-0.6000	0
36	LMAAVLAPL	145	-0.7000	0
37	LNADDPAVA	245	-0.7000	0
38	LLRAELRPG	470	-0.7000	0
39	VLAALAKLA	108	-0.8000	0
40	MQVTTRGDG	345	-0.8000	0
41	VVLNVGTAH	208	-0.9200	0
42	VVPPVAAPN	83	-1.0000	0
43	MAKLTAARV	255	-1.0000	0
44	VSRLVVVGT	418	-1.0000	0
45	VVVGTGRSI	422	-1.0000	0
46	VEFDSRAIG	33	-1.1000	0
47	MHHGAVLEG	433	-1.1000	0
48	ISAMHHGAV	430	-1.2000	0

49	LQALAWIAH	372	-1.2200	0
50	VLAARPVGV	71	-1.3000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	3.9000	48.75
2	FGSRE VIAQ	220	2.9000	36.25
3	LVADD TC GS	498	2.6000	32.50
4	VAAMA KLTA	252	2.4000	30.00
5	VLVKAS NAA	481	2.4000	30.00
6	IVGGAV ADI	11	2.2000	27.50
7	VVLVKAS NA	480	2.1000	26.25
8	VVLAAR PVG	70	1.9000	23.75
9	VRLGVC GDH	300	1.7800	22.25
10	LAARPV GVP	72	1.7000	21.25
11	VVGTGR SIS	423	1.7000	21.25
12	VLNVGT AHL	209	1.6000	20.00
13	MIELTVA QI	0	1.5000	18.75
14	IVVPPVA AP	82	1.5000	18.75
15	LAKLATA VA	112	1.5000	18.75
16	MAARHH GNI	187	1.4000	17.50
17	LILEMA ARH	183	1.1800	14.75
18	LTVAQIA EI	3	0.9000	11.25
19	MRAGLQ ALA	368	0.9000	11.25
20	LRPGDV VLV	475	0.9000	11.25
21	LFLALPG AR	45	0.8000	10.00
22	LTIIGIT GS	128	0.8000	10.00
23	IGRLAV RLD	409	0.8000	10.00
24	VRLDVS RLV	414	0.8000	10.00
25	ILEMAAR HH	184	0.6800	8.50
26	LEMAAR HHG	185	0.6000	7.50
27	LAALAK LAT	109	0.5000	6.25

28	VVRVSRDNT	263	0.5000	6.25
29	VTNALCAAA	310	0.5000	6.25
30	LVKASNAAG	482	0.5000	6.25
31	VLRATRRTD	173	0.4000	5.00
32	VIAQTKAEL	225	0.4000	5.00
33	LMAAVLAPL	145	0.3000	3.75
34	YLILEMAAR	182	0.3000	3.75
35	LNADDPAVA	245	0.3000	3.75
36	LLRAELRPG	470	0.3000	3.75
37	VLAALAKLA	108	0.2000	2.50
38	MQVTTRGDG	345	0.2000	2.50
39	VVLNVGTAH	208	0.0800	1.00
40	VEFDSRAIG	33	-0.1000	0
41	MHHGAVLEG	433	-0.1000	0
42	ISAMHHGAV	430	-0.2000	0
43	LQALAWIAH	372	-0.2200	0
44	VLAARPVGV	71	-0.3000	0
45	LCAAVALE	314	-0.5000	0

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	LVVVG TGRS	421	3.9000	45.35
2	FGSRE VIAQ	220	3.7000	43.02
3	IGRLAVRLD	409	3.5000	40.70
4	VVLAARPVG	70	3.2000	37.21
5	VLRATRRTD	173	3.1000	36.05
6	VRLGVCGDH	300	3.0000	34.88
7	VLNVGTAHL	209	2.6000	30.23
8	LVADDTCGS	498	2.6000	30.23
9	LCAAVALE	314	2.5000	29.07
10	IVGGAVADI	11	2.4000	27.91
11	LILEMAARH	183	2.4000	27.91

12	VAAMAKLTA	252	2.4000	27.91
13	VLVKASNAA	481	2.4000	27.91
14	LAARPVGVP	72	2.1000	24.42
15	VVLVKASNA	480	2.1000	24.42
16	VVPPVAAPN	83	2.0000	23.26
17	LRAELRPGD	471	2.0000	23.26
18	IVVPPVAAP	82	1.9000	22.09
19	ILEMAARHH	184	1.9000	22.09
20	LEMAARHHG	185	1.9000	22.09
21	LVKASNAAG	482	1.8000	20.93
22	MIELTVAQI	0	1.7000	19.77
23	VVGTGRSIS	423	1.7000	19.77
24	MAARHHGNI	187	1.6000	18.60
25	LLRAELRPG	470	1.6000	18.60
26	LAKLATAVA	112	1.5000	17.44
27	MQVTTRGDG	345	1.5000	17.44
28	LAALAKLAT	109	1.4000	16.28
29	VIAQTKAEL	225	1.4000	16.28
30	VVRVSRDNT	263	1.4000	16.28
31	LMAAVLAPL	145	1.3000	15.12
32	VVLNVGTAH	208	1.3000	15.12
33	VEFDSRAIG	33	1.2000	13.95
34	MHHGAVLEG	433	1.2000	13.95
35	LRPGDVVLV	475	1.2000	13.95
36	LTVAQIAEI	3	1.1000	12.79
37	VRLDVSRLV	414	1.1000	12.79
38	LQALAWIAH	372	1.0000	11.63
39	MRAGLQALA	368	0.9000	10.47
40	VSRLVVVGT	418	0.9000	10.47
41	VADALVADD	494	0.9000	10.47
42	LFLALPGAR	45	0.8000	9.30
43	LTIIGITGS	128	0.8000	9.30
44	FDSRAIGPG	35	0.7000	8.14
45	VAAQLVAGG	119	0.5000	5.81

46	VTNALCAAA	310	0.5000	5.81
47	LALPGARAD	47	0.4000	4.65
48	YLILEMAAR	182	0.3000	3.49
49	LNADDPAVA	245	0.3000	3.49
50	MAKLTAARV	255	0.3000	3.49
51	LAWIAHQPE	375	0.3000	3.49

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	FGSREVIAQ	220	4.7800	54.94
2	VLVKASNAA	481	3.4000	39.08
3	VVLVKASNA	480	2.9000	33.33
4	LTIIGITGS	128	2.6000	29.89
5	VVGTGRSIS	423	2.5000	28.74
6	LVVVGTGRS	421	2.2000	25.29
7	VAAMAKLTA	252	2.0000	22.99
8	VVLNVGTAH	208	1.8800	21.61
9	LVADDTCGS	498	1.6000	18.39
10	YLILEMAAR	182	1.3000	14.94
11	IVGGAVADI	11	1.2000	13.79
12	VVLAARPVG	70	1.1000	12.64
13	FLALPGARA	46	1.0000	11.49
14	LRPGDVVLV	475	0.9000	10.34
15	VVRVSRDNT	263	0.7000	8.05
16	WTVLRATTR	171	0.6000	6.90
17	LRATRRTDY	174	0.6000	6.90
18	VLNVGTAHL	209	0.6000	6.90
19	MIELTVAQI	0	0.5000	5.75
20	IVVPPVAAP	82	0.5000	5.75
21	LAKLATAVA	112	0.5000	5.75
22	LVAGGLTII	123	0.4000	4.60
23	LILEMAARH	183	0.1800	2.07



24	LAALAKLAT	109	0.1000	1.15
25	IGITGSSGK	131	0.1000	1.15
26	LEMAARHHG	185	0.1000	1.15
27	VRLGVCGDH	300	0.0800	0.92
28	LTVAQIAEI	3	-0.1000	0
29	MRAGLQALA	368	-0.1000	0
30	FDSRAIGPG	35	-0.3000	0
31	VLAARPVGV	71	-0.3000	0
32	MAARHHGNI	187	-0.3000	0
33	LQALAWIAH	372	-0.3400	0
34	VTNALCAA	310	-0.5000	0
35	IGRLAVRLD	409	-0.5000	0
36	VRLDVSRLV	414	-0.5000	0
37	MHHGAVLEG	433	-0.5000	0
38	LVKASNAAG	482	-0.5000	0
39	IIGITGSSG	130	-0.6000	0
40	VIAQTKAEL	225	-0.6000	0
41	LTAARVVRV	258	-0.6000	0
42	ILEMAARHH	184	-0.6200	0
43	LMAAVLAPL	145	-0.7000	0
44	LNADDPAVA	245	-0.7000	0
45	VGGAVADIS	12	-0.8000	0
46	FTLHAHDAQ	289	-0.8000	0
47	LFLALPGAR	45	-0.9000	0
48	VLRATRRTD	173	-0.9000	0

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	FGSREVIAQ	220	6.3000	62.38
2	VVLAARPVG	70	3.3500	33.17
3	VAAMAKLTA	252	3.2000	31.68
4	LVVVG TGRS	421	3.0000	29.70

5	IGRLAVRLD	409	2.7000	26.73
6	WAVLGEMAE	389	2.4000	23.76
7	VLRATRRTD	173	2.3000	22.77
8	LAALAKLAT	109	2.2000	21.78
9	LRAELRPGD	471	2.1500	21.29
10	VRLGVCGDH	300	2.1000	20.79
11	MHHGAVLEG	433	2.0000	19.80
12	WAGPVSLE	275	1.9000	18.81
13	FDSRAIGPG	35	1.8000	17.82
14	VLVKASNAA	481	1.7000	16.83
15	LEMAARHHG	185	1.6000	15.84
16	VLNVGTAHL	209	1.6000	15.84
17	LQALAWIAH	372	1.6000	15.84
18	LVADDTCS	498	1.6000	15.84
19	LCAAVALE	314	1.5000	14.85
20	IVGGAVADI	11	1.4000	13.86
21	LILEMAARH	183	1.4000	13.86
22	VVLNVGTAH	208	1.4000	13.86
23	YLILEMAAR	182	1.3000	12.87
24	LAARPVGVP	72	1.2000	11.88
25	ILEMAARHH	184	1.1000	10.89
26	LGEMAELE	392	1.1000	10.89
27	VVLVKASNA	480	1.1000	10.89
28	FLALPGARA	46	1.0000	9.90
29	VVPPVAAPN	83	1.0000	9.90
30	VAAPNVLAG	87	1.0000	9.90
31	IVVPPVAAP	82	0.9000	8.91
32	LTIIGITGS	128	0.9000	8.91
33	LLRAELRPG	470	0.8000	7.92
34	LVKASNAAG	482	0.8000	7.92
35	MIELTVAQI	0	0.7000	6.93
36	MAARHHGNI	187	0.7000	6.93
37	VVGTGRSIS	423	0.7000	6.93
38	LRPGDVVLV	475	0.7000	6.93

