MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Mar 15 20:33:19 2010
Length of input sequence	494 amino acids
Number of nanomers from input sequence	486
Number of nanomers with obligatory P1 anchor residue	153
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	49

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	MVGIGGAGM	14	1.5800	26.33
2	LRRVHMVGI	9	1.4500	24.17
3	IVPGGALVV	215	1.3000	21.67
4	YGSVEAYVA	198	1.1500	19.17
5	IVTMGAGDV	458	1.1000	18.33
6	LNALGALLA	299	1.0000	16.67
7	VHALRARGA	47	0.7900	13.17
8	VVLRPAVLA	100	0.7000	11.67

9	MVVFQPHLY	378	0.6800	11.33
10	VFVLDVYGA	406	0.6000	10.00
11	VTLLGPEIL	466	0.6000	10.00
12	IVALQHCGL	133	0.3000	5.00
13	FELVGTCGV	332	0.1500	2.50
14	YTPHVAVIT	180	0.1000	1.67
15	LLPGGATAV	68	-0.0100	0
16	IRLASELAT	273	-0.1000	0
17	FAAEFGRAL	392	-0.1100	0
18	VRANRSAPG	479	-0.1600	0
19	YGSVPGETM	247	-0.1700	0
20	IRVLRYGSV	242	-0.2000	0
21	VVFQPHLYS	379	-0.2000	0
22	YSRTKAFAA	386	-0.3000	0
23	VMRLSVPGR	287	-0.3300	0
24	MLIVALQHC	131	-0.3500	0
25	MRYVPDFSA	435	-0.4500	0
26	YVAVFDSFV	204	-0.5500	0
27	WQQQGVGAV	262	-0.6000	0
28	YVPDFSAVA	437	-0.6000	0
29	VAVITNIES	184	-0.8000	0
30	LAGVSGASV	419	-0.8500	0
31	MRLSVPGRH	288	-0.9000	0
32	VAQQVAAAA	444	-0.9000	0
33	LATAQGPRV	279	-0.9300	0
34	IRIGHDASS	57	-1.0000	0
35	VVTTHAAIP	76	-1.0000	0
36	VERIVPGGA	212	-1.0000	0
37	LVGTCGVGK	334	-1.0000	0
38	VGIGGAGMS	15	-1.1000	0
39	VLRYGSVPG	244	-1.1000	0
40	VQIGAPADE	309	-1.1000	0
41	ILTALRVRA	473	-1.1000	0
42	LVEARRRGI	90	-1.1100	0

43	LLQYTPHVA	177	-1.2000	0
44	LQYTPHVAV	178	-1.2000	0
45	LGALLAAVQ	302	-1.2000	0
46	LLAAVQIGA	305	-1.2000	0
47	MSGIARILL	22	-1.3000	0

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	MVGIGGAGM	14	2.5800	43.00
2	LRRVHMVGI	9	2.4500	40.83
3	IVPGGALVV	215	2.3000	38.33
4	IVTMGAGDV	458	2.1000	35.00
5	LNALGALLA	299	2.0000	33.33
6	VHALRARGA	47	1.7900	29.83
7	VVLRPAVLA	100	1.7000	28.33
8	MVVFQPHLY	378	1.6800	28.00
9	VFVLDVYGA	406	1.6000	26.67
10	VTLLGPEIL	466	1.6000	26.67
11	IVALQHCGL	133	1.3000	21.67
12	LRPAVLAKL	102	1.0000	16.67
13	LLPGGATAV	68	0.9900	16.50
14	IRLASELAT	273	0.9000	15.00
15	VRANRSAPG	479	0.8400	14.00
16	IRVLRYGSV	242	0.8000	13.33
17	VVFQPHLYS	379	0.8000	13.33
18	VMRLSVPGR	287	0.6700	11.17
19	MLIVALQHC	131	0.6500	10.83
20	MRYVPDFSA	435	0.5500	9.17
21	VAVITNIES	184	0.2000	3.33
22	YGSVEAYVA	198	0.1500	2.50
23	FELVGTCGV	332	0.1500	2.50
24	LAGVSGASV	419	0.1500	2.50

25	MRLSVPGRH	288	0.1000	1.67
26	VAQQVAAAA	444	0.1000	1.67
27	LATAQGPRV	279	0.0700	1.17
28	VGIGGAGMS	15	-0.1000	0
29	VLRYGSVPG	244	-0.1000	0
30	VQIGAPADE	309	-0.1000	0
31	ILTALRVRA	473	-0.1000	0
32	LVEARRRGI	90	-0.1100	0
33	FAAEFGRAL	392	-0.1100	0
34	LLQYTPHVA	177	-0.2000	0
35	LQYTPHVAV	178	-0.2000	0
36	LGALLAAVQ	302	-0.2000	0
37	LLAAVQIGA	305	-0.2000	0
38	MSGIARILL	22	-0.3000	0
39	LAGFEGVRR	322	-0.3200	0
40	LAKLMAGRT	107	-0.4000	0
41	MVLEQGDGG	367	-0.4000	0
42	LRVRANRSA	477	-0.4100	0
43	VRVFDDYAH	345	-0.5200	0
44	IGGAGMSGI	17	-0.6000	0

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	LRYGSVPGE	245	5.1000	53.68
2	VMRLSVPGR	287	4.2000	44.21
3	VVFQPHLYS	379	4.1000	43.16
4	ILLDRGGLV	28	4.0000	42.11
5	MRLSVPGRH	288	4.0000	42.11
6	VGIGGAGMS	15	3.7000	38.95
7	FVLDVYGAR	407	3.6000	37.89
8	YVPDFSAVA	437	3.6000	37.89
9	LMAGRTTLM	110	3.4000	35.79

10	IVPGGALVV	215	3.4000	35.79
11	VQIGAPADE	309	3.4000	35.79
12	MVGIGGAGM	14	3.2000	33.68
13	VHMVGIGGA	12	3.0000	31.58
14	IRIGHDASS	57	2.9000	30.53
15	VCTDDPGGA	223	2.9000	30.53
16	LRRVHMVGI	9	2.8000	29.47
17	LIRIGHDAS	56	2.7000	28.42
18	VPMRYVPDF	433	2.7000	28.42
19	VRANRSAPG	479	2.7000	28.42
20	LRPAVLAKL	102	2.6600	28.00
21	MLIVALQHC	131	2.6000	27.37
22	IESDHLDFY	190	2.5000	26.32
23	IVTMGAGDV	458	2.5000	26.32
24	VFVLDVYGA	406	2.4500	25.79
25	IGHDASSLD	59	2.3700	24.95
26	VVLRPAVLA	100	2.3000	24.21
27	ILTALRVRA	473	2.2000	23.16
28	MVTGTHGKT	118	2.1000	22.11
29	LQHCGLDPS	136	2.1000	22.11
30	MGAGDVTLL	461	2.0600	21.68
31	LLPGGATAV	68	2.0000	21.05
32	IPVVLRPAV	98	2.0000	21.05
33	IVALQHCGL	133	1.9600	20.63
34	LRARGALIR	50	1.9000	20.00
35	VLRPAVLAK	101	1.9000	20.00
36	VAVITNIES	184	1.9000	20.00
37	VERIVPGGA	212	1.9000	20.00
38	VFDSFVERI	207	1.8000	18.95
39	WQQQGVGAV	262	1.8000	18.95
40	VGTCGVGKA	335	1.8000	18.95
41	MSGIARILL	22	1.7600	18.53
42	LPPDLRRVH	5	1.7000	17.89
43	IRVLRYGSV	242	1.7000	17.89

44	VGKASVRVF	340	1.7000	17.89
45	LVEARRRGI	90	1.6000	16.84
46	MVVFQPHLY	378	1.6000	16.84
47	IRLASELAT	273	1.5000	15.79
48	MALNALGAL	297	1.4600	15.37
49	LQYTPHVAV	178	1.4000	14.74

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	YVPDFSAVA	437	4.6000	50.55
2	MRLSVPGRH	288	3.5800	39.34
3	FVLDVYGAR	407	3.1000	34.07
4	LRYGSVPGE	245	2.7000	29.67
5	VVFQPHLYS	379	2.7000	29.67
6	VGIGGAGMS	15	2.3000	25.27
7	VHMVGIGGA	12	2.0000	21.98
8	ILLDRGGLV	28	2.0000	21.98
9	VCTDDPGGA	223	1.9000	20.88
10	WQQQGVGAV	262	1.8000	19.78
11	VMRLSVPGR	287	1.7000	18.68
12	MLIVALQHC	131	1.6000	17.58
13	IRIGHDASS	57	1.5000	16.48
14	YAHHPTEIS	351	1.5000	16.48
15	VFVLDVYGA	406	1.4500	15.93
16	IVPGGALVV	215	1.4000	15.38
17	LIRIGHDAS	56	1.3000	14.29
18	VVLRPAVLA	100	1.3000	14.29
19	LPPDLRRVH	5	1.2800	14.07
20	FELVGTCGV	332	1.2000	13.19
21	ILTALRVRA	473	1.2000	13.19
22	VQIGAPADE	309	1.0000	10.99
23	LRRVHMVGI	9	0.9000	9.89

24	LMAGRTTLM	110	0.9000	9.89
25	VERIVPGGA	212	0.9000	9.89
26	VLRPAVLAK	101	0.8000	8.79
27	FVERIVPGG	211	0.8000	8.79
28	VGTCGVGKA	335	0.8000	8.79
29	MVGIGGAGM	14	0.7000	7.69
30	LRPAVLAKL	102	0.7000	7.69
31	LQHCGLDPS	136	0.7000	7.69
32	YGSVEAYVA	198	0.6500	7.14
33	VAVITNIES	184	0.5000	5.49
34	IVTMGAGDV	458	0.5000	5.49
35	MVTGTHGKT	118	0.4000	4.40
36	LYSRTKAFA	385	0.4000	4.40
37	VRANRSAPG	479	0.3000	3.30
38	IGHDASSLD	59	0.2700	2.97
39	IESDHLDFY	190	0.2000	2.20
40	VSGASVAEH	422	0.1800	1.98
41	LLAAVQIGA	305	0.1000	1.10
42	MRYVPDFSA	435	0.1000	1.10
43	MGAGDVTLL	461	0.1000	1.10
44	LLGPEILTA	468	0.1000	1.10

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	VVFQPHLYS	379	4.2000	47.73
2	YVPDFSAVA	437	3.6000	40.91
3	MRLSVPGRH	288	3.1800	36.14
4	IVPGGALVV	215	2.9000	32.95
5	MLIVALQHC	131	2.7000	30.68
6	LIRIGHDAS	56	2.6000	29.55
7	IRIGHDASS	57	2.5000	28.41
8	VLRPAVLAK	101	2.3000	26.14

9	LRYGSVPGE	245	2.3000	26.14
10	VVLRPAVLA	100	2.1800	24.77
11	ILTALRVRA	473	2.0800	23.64
12	LQHCGLDPS	136	2.0000	22.73
13	VQIGAPADE	309	2.0000	22.73
14	LPPDLRRVH	5	1.9800	22.50
15	VGIGGAGMS	15	1.9000	21.59
16	LMAGRTTLM	110	1.9000	21.59
17	LRRVHMVGI	9	1.7800	20.23
18	MVGIGGAGM	14	1.7000	19.32
19	LRPAVLAKL	102	1.7000	19.32
20	VHMVGIGGA	12	1.6000	18.18
21	ILLDRGGLV	28	1.6000	18.18
22	LLGPEILTA	468	1.6000	18.18
23	IESDHLDFY	190	1.5000	17.05
24	VCTDDPGGA	223	1.5000	17.05
25	LNALGALLA	299	1.5000	17.05
26	LYSRTKAFA	385	1.4000	15.91
27	VFDSFVERI	207	1.3000	14.77
28	IRLASELAT	273	1.3000	14.77
29	VMRLSVPGR	287	1.3000	14.77
30	VFVLDVYGA	406	1.3000	14.77
31	VRANRSAPG	479	1.3000	14.77
32	VAVITNIES	184	1.1800	13.41
33	VSGASVAEH	422	1.1800	13.41
34	LMVTGTHGK	117	1.1000	12.50
35	MVVFQPHLY	378	1.1000	12.50
36	MGAGDVTLL	461	1.1000	12.50
37	VSGSDAKES	36	1.0000	11.36
38	IGHDASSLD	59	1.0000	11.36
39	LLPGGATAV	68	1.0000	11.36
40	IVALQHCGL	133	1.0000	11.36
41	LGALLAAVQ	302	1.0000	11.36
42	LRARGALIR	50	0.9000	10.23

43	YAHHPTEIS	351	0.9000	10.23
44	LGEAGTNAH	151	0.7800	8.86
45	LLAAVQIGA	305	0.7800	8.86
46	FVLDVYGAR	407	0.7000	7.95
47	VTLLGPEIL	466	0.7000	7.95
48	LLQYTPHVA	177	0.5000	5.68
49	VERIVPGGA	212	0.5000	5.68

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	VVFQPHLYS	379	4.2000	47.73
2	YVPDFSAVA	437	3.6000	40.91
3	MRLSVPGRH	288	3.1800	36.14
4	IVPGGALVV	215	2.9000	32.95
5	MLIVALQHC	131	2.7000	30.68
6	LIRIGHDAS	56	2.6000	29.55
7	IRIGHDASS	57	2.5000	28.41
8	VLRPAVLAK	101	2.3000	26.14
9	LRYGSVPGE	245	2.3000	26.14
10	VVLRPAVLA	100	2.1800	24.77
11	ILTALRVRA	473	2.0800	23.64
12	LQHCGLDPS	136	2.0000	22.73
13	VQIGAPADE	309	2.0000	22.73
14	LPPDLRRVH	5	1.9800	22.50
15	VGIGGAGMS	15	1.9000	21.59
16	LMAGRTTLM	110	1.9000	21.59
17	LRRVHMVGI	9	1.7800	20.23
18	MVGIGGAGM	14	1.7000	19.32
19	LRPAVLAKL	102	1.7000	19.32
20	VHMVGIGGA	12	1.6000	18.18
21	ILLDRGGLV	28	1.6000	18.18
22	LLGPEILTA	468	1.6000	18.18

23	IESDHLDFY	190	1.5000	17.05
24	VCTDDPGGA	223	1.5000	17.05
25	LNALGALLA	299	1.5000	17.05
26	LYSRTKAFA	385	1.4000	15.91
27	VFDSFVERI	207	1.3000	14.77
28	IRLASELAT	273	1.3000	14.77
29	VMRLSVPGR	287	1.3000	14.77
30	VFVLDVYGA	406	1.3000	14.77
31	VRANRSAPG	479	1.3000	14.77
32	VAVITNIES	184	1.1800	13.41
33	VSGASVAEH	422	1.1800	13.41
34	LMVTGTHGK	117	1.1000	12.50
35	MVVFQPHLY	378	1.1000	12.50
36	MGAGDVTLL	461	1.1000	12.50
37	VSGSDAKES	36	1.0000	11.36
38	IGHDASSLD	59	1.0000	11.36
39	LLPGGATAV	68	1.0000	11.36
40	IVALQHCGL	133	1.0000	11.36
41	LGALLAAVQ	302	1.0000	11.36
42	LRARGALIR	50	0.9000	10.23
43	YAHHPTEIS	351	0.9000	10.23
44	LGEAGTNAH	151	0.7800	8.86
45	LLAAVQIGA	305	0.7800	8.86
46	FVLDVYGAR	407	0.7000	7.95
47	VTLLGPEIL	466	0.7000	7.95
48	LLQYTPHVA	177	0.5000	5.68
49	VERIVPGGA	212	0.5000	5.68

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	VVFQPHLYS	379	4.2000	47.73
2	YVPDFSAVA	437	3.6000	40.91

3	MRLSVPGRH	288	3.1800	36.14
4	IVPGGALVV	215	2.9000	32.95
5	MLIVALQHC	131	2.7000	30.68
6	LIRIGHDAS	56	2.6000	29.55
7	IRIGHDASS	57	2.5000	28.41
8	VLRPAVLAK	101	2.3000	26.14
9	LRYGSVPGE	245	2.3000	26.14
10	VVLRPAVLA	100	2.1800	24.77
11	ILTALRVRA	473	2.0800	23.64
12	LQHCGLDPS	136	2.0000	22.73
13	VQIGAPADE	309	2.0000	22.73
14	LPPDLRRVH	5	1.9800	22.50
15	VGIGGAGMS	15	1.9000	21.59
16	LMAGRTTLM	110	1.9000	21.59
17	LRRVHMVGI	9	1.7800	20.23
18	MVGIGGAGM	14	1.7000	19.32
19	LRPAVLAKL	102	1.7000	19.32
20	VHMVGIGGA	12	1.6000	18.18
21	ILLDRGGLV	28	1.6000	18.18
22	LLGPEILTA	468	1.6000	18.18
23	IESDHLDFY	190	1.5000	17.05
24	VCTDDPGGA	223	1.5000	17.05
25	LNALGALLA	299	1.5000	17.05
26	LYSRTKAFA	385	1.4000	15.91
27	VFDSFVERI	207	1.3000	14.77
28	IRLASELAT	273	1.3000	14.77
29	VMRLSVPGR	287	1.3000	14.77
30	VFVLDVYGA	406	1.3000	14.77
31	VRANRSAPG	479	1.3000	14.77
32	VAVITNIES	184	1.1800	13.41
33	VSGASVAEH	422	1.1800	13.41
34	LMVTGTHGK	117	1.1000	12.50
35	MVVFQPHLY	378	1.1000	12.50
36	MGAGDVTLL	461	1.1000	12.50

37	VSGSDAKES	36	1.0000	11.36
38	IGHDASSLD	59	1.0000	11.36
39	LLPGGATAV	68	1.0000	11.36
40	IVALQHCGL	133	1.0000	11.36
41	LGALLAAVQ	302	1.0000	11.36
42	LRARGALIR	50	0.9000	10.23
43	YAHHPTEIS	351	0.9000	10.23
44	LGEAGTNAH	151	0.7800	8.86
45	LLAAVQIGA	305	0.7800	8.86
46	FVLDVYGAR	407	0.7000	7.95
47	VTLLGPEIL	466	0.7000	7.95
48	LLQYTPHVA	177	0.5000	5.68
49	VERIVPGGA	212	0.5000	5.68

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	FVLDVYGAR	407	4.6000	48.42
2	YVPDFSAVA	437	4.6000	48.42
3	LRYGSVPGE	245	4.1000	43.16
4	VMRLSVPGR	287	3.2000	33.68
5	VVFQPHLYS	379	3.1000	32.63
6	ILLDRGGLV	28	3.0000	31.58
7	MRLSVPGRH	288	3.0000	31.58
8	WQQQGVGAV	262	2.8000	29.47
9	VGIGGAGMS	15	2.7000	28.42
10	LMAGRTTLM	110	2.4000	25.26
11	IVPGGALVV	215	2.4000	25.26
12	VQIGAPADE	309	2.4000	25.26
13	MVGIGGAGM	14	2.2000	23.16
14	FVERIVPGG	211	2.2000	23.16
15	FELVGTCGV	332	2.2000	23.16
16	VHMVGIGGA	12	2.0000	21.05

17	IRIGHDASS	57	1.9000	20.00
18	VCTDDPGGA	223	1.9000	20.00
19	YAHHPTEIS	351	1.9000	20.00
20	LRRVHMVGI	9	1.8000	18.95
21	LIRIGHDAS	56	1.7000	17.89
22	VPMRYVPDF	433	1.7000	17.89
23	VRANRSAPG	479	1.7000	17.89
24	LRPAVLAKL	102	1.6600	17.47
25	MLIVALQHC	131	1.6000	16.84
26	IESDHLDFY	190	1.5000	15.79
27	IVTMGAGDV	458	1.5000	15.79
28	VFVLDVYGA	406	1.4500	15.26
29	IGHDASSLD	59	1.3700	14.42
30	VVLRPAVLA	100	1.3000	13.68
31	ILTALRVRA	473	1.2000	12.63
32	MVTGTHGKT	118	1.1000	11.58
33	LQHCGLDPS	136	1.1000	11.58
34	MGAGDVTLL	461	1.0600	11.16
35	LLPGGATAV	68	1.0000	10.53
36	IPVVLRPAV	98	1.0000	10.53
37	IVALQHCGL	133	0.9600	10.11
38	LRARGALIR	50	0.9000	9.47
39	VLRPAVLAK	101	0.9000	9.47
40	VAVITNIES	184	0.9000	9.47
41	VERIVPGGA	212	0.9000	9.47
42	YGSVPGETM	247	0.9000	9.47
43	VFDSFVERI	207	0.8000	8.42
44	VGTCGVGKA	335	0.8000	8.42
45	MSGIARILL	22	0.7600	8.00
46	LPPDLRRVH	5	0.7000	7.37
47	FYGSVEAYV	197	0.7000	7.37
48	IRVLRYGSV	242	0.7000	7.37
49	VGKASVRVF	340	0.7000	7.37

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	VVFQPHLYS	379	4.2000	47.73
2	YVPDFSAVA	437	3.6000	40.91
3	MRLSVPGRH	288	3.1800	36.14
4	IVPGGALVV	215	2.9000	32.95
5	MLIVALQHC	131	2.7000	30.68
6	LIRIGHDAS	56	2.6000	29.55
7	IRIGHDASS	57	2.5000	28.41
8	VLRPAVLAK	101	2.3000	26.14
9	LRYGSVPGE	245	2.3000	26.14
10	VVLRPAVLA	100	2.1800	24.77
11	ILTALRVRA	473	2.0800	23.64
12	LQHCGLDPS	136	2.0000	22.73
13	VQIGAPADE	309	2.0000	22.73
14	LPPDLRRVH	5	1.9800	22.50
15	VGIGGAGMS	15	1.9000	21.59
16	LMAGRTTLM	110	1.9000	21.59
17	LRRVHMVGI	9	1.7800	20.23
18	MVGIGGAGM	14	1.7000	19.32
19	LRPAVLAKL	102	1.7000	19.32
20	VHMVGIGGA	12	1.6000	18.18
21	ILLDRGGLV	28	1.6000	18.18
22	LLGPEILTA	468	1.6000	18.18
23	IESDHLDFY	190	1.5000	17.05
24	VCTDDPGGA	223	1.5000	17.05
25	LNALGALLA	299	1.5000	17.05
26	LYSRTKAFA	385	1.4000	15.91
27	VFDSFVERI	207	1.3000	14.77
28	IRLASELAT	273	1.3000	14.77
29	VMRLSVPGR	287	1.3000	14.77
30	VFVLDVYGA	406	1.3000	14.77

31	VRANRSAPG	479	1.3000	14.77
32	VAVITNIES	184	1.1800	13.41
33	VSGASVAEH	422	1.1800	13.41
34	LMVTGTHGK	117	1.1000	12.50
35	MVVFQPHLY	378	1.1000	12.50
36	MGAGDVTLL	461	1.1000	12.50
37	VSGSDAKES	36	1.0000	11.36
38	IGHDASSLD	59	1.0000	11.36
39	LLPGGATAV	68	1.0000	11.36
40	IVALQHCGL	133	1.0000	11.36
41	LGALLAAVQ	302	1.0000	11.36
42	LRARGALIR	50	0.9000	10.23
43	YAHHPTEIS	351	0.9000	10.23
44	LGEAGTNAH	151	0.7800	8.86
45	LLAAVQIGA	305	0.7800	8.86
46	FVLDVYGAR	407	0.7000	7.95
47	VTLLGPEIL	466	0.7000	7.95
48	LLQYTPHVA	177	0.5000	5.68
49	VERIVPGGA	212	0.5000	5.68

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	YVPDFSAVA	437	4.8000	55.81
2	YAHHPTEIS	351	4.1000	47.67
3	LMVTGTHGK	117	2.9000	33.72
4	VVFQPHLYS	379	2.7000	31.40
5	VAVITNIES	184	2.3800	27.67
6	VRANRSAPG	479	2.1000	24.42
7	MRLSVPGRH	288	1.7800	20.70
8	FELVGTCGV	332	1.4000	16.28
9	LNALGALLA	299	1.3000	15.12
10	LASELATAQ	275	1.1000	12.79

11	FVAEADESD	166	1.0000	11.63
12	MAATLVSWQ	255	0.9000	10.47
13	WQQQGVGAV	262	0.9000	10.47
14	LGEAGTNAH	151	0.8800	10.23
15	VMRLSVPGR	287	0.8000	9.30
16	LGALLAAVQ	302	0.8000	9.30
17	MVLEQGDGG	367	0.8000	9.30
18	FGRALNAAD	396	0.8000	9.30
19	VFVLDVYGA	406	0.8000	9.30
20	IRIGHDASS	57	0.7000	8.14
21	FVLDVYGAR	407	0.7000	8.14
22	LIRIGHDAS	56	0.6000	6.98
23	VVTTHAAIP	76	0.5000	5.81
24	VAEHVTVPM	427	0.4800	5.58
25	VLRPAVLAK	101	0.4000	4.65
26	VVLRPAVLA	100	0.2800	3.26
27	YTPHVAVIT	180	0.2800	3.26
28	LVGTCGVGK	334	0.2800	3.26
29	MVGIGGAGM	14	0.2000	2.33
30	IGHDASSLD	59	0.2000	2.33
31	VSGSDAKES	36	0.1000	1.16
32	VFDSFVERI	207	0.1000	1.16
33	YSRTKAFAA	386	0.1000	1.16
34	LMAGRTTLM	110	-0.1000	0
35	LRVRANRSA	477	-0.1000	0
36	VTTHAAIPK	77	-0.1200	0
37	VSGASVAEH	422	-0.1200	0
38	IVPGGALVV	215	-0.2000	0
39	VAQQVAAAA	444	-0.2000	0
40	LQHCGLDPS	136	-0.3000	0
41	MVVFQPHLY	378	-0.3000	0
42	FQPHLYSRT	381	-0.3000	0
43	LRRVHMVGI	9	-0.3200	0
44	LQYTPHVAV	178	-0.3200	0

45	MLIVALQHC	131	-0.5000	0

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	LRVRANRSA	477	6.7000	69.79
2	VVLRPAVLA	100	4.3000	44.79
3	MAGRTTLMV	111	3.4000	35.42
4	LRARGALIR	50	3.2000	33.33
5	LMVTGTHGK	117	3.2000	33.33
6	VAVITNIES	184	3.0800	32.08
7	VRVFDDYAH	345	2.8800	30.00
8	LVSWQQQGV	259	2.8000	29.17
9	VVFQPHLYS	379	2.8000	29.17
10	IRIGHDASS	57	2.6000	27.08
11	LGIRVLRYG	240	2.6000	27.08
12	VFVLDVYGA	406	2.5000	26.04
13	MVVFQPHLY	378	2.4000	25.00
14	VGKASVRVF	340	2.1000	21.88
15	VLRPAVLAK	101	2.0000	20.83
16	LMAGRTTLM	110	2.0000	20.83
17	IVPGGALVV	215	2.0000	20.83
18	VHALRARGA	47	1.9000	19.79
19	LGEAGTNAH	151	1.8800	19.58
20	MLIVALQHC	131	1.8000	18.75
21	YAHHPTEIS	351	1.8000	18.75
22	VRANRSAPG	479	1.8000	18.75
23	VAEHVTVPM	427	1.7000	17.71
24	MRYVPDFSA	435	1.7000	17.71
25	VLRYGSVPG	244	1.5000	15.62
26	VRRRFELVG	328	1.5000	15.62
27	VTTHAAIPK	77	1.4000	14.58
28	LNALGALLA	299	1.2000	12.50

29	LLQYTPHVA	177	1.1000	11.46
30	LRRVHMVGI	9	1.0000	10.42
31	LDVYGAREQ	409	1.0000	10.42
32	LLDRGGLVS	29	0.9000	9.38
33	VSGASVAEH	422	0.8800	9.17
34	VPMRYVPDF	433	0.8000	8.33
35	LLGPEILTA	468	0.8000	8.33
36	LAQRATELG	233	0.7000	7.29
37	VAVFDSFVE	205	0.6000	6.25
38	IRLASELAT	273	0.6000	6.25
39	FELVGTCGV	332	0.6000	6.25
40	LTALRVRAN	474	0.6000	6.25
41	LRYGSVPGE	245	0.5000	5.21
42	MAATLVSWQ	255	0.5000	5.21
43	MVGIGGAGM	14	0.4800	5.00
44	LRPAVLAKL	102	0.4000	4.17
45	LGALLAAVQ	302	0.4000	4.17
46	VVTTHAAIP	76	0.3000	3.12
47	LDFYGSVEA	195	0.3000	3.12
48	VQIGAPADE	309	0.3000	3.12
49	LPGGATAVV	69	0.2000	2.08

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	VAVITNIES	184	3.6800	41.82
2	VFVLDVYGA	406	3.0000	34.09
3	VVFQPHLYS	379	2.5000	28.41
4	VRVFDDYAH	345	2.4800	28.18
5	MRYVPDFSA	435	2.3500	26.70
6	MVVFQPHLY	378	2.2000	25.00
7	LNALGALLA	299	2.1000	23.86
8	LGALLAAVQ	302	2.0000	22.73

9	IVTMGAGDV	458	2.0000	22.73
10	LGEAGTNAH	151	1.9800	22.50
11	LRRVHMVGI	9	1.9000	21.59
12	LMVTGTHGK	117	1.9000	21.59
13	FELVGTCGV	332	1.8000	20.45
14	MLIVALQHC	131	1.7000	19.32
15	VMRLSVPGR	287	1.7000	19.32
16	MVGIGGAGM	14	1.5000	17.05
17	VRANRSAPG	479	1.5000	17.05
18	VHMVGIGGA	12	1.4000	15.91
19	MRLSVPGRH	288	1.3800	15.68
20	VLRPAVLAK	101	1.3000	14.77
21	YVPDFSAVA	437	1.3000	14.77
22	VLRYGSVPG	244	1.2000	13.64
23	LIRIGHDAS	56	1.0000	11.36
24	MAATLVSWQ	255	1.0000	11.36
25	VHALRARGA	47	0.9000	10.23
26	IRIGHDASS	57	0.9000	10.23
27	VSGASVAEH	422	0.8800	10.00
28	VAVFDSFVE	205	0.7500	8.52
29	IVALQHCGL	133	0.7000	7.95
30	VERIVPGGA	212	0.7000	7.95
31	LRVRANRSA	477	0.7000	7.95
32	VVLRPAVLA	100	0.6000	6.82
33	LMAGRTTLM	110	0.6000	6.82
34	LRPAVLAKL	102	0.4000	4.55
35	ITNIESDHL	187	0.4000	4.55
36	YVAVFDSFV	204	0.3000	3.41
37	IRVLRYGSV	242	0.3000	3.41
38	VTLLGPEIL	466	0.3000	3.41
39	LLQYTPHVA	177	0.2000	2.27
40	VGTCGVGKA	335	0.2000	2.27
41	YAHHPTEIS	351	0.1000	1.14
42	LLGPEILTA	468	0.1000	1.14