39	MQVTTRGDG	345	0.6000	5.94
40	LAKLATAVA	112	0.5000	4.95
41	VIAQTKAEL	225	0.4000	3.96
42	VSRLVVVGT	418	0.4000	3.96
43	LMAAVLAPL	145	0.3000	2.97
44	VRLDVSRLV	414	0.3000	2.97
45	VEFDSRAIG	33	0.2000	1.98
46	LTVAQIAEI	3	0.1000	0.99
47	VAGGLTIIG	124	0.1000	0.99
48	VVRVSRDNT	263	0.1000	0.99
49	LFLALPGAR	45	-0.1000	0

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	LVVVGTGRS	421	3.1000	37.35
2	VAAMAKLTA	252	2.8000	33.73
3	FGSREVIAQ	220	2.5000	30.12
4	VVLAARPVG	70	2.0500	24.70
5	LAALAKLAT	109	1.7000	20.48
6	YLILEMAAR	182	1.7000	20.48
7	LTIIGITGS	128	1.5000	18.07
8	FLALPGARA	46	1.4000	16.87
9	VVLVKASNA	480	1.2000	14.46
10	VVGTGRSIS	423	1.1000	13.25
11	MIELTVAQI	0	0.9000	10.84
12	LAKLATAVA	112	0.9000	10.84
13	LVADDTCS	498	0.9000	10.84
14	LQALAWIAH	372	0.7800	9.40
15	VLNVGTAHL	209	0.7000	8.43
16	IVGGAVADI	11	0.5000	6.02
17	IGRLAVRLD	409	0.4000	4.82
18	LEMAARHHG	185	0.3000	3.61

19	VVLNVGTAH	208	0.1800	2.17
20	VRLGVCGDH	300	0.1800	2.17
21	LTVAQIAEI	3	-0.1000	0
22	LFLALPGAR	45	-0.1000	0
23	VSRLVVVGT	418	-0.1000	0
24	VPAIVVPPV	79	-0.1500	0
25	IVVPPVAAP	82	-0.2000	0
26	VLAALAKLA	108	-0.2000	0
27	WAVLGEMAE	389	-0.2000	0
28	MQVTTRGDG	345	-0.3000	0
29	LRPGDVVLV	475	-0.3000	0
30	VLRATRRTD	173	-0.4000	0
31	VTNALCAAA	310	-0.5000	0
32	LLRAELRPG	470	-0.5000	0
33	LVKASNAAG	482	-0.5000	0
34	LILEMAARH	183	-0.5200	0
35	ILEMAARHH	184	-0.5200	0
36	MAKLTAARV	255	-0.6000	0
37	LMAAVLAPL	145	-0.7000	0
38	WTVLRATRR	171	-0.7000	0
39	LRATRRTDY	174	-0.7000	0
40	VVRVSRDNT	263	-0.7000	0
41	VRLDVSRLV	414	-0.7000	0
42	VLAARPVGV	71	-0.8000	0
43	MRAGLQALA	368	-0.8000	0
44	VAAPNVLAG	87	-1.0000	0
45	LTAARVVRV	258	-1.1000	0
46	VLVKASNAA	481	-1.1000	0
47	LAEIAPPSI	198	-1.1500	0
48	VAAQLVAGG	119	-1.2000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	2.6000	30.95
2	VAAMAKLTA	252	2.5000	29.76
3	IGRLAVRLD	409	2.3000	27.38
4	VLVKASNAA	481	2.3000	27.38
5	VLRASTRRTD	173	2.2000	26.19
6	VRLDVSRLV	414	2.2000	26.19
7	LVADDTCS	498	2.2000	26.19
8	LLRAELRPG	470	2.1000	25.00
9	VIAQTKAEL	225	2.0000	23.81
10	VVGTGRSIS	423	2.0000	23.81
11	ILEMAARHH	184	1.8800	22.38
12	LEMAARHHG	185	1.8000	21.43
13	IVGGAVADI	11	1.7000	20.24
14	LVVVGTRGS	421	1.7000	20.24
15	VVLNVGTAH	208	1.6800	20.00
16	LTIIGITGS	128	1.4000	16.67
17	LRPGDVVLV	475	1.4000	16.67
18	VVVGTRSI	422	1.3000	15.48
19	VVLVKASNA	480	1.3000	15.48
20	MIELTVAQI	0	1.2000	14.29
21	LAKLATAVA	112	1.2000	14.29
22	FGSREVIAQ	220	1.1000	13.10
23	LILEMAARH	183	1.0800	12.86
24	IVVPPVAAP	82	1.0000	11.90
25	VLAALAKLA	108	1.0000	11.90
26	LTVAQIAEI	3	0.9000	10.71
27	LAALAKLAT	109	0.9000	10.71
28	VAAQLVAGG	119	0.8000	9.52
29	VLAARPVG	71	0.7000	8.33
30	VSRLVVVGT	418	0.7000	8.33
31	LGEFGSREV	217	0.5000	5.95
32	VTNALCAAA	310	0.5000	5.95
33	LVKASNAAG	482	0.5000	5.95

34	VLNVGTAHL	209	0.4000	4.76
35	LTAARVVRV	258	0.4000	4.76
36	FTLHAHDAQ	289	0.4000	4.76
37	MRAGLQALA	368	0.4000	4.76
38	LMAAVLAPL	145	0.3000	3.57
39	VRLGVCGDH	300	0.2800	3.33
40	LRATRRTDY	174	0.2000	2.38
41	VVRVSRDNT	263	0.2000	2.38
42	LHAHDAQAE	291	0.2000	2.38
43	IGPGGLFLA	40	0.1000	1.19
44	MHHGAVLEG	433	0.1000	1.19
45	VGGAVADIS	12	-0.1000	0
46	VLEHDNDGS	96	-0.1000	0
47	LNADDPAVA	245	-0.1000	0
48	WIAHQPEAT	377	-0.1000	0
49	LRAELRPGD	471	-0.1000	0

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	LVVVGTGRS	421	4.1000	49.40
2	VAAMAKLTA	252	3.8000	45.78
3	VVLAARPVG	70	3.0500	36.75
4	LAALAKLAT	109	2.7000	32.53
5	LTIIGITGS	128	2.5000	30.12
6	VVLVKASNA	480	2.2000	26.51
7	VVGTGRSIS	423	2.1000	25.30
8	MIELTVAQI	0	1.9000	22.89
9	LAKLATAVA	112	1.9000	22.89
10	LVADDTCGS	498	1.9000	22.89
11	LQALAWIAH	372	1.7800	21.45
12	VLNVGTAHL	209	1.7000	20.48
13	IVGGAVADI	11	1.5000	18.07

14	FGSREVIAQ	220	1.5000	18.07
15	IGRLAVRLD	409	1.4000	16.87
16	LEMAARHHG	185	1.3000	15.66
17	VVLNVGTAH	208	1.1800	14.22
18	VRLGVCGDH	300	1.1800	14.22
19	VIAQTKAEL	225	1.0000	12.05
20	MHHGAVLEG	433	1.0000	12.05
21	LTVAQIAEI	3	0.9000	10.84
22	LFLALPGAR	45	0.9000	10.84
23	VSRLVVVGT	418	0.9000	10.84
24	VPAIVVPPV	79	0.8500	10.24
25	IVVPPVAAP	82	0.8000	9.64
26	VLAALAKLA	108	0.8000	9.64
27	YLILEMAAR	182	0.7000	8.43
28	MQVTTRGDG	345	0.7000	8.43
29	LRPGDVVLV	475	0.7000	8.43
30	VLRATRRTD	173	0.6000	7.23
31	VTNALCAAA	310	0.5000	6.02
32	LLRAELRPG	470	0.5000	6.02
33	LVKASNAAG	482	0.5000	6.02
34	LILEMAARH	183	0.4800	5.78
35	ILEMAARHH	184	0.4800	5.78
36	FLALPGARA	46	0.4000	4.82
37	MAKLTAARV	255	0.4000	4.82
38	LMAAVLAPL	145	0.3000	3.61
39	LRATRRTDY	174	0.3000	3.61
40	VVRVSRDNT	263	0.3000	3.61
41	VRLDVSRLV	414	0.3000	3.61
42	VLAARPVGV	71	0.2000	2.41
43	MRAGLQALA	368	0.2000	2.41
44	LTAARVVRV	258	-0.1000	0
45	VLVKASNAA	481	-0.1000	0
46	LAEIAPPSI	198	-0.1500	0
47	VAAQLVAGG	119	-0.2000	0