43	VVTTHAAIP	76	-0.1000	0
44	IRLASELAT	273	-0.1000	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	FGRALNAAD	396	3.5000	37.23
2	FELVGTCGV	332	3.1000	32.98
3	VAVFDSFVE	205	2.7500	29.26
4	VRVFDDYAH	345	2.7000	28.72
5	VAVITNIES	184	2.6800	28.51
6	MVVFQPHLY	378	2.3000	24.47
7	YVPDFSAVA	437	2.3000	24.47
8	LGEAGTNAH	151	2.2000	23.40
9	VFVLDVYGA	406	2.0000	21.28
10	LGALLAAVQ	302	1.8000	19.15
11	VRANRSAPG	479	1.8000	19.15
12	MVGIGGAGM	14	1.6000	17.02
13	YVAVFDSFV	204	1.6000	17.02
14	MRLSVPGRH	288	1.6000	17.02
15	VLRYGSVPG	244	1.5000	15.96
16	VVFQPHLYS	379	1.5000	15.96
17	MRYVPDFSA	435	1.3500	14.36
18	IVTMGAGDV	458	1.3000	13.83
19	LRRVHMVGI	9	1.1000	11.70
20	IGHDASSLD	59	1.1000	11.70
21	LNALGALLA	299	1.1000	11.70
22	YAHHPTEIS	351	1.1000	11.70
23	VSGASVAEH	422	1.1000	11.70
24	YGSVEAYVA	198	1.0000	10.64
25	LRYGSVPGE	245	0.8000	8.51
26	MAATLVSWQ	255	0.8000	8.51
27	LMAGRTTLM	110	0.7000	7.45

28	MLIVALQHC	131	0.7000	7.45
29	IVALQHCGL	133	0.7000	7.45
30	VMRLSVPGR	287	0.7000	7.45
31	VQIGAPADE	309	0.6000	6.38
32	LTALRVRAN	474	0.6000	6.38
33	WQQQGVGAV	262	0.5000	5.32
34	VAHIRLASE	270	0.5000	5.32
35	VHMVGIGGA	12	0.4000	4.26
36	LRPAVLAKL	102	0.4000	4.26
37	ITNIESDHL	187	0.4000	4.26
38	VTLLGPEIL	466	0.3000	3.19
39	LMVTGTHGK	117	0.2000	2.13
40	FVAEADESD	166	0.2000	2.13
41	VHALRARGA	47	-0.1000	0
42	IRIGHDASS	57	-0.1000	0
43	VALQHCGLD	134	-0.2000	0
44	IRLASELAT	273	-0.2000	0
45	LASELATAQ	275	-0.2000	0
46	VERIVPGGA	212	-0.3000	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	FELVGTCGV	332	2.8000	31.82
2	VAVITNIES	184	2.6800	30.45
3	YVPDFSAVA	437	2.3000	26.14
4	VFVLDVYGA	406	2.0000	22.73
5	VVFQPHLYS	379	1.5000	17.05
6	VRVFDDYAH	345	1.4800	16.82
7	MRYVPDFSA	435	1.3500	15.34
8	YVAVFDSFV	204	1.3000	14.77
9	MVVFQPHLY	378	1.2000	13.64
10	LNALGALLA	299	1.1000	12.50

11	YAHHPTEIS	351	1.1000	12.50
12	YGSVEAYVA	198	1.0000	11.36
13	LGALLAAVQ	302	1.0000	11.36
14	IVTMGAGDV	458	1.0000	11.36
15	LGEAGTNAH	151	0.9800	11.14
16	LRRVHMVGI	9	0.9000	10.23
17	LMVTGTHGK	117	0.9000	10.23
18	FGRALNAAD	396	0.8000	9.09
19	MLIVALQHC	131	0.7000	7.95
20	VMRLSVPGR	287	0.7000	7.95
21	MVGIGGAGM	14	0.5000	5.68
22	VRANRSAPG	479	0.5000	5.68
23	VHMVGIGGA	12	0.4000	4.55
24	MRLSVPGRH	288	0.3800	4.32
25	VLRPAVLAK	101	0.3000	3.41
26	VLRYGSVPG	244	0.2000	2.27
27	WQQQGVGAV	262	0.2000	2.27
28	VHALRARGA	47	-0.1000	0
29	IRIGHDASS	57	-0.1000	0
30	VSGASVAEH	422	-0.1200	0
31	VAVFDSFVE	205	-0.2500	0
32	IVALQHCGL	133	-0.3000	0
33	VERIVPGGA	212	-0.3000	0
34	LRVRANRSA	477	-0.3000	0
35	VVLRPAVLA	100	-0.4000	0
36	LMAGRTTLM	110	-0.4000	0
37	YSRTKAFAA	386	-0.5500	0
38	LRPAVLAKL	102	-0.6000	0
39	ITNIESDHL	187	-0.6000	0
40	IRVLRYGSV	242	-0.7000	0
41	VTLLGPEIL	466	-0.7000	0
42	LLQYTPHVA	177	-0.8000	0
43	VGTCGVGKA	335	-0.8000	0
44	LLGPEILTA	468	-0.9000	0

45	LDFYGSVEA	195	-1.0000	0
46	LASELATAQ	275	-1.0000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VAVFDSFVE	205	3.7500	39.89
2	VRVFDDYAH	345	3.7000	39.36
3	VAVITNIES	184	3.6800	39.15
4	MVVFQPHLY	378	3.3000	35.11
5	LGEAGTNAH	151	3.2000	34.04
6	VFVLDVYGA	406	3.0000	31.91
7	LGALLAAVQ	302	2.8000	29.79
8	VRANRSAPG	479	2.8000	29.79
9	MVGIGGAGM	14	2.6000	27.66
10	MRLSVPGRH	288	2.6000	27.66
11	VLRYGSVPG	244	2.5000	26.60
12	VVFQPHLYS	379	2.5000	26.60
13	FGRALNAAD	396	2.5000	26.60
14	MRYVPDFSA	435	2.3500	25.00
15	IVTMGAGDV	458	2.3000	24.47
16	LRRVHMVGI	9	2.1000	22.34
17	IGHDASSLD	59	2.1000	22.34
18	LNALGALLA	299	2.1000	22.34
19	FELVGTCGV	332	2.1000	22.34
20	VSGASVAEH	422	2.1000	22.34
21	LRYGSVPGE	245	1.8000	19.15
22	MAATLVSWQ	255	1.8000	19.15
23	LMAGRTTLM	110	1.7000	18.09
24	MLIVALQHC	131	1.7000	18.09
25	IVALQHCGL	133	1.7000	18.09
26	VMRLSVPGR	287	1.7000	18.09
27	VQIGAPADE	309	1.6000	17.02

28	LTALRVRAN	474	1.6000	17.02
29	VAHIRLASE	270	1.5000	15.96
30	VHMVGIGGA	12	1.4000	14.89
31	LRPAVLAKL	102	1.4000	14.89
32	ITNIESDHL	187	1.4000	14.89
33	YVPDFSAVA	437	1.3000	13.83
34	VTLLGPEIL	466	1.3000	13.83
35	LMVTGTHGK	117	1.2000	12.77
36	LIRIGHDAS	56	1.0000	10.64
37	VAAAASPGD	448	1.0000	10.64
38	VHALRARGA	47	0.9000	9.57
39	IRIGHDASS	57	0.9000	9.57
40	VALQHCGLD	134	0.8000	8.51
41	IRLASELAT	273	0.8000	8.51
42	LASELATAQ	275	0.8000	8.51
43	VERIVPGGA	212	0.7000	7.45
44	LRVRANRSA	477	0.7000	7.45
45	VVLRPAVLA	100	0.6000	6.38
46	VLRPAVLAK	101	0.6000	6.38
47	VEAYVAVFD	201	0.6000	6.38
48	YVAVFDSFV	204	0.6000	6.38
49	LVVCTDDPG	221	0.6000	6.38

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	YVPDFSAVA	437	4.8000	53.33
2	YAHHPTEIS	351	4.5000	50.00
3	VRANRSAPG	479	3.5000	38.89
4	VVFQPHLYS	379	3.1000	34.44
5	LMVTGTHGK	117	3.0000	33.33
6	VAVITNIES	184	2.7800	30.89
7	FELVGTCGV	332	2.4000	26.67

8	VMRLSVPGR	287	2.3000	25.56
9	MVLEQGDGG	367	2.2000	24.44
10	FVLDVYGAR	407	2.2000	24.44
11	FVAEADESD	166	2.1000	23.33
12	VAEHVTVPM	427	1.9800	22.00
13	WQQQGVGAV	262	1.9000	21.11
14	FGRALNAAD	396	1.9000	21.11
15	MVGIGGAGM	14	1.7000	18.89
16	VVTTHAAIP	76	1.5000	16.67
17	LMAGRTTLM	110	1.4000	15.56
18	IGHDASSLD	59	1.3000	14.44
19	LNALGALLA	299	1.3000	14.44
20	MRLSVPGRH	288	1.2000	13.33
21	IRIGHDASS	57	1.1000	12.22
22	LIRIGHDAS	56	1.0000	11.11
23	VFDSFVERI	207	1.0000	11.11
24	MVVFQPHLY	378	1.0000	11.11
25	IVTMGAGDV	458	1.0000	11.11
26	YTPHVAVIT	180	0.9800	10.89
27	ITNIESDHL	187	0.9600	10.67
28	VTLLGPEIL	466	0.9600	10.67
29	IVPGGALVV	215	0.8000	8.89
30	VFVLDVYGA	406	0.8000	8.89
31	LQYTPHVAV	178	0.6800	7.56
32	LVVCTDDPG	221	0.6000	6.67
33	LRRVHMVGI	9	0.5800	6.44
34	VLRYGSVPG	244	0.5800	6.44
35	VSGSDAKES	36	0.5000	5.56
36	LRARGALIR	50	0.5000	5.56
37	VLRPAVLAK	101	0.5000	5.56
38	IVALQHCGL	133	0.4600	5.11
39	VVCTDDPGG	222	0.4000	4.44
40	LASELATAQ	275	0.4000	4.44
41	FQPHLYSRT	381	0.4000	4.44

42	LVGTCGVGK	334	0.3800	4.22
43	LRPAVLAKL	102	0.3600	4.00
44	VGGELGEAG	147	0.3000	3.33
45	LGEAGTNAH	151	0.3000	3.33
46	LRYGSVPGE	245	0.3000	3.33
47	VVLRPAVLA	100	0.2800	3.11
48	MAGRTTLMV	111	0.2000	2.22
49	YVAVFDSFV	204	0.2000	2.22

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	VAVITNIES	184	3.6800	41.82
2	VFVLDVYGA	406	3.0000	34.09
3	VVFQPHLYS	379	2.5000	28.41
4	VRVFDDYAH	345	2.4800	28.18
5	MRYVPDFSA	435	2.3500	26.70
6	MVVFQPHLY	378	2.2000	25.00
7	LNALGALLA	299	2.1000	23.86
8	LGALLAAVQ	302	2.0000	22.73
9	IVTMGAGDV	458	2.0000	22.73
10	LGEAGTNAH	151	1.9800	22.50
11	LRRVHMVGI	9	1.9000	21.59
12	LMVTGTHGK	117	1.9000	21.59
13	FELVGTCGV	332	1.8000	20.45
14	MLIVALQHC	131	1.7000	19.32
15	VMRLSVPGR	287	1.7000	19.32
16	MVGIGGAGM	14	1.5000	17.05
17	VRANRSAPG	479	1.5000	17.05
18	VHMVGIGGA	12	1.4000	15.91
19	MRLSVPGRH	288	1.3800	15.68
20	VLRPAVLAK	101	1.3000	14.77
21	YVPDFSAVA	437	1.3000	14.77

22	VLRYGSVPG	244	1.2000	13.64
23	LIRIGHDAS	56	1.0000	11.36
24	MAATLVSWQ	255	1.0000	11.36
25	VHALRARGA	47	0.9000	10.23
26	IRIGHDASS	57	0.9000	10.23
27	VSGASVAEH	422	0.8800	10.00
28	VAVFDSFVE	205	0.7500	8.52
29	IVALQHCGL	133	0.7000	7.95
30	VERIVPGGA	212	0.7000	7.95
31	LRVRANRSA	477	0.7000	7.95
32	VVLRPAVLA	100	0.6000	6.82
33	LMAGRTTLM	110	0.6000	6.82
34	LRPAVLAKL	102	0.4000	4.55
35	ITNIESDHL	187	0.4000	4.55
36	YVAVFDSFV	204	0.3000	3.41
37	IRVLRYGSV	242	0.3000	3.41
38	VTLLGPEIL	466	0.3000	3.41
39	LLQYTPHVA	177	0.2000	2.27
40	VGTCGVGKA	335	0.2000	2.27
41	YAHHPTEIS	351	0.1000	1.14
42	LLGPEILTA	468	0.1000	1.14
43	VVTTHAAIP	76	-0.1000	0
44	IRLASELAT	273	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVPDFSAVA	437	4.8000	55.81
2	YAHHPTEIS	351	4.1000	47.67
3	LMVTGTHGK	117	2.9000	33.72
4	VVFQPHLYS	379	2.7000	31.40
5	VAVITNIES	184	2.3800	27.67
6	VRANRSAPG	479	2.1000	24.42

7	MRLSVPGRH	288	1.7800	20.70
8	FELVGTCGV	332	1.4000	16.28
9	LNALGALLA	299	1.3000	15.12
10	LASELATAQ	275	1.1000	12.79
11	FVAEADESD	166	1.0000	11.63
12	MAATLVSWQ	255	0.9000	10.47
13	WQQQGVGAV	262	0.9000	10.47
14	LGEAGTNAH	151	0.8800	10.23
15	VMRLSVPGR	287	0.8000	9.30
16	LGALLAAVQ	302	0.8000	9.30
17	MVLEQGDGG	367	0.8000	9.30
18	FGRALNAAD	396	0.8000	9.30
19	VFVLDVYGA	406	0.8000	9.30
20	IRIGHDASS	57	0.7000	8.14
21	FVLDVYGAR	407	0.7000	8.14
22	LIRIGHDAS	56	0.6000	6.98
23	VVTTHAAIP	76	0.5000	5.81
24	VAEHVTVPM	427	0.4800	5.58
25	VLRPAVLAK	101	0.4000	4.65
26	VVLRPAVLA	100	0.2800	3.26
27	YTPHVAVIT	180	0.2800	3.26
28	LVGTCGVGK	334	0.2800	3.26
29	MVGIGGAGM	14	0.2000	2.33
30	IGHDASSLD	59	0.2000	2.33
31	VSGSDAKES	36	0.1000	1.16
32	VFDSFVERI	207	0.1000	1.16
33	YSRTKAFAA	386	0.1000	1.16
34	LMAGRTTLM	110	-0.1000	0
35	LRVRANRSA	477	-0.1000	0
36	VTTHAAIPK	77	-0.1200	0
37	VSGASVAEH	422	-0.1200	0
38	IVPGGALVV	215	-0.2000	0
39	VAQQVAAAA	444	-0.2000	0
40	LQHCGLDPS	136	-0.3000	0