48	LALLRAELR	468	-0.2000	0
49	LRAELRPGD	471	-0.2500	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	4.1000	49.40
2	VAAMAKLTA	252	3.8000	45.78
3	VVLAARPVG	70	3.0500	36.75
4	LAALAKLAT	109	2.7000	32.53
5	LTIIGITGS	128	2.5000	30.12
6	VVLVKASNA	480	2.2000	26.51
7	VVGTGRSIS	423	2.1000	25.30
8	MIELTVAQI	0	1.9000	22.89
9	LAKLATAVA	112	1.9000	22.89
10	LVADDTCS	498	1.9000	22.89
11	LQALAWIAH	372	1.7800	21.45
12	VLNVGTAHL	209	1.7000	20.48
13	IVGGAVADI	11	1.5000	18.07
14	FGSREVIAQ	220	1.5000	18.07
15	IGRLAVRLD	409	1.4000	16.87
16	LEMAARHHG	185	1.3000	15.66
17	VVLNVGTAH	208	1.1800	14.22
18	VRLGVCGDH	300	1.1800	14.22
19	VIAQTKAEL	225	1.0000	12.05
20	MHHGAVLEG	433	1.0000	12.05
21	LTVAQIAEI	3	0.9000	10.84
22	LFLALPGAR	45	0.9000	10.84
23	VSRLVVVGT	418	0.9000	10.84
24	VPAIVPPV	79	0.8500	10.24
25	IVVPPVAAP	82	0.8000	9.64
26	VLAALAKLA	108	0.8000	9.64
27	YLILEMAAR	182	0.7000	8.43



28	MQVTTRGDG	345	0.7000	8.43
29	LRPGDVVLV	475	0.7000	8.43
30	VLRATRRTD	173	0.6000	7.23
31	VTNALCAAA	310	0.5000	6.02
32	LLRAELRPG	470	0.5000	6.02
33	LVKASNAAG	482	0.5000	6.02
34	LILEMAARH	183	0.4800	5.78
35	ILEMAARHH	184	0.4800	5.78
36	FLALPGARA	46	0.4000	4.82
37	MAKLTAARV	255	0.4000	4.82
38	LMAAVLAPL	145	0.3000	3.61
39	LRATRRTDY	174	0.3000	3.61
40	VVRVSRDNT	263	0.3000	3.61
41	VRLDVSRLV	414	0.3000	3.61
42	VLAARPVG	71	0.2000	2.41
43	MRAGLQALA	368	0.2000	2.41
44	LTAARVVRV	258	-0.1000	0
45	VLVKASNAA	481	-0.1000	0
46	LAEIAPPSI	198	-0.1500	0
47	VAAQLVAGG	119	-0.2000	0
48	LALLRAELR	468	-0.2000	0
49	LRAELRPGD	471	-0.2500	0

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVADDTCS	498	5.9000	64.84
2	LVVVGTRGS	421	4.2000	46.15
3	VRLGVCGDH	300	3.8800	42.64
4	VVLAARPVG	70	3.8000	41.76
5	VRLDVSRLV	414	3.8000	41.76
6	IVGGAVADI	11	3.7000	40.66
7	LRPGDVVLV	475	3.7000	40.66

8	LNADDDPAVA	245	3.6000	39.56
9	LTIIGITGS	128	3.3000	36.26
10	VEFDSRAIG	33	3.2000	35.16
11	VVLVKASNA	480	3.1700	34.84
12	VVGTGRSIS	423	3.0700	33.74
13	VSRDNTGDV	266	2.9000	31.87
14	VVLNVGTAH	208	2.5800	28.35
15	LVAGGLTII	123	2.4000	26.37
16	MRAGLQALA	368	2.4000	26.37
17	LGEDAIAEH	398	2.3800	26.15
18	IGPGGLFLA	40	2.0000	21.98
19	VVRVSRDNT	263	2.0000	21.98
20	VSLDELARP	279	1.9000	20.88
21	MHHGAVLEG	433	1.9000	20.88
22	IVVPPVAAP	82	1.5000	16.48
23	VAAMAKLTA	252	1.5000	16.48
24	LFLALPGAR	45	1.4000	15.38
25	VIAQTKAEL	225	1.4000	15.38
26	VLNVGTAHL	209	1.3000	14.29
27	VGTGRSISA	424	1.3000	14.29
28	VPAIVVPPV	79	1.2000	13.19
29	LECGASVEQ	321	1.2000	13.19
30	VVVGTRSI	422	1.2000	13.19
31	LRAELRPGD	471	1.2000	13.19
32	LILEMAARH	183	1.1800	12.97
33	LRATRRTDY	174	1.1000	12.09
34	VLAARPVGV	71	1.0000	10.99
35	VCGDHQVTN	304	1.0000	10.99
36	LTVAQIAEI	3	0.9000	9.89
37	VAGGLTIIG	124	0.9000	9.89
38	MIELTVAQI	0	0.8000	8.79
39	VGGAVADIS	12	0.8000	8.79
40	LAKLATAVA	112	0.8000	8.79
41	FGSREVIAQ	220	0.8000	8.79

42	MQVTTRGDG	345	0.8000	8.79
43	VKASNAAGL	483	0.8000	8.79
44	LEMAARHHG	185	0.7000	7.69
45	LTAARVVRV	258	0.7000	7.69
46	IGITGSSGK	131	0.6700	7.36
47	VSRLVVVGT	418	0.6000	6.59
48	VTNALCAA	310	0.5000	5.49
49	LVKASNAAG	482	0.5000	5.49
50	VADDTCGSV	499	0.4000	4.40
51	VLVKASNAA	481	0.3100	3.41

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	FGSREVIAQ	220	2.1000	25.00
2	VVLAARPVG	70	1.6000	19.05
3	VAAMAKLTA	252	1.5000	17.86
4	FTLHAHDAQ	289	1.4000	16.67
5	IGRLAVRLD	409	1.3000	15.48
6	VLVKASNAA	481	1.3000	15.48
7	VLRAATRTD	173	1.2000	14.29
8	VRLDVSRLV	414	1.2000	14.29
9	LVADDTCGS	498	1.2000	14.29
10	LLRAELRPG	470	1.1000	13.10
11	YLILEMAAR	182	1.0000	11.90
12	VIAQTKAEL	225	1.0000	11.90
13	VVGTGRSIS	423	1.0000	11.90
14	WIAHQPEAT	377	0.9000	10.71
15	ILEMAARHH	184	0.8800	10.48
16	LEMAARHHG	185	0.8000	9.52
17	IVGGAVADI	11	0.7000	8.33
18	FLALPGARA	46	0.7000	8.33
19	LVVVGTGRS	421	0.7000	8.33

20	VVLNVGTAH	208	0.6800	8.10
21	LTIIGITGS	128	0.4000	4.76
22	LRPGDVVLV	475	0.4000	4.76
23	VVVG TGRSI	422	0.3000	3.57
24	VVLVKASNA	480	0.3000	3.57
25	MIELTVAQI	0	0.2000	2.38
26	LAKLATAVA	112	0.2000	2.38
27	LILEMAARH	183	0.0800	0.95
28	LTVAQIAEI	3	-0.1000	0
29	LAALAKLAT	109	-0.1000	0
30	VAAQLVAGG	119	-0.2000	0
31	VLAARVPGV	71	-0.3000	0
32	VSRLVVVGT	418	-0.3000	0
33	LGEFGSREV	217	-0.5000	0
34	VTNALCAAA	310	-0.5000	0
35	LVKASNAAG	482	-0.5000	0
36	VLNVGTAHL	209	-0.6000	0
37	LTAARVVRV	258	-0.6000	0
38	MRAGLQALA	368	-0.6000	0
39	LMAAVLAPL	145	-0.7000	0
40	VRLGVCGDH	300	-0.7200	0
41	LRATRRTDY	174	-0.8000	0
42	VVRVSRDNT	263	-0.8000	0
43	LHAHDAQAE	291	-0.8000	0
44	IGPGGLFLA	40	-0.9000	0
45	MHHGAVLEG	433	-0.9000	0
46	WTVLRATRR	171	-1.0000	0
47	VGGAVADIS	12	-1.1000	0
48	VLEHDNDGS	96	-1.1000	0

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	VVLAARPVG	70	3.0000	34.09
2	YLILEMAAR	182	2.5000	28.41
3	LLRAELRPG	470	2.5000	28.41
4	IGRLAVRLD	409	2.4000	27.27
5	VLRATRRTD	173	2.3000	26.14
6	LEMAARHHG	185	2.2000	25.00
7	VRLDVSRLV	414	2.2000	25.00
8	VIAQTKAEL	225	1.9600	22.27
9	IVGGAVADI	11	1.6000	18.18
10	WIAHQPEAT	377	1.6000	18.18
11	LVADDTCS	498	1.6000	18.18
12	VAAMAKLTA	252	1.5000	17.05
13	FGSREVIAQ	220	1.4000	15.91
14	VVGTGRSIS	423	1.4000	15.91
15	LRPGDVVLV	475	1.4000	15.91
16	VLVKASNAA	481	1.3000	14.77
17	VAAQLVAGG	119	1.2000	13.64
18	VVVGTGRSI	422	1.2000	13.64
19	MIELTVAQI	0	1.1000	12.50
20	LVVVGTGRS	421	1.1000	12.50
21	IVVPPVAAP	82	1.0000	11.36
22	LVKASNAAG	482	0.9000	10.23
23	LTVAQIAEI	3	0.8000	9.09
24	LTIIGITGS	128	0.8000	9.09
25	FLALPGARA	46	0.7000	7.95
26	VLAARPVGV	71	0.7000	7.95
27	FTLHAHDAQ	289	0.7000	7.95
28	LAALAKLAT	109	0.6000	6.82
29	LHAHDAQAE	291	0.6000	6.82
30	WTVLRATTR	171	0.5000	5.68
31	LRATRRTDY	174	0.5000	5.68
32	LGEFGSREV	217	0.5000	5.68
33	MHHGAVLEG	433	0.5000	5.68
34	LTAARVVRV	258	0.4000	4.55