41	MVVFQPHLY	378	-0.3000	0
42	FQPHLYSRT	381	-0.3000	0
43	LRRVHMVGI	9	-0.3200	0
44	LQYTPHVAV	178	-0.3200	0
45	MLIVALQHC	131	-0.5000	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	LRRVHMVGI	9	7.0000	60.34
2	VGAVAHIRL	267	5.4000	46.55
3	LQYTPHVAV	178	5.2000	44.83
4	MSGIARILL	22	4.7000	40.52
5	IVPGGALVV	215	4.5000	38.79
6	VFDSFVERI	207	4.4000	37.93
7	LRPAVLAKL	102	4.0000	34.48
8	FELVGTCGV	332	3.9200	33.79
9	YGSVPGETM	247	3.9000	33.62
10	YSRTKAFAA	386	3.9000	33.62
11	MVGIGGAGM	14	3.8000	32.76
12	ITNIESDHL	187	3.3000	28.45
13	YGSVEAYVA	198	3.3000	28.45
14	MVVFQPHLY	378	3.3000	28.45
15	MRLSVPGRH	288	3.0000	25.86
16	VTLLGPEIL	466	3.0000	25.86
17	LVEARRRGI	90	2.9000	25.00
18	IVALQHCGL	133	2.9000	25.00
19	YVAVFDSFV	204	2.9000	25.00
20	MGAGDVTLL	461	2.8000	24.14
21	IGGAGMSGI	17	2.7000	23.28
22	IVTMGAGDV	458	2.7000	23.28
23	VVLRPAVLA	100	2.6000	22.41
24	MLIVALQHC	131	2.6000	22.41

25	LVGTCGVGK	334	2.6000	22.41
26	MRYVPDFSA	435	2.5000	21.55
27	YTPHVAVIT	180	2.4000	20.69
28	VGKASVRVF	340	2.4000	20.69
29	IPKTNPELV	83	2.3000	19.83
30	IRLASELAT	273	2.3000	19.83
31	MAGRTTLMV	111	2.2200	19.14
32	LVSWQQQGV	259	2.2000	18.97
33	LLPGGATAV	68	2.1000	18.10
34	VAVITNIES	184	2.1000	18.10
35	FYGSVEAYV	197	2.1000	18.10
36	VAVFDSFVE	205	2.1000	18.10
37	FAAEFGRAL	392	2.1000	18.10
38	VYGAREQPL	411	2.1000	18.10
39	VVTTHAAIP	76	1.9000	16.38
40	IRVLRYGSV	242	1.9000	16.38
41	LMAGRTTLM	110	1.8200	15.69
42	WQQQGVGAV	262	1.8000	15.52
43	LGPEILTAL	469	1.8000	15.52
44	LMVTGTHGK	117	1.7200	14.83
45	VHMVGIGGA	12	1.6000	13.79
46	LRARGALIR	50	1.5000	12.93
47	VVFQPHLYS	379	1.5000	12.93
48	LAGVSGASV	419	1.5000	12.93
49	VAEHVTVPM	427	1.4200	12.24

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRRVHMVGI	9	7.0000	60.34
2	VGAVAHIRL	267	5.4000	46.55
3	LQYTPHVAV	178	5.2000	44.83
4	MSGIARILL	22	4.7000	40.52

5	IVPGGALVV	215	4.5000	38.79
6	VFDSFVERI	207	4.4000	37.93
7	LRPAVLAKL	102	4.0000	34.48
8	FELVGTCGV	332	3.9200	33.79
9	YGSVPGETM	247	3.9000	33.62
10	YSRTKAFAA	386	3.9000	33.62
11	MVGIGGAGM	14	3.8000	32.76
12	ITNIESDHL	187	3.3000	28.45
13	YGSVEAYVA	198	3.3000	28.45
14	MVVFQPHLY	378	3.3000	28.45
15	MRLSVPGRH	288	3.0000	25.86
16	VTLLGPEIL	466	3.0000	25.86
17	LVEARRRGI	90	2.9000	25.00
18	IVALQHCGL	133	2.9000	25.00
19	YVAVFDSFV	204	2.9000	25.00
20	MGAGDVTLL	461	2.8000	24.14
21	IGGAGMSGI	17	2.7000	23.28
22	IVTMGAGDV	458	2.7000	23.28
23	VVLRPAVLA	100	2.6000	22.41
24	MLIVALQHC	131	2.6000	22.41
25	LVGTCGVGK	334	2.6000	22.41
26	MRYVPDFSA	435	2.5000	21.55
27	YTPHVAVIT	180	2.4000	20.69
28	VGKASVRVF	340	2.4000	20.69
29	IPKTNPELV	83	2.3000	19.83
30	IRLASELAT	273	2.3000	19.83
31	MAGRTTLMV	111	2.2200	19.14
32	LVSWQQQGV	259	2.2000	18.97
33	LLPGGATAV	68	2.1000	18.10
34	VAVITNIES	184	2.1000	18.10
35	FYGSVEAYV	197	2.1000	18.10
36	VAVFDSFVE	205	2.1000	18.10
37	FAAEFGRAL	392	2.1000	18.10
38	VYGAREQPL	411	2.1000	18.10

39	VVTTHAAIP	76	1.9000	16.38
40	IRVLRYGSV	242	1.9000	16.38
41	LMAGRTTLM	110	1.8200	15.69
42	WQQQGVGAV	262	1.8000	15.52
43	LGPEILTAL	469	1.8000	15.52
44	LMVTGTHGK	117	1.7200	14.83
45	VHMVGIGGA	12	1.6000	13.79
46	LRARGALIR	50	1.5000	12.93
47	VVFQPHLYS	379	1.5000	12.93
48	LAGVSGASV	419	1.5000	12.93
49	VAEHVTVPM	427	1.4200	12.24

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	LYSRTKAFA	385	3.7000	43.02
2	FVERIVPGG	211	3.5000	40.70
3	VVLRPAVLA	100	3.3000	38.37
4	LGIRVLRYG	240	3.2000	37.21
5	VRRRFELVG	328	2.8000	32.56
6	LRVRANRSA	477	2.8000	32.56
7	MRLSVPGRH	288	2.5000	29.07
8	VQIGAPADE	309	2.5000	29.07
9	LRYGSVPGE	245	2.3000	26.74
10	FEGVRRRFE	325	2.3000	26.74
11	LRARGALIR	50	2.2000	25.58
12	VPMRYVPDF	433	2.1000	24.42
13	VLRYGSVPG	244	2.0000	23.26
14	LLQYTPHVA	177	1.8000	20.93
15	FELVGTCGV	332	1.8000	20.93
16	MVVFQPHLY	378	1.8000	20.93
17	VHMVGIGGA	12	1.7000	19.77
18	LRPAVLAKL	102	1.7000	19.77

19	IVALQHCGL	133	1.7000	19.77
20	MVGIGGAGM	14	1.6000	18.60
21	MAGRTTLMV	111	1.6000	18.60
22	FGRALNAAD	396	1.6000	18.60
23	IVTMGAGDV	458	1.6000	18.60
24	LGALLAAVQ	302	1.5000	17.44
25	VSGASVAEH	422	1.4000	16.28
26	VRANRSAPG	479	1.4000	16.28
27	YGAREQPLA	412	1.3000	15.12
28	YVPDFSAVA	437	1.3000	15.12
29	VEAYVAVFD	201	1.2000	13.95
30	VVFQPHLYS	379	1.2000	13.95
31	VFVLDVYGA	406	1.1000	12.79
32	LDVYGAREQ	409	1.1000	12.79
33	VEARRRGIP	91	1.0000	11.63
34	VAHIRLASE	270	1.0000	11.63
35	LTALRVRAN	474	0.9000	10.47
36	MLIVALQHC	131	0.8000	9.30
37	LLDRGGLVS	29	0.7000	8.14
38	VPGRHMALN	292	0.7000	8.14
39	WQQQGVGAV	262	0.5000	5.81
40	VMRLSVPGR	287	0.5000	5.81
41	VLAKLMAGR	106	0.4000	4.65
42	VAVFDSFVE	205	0.3000	3.49
43	VGIGGAGMS	15	0.2000	2.33
44	LVEARRRGI	90	0.2000	2.33
45	IRLASELAT	273	0.2000	2.33
46	LNALGALLA	299	0.2000	2.33
47	VGTCGVGKA	335	0.2000	2.33
48	LRRVHMVGI	9	0.1000	1.16
49	VERIVPGGA	212	0.1000	1.16

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

	1.0	

Rank	Sequence	At Position	Score	% of Highest Score
1	LYSRTKAFA	385	3.7000	46.25
2	VVLRPAVLA	100	3.3000	41.25
3	LRVRANRSA	477	2.8000	35.00
4	LRARGALIR	50	2.2000	27.50
5	FVERIVPGG	211	2.2000	27.50
6	LGIRVLRYG	240	1.9000	23.75
7	LLQYTPHVA	177	1.8000	22.50
8	VHMVGIGGA	12	1.7000	21.25
9	VRRRFELVG	328	1.5000	18.75
10	FELVGTCGV	332	1.5000	18.75
11	MAGRTTLMV	111	1.3000	16.25
12	YGAREQPLA	412	1.3000	16.25
13	YVPDFSAVA	437	1.3000	16.25
14	IVTMGAGDV	458	1.3000	16.25
15	MRLSVPGRH	288	1.2800	16.00
16	VVFQPHLYS	379	1.2000	15.00
17	VPMRYVPDF	433	1.2000	15.00
18	VFVLDVYGA	406	1.1000	13.75
19	MLIVALQHC	131	0.8000	10.00
20	LLDRGGLVS	29	0.7000	8.75
21	LRPAVLAKL	102	0.7000	8.75
22	IVALQHCGL	133	0.7000	8.75
23	VLRYGSVPG	244	0.7000	8.75
24	LGALLAAVQ	302	0.7000	8.75
25	MVVFQPHLY	378	0.7000	8.75
26	VEARRRGIP	91	0.6000	7.50
27	MVGIGGAGM	14	0.5000	6.25
28	VMRLSVPGR	287	0.5000	6.25
29	VLAKLMAGR	106	0.4000	5.00
30	VLRPAVLAK	101	0.3000	3.75
31	LDVYGAREQ	409	0.3000	3.75
32	VGIGGAGMS	15	0.2000	2.50

33	WQQQGVGAV	262	0.2000	2.50
34	LNALGALLA	299	0.2000	2.50
35	VGTCGVGKA	335	0.2000	2.50
36	VSGASVAEH	422	0.1800	2.25
37	VERIVPGGA	212	0.1000	1.25
38	VRANRSAPG	479	0.1000	1.25
39	LRRVHMVGI	9	-0.1000	0
40	VHALRARGA	47	-0.1000	0
41	YGSVEAYVA	198	-0.1000	0
42	ILTALRVRA	473	-0.1000	0
43	IRVLRYGSV	242	-0.2000	0
44	LLGPEILTA	468	-0.4000	0
45	LDFYGSVEA	195	-0.5000	0
46	VQIGAPADE	309	-0.5000	0

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	LYSRTKAFA	385	4.7000	58.75
2	VVLRPAVLA	100	4.3000	53.75
3	LRVRANRSA	477	3.8000	47.50
4	LRARGALIR	50	3.2000	40.00
5	LGIRVLRYG	240	2.9000	36.25
6	LLQYTPHVA	177	2.8000	35.00
7	VHMVGIGGA	12	2.7000	33.75
8	VRRRFELVG	328	2.5000	31.25
9	MAGRTTLMV	111	2.3000	28.75
10	IVTMGAGDV	458	2.3000	28.75
11	MRLSVPGRH	288	2.2800	28.50
12	VVFQPHLYS	379	2.2000	27.50
13	VPMRYVPDF	433	2.2000	27.50
14	VFVLDVYGA	406	2.1000	26.25
15	MLIVALQHC	131	1.8000	22.50

16	LLDRGGLVS	29	1.7000	21.25
17	LRPAVLAKL	102	1.7000	21.25
18	IVALQHCGL	133	1.7000	21.25
19	VLRYGSVPG	244	1.7000	21.25
20	LGALLAAVQ	302	1.7000	21.25
21	MVVFQPHLY	378	1.7000	21.25
22	VEARRRGIP	91	1.6000	20.00
23	MVGIGGAGM	14	1.5000	18.75
24	VMRLSVPGR	287	1.5000	18.75
25	VLAKLMAGR	106	1.4000	17.50
26	VLRPAVLAK	101	1.3000	16.25
27	LDVYGAREQ	409	1.3000	16.25
28	VGIGGAGMS	15	1.2000	15.00
29	FVERIVPGG	211	1.2000	15.00
30	LNALGALLA	299	1.2000	15.00
31	VGTCGVGKA	335	1.2000	15.00
32	VSGASVAEH	422	1.1800	14.75
33	VERIVPGGA	212	1.1000	13.75
34	VRANRSAPG	479	1.1000	13.75
35	IRIGHDASS	57	1.0000	12.50
36	LVEARRRGI	90	1.0000	12.50
37	LRRVHMVGI	9	0.9000	11.25
38	VHALRARGA	47	0.9000	11.25
39	ILTALRVRA	473	0.9000	11.25
40	IRVLRYGSV	242	0.8000	10.00
41	LLGPEILTA	468	0.6000	7.50
42	LDFYGSVEA	195	0.5000	6.25
43	VQIGAPADE	309	0.5000	6.25
44	FELVGTCGV	332	0.5000	6.25
45	IVPGGALVV	215	0.4000	5.00
46	LIRIGHDAS	56	0.3000	3.75
47	LRYGSVPGE	245	0.3000	3.75
48	IRLASELAT	273	0.3000	3.75
49	YGAREQPLA	412	0.3000	3.75

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	LYSRTKAFA	385	4.7000	54.65
2	VVLRPAVLA	100	4.3000	50.00
3	LGIRVLRYG	240	4.2000	48.84
4	VRRRFELVG	328	3.8000	44.19
5	LRVRANRSA	477	3.8000	44.19
6	MRLSVPGRH	288	3.5000	40.70
7	VQIGAPADE	309	3.5000	40.70
8	LRYGSVPGE	245	3.3000	38.37
9	LRARGALIR	50	3.2000	37.21
10	VPMRYVPDF	433	3.1000	36.05
11	VLRYGSVPG	244	3.0000	34.88
12	LLQYTPHVA	177	2.8000	32.56
13	MVVFQPHLY	378	2.8000	32.56
14	VHMVGIGGA	12	2.7000	31.40
15	LRPAVLAKL	102	2.7000	31.40
16	IVALQHCGL	133	2.7000	31.40
17	MVGIGGAGM	14	2.6000	30.23
18	MAGRTTLMV	111	2.6000	30.23
19	IVTMGAGDV	458	2.6000	30.23
20	FVERIVPGG	211	2.5000	29.07
21	LGALLAAVQ	302	2.5000	29.07
22	VSGASVAEH	422	2.4000	27.91
23	VRANRSAPG	479	2.4000	27.91
24	VEAYVAVFD	201	2.2000	25.58
25	VVFQPHLYS	379	2.2000	25.58
26	VFVLDVYGA	406	2.1000	24.42
27	LDVYGAREQ	409	2.1000	24.42
28	VEARRRGIP	91	2.0000	23.26
29	VAHIRLASE	270	2.0000	23.26
30	LTALRVRAN	474	1.9000	22.09

31	MLIVALQHC	131	1.8000	20.93
32	LLDRGGLVS	29	1.7000	19.77
33	VPGRHMALN	292	1.7000	19.77
34	VMRLSVPGR	287	1.5000	17.44
35	VLAKLMAGR	106	1.4000	16.28
36	VAVFDSFVE	205	1.3000	15.12
37	FEGVRRRFE	325	1.3000	15.12
38	VGIGGAGMS	15	1.2000	13.95
39	LVEARRRGI	90	1.2000	13.95
40	IRLASELAT	273	1.2000	13.95
41	LNALGALLA	299	1.2000	13.95
42	VGTCGVGKA	335	1.2000	13.95
43	LRRVHMVGI	9	1.1000	12.79
44	VERIVPGGA	212	1.1000	12.79
45	IRVLRYGSV	242	1.1000	12.79
46	IRIGHDASS	57	1.0000	11.63
47	LAQRATELG	233	1.0000	11.63
48	VGKASVRVF	340	1.0000	11.63
49	VRVFDDYAH	345	1.0000	11.63