35	VSRLVVVGT	418	0.4000	4.55
36	VLNVGTAHL	209	0.3600	4.09
37	LFLALPGAR	45	0.3000	3.41
38	ILEMAARHH	184	0.3000	3.41
39	IAEHDRIGR	403	0.3000	3.41
40	VVLVKASNA	480	0.3000	3.41
41	LMAAVLAPL	145	0.2600	2.95
42	LAKLATAVA	112	0.2000	2.27
43	ISPQDAAHR	19	0.1000	1.14
44	VVLNVGTAH	208	0.1000	1.14
45	VEFDSRAIG	33	-0.1000	0
46	VVRVSRDNT	263	-0.1000	0
47	LCAAVALE	314	-0.1000	0
48	LTAAPPVSR	334	-0.1000	0

ALLELE: DRB1_1121	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	2.6000	30.95
2	VAAMAKLTA	252	2.5000	29.76
3	IGRLAVRLD	409	2.3000	27.38
4	VLVKASNAA	481	2.3000	27.38
5	VLRATRRTD	173	2.2000	26.19
6	VRLDVSRV	414	2.2000	26.19
7	LVADDTCS	498	2.2000	26.19
8	LLRAELRPG	470	2.1000	25.00
9	VIAQTKAEL	225	2.0000	23.81
10	VVGTGRSIS	423	2.0000	23.81
11	ILEMAARHH	184	1.8800	22.38
12	LEMAARHHG	185	1.8000	21.43
13	IVGGAVADI	11	1.7000	20.24
14	LVVVGTGRS	421	1.7000	20.24
15	VVLNVGTAH	208	1.6800	20.00

16	LTIIGITGS	128	1.4000	16.67
17	LRPGDVVLV	475	1.4000	16.67
18	VVVGTRSI	422	1.3000	15.48
19	VVLVKASNA	480	1.3000	15.48
20	MIELTVAQI	0	1.2000	14.29
21	LAKLATAVA	112	1.2000	14.29
22	FGSREVIAQ	220	1.1000	13.10
23	LILEMAARH	183	1.0800	12.86
24	IVVPPVAAP	82	1.0000	11.90
25	VLAALAKLA	108	1.0000	11.90
26	LTVAQIAEI	3	0.9000	10.71
27	LAALAKLAT	109	0.9000	10.71
28	VAAQLVAGG	119	0.8000	9.52
29	VLAARPVGV	71	0.7000	8.33
30	VSRLVVVGT	418	0.7000	8.33
31	LGEFGSREV	217	0.5000	5.95
32	VTNALCAAA	310	0.5000	5.95
33	LVKASNAAG	482	0.5000	5.95
34	VLNVGTAHL	209	0.4000	4.76
35	LTAARVVRV	258	0.4000	4.76
36	FTLHAHDAQ	289	0.4000	4.76
37	MRAGLQALA	368	0.4000	4.76
38	LMAAVLAPL	145	0.3000	3.57
39	VRLGVCGDH	300	0.2800	3.33
40	LRATRRTDY	174	0.2000	2.38
41	VVRVSRDNT	263	0.2000	2.38
42	LHAHDAQAE	291	0.2000	2.38
43	IGPGGLFLA	40	0.1000	1.19
44	MHHGAVLEG	433	0.1000	1.19
45	VGGAVADIS	12	-0.1000	0
46	VLEHDNDGS	96	-0.1000	0
47	LNADDPAVA	245	-0.1000	0
48	WIAHQPEAT	377	-0.1000	0
49	LRAELRPGD	471	-0.1000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	3.5000	40.23
2	VVLAAR PVG	70	3.4500	39.66
3	YLILEMAAR	182	3.2000	36.78
4	VAAMAKLTA	252	2.8000	32.18
5	LAALAKLAT	109	2.4000	27.59
6	LTIIGITGS	128	1.9000	21.84
7	MIELTVAQI	0	1.8000	20.69
8	FGSREVIAQ	220	1.8000	20.69
9	LEMAARHHG	185	1.7000	19.54
10	VLNVGTAHL	209	1.6600	19.08
11	IGRLAVRLD	409	1.5000	17.24
12	VVGTGRSIS	423	1.5000	17.24
13	IVGGAVADI	11	1.4000	16.09
14	LFLALPGAR	45	1.4000	16.09
15	FLALPGARA	46	1.4000	16.09
16	MHHGAVLEG	433	1.4000	16.09
17	LVADDT CGS	498	1.3000	14.94
18	WAVLGEMAE	389	1.2000	13.79
19	VVLVKASNA	480	1.2000	13.79
20	MQVTTRGDG	345	1.1000	12.64
21	VIAQTKAEL	225	0.9600	11.03
22	LAKLATAVA	112	0.9000	10.34
23	LLRAELRPG	470	0.9000	10.34
24	LVKASNAAG	482	0.9000	10.34
25	VPAIVVPPV	79	0.8500	9.77
26	LTVAQIAEI	3	0.8000	9.20
27	IVVPPVAAP	82	0.8000	9.20
28	WTVLRATRR	171	0.8000	9.20
29	VLRATRRTD	173	0.7000	8.05
30	LRPGDVVLV	475	0.7000	8.05



31	LRATRRTDY	174	0.6000	6.90
32	VSRLVVVGT	418	0.6000	6.90
33	VAAPNVLAG	87	0.4000	4.60
34	MAKLTAARV	255	0.4000	4.60
35	VRLDVSRLV	414	0.3000	3.45
36	LALLRAELR	468	0.3000	3.45
37	LMAAVLAPL	145	0.2600	2.99
38	VLAARPVG	71	0.2000	2.30
39	VAAQLVAGG	119	0.2000	2.30
40	VGTAHLGEF	212	0.2000	2.30
41	LQALAWIAH	372	0.2000	2.30
42	LTAARVVRV	258	-0.1000	0
43	LCAAVALE	314	-0.1000	0
44	LRAELRPGD	471	-0.1500	0
45	VLAALAKLA	108	-0.2000	0
46	MAAVLAPLG	146	-0.2500	0
47	LAEIAPPSI	198	-0.2500	0
48	VAQIAEIVG	5	-0.3000	0
49	VEFDSRAIG	33	-0.4000	0

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	VVLAARPVG	70	4.0000	45.45
2	LLRAELRPG	470	3.5000	39.77
3	IGRLAVRLD	409	3.4000	38.64
4	VLRATRRTD	173	3.3000	37.50
5	LEMAARHHG	185	3.2000	36.36
6	VRLDVSRLV	414	3.2000	36.36
7	VIAQTKAEL	225	2.9600	33.64
8	IVGGAVADI	11	2.6000	29.55
9	LVADDTCS	498	2.6000	29.55
10	VAAMAKLTA	252	2.5000	28.41

11	VVGTGRSIS	423	2.4000	27.27
12	LRPGDVVLV	475	2.4000	27.27
13	VLVKASNAA	481	2.3000	26.14
14	VAAQLVAGG	119	2.2000	25.00
15	VVVGTGRSI	422	2.2000	25.00
16	MIELTVAQI	0	2.1000	23.86
17	LVVVGTGRS	421	2.1000	23.86
18	IVVPPVAAP	82	2.0000	22.73
19	LVKASNAA	482	1.9000	21.59
20	LTVAQIAEI	3	1.8000	20.45
21	LTIIGITGS	128	1.8000	20.45
22	VLAARPVGV	71	1.7000	19.32
23	LAALAKLAT	109	1.6000	18.18
24	LHAHDAQAE	291	1.6000	18.18
25	LRATRRTDY	174	1.5000	17.05
26	YLILEMAAR	182	1.5000	17.05
27	LGEFGSREV	217	1.5000	17.05
28	MHHGAVLEG	433	1.5000	17.05
29	LTAARVVRV	258	1.4000	15.91
30	VSRLVVVGT	418	1.4000	15.91
31	VLNVGTAHL	209	1.3600	15.45
32	LFLALPGAR	45	1.3000	14.77
33	ILEMAARHH	184	1.3000	14.77
34	IAEHDRIGR	403	1.3000	14.77
35	VVLVKASNA	480	1.3000	14.77
36	LMAAVLAPL	145	1.2600	14.32
37	LAKLATAVA	112	1.2000	13.64
38	ISPQDAAHR	19	1.1000	12.50
39	VVLNVGTAH	208	1.1000	12.50
40	VLAALAKLA	108	1.0000	11.36
41	LRAELRPGD	471	1.0000	11.36
42	VEFDSRAIG	33	0.9000	10.23
43	VVRVSRDNT	263	0.9000	10.23
44	LCAAVALE	314	0.9000	10.23

45	LTAAPPVSR	334	0.9000	10.23
46	LALLRAELR	468	0.9000	10.23
47	LPQAVPHSG	233	0.7000	7.95
48	MAKLTAARV	255	0.7000	7.95
49	WIAHQPEAT	377	0.6000	6.82
50	VAAPNVLG	87	0.5000	5.68
51	LVAGGLTII	123	0.5000	5.68

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	VVLAARPVG	70	3.0000	34.09
2	YLILEMAAR	182	2.5000	28.41
3	LLRAELRPG	470	2.5000	28.41
4	IGRLAVRLD	409	2.4000	27.27
5	VLRATRRTD	173	2.3000	26.14
6	LEMAARHHG	185	2.2000	25.00
7	VRLDVSRLV	414	2.2000	25.00
8	VIAQTKAEL	225	1.9600	22.27
9	IVGGAVADI	11	1.6000	18.18
10	WIAHQPEAT	377	1.6000	18.18
11	LVADDTCS	498	1.6000	18.18
12	VAAMAKLTA	252	1.5000	17.05
13	FGSREVIAQ	220	1.4000	15.91
14	VVGTGRSIS	423	1.4000	15.91
15	LRPGDVVLV	475	1.4000	15.91
16	VLVKASNAA	481	1.3000	14.77
17	VAAQLVAGG	119	1.2000	13.64
18	VVVGTGRSI	422	1.2000	13.64
19	MIELTVAQI	0	1.1000	12.50
20	LVVVGTGRS	421	1.1000	12.50
21	IVVPPVAAP	82	1.0000	11.36
22	LVKASNAAG	482	0.9000	10.23

23	LTVAQIAEI	3	0.8000	9.09
24	LTIIGITGS	128	0.8000	9.09
25	FLALPGARA	46	0.7000	7.95
26	VLAARPVGV	71	0.7000	7.95
27	FTLHAHDAQ	289	0.7000	7.95
28	LAALAKLAT	109	0.6000	6.82
29	LHAHDAQAE	291	0.6000	6.82
30	WTVLRATRR	171	0.5000	5.68
31	LRATRRTDY	174	0.5000	5.68
32	LGEFGSREV	217	0.5000	5.68
33	MHHGAVLEG	433	0.5000	5.68
34	LTAARVVRV	258	0.4000	4.55
35	VSRLVVVGT	418	0.4000	4.55
36	VLNVGTAHL	209	0.3600	4.09
37	LFLALPGAR	45	0.3000	3.41
38	ILEMAARHH	184	0.3000	3.41
39	IAEHDRIGR	403	0.3000	3.41
40	VVLVKASNA	480	0.3000	3.41
41	LMAAVLAPL	145	0.2600	2.95
42	LAKLATAVA	112	0.2000	2.27
43	ISPQDAAHR	19	0.1000	1.14
44	VVLNVGTAH	208	0.1000	1.14
45	VEFDSRAIG	33	-0.1000	0
46	VVRVSRDNT	263	-0.1000	0
47	LCAAVALE	314	-0.1000	0
48	LTAAPPVSR	334	-0.1000	0

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	IGRLAVRLD	409	5.0000	55.56
2	VLRATRRTD	173	4.9000	54.44
3	VVLAARPVG	70	3.9000	43.33

4	LLRAELRPG	470	3.4000	37.78
5	LHAHDAQAE	291	3.2000	35.56
6	ILEMAARHH	184	3.1000	34.44
7	LEMAARHHG	185	3.1000	34.44
8	VIAQTKAEL	225	3.0000	33.33
9	VVLNVGTAH	208	2.9000	32.22
10	LRAELRPGD	471	2.6000	28.89
11	VAAMAKLTA	252	2.5000	27.78
12	LCAAVALE	314	2.5000	27.78
13	VRLDVSRLV	414	2.5000	27.78
14	LILEMAARH	183	2.3000	25.56
15	VLVKASNAA	481	2.3000	25.56
16	LVADDTCGS	498	2.2000	24.44
17	VAAQLVAGG	119	2.1000	23.33
18	VVGTGRSIS	423	2.0000	22.22
19	IVGGAVADI	11	1.9000	21.11
20	FGSREVIAQ	220	1.9000	21.11
21	LAALAKLAT	109	1.8000	20.00
22	LVKASNAAG	482	1.8000	20.00
23	LALPGARAD	47	1.7000	18.89
24	LVVVGTGRS	421	1.7000	18.89
25	LRPGDVVLV	475	1.7000	18.89
26	VSRLVVVGT	418	1.6000	17.78
27	VVPPVAAPN	83	1.5000	16.67
28	VRLGVCGDH	300	1.5000	16.67
29	VVVGTGRSI	422	1.5000	16.67
30	MIELTVAQI	0	1.4000	15.56
31	IVVPPVAAP	82	1.4000	15.56
32	LTIIGITGS	128	1.4000	15.56
33	VLNVGTAHL	209	1.4000	15.56
34	MHHGAVLEG	433	1.4000	15.56
35	LMAAVLAPL	145	1.3000	14.44
36	LRATRRTDY	174	1.3000	14.44
37	VVLVKASNA	480	1.3000	14.44

38	LAKLATAVA	112	1.2000	13.33
39	FTLHAHDAQ	289	1.2000	13.33
40	LTVAQIAEI	3	1.1000	12.22
41	VVRVSRDNT	263	1.1000	12.22
42	VLAARPVGV	71	1.0000	11.11
43	VLAALAKLA	108	1.0000	11.11
44	LQALAWIAH	372	1.0000	11.11
45	VADALVADD	494	0.9000	10.00
46	VEFDSRAIG	33	0.8000	8.89
47	LGEFGSREV	217	0.8000	8.89
48	WIAHQPEAT	377	0.8000	8.89
49	LTAARVVRV	258	0.7000	7.78
50	LPQAVPHSG	233	0.6000	6.67
51	VTNALCAAA	310	0.5000	5.56

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	3.5000	40.23
2	VVLAARPVG	70	3.4500	39.66
3	YLILEMAAR	182	3.2000	36.78
4	VAAMAKLTA	252	2.8000	32.18
5	LAALAKLAT	109	2.4000	27.59
6	LTIIGITGS	128	1.9000	21.84
7	MIELTVAQI	0	1.8000	20.69
8	FGSREVIAQ	220	1.8000	20.69
9	LEMAARHHG	185	1.7000	19.54
10	VLNVGTAHL	209	1.6600	19.08
11	IGRLAVRLD	409	1.5000	17.24
12	VVGTGRSIS	423	1.5000	17.24
13	IVGGAVADI	11	1.4000	16.09
14	LFLALPGAR	45	1.4000	16.09
15	FLALPGARA	46	1.4000	16.09

16	MHHGAVLEG	433	1.4000	16.09
17	LVADDTCS	498	1.3000	14.94
18	WAVLGEMAE	389	1.2000	13.79
19	VVLVKASNA	480	1.2000	13.79
20	MQVTTRGDG	345	1.1000	12.64
21	VIAQTKAEL	225	0.9600	11.03
22	LAKLATAVA	112	0.9000	10.34
23	LLRAELRPG	470	0.9000	10.34
24	LVKASNAAG	482	0.9000	10.34
25	VPAIVVPPV	79	0.8500	9.77
26	LTVAQIAEI	3	0.8000	9.20
27	IVVPPVAAP	82	0.8000	9.20
28	WTVLRATRR	171	0.8000	9.20
29	VLRATRRTD	173	0.7000	8.05
30	LRPGDVVLV	475	0.7000	8.05
31	LRATRRTDY	174	0.6000	6.90
32	VSRLVVVGT	418	0.6000	6.90
33	VAAPNVLAG	87	0.4000	4.60
34	MAKLTAARV	255	0.4000	4.60
35	VRLDVSRLV	414	0.3000	3.45
36	LALLRAELR	468	0.3000	3.45
37	LMAAVLAPL	145	0.2600	2.99
38	VLAARPVG	71	0.2000	2.30
39	VAAQLVAGG	119	0.2000	2.30
40	VGTAHLGEF	212	0.2000	2.30
41	LQALAWIAH	372	0.2000	2.30
42	LTAARVVRV	258	-0.1000	0
43	LCAAVALE	314	-0.1000	0
44	LRAELRPGD	471	-0.1500	0
45	VLAALAKLA	108	-0.2000	0
46	MAAVLAPLG	146	-0.2500	0
47	LAEIAPPSI	198	-0.2500	0
48	VAQIAEIVG	5	-0.3000	0
49	VEFDSRAIG	33	-0.4000	0

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	3.0000	44.12
2	YLILEMAAR	182	1.7000	25.00
3	FLALPGARA	46	1.4000	20.59
4	VVLVKASNA	480	1.2000	17.65
5	VVGTGRSIS	423	1.1000	16.18
6	VAAMAKLTA	252	1.0000	14.71
7	MIELTVAQI	0	0.9000	13.24
8	VVLAARPVG	70	0.9000	13.24
9	LAKLATAVA	112	0.9000	13.24
10	FGSREVIAQ	220	0.9000	13.24
11	LVADDTCS	498	0.9000	13.24
12	VLNVGTAHL	209	0.7000	10.29
13	IVGGAVADI	11	0.5000	7.35
14	LTIIGITGS	128	0.4000	5.88
15	IGRLAVRLD	409	0.2000	2.94
16	VRLGVCGDH	300	0.0800	1.18
17	LTVAQIAEI	3	-0.1000	0
18	LAALAKLAT	109	-0.1000	0
19	LFLALPGAR	45	-0.2000	0
20	IVVPPVAAP	82	-0.2000	0
21	LEMAARHHG	185	-0.4000	0
22	VVRVSRDNT	263	-0.4000	0
23	MQVTTRGDG	345	-0.4000	0
24	VTNALCAA	310	-0.5000	0
25	LVKASNAAG	482	-0.5000	0
26	LILEMAARH	183	-0.5200	0
27	VLRA TRTD	173	-0.6000	0
28	MAKLTAARV	255	-0.6000	0
29	VSRLVVVGT	418	-0.6000	0
30	LMAAVLAPL	145	-0.7000	0



31	LLRAELRPG	470	-0.7000	0
32	ILEMAARHH	184	-0.7200	0
33	VLAALAKLA	108	-0.8000	0
34	MRAGLQALA	368	-0.8000	0
35	LRPGDVVLV	475	-0.8000	0
36	LQALAWIAH	372	-0.8200	0
37	VRLDVSRLV	414	-0.9000	0
38	VVLNVGTAH	208	-0.9200	0
39	VAAQLVAGG	119	-1.2000	0
40	VLAARPVG	71	-1.3000	0
41	VPAIVVPPV	79	-1.3000	0
42	IGITGSSGK	131	-1.3000	0
43	LNADDPAVA	245	-1.4000	0
44	VLVKASNAA	481	-1.4000	0
45	LCAAVALE	314	-1.5000	0
46	VAAALTAAP	330	-1.5000	0
47	LTAARVVRV	258	-1.6000	0
48	FTLHAHDAQ	289	-1.6000	0
49	ISAMHHGAV	430	-1.6000	0

ALLELE: DRB1\_1311    Threshold for 3 % with score: 2.0    Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVVG TGRS	421	4.1000	49.40
2	VAAMAKLTA	252	3.8000	45.78
3	VVLAARPVG	70	3.0500	36.75
4	LAALAKLAT	109	2.7000	32.53
5	LTIIGITGS	128	2.5000	30.12
6	VVLVKASNA	480	2.2000	26.51
7	VVGTGRSIS	423	2.1000	25.30
8	MIELTVAQI	0	1.9000	22.89
9	LAKLATAVA	112	1.9000	22.89
10	LVADDTCS	498	1.9000	22.89