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	VVLRPAVLA	100	4.3000	49.43
2	LYSRTKAFA	385	3.7000	42.53
3	LRARGALIR	50	2.8000	32.18
4	LRVRANRSA	477	2.5000	28.74
5	FVERIVPGG	211	2.4000	27.59
6	LLQYTPHVA	177	2.3000	26.44
7	VRRRFELVG	328	2.1000	24.14
8	VFVLDVYGA	406	2.0000	22.99
9	MAGRTTLMV	111	1.9000	21.84
10	MLIVALQHC	131	1.8000	20.69

11	VVFQPHLYS	379	1.8000	20.69
12	VLRYGSVPG	244	1.7000	19.54
13	LGIRVLRYG	240	1.6000	18.39
14	FELVGTCGV	332	1.5000	17.24
15	YGAREQPLA	412	1.5000	17.24
16	VPMRYVPDF	433	1.4000	16.09
17	LLDRGGLVS	29	1.3000	14.94
18	YVPDFSAVA	437	1.3000	14.94
19	MVVFQPHLY	378	1.2000	13.79
20	VHMVGIGGA	12	1.0000	11.49
21	LRRVHMVGI	9	0.9000	10.34
22	VLRPAVLAK	101	0.9000	10.34
23	ILTALRVRA	473	0.9000	10.34
24	YGSVEAYVA	198	0.8000	9.20
25	LNALGALLA	299	0.8000	9.20
26	LRPAVLAKL	102	0.7000	8.05
27	IVALQHCGL	133	0.7000	8.05
28	VMRLSVPGR	287	0.7000	8.05
29	LGALLAAVQ	302	0.7000	8.05
30	IVTMGAGDV	458	0.6000	6.90
31	MRLSVPGRH	288	0.5800	6.67
32	MVGIGGAGM	14	0.5000	5.75
33	LIRIGHDAS	56	0.5000	5.75
34	LDFYGSVEA	195	0.5000	5.75
35	VLAKLMAGR	106	0.4000	4.60
36	LAQRATELG	233	0.4000	4.60
37	MAATLVSWQ	255	0.2000	2.30
38	LLGPEILTA	468	0.2000	2.30
39	VSGASVAEH	422	0.1800	2.07
40	LQHCGLDPS	136	0.1000	1.15
41	LVSWQQQGV	259	0.1000	1.15
42	VRANRSAPG	479	0.1000	1.15
43	VAVITNIES	184	-0.0200	0
44	VEARRRGIP	91	-0.1000	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	FVERIVPGG	211	4.6500	46.04
2	VRRRFELVG	328	4.6000	45.54
3	LRARGALIR	50	4.0000	39.60
4	VVLRPAVLA	100	3.8000	37.62
5	LYSRTKAFA	385	3.7000	36.63
6	LRYGSVPGE	245	3.4500	34.16
7	MAGRTTLMV	111	3.4000	33.66
8	LGIRVLRYG	240	3.4000	33.66
9	VPMRYVPDF	433	3.2500	32.18
10	VVFQPHLYS	379	3.0000	29.70
11	LRVRANRSA	477	3.0000	29.70
12	MRLSVPGRH	288	2.6000	25.74
13	LLDRGGLVS	29	2.5000	24.75
14	LLQYTPHVA	177	2.5000	24.75
15	VLRYGSVPG	244	2.5000	24.75
16	VQIGAPADE	309	2.5000	24.75
17	FEGVRRRFE	325	2.5000	24.75
18	MVVFQPHLY	378	2.5000	24.75
19	YGAREQPLA	412	2.4500	24.26
20	IRLASELAT	273	2.0000	19.80
21	LNALGALLA	299	2.0000	19.80
22	VHMVGIGGA	12	1.8000	17.82
23	FELVGTCGV	332	1.8000	17.82
24	VFVLDVYGA	406	1.8000	17.82
25	LRPAVLAKL	102	1.7000	16.83
26	IVALQHCGL	133	1.7000	16.83
27	VEAYVAVFD	201	1.7000	16.83
28	IVTMGAGDV	458	1.7000	16.83
29	VMRLSVPGR	287	1.6500	16.34
30	MVGIGGAGM	14	1.6000	15.84

31	FGRALNAAD	396	1.6000	15.84
32	IVPGGALVV	215	1.5000	14.85
33	LGALLAAVQ	302	1.5000	14.85
34	VLRPAVLAK	101	1.4000	13.86
35	VSGASVAEH	422	1.4000	13.86
36	LLGPEILTA	468	1.4000	13.86
37	VRANRSAPG	479	1.4000	13.86
38	LDVYGAREQ	409	1.3000	12.87
39	YVPDFSAVA	437	1.3000	12.87
40	VEARRRGIP	91	1.1000	10.89
41	LAQRATELG	233	1.1000	10.89
42	LTALRVRAN	474	1.1000	10.89
43	MSGIARILL	22	1.0000	9.90
44	VAHIRLASE	270	1.0000	9.90
45	MLIVALQHC	131	0.9000	8.91
46	FAVGGELGE	145	0.9000	8.91
47	VAVFDSFVE	205	0.8000	7.92
48	VAVITNIES	184	0.7000	6.93
49	VPGRHMALN	292	0.7000	6.93

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	VVFQPHLYS	379	3.6000	43.37
2	LNALGALLA	299	2.4000	28.92
3	VFVLDVYGA	406	2.2000	26.51
4	VMRLSVPGR	287	2.0500	24.70
5	VHMVGIGGA	12	1.9000	22.89
6	MRLSVPGRH	288	1.6800	20.24
7	FELVGTCGV	332	1.6000	19.28
8	VLRPAVLAK	101	1.4000	16.87
9	VAVITNIES	184	1.3000	15.66
10	MVVFQPHLY	378	1.3000	15.66

11	MVGIGGAGM	14	1.1000	13.25
12	IVALQHCGL	133	1.1000	13.25
13	IRLASELAT	273	1.1000	13.25
14	LGALLAAVQ	302	1.1000	13.25
15	LRARGALIR	50	1.0000	12.05
16	MLIVALQHC	131	1.0000	12.05
17	IVTMGAGDV	458	1.0000	12.05
18	WQQQGVGAV	262	0.9000	10.84
19	VVLRPAVLA	100	0.8000	9.64
20	VERIVPGGA	212	0.8000	9.64
21	LRPAVLAKL	102	0.7000	8.43
22	YGSVEAYVA	198	0.7000	8.43
23	LYSRTKAFA	385	0.7000	8.43
24	LLGPEILTA	468	0.7000	8.43
25	MSGIARILL	22	0.6000	7.23
26	YVPDFSAVA	437	0.6000	7.23
27	LRRVHMVGI	9	0.5000	6.02
28	VHALRARGA	47	0.5000	6.02
29	IVPGGALVV	215	0.5000	6.02
30	LLAAVQIGA	305	0.5000	6.02
31	ILTALRVRA	473	0.4000	4.82
32	FVERIVPGG	211	0.3500	4.22
33	LMVTGTHGK	117	0.3000	3.61
34	IRVLRYGSV	242	0.3000	3.61
35	VRRRFELVG	328	0.3000	3.61
36	VGTCGVGKA	335	0.3000	3.61
37	LVEARRRGI	90	0.2000	2.41
38	VSGASVAEH	422	0.1800	2.17
39	MAGRTTLMV	111	0.1000	1.20
40	VRANRSAPG	479	0.1000	1.20
41	YAHHPTEIS	351	-0.2000	0
42	LRYGSVPGE	245	-0.2500	0
43	IPVVLRPAV	98	-0.3500	0
44	VGIGGAGMS	15	-0.4000	0

45	LIRIGHDAS	56	-0.4000	0
46	LLQYTPHVA	177	-0.4000	0
47	VGAVAHIRL	267	-0.4000	0

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	VVFQPHLYS	379	4.5000	53.57
2	LRVRANRSA	477	3.5000	41.67
3	VVLRPAVLA	100	3.2000	38.10
4	MVVFQPHLY	378	3.2000	38.10
5	LVEARRRGI	90	2.8000	33.33
6	VFVLDVYGA	406	2.7000	32.14
7	LGIRVLRYG	240	2.6000	30.95
8	LYSRTKAFA	385	2.6000	30.95
9	VHALRARGA	47	2.4000	28.57
10	LLQYTPHVA	177	2.2000	26.19
11	VMRLSVPGR	287	1.9000	22.62
12	VGKASVRVF	340	1.9000	22.62
13	ILTALRVRA	473	1.9000	22.62
14	LRARGALIR	50	1.8000	21.43
15	LRPAVLAKL	102	1.7000	20.24
16	MRLSVPGRH	288	1.6800	20.00
17	LVSWQQQGV	259	1.6000	19.05
18	LNALGALLA	299	1.6000	19.05
19	VLRPAVLAK	101	1.5000	17.86
20	MLIVALQHC	131	1.4000	16.67
21	IVALQHCGL	133	1.4000	16.67
22	LGALLAAVQ	302	1.4000	16.67
23	LTALRVRAN	474	1.4000	16.67
24	LMVTGTHGK	117	1.3000	15.48
25	LDVYGAREQ	409	1.3000	15.48
26	YAHHPTEIS	351	1.2000	14.29

27	VRANRSAPG	479	1.2000	14.29
28	VSGASVAEH	422	1.1800	14.05
29	VRRRFELVG	328	1.1000	13.10
30	IRLASELAT	273	1.0000	11.90
31	VRVFDDYAH	345	0.9800	11.67
32	MAGRTTLMV	111	0.9000	10.71
33	VLRYGSVPG	244	0.9000	10.71
34	LQHCGLDPS	136	0.8000	9.52
35	VPMRYVPDF	433	0.8000	9.52
36	LLGPEILTA	468	0.8000	9.52
37	LRRVHMVGI	9	0.7000	8.33
38	VTTHAAIPK	77	0.7000	8.33
39	IVTMGAGDV	458	0.7000	8.33
40	LPPDLRRVH	5	0.6800	8.10
41	MVGIGGAGM	14	0.6000	7.14
42	LIVALQHCG	132	0.6000	7.14
43	IVPGGALVV	215	0.6000	7.14
44	VAEHVTVPM	427	0.6000	7.14
45	VAQQVAAAA	444	0.6000	7.14
46	VHMVGIGGA	12	0.5000	5.95
47	IRIGHDASS	57	0.5000	5.95
48	LRYGSVPGE	245	0.5000	5.95
49	LLDRGGLVS	29	0.3000	3.57

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	VVFQPHLYS	379	4.6000	55.42
2	LNALGALLA	299	3.4000	40.96
3	VFVLDVYGA	406	3.2000	38.55
4	VMRLSVPGR	287	3.0500	36.75
5	VHMVGIGGA	12	2.9000	34.94
6	MRLSVPGRH	288	2.6800	32.29

7	VLRPAVLAK	101	2.4000	28.92
8	VAVITNIES	184	2.3000	27.71
9	MVVFQPHLY	378	2.3000	27.71
10	MVGIGGAGM	14	2.1000	25.30
11	IVALQHCGL	133	2.1000	25.30
12	IRLASELAT	273	2.1000	25.30
13	LGALLAAVQ	302	2.1000	25.30
14	LRARGALIR	50	2.0000	24.10
15	MLIVALQHC	131	2.0000	24.10
16	IVTMGAGDV	458	2.0000	24.10
17	VVLRPAVLA	100	1.8000	21.69
18	VERIVPGGA	212	1.8000	21.69
19	LRPAVLAKL	102	1.7000	20.48
20	LYSRTKAFA	385	1.7000	20.48
21	LLGPEILTA	468	1.7000	20.48
22	MSGIARILL	22	1.6000	19.28
23	LRRVHMVGI	9	1.5000	18.07
24	VHALRARGA	47	1.5000	18.07
25	IVPGGALVV	215	1.5000	18.07
26	LLAAVQIGA	305	1.5000	18.07
27	ILTALRVRA	473	1.4000	16.87
28	LMVTGTHGK	117	1.3000	15.66
29	IRVLRYGSV	242	1.3000	15.66
30	VRRRFELVG	328	1.3000	15.66
31	VGTCGVGKA	335	1.3000	15.66
32	LVEARRRGI	90	1.2000	14.46
33	VSGASVAEH	422	1.1800	14.22
34	MAGRTTLMV	111	1.1000	13.25
35	VRANRSAPG	479	1.1000	13.25
36	LRVRANRSA	477	1.0000	12.05
37	LRYGSVPGE	245	0.7500	9.04
38	IPVVLRPAV	98	0.6500	7.83
39	VGIGGAGMS	15	0.6000	7.23
40	LIRIGHDAS	56	0.6000	7.23

41	LLQYTPHVA	177	0.6000	7.23
42	VGAVAHIRL	267	0.6000	7.23
43	FELVGTCGV	332	0.6000	7.23
44	MRYVPDFSA	435	0.6000	7.23
45	LLDRGGLVS	29	0.5000	6.02
46	LTALRVRAN	474	0.5000	6.02
47	VRVFDDYAH	345	0.3800	4.58
48	VPMRYVPDF	433	0.3500	4.22
49	IRIGHDASS	57	0.3000	3.61

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	VVFQPHLYS	379	4.6000	55.42
2	LNALGALLA	299	3.4000	40.96
3	VFVLDVYGA	406	3.2000	38.55
4	VMRLSVPGR	287	3.0500	36.75
5	VHMVGIGGA	12	2.9000	34.94
6	MRLSVPGRH	288	2.6800	32.29
7	VLRPAVLAK	101	2.4000	28.92
8	VAVITNIES	184	2.3000	27.71
9	MVVFQPHLY	378	2.3000	27.71
10	MVGIGGAGM	14	2.1000	25.30
11	IVALQHCGL	133	2.1000	25.30
12	IRLASELAT	273	2.1000	25.30
13	LGALLAAVQ	302	2.1000	25.30
14	LRARGALIR	50	2.0000	24.10
15	MLIVALQHC	131	2.0000	24.10
16	IVTMGAGDV	458	2.0000	24.10
17	VVLRPAVLA	100	1.8000	21.69
18	VERIVPGGA	212	1.8000	21.69
19	LRPAVLAKL	102	1.7000	20.48
20	LYSRTKAFA	385	1.7000	20.48

21	LLGPEILTA	468	1.7000	20.48
22	MSGIARILL	22	1.6000	19.28
23	LRRVHMVGI	9	1.5000	18.07
24	VHALRARGA	47	1.5000	18.07
25	IVPGGALVV	215	1.5000	18.07
26	LLAAVQIGA	305	1.5000	18.07
27	ILTALRVRA	473	1.4000	16.87
28	LMVTGTHGK	117	1.3000	15.66
29	IRVLRYGSV	242	1.3000	15.66
30	VRRRFELVG	328	1.3000	15.66
31	VGTCGVGKA	335	1.3000	15.66
32	LVEARRRGI	90	1.2000	14.46
33	VSGASVAEH	422	1.1800	14.22
34	MAGRTTLMV	111	1.1000	13.25
35	VRANRSAPG	479	1.1000	13.25
36	LRVRANRSA	477	1.0000	12.05
37	LRYGSVPGE	245	0.7500	9.04
38	IPVVLRPAV	98	0.6500	7.83
39	VGIGGAGMS	15	0.6000	7.23
40	LIRIGHDAS	56	0.6000	7.23
41	LLQYTPHVA	177	0.6000	7.23
42	VGAVAHIRL	267	0.6000	7.23
43	FELVGTCGV	332	0.6000	7.23
44	MRYVPDFSA	435	0.6000	7.23
45	LLDRGGLVS	29	0.5000	6.02
46	LTALRVRAN	474	0.5000	6.02
47	VRVFDDYAH	345	0.3800	4.58
48	VPMRYVPDF	433	0.3500	4.22
49	IRIGHDASS	57	0.3000	3.61

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	MRLSVPGRH	288	4.5800	50.33
2	LRYGSVPGE	245	3.7000	40.66
3	VVFQPHLYS	379	3.7000	40.66
4	YVPDFSAVA	437	3.6000	39.56
5	VGIGGAGMS	15	3.3000	36.26
6	VHMVGIGGA	12	3.0000	32.97
7	ILLDRGGLV	28	3.0000	32.97
8	VCTDDPGGA	223	2.9000	31.87
9	VMRLSVPGR	287	2.7000	29.67
10	MLIVALQHC	131	2.6000	28.57
11	IRIGHDASS	57	2.5000	27.47
12	VFVLDVYGA	406	2.4500	26.92
13	IVPGGALVV	215	2.4000	26.37
14	LIRIGHDAS	56	2.3000	25.27
15	VVLRPAVLA	100	2.3000	25.27
16	LPPDLRRVH	5	2.2800	25.05
17	ILTALRVRA	473	2.2000	24.18
18	FVLDVYGAR	407	2.1000	23.08
19	VQIGAPADE	309	2.0000	21.98
20	LRRVHMVGI	9	1.9000	20.88
21	LMAGRTTLM	110	1.9000	20.88
22	VERIVPGGA	212	1.9000	20.88
23	VLRPAVLAK	101	1.8000	19.78
24	VGTCGVGKA	335	1.8000	19.78
25	MVGIGGAGM	14	1.7000	18.68
26	LRPAVLAKL	102	1.7000	18.68
27	LQHCGLDPS	136	1.7000	18.68
28	VAVITNIES	184	1.5000	16.48
29	IVTMGAGDV	458	1.5000	16.48
30	MVTGTHGKT	118	1.4000	15.38
31	LYSRTKAFA	385	1.4000	15.38
32	VRANRSAPG	479	1.3000	14.29
33	IGHDASSLD	59	1.2700	13.96
34	IESDHLDFY	190	1.2000	13.19

35	VSGASVAEH	422	1.1800	12.97
36	LLAAVQIGA	305	1.1000	12.09
37	MRYVPDFSA	435	1.1000	12.09
38	MGAGDVTLL	461	1.1000	12.09
39	LLGPEILTA	468	1.1000	12.09
40	LLPGGATAV	68	1.0000	10.99
41	IPVVLRPAV	98	1.0000	10.99
42	IVALQHCGL	133	1.0000	10.99
43	LNALGALLA	299	1.0000	10.99
44	LGALLAAVQ	302	1.0000	10.99
45	VFDSFVERI	207	0.9000	9.89
46	MSGIARILL	22	0.8000	8.79
47	WQQQGVGAV	262	0.8000	8.79
48	IRLASELAT	273	0.8000	8.79
49	VPMRYVPDF	433	0.8000	8.79

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	VVFQPHLYS	379	3.5000	41.67
2	LRVRANRSA	477	2.5000	29.76
3	VVLRPAVLA	100	2.2000	26.19
4	YAHHPTEIS	351	2.2000	26.19
5	MVVFQPHLY	378	2.2000	26.19
6	LVEARRRGI	90	1.8000	21.43
7	VFVLDVYGA	406	1.7000	20.24
8	LGIRVLRYG	240	1.6000	19.05
9	LYSRTKAFA	385	1.6000	19.05
10	VHALRARGA	47	1.4000	16.67
11	LLQYTPHVA	177	1.2000	14.29
12	VMRLSVPGR	287	0.9000	10.71
13	VGKASVRVF	340	0.9000	10.71
14	YVPDFSAVA	437	0.9000	10.71

15	ILTALRVRA	473	0.9000	10.71
16	LRARGALIR	50	0.8000	9.52
17	FVERIVPGG	211	0.8000	9.52
18	WQQQGVGAV	262	0.8000	9.52
19	LRPAVLAKL	102	0.7000	8.33
20	MRLSVPGRH	288	0.6800	8.10
21	LVSWQQQGV	259	0.6000	7.14
22	LNALGALLA	299	0.6000	7.14
23	VLRPAVLAK	101	0.5000	5.95
24	YTPHVAVIT	180	0.5000	5.95
25	MLIVALQHC	131	0.4000	4.76
26	IVALQHCGL	133	0.4000	4.76
27	LGALLAAVQ	302	0.4000	4.76
28	LTALRVRAN	474	0.4000	4.76
29	LMVTGTHGK	117	0.3000	3.57
30	FELVGTCGV	332	0.3000	3.57
31	LDVYGAREQ	409	0.3000	3.57
32	VRANRSAPG	479	0.2000	2.38
33	VSGASVAEH	422	0.1800	2.14
34	VRRRFELVG	328	0.1000	1.19
35	VRVFDDYAH	345	-0.0200	0
36	MAGRTTLMV	111	-0.1000	0
37	VLRYGSVPG	244	-0.1000	0
38	FEGVRRRFE	325	-0.1000	0
39	YSRTKAFAA	386	-0.1000	0
40	YGAREQPLA	412	-0.1000	0
41	LQHCGLDPS	136	-0.2000	0
42	VPMRYVPDF	433	-0.2000	0
43	LLGPEILTA	468	-0.2000	0
44	LRRVHMVGI	9	-0.3000	0
45	VTTHAAIPK	77	-0.3000	0
46	IVTMGAGDV	458	-0.3000	0
47	LPPDLRRVH	5	-0.3200	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	VVFQPHLYS	379	3.9000	44.32
2	MVVFQPHLY	378	3.5000	39.77
3	LGIRVLRYG	240	3.0000	34.09
4	VGKASVRVF	340	2.8000	31.82
5	LVEARRRGI	90	2.7000	30.68
6	YAHHPTEIS	351	2.6000	29.55
7	LRVRANRSA	477	2.5000	28.41
8	VMRLSVPGR	287	2.4000	27.27
9	LRARGALIR	50	2.3000	26.14
10	VVLRPAVLA	100	2.2000	25.00
11	FVERIVPGG	211	2.2000	25.00
12	WQQQGVGAV	262	1.8000	20.45
13	VFVLDVYGA	406	1.7000	19.32
14	VPMRYVPDF	433	1.7000	19.32
15	LRPAVLAKL	102	1.6600	18.86
16	LVSWQQQGV	259	1.6000	18.18
17	LYSRTKAFA	385	1.6000	18.18
18	VRANRSAPG	479	1.6000	18.18
19	VRRRFELVG	328	1.5000	17.05
20	VHALRARGA	47	1.4000	15.91
21	IVALQHCGL	133	1.3600	15.45
22	VLRYGSVPG	244	1.3000	14.77
23	FEGVRRRFE	325	1.3000	14.77
24	FELVGTCGV	332	1.3000	14.77
25	LLQYTPHVA	177	1.2000	13.64
26	YTPHVAVIT	180	1.2000	13.64
27	LTALRVRAN	474	1.2000	13.64
28	MVGIGGAGM	14	1.1000	12.50
29	VAEHVTVPM	427	1.1000	12.50
30	LIVALQHCG	132	1.0000	11.36

31	MAGRTTLMV	111	0.9000	10.23
32	LRYGSVPGE	245	0.9000	10.23
33	YVPDFSAVA	437	0.9000	10.23
34	ILTALRVRA	473	0.9000	10.23
35	IRLASELAT	273	0.7000	7.95
36	IVTMGAGDV	458	0.7000	7.95
37	LRRVHMVGI	9	0.6000	6.82
38	VLRPAVLAK	101	0.6000	6.82
39	IVPGGALVV	215	0.6000	6.82
40	LNALGALLA	299	0.6000	6.82
41	VAVFDSFVE	205	0.5000	5.68
42	VLAKLMAGR	106	0.4000	4.55
43	LMVTGTHGK	117	0.4000	4.55
44	MLIVALQHC	131	0.4000	4.55
45	VQIGAPADE	309	0.4000	4.55
46	LQHCGLDPS	136	0.2000	2.27
47	FQPHLYSRT	381	0.2000	2.27
48	MRLSVPGRH	288	0.1000	1.14

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	VVFQPHLYS	379	4.5000	53.57
2	LRVRANRSA	477	3.5000	41.67
3	VVLRPAVLA	100	3.2000	38.10
4	MVVFQPHLY	378	3.2000	38.10
5	LVEARRRGI	90	2.8000	33.33
6	VFVLDVYGA	406	2.7000	32.14
7	LGIRVLRYG	240	2.6000	30.95
8	LYSRTKAFA	385	2.6000	30.95
9	VHALRARGA	47	2.4000	28.57
10	LLQYTPHVA	177	2.2000	26.19
11	VMRLSVPGR	287	1.9000	22.62

12	VGKASVRVF	340	1.9000	22.62
13	ILTALRVRA	473	1.9000	22.62
14	LRARGALIR	50	1.8000	21.43
15	LRPAVLAKL	102	1.7000	20.24
16	MRLSVPGRH	288	1.6800	20.00
17	LVSWQQQGV	259	1.6000	19.05
18	LNALGALLA	299	1.6000	19.05
19	VLRPAVLAK	101	1.5000	17.86
20	MLIVALQHC	131	1.4000	16.67
21	IVALQHCGL	133	1.4000	16.67
22	LGALLAAVQ	302	1.4000	16.67
23	LTALRVRAN	474	1.4000	16.67
24	LMVTGTHGK	117	1.3000	15.48
25	LDVYGAREQ	409	1.3000	15.48
26	YAHHPTEIS	351	1.2000	14.29
27	VRANRSAPG	479	1.2000	14.29
28	VSGASVAEH	422	1.1800	14.05
29	VRRRFELVG	328	1.1000	13.10
30	IRLASELAT	273	1.0000	11.90
31	VRVFDDYAH	345	0.9800	11.67
32	MAGRTTLMV	111	0.9000	10.71
33	VLRYGSVPG	244	0.9000	10.71
34	LQHCGLDPS	136	0.8000	9.52
35	VPMRYVPDF	433	0.8000	9.52
36	LLGPEILTA	468	0.8000	9.52
37	LRRVHMVGI	9	0.7000	8.33
38	VTTHAAIPK	77	0.7000	8.33
39	IVTMGAGDV	458	0.7000	8.33
40	LPPDLRRVH	5	0.6800	8.10
41	MVGIGGAGM	14	0.6000	7.14
42	LIVALQHCG	132	0.6000	7.14
43	IVPGGALVV	215	0.6000	7.14
44	VAEHVTVPM	427	0.6000	7.14
45	VAQQVAAAA	444	0.6000	7.14

46	VHMVGIGGA	12	0.5000	5.95
47	IRIGHDASS	57	0.5000	5.95
48	LRYGSVPGE	245	0.5000	5.95
49	LLDRGGLVS	29	0.3000	3.57

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	VVFQPHLYS	379	4.0000	45.98
2	VMRLSVPGR	287	3.5500	40.80
3	MVGIGGAGM	14	2.6000	29.89
4	FELVGTCGV	332	2.6000	29.89
5	MVVFQPHLY	378	2.6000	29.89
6	LRARGALIR	50	2.5000	28.74
7	LNALGALLA	299	2.4000	27.59
8	VFVLDVYGA	406	2.2000	25.29
9	IVALQHCGL	133	2.0600	23.68
10	IVTMGAGDV	458	2.0000	22.99
11	VHMVGIGGA	12	1.9000	21.84
12	WQQQGVGAV	262	1.9000	21.84
13	IRLASELAT	273	1.8000	20.69
14	FVERIVPGG	211	1.7500	20.11
15	VAVITNIES	184	1.7000	19.54
16	VRRRFELVG	328	1.7000	19.54
17	LRPAVLAKL	102	1.6600	19.08
18	MSGIARILL	22	1.5600	17.93
19	VLRPAVLAK	101	1.5000	17.24
20	IVPGGALVV	215	1.5000	17.24
21	VRANRSAPG	479	1.5000	17.24
22	LRRVHMVGI	9	1.4000	16.09
23	IRVLRYGSV	242	1.3000	14.94
24	VPMRYVPDF	433	1.2500	14.37
25	VGKASVRVF	340	1.2000	13.79

26	LRYGSVPGE	245	1.1500	13.22
27	LVEARRRGI	90	1.1000	12.64
28	MAGRTTLMV	111	1.1000	12.64
29	MRLSVPGRH	288	1.1000	12.64
30	MLIVALQHC	131	1.0000	11.49
31	FEGVRRRFE	325	1.0000	11.49
32	VVLRPAVLA	100	0.8000	9.20
33	VERIVPGGA	212	0.8000	9.20
34	YGSVEAYVA	198	0.7000	8.05
35	LYSRTKAFA	385	0.7000	8.05
36	LLGPEILTA	468	0.7000	8.05
37	IPVVLRPAV	98	0.6500	7.47
38	YVPDFSAVA	437	0.6000	6.90
39	VGAVAHIRL	267	0.5600	6.44
40	VHALRARGA	47	0.5000	5.75
41	LIVALQHCG	132	0.5000	5.75
42	LGIRVLRYG	240	0.5000	5.75
43	LLAAVQIGA	305	0.5000	5.75
44	LMVTGTHGK	117	0.4000	4.60
45	LGALLAAVQ	302	0.4000	4.60
46	ILTALRVRA	473	0.4000	4.60
47	VGTCGVGKA	335	0.3000	3.45
48	LTALRVRAN	474	0.3000	3.45
49	VTLLGPEIL	466	0.2600	2.99

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVFQPHLYS	379	4.9000	55.68
2	MVVFQPHLY	378	4.5000	51.14
3	LGIRVLRYG	240	4.0000	45.45
4	VGKASVRVF	340	3.8000	43.18
5	LVEARRRGI	90	3.7000	42.05

6	LRVRANRSA	477	3.5000	39.77
7	VMRLSVPGR	287	3.4000	38.64
8	LRARGALIR	50	3.3000	37.50
9	VVLRPAVLA	100	3.2000	36.36
10	VFVLDVYGA	406	2.7000	30.68
11	VPMRYVPDF	433	2.7000	30.68
12	LRPAVLAKL	102	2.6600	30.23
13	LVSWQQQGV	259	2.6000	29.55
14	LYSRTKAFA	385	2.6000	29.55
15	VRANRSAPG	479	2.6000	29.55
16	VRRRFELVG	328	2.5000	28.41
17	VHALRARGA	47	2.4000	27.27
18	IVALQHCGL	133	2.3600	26.82
19	VLRYGSVPG	244	2.3000	26.14
20	LLQYTPHVA	177	2.2000	25.00
21	LTALRVRAN	474	2.2000	25.00
22	MVGIGGAGM	14	2.1000	23.86
23	VAEHVTVPM	427	2.1000	23.86
24	LIVALQHCG	132	2.0000	22.73
25	MAGRTTLMV	111	1.9000	21.59
26	LRYGSVPGE	245	1.9000	21.59
27	ILTALRVRA	473	1.9000	21.59
28	IRLASELAT	273	1.7000	19.32
29	IVTMGAGDV	458	1.7000	19.32
30	LRRVHMVGI	9	1.6000	18.18
31	VLRPAVLAK	101	1.6000	18.18
32	IVPGGALVV	215	1.6000	18.18
33	LNALGALLA	299	1.6000	18.18
34	YAHHPTEIS	351	1.6000	18.18
35	VAVFDSFVE	205	1.5000	17.05
36	VLAKLMAGR	106	1.4000	15.91
37	LMVTGTHGK	117	1.4000	15.91
38	MLIVALQHC	131	1.4000	15.91
39	VQIGAPADE	309	1.4000	15.91