11	LQALAWIAH	372	1.7800	21.45
12	VLNVGTAHL	209	1.7000	20.48
13	IVGGAVADI	11	1.5000	18.07
14	FGSREVIAQ	220	1.5000	18.07
15	IGRLAVRLD	409	1.4000	16.87
16	LEMAARHHG	185	1.3000	15.66
17	VVLNVGTAH	208	1.1800	14.22
18	VRLGVCGDH	300	1.1800	14.22
19	VIAQTKAEL	225	1.0000	12.05
20	MHHGAVLEG	433	1.0000	12.05
21	LTVAQIAEI	3	0.9000	10.84
22	LFLALPGAR	45	0.9000	10.84
23	VSRLVVVGT	418	0.9000	10.84
24	VPAIVVPPV	79	0.8500	10.24
25	IVVPPVAAP	82	0.8000	9.64
26	VLAALAKLA	108	0.8000	9.64
27	YLILEMAAR	182	0.7000	8.43
28	MQVTTRGDG	345	0.7000	8.43
29	LRPGDVVLV	475	0.7000	8.43
30	VLRATRRTD	173	0.6000	7.23
31	VTNALCAAA	310	0.5000	6.02
32	LLRAELRPG	470	0.5000	6.02
33	LVKASNAAG	482	0.5000	6.02
34	LILEMAARH	183	0.4800	5.78
35	ILEMAARHH	184	0.4800	5.78
36	FLALPGARA	46	0.4000	4.82
37	MAKLTAARV	255	0.4000	4.82
38	LMAAVLAPL	145	0.3000	3.61
39	LRATRRTDY	174	0.3000	3.61
40	VVRVSRDNT	263	0.3000	3.61
41	VRLDVSRLV	414	0.3000	3.61
42	VLAARPVGV	71	0.2000	2.41
43	MRAGLQALA	368	0.2000	2.41
44	LTAARVVRV	258	-0.1000	0

45	VLVKASNAA	481	-0.1000	0
46	LAEIAPPSI	198	-0.1500	0
47	VAAQLVAGG	119	-0.2000	0
48	LALLRAELR	468	-0.2000	0
49	LRAELRPGD	471	-0.2500	0

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	3.3500	37.64
2	FGSREVIAQ	220	3.3000	37.08
3	IGRLAVRLD	409	3.1000	34.83
4	LVVVG TGRS	421	3.1000	34.83
5	VAAMAKLTA	252	2.8000	31.46
6	WAVLGEMAE	389	2.8000	31.46
7	LAALAKLAT	109	2.6000	29.21
8	VLRA TRTD	173	2.3000	25.84
9	LQALAWIAH	372	2.0000	22.47
10	YLILEMAAR	182	1.7000	19.10
11	VLNVGTAHL	209	1.7000	19.10
12	LEMAARHHG	185	1.6000	17.98
13	LTIIGITGS	128	1.5000	16.85
14	LCAA VALE	314	1.5000	16.85
15	LRAELRPGD	471	1.4500	16.29
16	FLALPGARA	46	1.4000	15.73
17	VVLNVGTAH	208	1.4000	15.73
18	VRLGVCGDH	300	1.4000	15.73
19	MHHGAVLEG	433	1.3000	14.61
20	WAGPVS LDE	275	1.2000	13.48
21	VVLVKASNA	480	1.2000	13.48
22	MIELTVAQI	0	1.1000	12.36
23	VVGTGRSIS	423	1.1000	12.36
24	VIAQTKAEL	225	1.0000	11.24

25	MQVTTRGDG	345	1.0000	11.24
26	LAKLATAVA	112	0.9000	10.11
27	LVADDTCS	498	0.9000	10.11
28	VSRLVVVGT	418	0.8000	8.99
29	LLRAELRPG	470	0.8000	8.99
30	LVKASNAAG	482	0.8000	8.99
31	IVGGAVADI	11	0.7000	7.87
32	LILEMAARH	183	0.7000	7.87
33	ILEMAARHH	184	0.7000	7.87
34	LGEMAEELGE	392	0.7000	7.87
35	LRATRRTDY	174	0.4000	4.49
36	VVPPVAAPN	83	0.3000	3.37
37	VAAPNVLG	87	0.3000	3.37
38	LMAAVLAPL	145	0.3000	3.37
39	IVVPPVAAP	82	0.2000	2.25
40	VVRVSRDNT	263	0.2000	2.25
41	VPAIVVPPV	79	0.1500	1.69
42	LTVAQIAEI	3	0.1000	1.12
43	VAAQLVAGG	119	0.1000	1.12
44	LFLALPGAR	45	-0.1000	0
45	VADALVADD	494	-0.1000	0
46	VLAALAKLA	108	-0.2000	0
47	MAKLTAARV	255	-0.3000	0
48	MAAVLAPLG	146	-0.3500	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4		
Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	2.6000	30.95
2	VAAMAKLTA	252	2.5000	29.76
3	IGRLAVRLD	409	2.3000	27.38
4	VLVKASNAA	481	2.3000	27.38
5	VLRATRRTD	173	2.2000	26.19

6	VRLDVSRLV	414	2.2000	26.19
7	LVADDTCGS	498	2.2000	26.19
8	LLRAELRPG	470	2.1000	25.00
9	VIAQTKAEL	225	2.0000	23.81
10	VVGTGRSIS	423	2.0000	23.81
11	ILEMAARHH	184	1.8800	22.38
12	LEMAARHHG	185	1.8000	21.43
13	IVGGAVADI	11	1.7000	20.24
14	LVVVGTGRS	421	1.7000	20.24
15	VVLNVGTAH	208	1.6800	20.00
16	LTIIGITGS	128	1.4000	16.67
17	LRPGDVVLV	475	1.4000	16.67
18	VVVGTGRSI	422	1.3000	15.48
19	VVLVKASNA	480	1.3000	15.48
20	MIELTVAQI	0	1.2000	14.29
21	LAKLATAVA	112	1.2000	14.29
22	FGSREVIAQ	220	1.1000	13.10
23	LILEMAARH	183	1.0800	12.86
24	IVVPPVAAP	82	1.0000	11.90
25	VLAALAKLA	108	1.0000	11.90
26	LTVAQIAEI	3	0.9000	10.71
27	LAALAKLAT	109	0.9000	10.71
28	VAAQLVAGG	119	0.8000	9.52
29	VLAARPVGV	71	0.7000	8.33
30	VSRLVVVGT	418	0.7000	8.33
31	LGEFGSREV	217	0.5000	5.95
32	VTNALCAAA	310	0.5000	5.95
33	LVKASNAAG	482	0.5000	5.95
34	VLNVGTAHL	209	0.4000	4.76
35	LTAARVVRV	258	0.4000	4.76
36	FTLHAHDAQ	289	0.4000	4.76
37	MRAGLQALA	368	0.4000	4.76
38	LMAAVLAPL	145	0.3000	3.57
39	VRLGVCGDH	300	0.2800	3.33

40	LRATRRTDY	174	0.2000	2.38
41	VVRVSRDNT	263	0.2000	2.38
42	LHAHDAQAE	291	0.2000	2.38
43	IGPGGLFLA	40	0.1000	1.19
44	MHHGAVLEG	433	0.1000	1.19
45	VGGAVADIS	12	-0.1000	0
46	VLEHDNDGS	96	-0.1000	0
47	LNADDPAVA	245	-0.1000	0
48	WIAHQPEAT	377	-0.1000	0
49	LRAELRPGD	471	-0.1000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	FGSREVIAQ	220	2.1000	25.00
2	VVLAARPVG	70	1.6000	19.05
3	VAAMAKLTA	252	1.5000	17.86
4	FTLHAHDAQ	289	1.4000	16.67
5	IGRLAVRLD	409	1.3000	15.48
6	VLVKASNAA	481	1.3000	15.48
7	VLRATRRTD	173	1.2000	14.29
8	VRLDVSRLV	414	1.2000	14.29
9	LVADDTCSG	498	1.2000	14.29
10	LLRAELRPG	470	1.1000	13.10
11	YLILEMAAR	182	1.0000	11.90
12	VIAQTKAEL	225	1.0000	11.90
13	VVGTGRSIS	423	1.0000	11.90
14	WIAHQPEAT	377	0.9000	10.71
15	ILEMAARHH	184	0.8800	10.48
16	LEMAARHHG	185	0.8000	9.52
17	IVGGAVADI	11	0.7000	8.33
18	FLALPGARA	46	0.7000	8.33
19	LVVVTGRS	421	0.7000	8.33

20	VVLNVGTAH	208	0.6800	8.10
21	LTIIGITGS	128	0.4000	4.76
22	LRPGDVVLV	475	0.4000	4.76
23	VVVGTRSI	422	0.3000	3.57
24	VVLVKASNA	480	0.3000	3.57
25	MIELTVAQI	0	0.2000	2.38
26	LAKLATAVA	112	0.2000	2.38
27	LILEMAARH	183	0.0800	0.95
28	LTVAQIAEI	3	-0.1000	0
29	LAALAKLAT	109	-0.1000	0
30	VAAQLVAGG	119	-0.2000	0
31	VLAARVPGV	71	-0.3000	0
32	VSRLVVVGT	418	-0.3000	0
33	LGEFGSREV	217	-0.5000	0
34	VTNALCAAA	310	-0.5000	0
35	LVKASNAAG	482	-0.5000	0
36	VLNVGTAHL	209	-0.6000	0
37	LTAARVVRV	258	-0.6000	0
38	MRAGLQALA	368	-0.6000	0
39	LMAAVLAPL	145	-0.7000	0
40	VRLGVCGDH	300	-0.7200	0
41	LRATRRTDY	174	-0.8000	0
42	VVRVSRDNT	263	-0.8000	0
43	LHAHDAQAE	291	-0.8000	0
44	IGPGGLFLA	40	-0.9000	0
45	MHHGAVLEG	433	-0.9000	0
46	WTVLRATRR	171	-1.0000	0
47	VGGAVADIS	12	-1.1000	0
48	VLEHDNDGS	96	-1.1000	0

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	VVLAARPVG	70	4.0000	45.45
2	LLRAELRPG	470	3.5000	39.77
3	IGRLAVRLD	409	3.4000	38.64
4	VLRAATRRTD	173	3.3000	37.50
5	LEMAARHHG	185	3.2000	36.36
6	VRLDVSRLV	414	3.2000	36.36
7	VIAQTKAEL	225	2.9600	33.64
8	IVGGAVADI	11	2.6000	29.55
9	LVADDTCGS	498	2.6000	29.55
10	VAAMAKLTA	252	2.5000	28.41
11	VVGTGRSIS	423	2.4000	27.27
12	LRPGDVVLV	475	2.4000	27.27
13	VLVKASNAA	481	2.3000	26.14
14	VAAQLVAGG	119	2.2000	25.00
15	VVVTGRSI	422	2.2000	25.00
16	MIELTVAQI	0	2.1000	23.86
17	LVVVGTGRS	421	2.1000	23.86
18	IVVPPVAAP	82	2.0000	22.73
19	LVKASNAAG	482	1.9000	21.59
20	LTVAQIAEI	3	1.8000	20.45
21	LTIIGITGS	128	1.8000	20.45
22	VLAARPVGV	71	1.7000	19.32
23	LAALAKLAT	109	1.6000	18.18
24	LHAHDAQAE	291	1.6000	18.18
25	LRATRRTDY	174	1.5000	17.05
26	YLILEMAAR	182	1.5000	17.05
27	LGEFGSREV	217	1.5000	17.05
28	MHHGAVLEG	433	1.5000	17.05
29	LTAARVVRV	258	1.4000	15.91
30	VSRLVVVGT	418	1.4000	15.91
31	VLNVGTAHL	209	1.3600	15.45
32	LFLALPGAR	45	1.3000	14.77
33	ILEMAARHH	184	1.3000	14.77
34	IAEHDRIGR	403	1.3000	14.77



35	VVLVKASNA	480	1.3000	14.77
36	LMAAVLAPL	145	1.2600	14.32
37	LAKLATAVA	112	1.2000	13.64
38	ISPQDAAHR	19	1.1000	12.50
39	VVLNVGTAH	208	1.1000	12.50
40	VLAALAKLA	108	1.0000	11.36
41	LRAELRPGD	471	1.0000	11.36
42	VEFDSRAIG	33	0.9000	10.23
43	VVRVSRDNT	263	0.9000	10.23
44	LCAAAVALE	314	0.9000	10.23
45	LTAAPPVSR	334	0.9000	10.23
46	LALLRAELR	468	0.9000	10.23
47	LPQAVPHSG	233	0.7000	7.95
48	MAKLTAARV	255	0.7000	7.95
49	WIAHQPEAT	377	0.6000	6.82
50	VAAPNVLAG	87	0.5000	5.68
51	LVAGGLTII	123	0.5000	5.68

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	VVLAARPVG	70	4.0000	45.45
2	LLRAELRPG	470	3.5000	39.77
3	IGRLAVRLD	409	3.4000	38.64
4	VLRATRRTD	173	3.3000	37.50
5	LEMAARHHG	185	3.2000	36.36
6	VRLDVSRLV	414	3.2000	36.36
7	VIAQTKAEL	225	2.9600	33.64
8	IVGGAVADI	11	2.6000	29.55
9	LVADDTCGS	498	2.6000	29.55
10	VAAMAKLTA	252	2.5000	28.41
11	VVGTGRSIS	423	2.4000	27.27
12	LRPGDVVLV	475	2.4000	27.27

13	VLVKASNAA	481	2.3000	26.14
14	VAAQLVAGG	119	2.2000	25.00
15	VVVGTRSI	422	2.2000	25.00
16	MIELTVAQI	0	2.1000	23.86
17	LVVVGTRGS	421	2.1000	23.86
18	IVVPPVAAP	82	2.0000	22.73
19	LVKASNAAAG	482	1.9000	21.59
20	LTVAQIAEI	3	1.8000	20.45
21	LTIIGITGS	128	1.8000	20.45
22	VLAARPVGV	71	1.7000	19.32
23	LAALAKLAT	109	1.6000	18.18
24	LHAHDAQAE	291	1.6000	18.18
25	LRATRRTDY	174	1.5000	17.05
26	YLILEMAAR	182	1.5000	17.05
27	LGEFGSREV	217	1.5000	17.05
28	MHHGAVLEG	433	1.5000	17.05
29	LTAARVVRV	258	1.4000	15.91
30	VSRLVVVGT	418	1.4000	15.91
31	VLNVGTAHL	209	1.3600	15.45
32	LFLALPGAR	45	1.3000	14.77
33	ILEMAARHH	184	1.3000	14.77
34	IAEHDRIGR	403	1.3000	14.77
35	VVLVKASNA	480	1.3000	14.77
36	LMAAVLAPL	145	1.2600	14.32
37	LAKLATAVA	112	1.2000	13.64
38	ISPQDAAHR	19	1.1000	12.50
39	VVLNVGTAH	208	1.1000	12.50
40	VLAALAKLA	108	1.0000	11.36
41	LRAELRPGD	471	1.0000	11.36
42	VEFDSRAIG	33	0.9000	10.23
43	VVRVSRDNT	263	0.9000	10.23
44	LCAAAVALE	314	0.9000	10.23
45	LTAAPPVSR	334	0.9000	10.23
46	LALLRAELR	468	0.9000	10.23

47	LPQAVPHSG	233	0.7000	7.95
48	MAKLTAARV	255	0.7000	7.95
49	WIAHQPEAT	377	0.6000	6.82
50	VAAPNVLAG	87	0.5000	5.68
51	LVAGGLTII	123	0.5000	5.68

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	3.6000	36.73
2	VVLVKASNA	480	3.6000	36.73
3	VVVG TGRSI	422	3.3000	33.67
4	LVAGGLTII	123	3.2000	32.65
5	VRLDVSRLV	414	3.2000	32.65
6	VVRVSRDNT	263	3.1000	31.63
7	VVGTGRSIS	423	3.0000	30.61
8	LRPGDVVLV	475	2.8000	28.57
9	IVGGAVADI	11	2.7000	27.55
10	VAAMAKLTA	252	2.6000	26.53
11	VGTGRSISA	424	2.6000	26.53
12	VVLNVGTAH	208	2.5000	25.51
13	LVVVG TGRS	421	2.4600	25.10
14	IGPGGLFLA	40	2.4000	24.49
15	LEMAARHHG	185	2.3000	23.47
16	LRATRRTDY	174	2.2000	22.45
17	VLNVGTAHL	209	2.1600	22.04
18	LGEFGSREV	217	2.1000	21.43
19	VRLGVCGDH	300	2.1000	21.43
20	VLVKASNAA	481	2.1000	21.43
21	LTIIGITGS	128	2.0500	20.92
22	IGVVLNVGT	206	2.0000	20.41
23	LVKASNAAG	482	2.0000	20.41
24	LAALAKLAT	109	1.9000	19.39

25	IIGITGSSG	130	1.9000	19.39
26	VRVSRDNTG	264	1.9000	19.39
27	LMAAVLAPL	145	1.8000	18.37
28	VVLNADDDPA	243	1.8000	18.37
29	MHHGAVLEG	433	1.8000	18.37
30	VLNADDDPAV	244	1.7000	17.35
31	LQALAWIAH	372	1.7000	17.35
32	MQVTTRGDG	345	1.6000	16.33
33	LGVCGDHQV	302	1.5000	15.31
34	VLAARPVGV	71	1.4000	14.29
35	VVAPPGSFN	156	1.4000	14.29
36	MRAGLQALA	368	1.4000	14.29
37	IAEHDRIGR	403	1.4000	14.29
38	LVADDTCS	498	1.3600	13.88
39	VKASNAAGL	483	1.3000	13.27
40	LTVAQIAEI	3	1.2500	12.76
41	VALECGASV	319	1.2000	12.24
42	YLILEMAAR	182	1.1000	11.22
43	LNVTGTAHLG	210	1.1000	11.22
44	VSRHRMQVT	340	1.1000	11.22
45	VNVADGDAA	459	1.1000	11.22
46	FLALPGARA	46	1.0000	10.20
47	LRAELRPGD	471	1.0000	10.20
48	IVVPPVAAP	82	0.9000	9.18
49	VVPPVAAPN	83	0.9000	9.18
50	IGITGSSGK	131	0.9000	9.18
51	VAGGLTIIG	124	0.8600	8.78

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	2.6000	26.53
2	VVLVKASNA	480	2.6000	26.53