40	LQHCGLDPS	136	1.2000	13.64
41	FVERIVPGG	211	1.2000	13.64
42	MRLSVPGRH	288	1.1000	12.50
43	LQYTPHVAV	178	1.0000	11.36
44	IRIGHDASS	57	0.9000	10.23
45	VTLLGPEIL	466	0.8600	9.77
46	VTTHAAIPK	77	0.8000	9.09
47	WQQQGVGAV	262	0.8000	9.09
48	LLGPEILTA	468	0.8000	9.09
49	LLDRGGLVS	29	0.7000	7.95

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	VVFQPHLYS	379	3.9000	44.32
2	MVVFQPHLY	378	3.5000	39.77
3	LGIRVLRYG	240	3.0000	34.09
4	VGKASVRVF	340	2.8000	31.82
5	LVEARRRGI	90	2.7000	30.68
6	YAHHPTEIS	351	2.6000	29.55
7	LRVRANRSA	477	2.5000	28.41
8	VMRLSVPGR	287	2.4000	27.27
9	LRARGALIR	50	2.3000	26.14
10	VVLRPAVLA	100	2.2000	25.00
11	FVERIVPGG	211	2.2000	25.00
12	WQQQGVGAV	262	1.8000	20.45
13	VFVLDVYGA	406	1.7000	19.32
14	VPMRYVPDF	433	1.7000	19.32
15	LRPAVLAKL	102	1.6600	18.86
16	LVSWQQQGV	259	1.6000	18.18
17	LYSRTKAFA	385	1.6000	18.18
18	VRANRSAPG	479	1.6000	18.18
19	VRRRFELVG	328	1.5000	17.05

20	VHALRARGA	47	1.4000	15.91
21	IVALQHCGL	133	1.3600	15.45
22	VLRYGSVPG	244	1.3000	14.77
23	FEGVRRRFE	325	1.3000	14.77
24	FELVGTCGV	332	1.3000	14.77
25	LLQYTPHVA	177	1.2000	13.64
26	YTPHVAVIT	180	1.2000	13.64
27	LTALRVRAN	474	1.2000	13.64
28	MVGIGGAGM	14	1.1000	12.50
29	VAEHVTVPM	427	1.1000	12.50
30	LIVALQHCG	132	1.0000	11.36
31	MAGRTTLMV	111	0.9000	10.23
32	LRYGSVPGE	245	0.9000	10.23
33	YVPDFSAVA	437	0.9000	10.23
34	ILTALRVRA	473	0.9000	10.23
35	IRLASELAT	273	0.7000	7.95
36	IVTMGAGDV	458	0.7000	7.95
37	LRRVHMVGI	9	0.6000	6.82
38	VLRPAVLAK	101	0.6000	6.82
39	IVPGGALVV	215	0.6000	6.82
40	LNALGALLA	299	0.6000	6.82
41	VAVFDSFVE	205	0.5000	5.68
42	VLAKLMAGR	106	0.4000	4.55
43	LMVTGTHGK	117	0.4000	4.55
44	MLIVALQHC	131	0.4000	4.55
45	VQIGAPADE	309	0.4000	4.55
46	LQHCGLDPS	136	0.2000	2.27
47	FQPHLYSRT	381	0.2000	2.27
48	MRLSVPGRH	288	0.1000	1.14

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	VVFQPHLYS	379	4.5000	50.00
2	MVVFQPHLY	378	4.3000	47.78
3	LGIRVLRYG	240	3.9000	43.33
4	LRYGSVPGE	245	3.5000	38.89
5	LRVRANRSA	477	3.5000	38.89
6	LTALRVRAN	474	3.4000	37.78
7	VVLRPAVLA	100	3.2000	35.56
8	VAVFDSFVE	205	3.1000	34.44
9	LVEARRRGI	90	3.0000	33.33
10	VQIGAPADE	309	3.0000	33.33
11	MRLSVPGRH	288	2.9000	32.22
12	VGKASVRVF	340	2.8000	31.11
13	LRPAVLAKL	102	2.7000	30.00
14	VFVLDVYGA	406	2.7000	30.00
15	LYSRTKAFA	385	2.6000	28.89
16	VRANRSAPG	479	2.5000	27.78
17	VHALRARGA	47	2.4000	26.67
18	IVALQHCGL	133	2.4000	26.67
19	VRRRFELVG	328	2.4000	26.67
20	VSGASVAEH	422	2.4000	26.67
21	LLQYTPHVA	177	2.2000	24.44
22	VLRYGSVPG	244	2.2000	24.44
23	LGALLAAVQ	302	2.2000	24.44
24	VRVFDDYAH	345	2.2000	24.44
25	LDVYGAREQ	409	2.1000	23.33
26	LPPDLRRVH	5	1.9000	21.11
27	LIVALQHCG	132	1.9000	21.11
28	LVSWQQQGV	259	1.9000	21.11
29	IRLASELAT	273	1.9000	21.11
30	VMRLSVPGR	287	1.9000	21.11
31	FEGVRRRFE	325	1.9000	21.11
32	ILTALRVRA	473	1.9000	21.11
33	LRARGALIR	50	1.8000	20.00
34	MVGIGGAGM	14	1.7000	18.89

35	VAEHVTVPM	427	1.7000	18.89
36	VPMRYVPDF	433	1.7000	18.89
37	LNALGALLA	299	1.6000	17.78
38	LGEAGTNAH	151	1.5000	16.67
39	MLIVALQHC	131	1.4000	15.56
40	VEAYVAVFD	201	1.4000	15.56
41	MAGRTTLMV	111	1.2000	13.33
42	YAHHPTEIS	351	1.2000	13.33
43	VALQHCGLD	134	1.1000	12.22
44	FVERIVPGG	211	1.1000	12.22
45	VAHIRLASE	270	1.1000	12.22
46	IVTMGAGDV	458	1.0000	11.11
47	LRRVHMVGI	9	0.9000	10.00
48	IVPGGALVV	215	0.9000	10.00
49	VTLLGPEIL	466	0.9000	10.00

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	VVFQPHLYS	379	4.0000	45.98
2	VMRLSVPGR	287	3.5500	40.80
3	MVGIGGAGM	14	2.6000	29.89
4	FELVGTCGV	332	2.6000	29.89
5	MVVFQPHLY	378	2.6000	29.89
6	LRARGALIR	50	2.5000	28.74
7	LNALGALLA	299	2.4000	27.59
8	VFVLDVYGA	406	2.2000	25.29
9	IVALQHCGL	133	2.0600	23.68
10	IVTMGAGDV	458	2.0000	22.99
11	VHMVGIGGA	12	1.9000	21.84
12	WQQQGVGAV	262	1.9000	21.84
13	IRLASELAT	273	1.8000	20.69
14	FVERIVPGG	211	1.7500	20.11

15	VAVITNIES	184	1.7000	19.54
16	VRRRFELVG	328	1.7000	19.54
17	LRPAVLAKL	102	1.6600	19.08
18	MSGIARILL	22	1.5600	17.93
19	VLRPAVLAK	101	1.5000	17.24
20	IVPGGALVV	215	1.5000	17.24
21	VRANRSAPG	479	1.5000	17.24
22	LRRVHMVGI	9	1.4000	16.09
23	IRVLRYGSV	242	1.3000	14.94
24	VPMRYVPDF	433	1.2500	14.37
25	VGKASVRVF	340	1.2000	13.79
26	LRYGSVPGE	245	1.1500	13.22
27	LVEARRRGI	90	1.1000	12.64
28	MAGRTTLMV	111	1.1000	12.64
29	MRLSVPGRH	288	1.1000	12.64
30	MLIVALQHC	131	1.0000	11.49
31	FEGVRRRFE	325	1.0000	11.49
32	VVLRPAVLA	100	0.8000	9.20
33	VERIVPGGA	212	0.8000	9.20
34	YGSVEAYVA	198	0.7000	8.05
35	LYSRTKAFA	385	0.7000	8.05
36	LLGPEILTA	468	0.7000	8.05
37	IPVVLRPAV	98	0.6500	7.47
38	YVPDFSAVA	437	0.6000	6.90
39	VGAVAHIRL	267	0.5600	6.44
40	VHALRARGA	47	0.5000	5.75
41	LIVALQHCG	132	0.5000	5.75
42	LGIRVLRYG	240	0.5000	5.75
43	LLAAVQIGA	305	0.5000	5.75
44	LMVTGTHGK	117	0.4000	4.60
45	LGALLAAVQ	302	0.4000	4.60
46	ILTALRVRA	473	0.4000	4.60
47	VGTCGVGKA	335	0.3000	3.45
48	LTALRVRAN	474	0.3000	3.45

49	VTLLGPEIL	466	0.2600	2.99

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	VHMVGIGGA	12	1.8000	26.47
2	VVFQPHLYS	379	1.8000	26.47
3	FELVGTCGV	332	1.6000	23.53
4	MRLSVPGRH	288	1.5800	23.24
5	VFVLDVYGA	406	1.5000	22.06
6	MVGIGGAGM	14	1.1000	16.18
7	IVALQHCGL	133	1.1000	16.18
8	LGALLAAVQ	302	1.1000	16.18
9	MLIVALQHC	131	0.9000	13.24
10	VMRLSVPGR	287	0.9000	13.24
11	IVTMGAGDV	458	0.9000	13.24
12	WQQQGVGAV	262	0.8000	11.76
13	LRPAVLAKL	102	0.7000	10.29
14	VERIVPGGA	212	0.7000	10.29
15	LYSRTKAFA	385	0.7000	10.29
16	LNALGALLA	299	0.6000	8.82
17	MVVFQPHLY	378	0.6000	8.82
18	YVPDFSAVA	437	0.6000	8.82
19	VHALRARGA	47	0.3000	4.41
20	VVLRPAVLA	100	0.3000	4.41
21	IRVLRYGSV	242	0.2000	2.94
22	VGTCGVGKA	335	0.2000	2.94
23	VSGASVAEH	422	0.1800	2.65
24	VRANRSAPG	479	0.1000	1.47
25	LIRIGHDAS	56	-0.1000	0
26	ILTALRVRA	473	-0.1000	0
27	LRVRANRSA	477	-0.2000	0
28	VAVITNIES	184	-0.3000	0

29	VLRPAVLAK	101	-0.4000	0
30	LMVTGTHGK	117	-0.4000	0
31	VGIGGAGMS	15	-0.5000	0
32	FEGVRRRFE	325	-0.6000	0
33	IRIGHDASS	57	-0.7000	0
34	IRLASELAT	273	-0.7000	0
35	LTALRVRAN	474	-0.7000	0
36	LRARGALIR	50	-0.8000	0
37	VVTTHAAIP	76	-0.8000	0
38	FVERIVPGG	211	-0.8000	0
39	VGKASVRVF	340	-0.9000	0
40	MRYVPDFSA	435	-0.9000	0
41	MSGIARILL	22	-1.0000	0
42	LVSWQQQGV	259	-1.0000	0
43	LQHCGLDPS	136	-1.1000	0
44	LLQYTPHVA	177	-1.1000	0
45	LGIRVLRYG	240	-1.1000	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	VVFQPHLYS	379	4.6000	55.42
2	LNALGALLA	299	3.4000	40.96
3	VFVLDVYGA	406	3.2000	38.55
4	VMRLSVPGR	287	3.0500	36.75
5	VHMVGIGGA	12	2.9000	34.94
6	MRLSVPGRH	288	2.6800	32.29
7	VLRPAVLAK	101	2.4000	28.92
8	VAVITNIES	184	2.3000	27.71
9	MVVFQPHLY	378	2.3000	27.71
10	MVGIGGAGM	14	2.1000	25.30
11	IVALQHCGL	133	2.1000	25.30
12	IRLASELAT	273	2.1000	25.30

13	LGALLAAVQ	302	2.1000	25.30
14	LRARGALIR	50	2.0000	24.10
15	MLIVALQHC	131	2.0000	24.10
16	IVTMGAGDV	458	2.0000	24.10
17	VVLRPAVLA	100	1.8000	21.69
18	VERIVPGGA	212	1.8000	21.69
19	LRPAVLAKL	102	1.7000	20.48
20	LYSRTKAFA	385	1.7000	20.48
21	LLGPEILTA	468	1.7000	20.48
22	MSGIARILL	22	1.6000	19.28
23	LRRVHMVGI	9	1.5000	18.07
24	VHALRARGA	47	1.5000	18.07
25	IVPGGALVV	215	1.5000	18.07
26	LLAAVQIGA	305	1.5000	18.07
27	ILTALRVRA	473	1.4000	16.87
28	LMVTGTHGK	117	1.3000	15.66
29	IRVLRYGSV	242	1.3000	15.66
30	VRRRFELVG	328	1.3000	15.66
31	VGTCGVGKA	335	1.3000	15.66
32	LVEARRRGI	90	1.2000	14.46
33	VSGASVAEH	422	1.1800	14.22
34	MAGRTTLMV	111	1.1000	13.25
35	VRANRSAPG	479	1.1000	13.25
36	LRVRANRSA	477	1.0000	12.05
37	LRYGSVPGE	245	0.7500	9.04
38	IPVVLRPAV	98	0.6500	7.83
39	VGIGGAGMS	15	0.6000	7.23
40	LIRIGHDAS	56	0.6000	7.23
41	LLQYTPHVA	177	0.6000	7.23
42	VGAVAHIRL	267	0.6000	7.23
43	FELVGTCGV	332	0.6000	7.23
44	MRYVPDFSA	435	0.6000	7.23
45	LLDRGGLVS	29	0.5000	6.02
46	LTALRVRAN	474	0.5000	6.02

47	VRVFDDYAH	345	0.3800	4.58
48	VPMRYVPDF	433	0.3500	4.22
49	IRIGHDASS	57	0.3000	3.61

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	VVFQPHLYS	379	3.6000	40.45
2	MRLSVPGRH	288	2.9000	32.58
3	LRYGSVPGE	245	2.7500	30.90
4	FEGVRRRFE	325	2.6000	29.21
5	LNALGALLA	299	2.4000	26.97
6	MVVFQPHLY	378	2.4000	26.97
7	MVGIGGAGM	14	2.2000	24.72
8	VFVLDVYGA	406	2.2000	24.72
9	IVALQHCGL	133	2.1000	23.60
10	VMRLSVPGR	287	2.0500	23.03
11	IRLASELAT	273	2.0000	22.47
12	VHMVGIGGA	12	1.9000	21.35
13	LGALLAAVQ	302	1.9000	21.35
14	FELVGTCGV	332	1.9000	21.35
15	VQIGAPADE	309	1.8000	20.22
16	LRPAVLAKL	102	1.7000	19.10
17	FVERIVPGG	211	1.6500	18.54
18	MSGIARILL	22	1.6000	17.98
19	VAHIRLASE	270	1.6000	17.98
20	VRRRFELVG	328	1.6000	17.98
21	FGRALNAAD	396	1.6000	17.98
22	LTALRVRAN	474	1.5000	16.85
23	VSGASVAEH	422	1.4000	15.73
24	VRANRSAPG	479	1.4000	15.73
25	VAVITNIES	184	1.3000	14.61
26	IVTMGAGDV	458	1.3000	14.61

27	WQQQGVGAV	262	1.2000	13.48
28	LRARGALIR	50	1.0000	11.24
29	MLIVALQHC	131	1.0000	11.24
30	VVLRPAVLA	100	0.8000	8.99
31	VERIVPGGA	212	0.8000	8.99
32	IVPGGALVV	215	0.8000	8.99
33	LRRVHMVGI	9	0.7000	7.87
34	VLRPAVLAK	101	0.7000	7.87
35	YGSVEAYVA	198	0.7000	7.87
36	VAVFDSFVE	205	0.7000	7.87
37	LYSRTKAFA	385	0.7000	7.87
38	LLGPEILTA	468	0.7000	7.87
39	IRVLRYGSV	242	0.6000	6.74
40	VGAVAHIRL	267	0.6000	6.74
41	VRVFDDYAH	345	0.6000	6.74
42	YVPDFSAVA	437	0.6000	6.74
43	VHALRARGA	47	0.5000	5.62
44	LLAAVQIGA	305	0.5000	5.62
45	LVEARRRGI	90	0.4000	4.49
46	MAGRTTLMV	111	0.4000	4.49
47	LIVALQHCG	132	0.4000	4.49
48	LGIRVLRYG	240	0.4000	4.49
49	ILTALRVRA	473	0.4000	4.49