3	VVVG TGRSI	422	2.3000	23.47
4	LVAGGLTII	123	2.2000	22.45
5	VRLDVSRLV	414	2.2000	22.45
6	YLILEMAAR	182	2.1000	21.43
7	VVRVSRDNT	263	2.1000	21.43
8	FLALPGARA	46	2.0000	20.41
9	VVGTGRSIS	423	2.0000	20.41
10	LRPGDVVLV	475	1.8000	18.37
11	IVGGAVADI	11	1.7000	17.35
12	VAAMAKLTA	252	1.6000	16.33
13	VGTGRSISA	424	1.6000	16.33
14	VVLNVGTAH	208	1.5000	15.31
15	LVVVGTGRS	421	1.4600	14.90
16	IGPGGLFLA	40	1.4000	14.29
17	LEMAARHHG	185	1.3000	13.27
18	LRATRRTDY	174	1.2000	12.24
19	VLNVGTAHL	209	1.1600	11.84
20	LGEFGSREV	217	1.1000	11.22
21	VRLGVCGDH	300	1.1000	11.22
22	WIAHQPEAT	377	1.1000	11.22
23	VLVKASNAA	481	1.1000	11.22
24	LTIIGITGS	128	1.0500	10.71
25	IGVVVLNVGT	206	1.0000	10.20
26	LVKASNAAG	482	1.0000	10.20
27	LAALAKLAT	109	0.9000	9.18
28	IIGITGSSG	130	0.9000	9.18
29	VRVSRDNTG	264	0.9000	9.18
30	LMAAVLAPL	145	0.8000	8.16
31	VVLNADDPA	243	0.8000	8.16
32	MHHGAVLEG	433	0.8000	8.16
33	VLNADDPAV	244	0.7000	7.14
34	LQALAWIAH	372	0.7000	7.14
35	MQVTTRGDG	345	0.6000	6.12
36	FGSREVIAQ	220	0.5000	5.10

37	WAGPVS LDE	275	0.5000	5.10
38	LGVCGD HQV	302	0.5000	5.10
39	VLAARPVGV	71	0.4000	4.08
40	VVAPPGSFN	156	0.4000	4.08
41	FNNELGHPW	163	0.4000	4.08
42	MRAGLQALA	368	0.4000	4.08
43	IAEHDRIGR	403	0.4000	4.08
44	LVADDT CGS	498	0.3600	3.67
45	VKASNAAGL	483	0.3000	3.06
46	LTVAQIAEI	3	0.2500	2.55
47	WTVLRATRR	171	0.2000	2.04
48	VALECGASV	319	0.2000	2.04
49	LNVTGTAHLG	210	0.1000	1.02
50	VSRHRMQVT	340	0.1000	1.02
51	VNVADGDAA	459	0.1000	1.02

ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	VVLAARPVG	70	3.6000	36.73
2	VVLVKASNA	480	3.6000	36.73
3	VVVG TGRSI	422	3.3000	33.67
4	LVAGGLTII	123	3.2000	32.65
5	VRLDVSR LV	414	3.2000	32.65
6	VVRVSRDNT	263	3.1000	31.63
7	VVGTGRSIS	423	3.0000	30.61
8	LRPGDVVLV	475	2.8000	28.57
9	IVGGAVADI	11	2.7000	27.55
10	VAAMAKLTA	252	2.6000	26.53
11	VGTGRSISA	424	2.6000	26.53
12	VVLNVGTAH	208	2.5000	25.51
13	LVVVG TGRS	421	2.4600	25.10
14	IGPGGLFLA	40	2.4000	24.49

15	LEMAARHHG	185	2.3000	23.47
16	LRATRRTDY	174	2.2000	22.45
17	VLNVGTAHL	209	2.1600	22.04
18	LGEFGSREV	217	2.1000	21.43
19	VRLGVCGDH	300	2.1000	21.43
20	VLVKASNAA	481	2.1000	21.43
21	LTIIGITGS	128	2.0500	20.92
22	IGVVLVNVT	206	2.0000	20.41
23	LVKASNAAG	482	2.0000	20.41
24	LAALAKLAT	109	1.9000	19.39
25	IIGITGSSG	130	1.9000	19.39
26	VRVSRDNTG	264	1.9000	19.39
27	LMAAVLAPL	145	1.8000	18.37
28	VVLNADDDPA	243	1.8000	18.37
29	MHHGAVLEG	433	1.8000	18.37
30	VLNADDDPAV	244	1.7000	17.35
31	LQALAWIAH	372	1.7000	17.35
32	MQVTTRGDG	345	1.6000	16.33
33	LGVCGDHQV	302	1.5000	15.31
34	VLAARVPGV	71	1.4000	14.29
35	VVAPPGSFN	156	1.4000	14.29
36	MRAGLQALA	368	1.4000	14.29
37	IAEHDRIGR	403	1.4000	14.29
38	LVADDTCS	498	1.3600	13.88
39	VKASNAAGL	483	1.3000	13.27
40	LTVAQIAEI	3	1.2500	12.76
41	VALECGASV	319	1.2000	12.24
42	YLILEMAAR	182	1.1000	11.22
43	LNVGTAHLG	210	1.1000	11.22
44	VSRHRMQVT	340	1.1000	11.22
45	VNVADGDAA	459	1.1000	11.22
46	FLALPGARA	46	1.0000	10.20
47	LRAELRPGD	471	1.0000	10.20
48	IVVPPVAAP	82	0.9000	9.18

49	VVPPVAAPN	83	0.9000	9.18
50	IGITGSSGK	131	0.9000	9.18
51	VAGGLTIIG	124	0.8600	8.78

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LFLALPGAR	45	4.1000	41.84
2	YLILEMAAR	182	4.1000	41.84
3	WTVLRATRR	171	3.9000	39.80
4	IGITGSSGK	131	3.3000	33.67
5	LVVVGTGRS	421	3.2000	32.65
6	VVLVKASNA	480	3.0000	30.61
7	ILEMAARHH	184	2.8000	28.57
8	VRLGVCGDH	300	2.2000	22.45
9	VVVGTRSI	422	2.2000	22.45
10	LALLRAELR	468	2.2000	22.45
11	VLNVGTAHL	209	2.1000	21.43
12	LRATRRTDY	174	1.8000	18.37
13	IIGITGSSG	130	1.5000	15.31
14	LTIIGITGS	128	1.4000	14.29
15	VVLNVGTAH	208	1.4000	14.29
16	LTAAPPVSR	334	1.4000	14.29
17	LLRAELRPG	470	1.4000	14.29
18	FLALPGARA	46	1.3000	13.27
19	LQALAWIAH	372	1.3000	13.27
20	IELTVAQIA	1	1.1000	11.22
21	VLAALAKLA	108	0.9000	9.18
22	VRLDVSRLV	414	0.9000	9.18
23	VKASNAAGL	483	0.9000	9.18
24	ISPQDAAHR	19	0.8000	8.16
25	LILEMAARH	183	0.8000	8.16
26	LEMAARHHG	185	0.8000	8.16



27	VVGTGRSIS	423	0.8000	8.16
28	MQVTTRGDG	345	0.7000	7.14
29	VVLAARPVG	70	0.6000	6.12
30	LMAAVLAPL	145	0.4000	4.08
31	LATAVAAQL	115	0.3000	3.06
32	LNVGTAHLG	210	0.3000	3.06
33	VGTAHLGEF	212	0.3000	3.06
34	LPQAVPHSG	233	0.3000	3.06
35	FNNELGHPW	163	0.2000	2.04
36	LVKASNAAG	482	0.2000	2.04
37	VRVSRDNTG	264	0.1000	1.02
38	VAQIAEIVG	5	-0.1000	0
39	VADISPQDA	16	-0.1000	0
40	VVPPVAAPN	83	-0.1000	0
41	MAAVLAPLG	146	-0.1000	0
42	LAEIAPPSI	198	-0.1000	0
43	VVRVSRDNT	263	-0.1000	0
44	VAAMAKLTA	252	-0.2000	0
45	VTGTVEFDS	29	-0.3000	0
46	VLAARPVGV	71	-0.3000	0
47	IVGGAVADI	11	-0.4000	0

ALLELE: DRB5_0105		Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8	
Rank	Sequence	At Position	Score	% of Highest Score
1	LFLALPGAR	45	4.1000	41.84
2	YLILEMAAR	182	4.1000	41.84
3	WTVLRATRR	171	3.9000	39.80
4	IGITGSSGK	131	3.3000	33.67
5	LVVVG TGRS	421	3.2000	32.65
6	VVLVKASNA	480	3.0000	30.61
7	ILEMAARHH	184	2.8000	28.57
8	VRLGVC GDH	300	2.2000	22.45

9	VVVGTRSI	422	2.2000	22.45
10	LALLRAELR	468	2.2000	22.45
11	VLNVGTAHL	209	2.1000	21.43
12	LRATRRTDY	174	1.8000	18.37
13	IIGITGSSG	130	1.5000	15.31
14	LTIIGITGS	128	1.4000	14.29
15	VVLNVGTAH	208	1.4000	14.29
16	LTAAPPVSR	334	1.4000	14.29
17	LLRAELRPG	470	1.4000	14.29
18	FLALPGARA	46	1.3000	13.27
19	LQALAWIAH	372	1.3000	13.27
20	IELTVAQIA	1	1.1000	11.22
21	VLAALAKLA	108	0.9000	9.18
22	VRLDVSRLV	414	0.9000	9.18
23	VKASNAAGL	483	0.9000	9.18
24	ISPQDAAHR	19	0.8000	8.16
25	LILEMAARH	183	0.8000	8.16
26	LEMAARHHG	185	0.8000	8.16
27	VVGTGRSIS	423	0.8000	8.16
28	MQVTTRGDG	345	0.7000	7.14
29	VVLAARPVG	70	0.6000	6.12
30	LMAAVLAPL	145	0.4000	4.08
31	LATAVAAQL	115	0.3000	3.06
32	LNVGTAHLG	210	0.3000	3.06
33	VGTAHLGEF	212	0.3000	3.06
34	LPQAVPHSG	233	0.3000	3.06
35	FNNELGHPW	163	0.2000	2.04
36	LVKASNAAG	482	0.2000	2.04
37	VRVSRDNTG	264	0.1000	1.02
38	VAQIAEIVG	5	-0.1000	0
39	VADISPQDA	16	-0.1000	0
40	VVPPVAAPN	83	-0.1000	0
41	MAAVLAPLG	146	-0.1000	0
42	LAEIAPPSI	198	-0.1000	0

43	VVRVSRDNT	263	-0.1000	0
44	VAAMAKLTA	252	-0.2000	0
45	VTGTVEFDS	29	-0.3000	0
46	VLAARPVGV	71	-0.3000	0
47	IVGGAVADI	11	-0.4000	0