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	VVFQPHLYS	379	4.5000	53.57
2	LRVRANRSA	477	3.5000	41.67
3	VVLRPAVLA	100	3.2000	38.10
4	MVVFQPHLY	378	3.2000	38.10
5	LVEARRRGI	90	2.8000	33.33
6	VFVLDVYGA	406	2.7000	32.14

7	LGIRVLRYG	240	2.6000	30.95
8	LYSRTKAFA	385	2.6000	30.95
9	VHALRARGA	47	2.4000	28.57
10	LLQYTPHVA	177	2.2000	26.19
11	VMRLSVPGR	287	1.9000	22.62
12	VGKASVRVF	340	1.9000	22.62
13	ILTALRVRA	473	1.9000	22.62
14	LRARGALIR	50	1.8000	21.43
15	LRPAVLAKL	102	1.7000	20.24
16	MRLSVPGRH	288	1.6800	20.00
17	LVSWQQQGV	259	1.6000	19.05
18	LNALGALLA	299	1.6000	19.05
19	VLRPAVLAK	101	1.5000	17.86
20	MLIVALQHC	131	1.4000	16.67
21	IVALQHCGL	133	1.4000	16.67
22	LGALLAAVQ	302	1.4000	16.67
23	LTALRVRAN	474	1.4000	16.67
24	LMVTGTHGK	117	1.3000	15.48
25	LDVYGAREQ	409	1.3000	15.48
26	YAHHPTEIS	351	1.2000	14.29
27	VRANRSAPG	479	1.2000	14.29
28	VSGASVAEH	422	1.1800	14.05
29	VRRRFELVG	328	1.1000	13.10
30	IRLASELAT	273	1.0000	11.90
31	VRVFDDYAH	345	0.9800	11.67
32	MAGRTTLMV	111	0.9000	10.71
33	VLRYGSVPG	244	0.9000	10.71
34	LQHCGLDPS	136	0.8000	9.52
35	VPMRYVPDF	433	0.8000	9.52
36	LLGPEILTA	468	0.8000	9.52
37	LRRVHMVGI	9	0.7000	8.33
38	VTTHAAIPK	77	0.7000	8.33
39	IVTMGAGDV	458	0.7000	8.33
40	LPPDLRRVH	5	0.6800	8.10

41	MVGIGGAGM	14	0.6000	7.14
42	LIVALQHCG	132	0.6000	7.14
43	IVPGGALVV	215	0.6000	7.14
44	VAEHVTVPM	427	0.6000	7.14
45	VAQQVAAAA	444	0.6000	7.14
46	VHMVGIGGA	12	0.5000	5.95
47	IRIGHDASS	57	0.5000	5.95
48	LRYGSVPGE	245	0.5000	5.95
49	LLDRGGLVS	29	0.3000	3.57

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	VVFQPHLYS	379	3.5000	41.67
2	LRVRANRSA	477	2.5000	29.76
3	VVLRPAVLA	100	2.2000	26.19
4	YAHHPTEIS	351	2.2000	26.19
5	MVVFQPHLY	378	2.2000	26.19
6	LVEARRRGI	90	1.8000	21.43
7	VFVLDVYGA	406	1.7000	20.24
8	LGIRVLRYG	240	1.6000	19.05
9	LYSRTKAFA	385	1.6000	19.05
10	VHALRARGA	47	1.4000	16.67
11	LLQYTPHVA	177	1.2000	14.29
12	VMRLSVPGR	287	0.9000	10.71
13	VGKASVRVF	340	0.9000	10.71
14	YVPDFSAVA	437	0.9000	10.71
15	ILTALRVRA	473	0.9000	10.71
16	LRARGALIR	50	0.8000	9.52
17	FVERIVPGG	211	0.8000	9.52
18	WQQQGVGAV	262	0.8000	9.52
19	LRPAVLAKL	102	0.7000	8.33
20	MRLSVPGRH	288	0.6800	8.10

21	LVSWQQQGV	259	0.6000	7.14
22	LNALGALLA	299	0.6000	7.14
23	VLRPAVLAK	101	0.5000	5.95
24	YTPHVAVIT	180	0.5000	5.95
25	MLIVALQHC	131	0.4000	4.76
26	IVALQHCGL	133	0.4000	4.76
27	LGALLAAVQ	302	0.4000	4.76
28	LTALRVRAN	474	0.4000	4.76
29	LMVTGTHGK	117	0.3000	3.57
30	FELVGTCGV	332	0.3000	3.57
31	LDVYGAREQ	409	0.3000	3.57
32	VRANRSAPG	479	0.2000	2.38
33	VSGASVAEH	422	0.1800	2.14
34	VRRRFELVG	328	0.1000	1.19
35	VRVFDDYAH	345	-0.0200	0
36	MAGRTTLMV	111	-0.1000	0
37	VLRYGSVPG	244	-0.1000	0
38	FEGVRRRFE	325	-0.1000	0
39	YSRTKAFAA	386	-0.1000	0
40	YGAREQPLA	412	-0.1000	0
41	LQHCGLDPS	136	-0.2000	0
42	VPMRYVPDF	433	-0.2000	0
43	LLGPEILTA	468	-0.2000	0
44	LRRVHMVGI	9	-0.3000	0
45	VTTHAAIPK	77	-0.3000	0
46	IVTMGAGDV	458	-0.3000	0
47	LPPDLRRVH	5	-0.3200	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	VVFQPHLYS	379	4.9000	55.68
2	MVVFQPHLY	378	4.5000	51.14

3	LGIRVLRYG	240	4.0000	45.45
4	VGKASVRVF	340	3.8000	43.18
5	LVEARRRGI	90	3.7000	42.05
6	LRVRANRSA	477	3.5000	39.77
7	VMRLSVPGR	287	3.4000	38.64
8	LRARGALIR	50	3.3000	37.50
9	VVLRPAVLA	100	3.2000	36.36
10	VFVLDVYGA	406	2.7000	30.68
11	VPMRYVPDF	433	2.7000	30.68
12	LRPAVLAKL	102	2.6600	30.23
13	LVSWQQQGV	259	2.6000	29.55
14	LYSRTKAFA	385	2.6000	29.55
15	VRANRSAPG	479	2.6000	29.55
16	VRRRFELVG	328	2.5000	28.41
17	VHALRARGA	47	2.4000	27.27
18	IVALQHCGL	133	2.3600	26.82
19	VLRYGSVPG	244	2.3000	26.14
20	LLQYTPHVA	177	2.2000	25.00
21	LTALRVRAN	474	2.2000	25.00
22	MVGIGGAGM	14	2.1000	23.86
23	VAEHVTVPM	427	2.1000	23.86
24	LIVALQHCG	132	2.0000	22.73
25	MAGRTTLMV	111	1.9000	21.59
26	LRYGSVPGE	245	1.9000	21.59
27	ILTALRVRA	473	1.9000	21.59
28	IRLASELAT	273	1.7000	19.32
29	IVTMGAGDV	458	1.7000	19.32
30	LRRVHMVGI	9	1.6000	18.18
31	VLRPAVLAK	101	1.6000	18.18
32	IVPGGALVV	215	1.6000	18.18
33	LNALGALLA	299	1.6000	18.18
34	YAHHPTEIS	351	1.6000	18.18
35	VAVFDSFVE	205	1.5000	17.05
36	VLAKLMAGR	106	1.4000	15.91

37	LMVTGTHGK	117	1.4000	15.91
38	MLIVALQHC	131	1.4000	15.91
39	VQIGAPADE	309	1.4000	15.91
40	LQHCGLDPS	136	1.2000	13.64
41	FVERIVPGG	211	1.2000	13.64
42	MRLSVPGRH	288	1.1000	12.50
43	LQYTPHVAV	178	1.0000	11.36
44	IRIGHDASS	57	0.9000	10.23
45	VTLLGPEIL	466	0.8600	9.77
46	VTTHAAIPK	77	0.8000	9.09
47	WQQQGVGAV	262	0.8000	9.09
48	LLGPEILTA	468	0.8000	9.09
49	LLDRGGLVS	29	0.7000	7.95

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	VVFQPHLYS	379	4.9000	55.68
2	MVVFQPHLY	378	4.5000	51.14
3	LGIRVLRYG	240	4.0000	45.45
4	VGKASVRVF	340	3.8000	43.18
5	LVEARRRGI	90	3.7000	42.05
6	LRVRANRSA	477	3.5000	39.77
7	VMRLSVPGR	287	3.4000	38.64
8	LRARGALIR	50	3.3000	37.50
9	VVLRPAVLA	100	3.2000	36.36
10	VFVLDVYGA	406	2.7000	30.68
11	VPMRYVPDF	433	2.7000	30.68
12	LRPAVLAKL	102	2.6600	30.23
13	LVSWQQQGV	259	2.6000	29.55
14	LYSRTKAFA	385	2.6000	29.55
15	VRANRSAPG	479	2.6000	29.55
16	VRRRFELVG	328	2.5000	28.41

17	VHALRARGA	47	2.4000	27.27
18	IVALQHCGL	133	2.3600	26.82
19	VLRYGSVPG	244	2.3000	26.14
20	LLQYTPHVA	177	2.2000	25.00
21	LTALRVRAN	474	2.2000	25.00
22	MVGIGGAGM	14	2.1000	23.86
23	VAEHVTVPM	427	2.1000	23.86
24	LIVALQHCG	132	2.0000	22.73
25	MAGRTTLMV	111	1.9000	21.59
26	LRYGSVPGE	245	1.9000	21.59
27	ILTALRVRA	473	1.9000	21.59
28	IRLASELAT	273	1.7000	19.32
29	IVTMGAGDV	458	1.7000	19.32
30	LRRVHMVGI	9	1.6000	18.18
31	VLRPAVLAK	101	1.6000	18.18
32	IVPGGALVV	215	1.6000	18.18
33	LNALGALLA	299	1.6000	18.18
34	YAHHPTEIS	351	1.6000	18.18
35	VAVFDSFVE	205	1.5000	17.05
36	VLAKLMAGR	106	1.4000	15.91
37	LMVTGTHGK	117	1.4000	15.91
38	MLIVALQHC	131	1.4000	15.91
39	VQIGAPADE	309	1.4000	15.91
40	LQHCGLDPS	136	1.2000	13.64
41	FVERIVPGG	211	1.2000	13.64
42	MRLSVPGRH	288	1.1000	12.50
43	LQYTPHVAV	178	1.0000	11.36
44	IRIGHDASS	57	0.9000	10.23
45	VTLLGPEIL	466	0.8600	9.77
46	VTTHAAIPK	77	0.8000	9.09
47	WQQQGVGAV	262	0.8000	9.09
48	LLGPEILTA	468	0.8000	9.09
49	LLDRGGLVS	29	0.7000	7.95

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	IVPGGALVV	215	4.6000	46.94
2	MVVFQPHLY	378	4.5000	45.92
3	VLRYGSVPG	244	4.3000	43.88
4	VRVFDDYAH	345	4.3000	43.88
5	LRRVHMVGI	9	4.2000	42.86
6	MRYVPDFSA	435	4.2000	42.86
7	LLQYTPHVA	177	3.9000	39.80
8	IRVLRYGSV	242	3.9000	39.80
9	IRLASELAT	273	3.9000	39.80
10	VVLRPAVLA	100	3.6000	36.73
11	MSGIARILL	22	3.5000	35.71
12	MVGIGGAGM	14	3.4800	35.51
13	IVTMGAGDV	458	3.4000	34.69
14	LRARGALIR	50	3.3000	33.67
15	LRPAVLAKL	102	3.2000	32.65
16	LNALGALLA	299	3.2000	32.65
17	VRRRFELVG	328	3.2000	32.65
18	VVFQPHLYS	379	3.2000	32.65
19	LRVRANRSA	477	3.1000	31.63
20	IRIGHDASS	57	3.0000	30.61
21	VAVITNIES	184	3.0000	30.61
22	VAVFDSFVE	205	3.0000	30.61
23	LDFYGSVEA	195	2.9000	29.59
24	LLGPEILTA	468	2.8500	29.08
25	MLIVALQHC	131	2.6000	26.53
26	IVALQHCGL	133	2.6000	26.53
27	MAGRTTLMV	111	2.5600	26.12
28	VHMVGIGGA	12	2.4500	25.00
29	ILLDRGGLV	28	2.4000	24.49
30	LAGFEGVRR	322	2.4000	24.49

31	ILTALRVRA	473	2.3000	23.47
32	VGAVAHIRL	267	2.2000	22.45
33	VFVLDVYGA	406	2.2000	22.45
34	LVEARRRGI	90	2.1000	21.43
35	FQPHLYSRT	381	2.1000	21.43
36	LLDRGGLVS	29	2.0000	20.41
37	LVSWQQQGV	259	1.9000	19.39
38	IGGAGMSGI	17	1.8000	18.37
39	LLPGGATAV	68	1.8000	18.37
40	IPVVLRPAV	98	1.8000	18.37
41	LQYTPHVAV	178	1.8000	18.37
42	VRANRSAPG	479	1.8000	18.37
43	VGIGGAGMS	15	1.7000	17.35
44	LLAAVQIGA	305	1.7000	17.35
45	MRLSVPGRH	288	1.6000	16.33
46	YVPDFSAVA	437	1.6000	16.33
47	ITNIESDHL	187	1.5000	15.31
48	YVAVFDSFV	204	1.5000	15.31
49	LSVPGRHMA	290	1.5000	15.31

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	IVPGGALVV	215	3.6000	36.73
2	MVVFQPHLY	378	3.5000	35.71
3	VLRYGSVPG	244	3.3000	33.67
4	VRVFDDYAH	345	3.3000	33.67
5	LRRVHMVGI	9	3.2000	32.65
6	MRYVPDFSA	435	3.2000	32.65
7	FQPHLYSRT	381	3.1000	31.63
8	LLQYTPHVA	177	2.9000	29.59
9	IRVLRYGSV	242	2.9000	29.59
10	IRLASELAT	273	2.9000	29.59

11	VVLRPAVLA	100	2.6000	26.53
12	YVPDFSAVA	437	2.6000	26.53
13	MSGIARILL	22	2.5000	25.51
14	YVAVFDSFV	204	2.5000	25.51
15	MVGIGGAGM	14	2.4800	25.31
16	IVTMGAGDV	458	2.4000	24.49
17	LRARGALIR	50	2.3000	23.47
18	LRPAVLAKL	102	2.2000	22.45
19	LNALGALLA	299	2.2000	22.45
20	VRRRFELVG	328	2.2000	22.45
21	VVFQPHLYS	379	2.2000	22.45
22	FVLDVYGAR	407	2.1000	21.43
23	LRVRANRSA	477	2.1000	21.43
24	IRIGHDASS	57	2.0000	20.41
25	VAVITNIES	184	2.0000	20.41
26	VAVFDSFVE	205	2.0000	20.41
27	LDFYGSVEA	195	1.9000	19.39
28	LLGPEILTA	468	1.8500	18.88
29	MLIVALQHC	131	1.6000	16.33
30	IVALQHCGL	133	1.6000	16.33
31	YGSVEAYVA	198	1.6000	16.33
32	MAGRTTLMV	111	1.5600	15.92
33	FELVGTCGV	332	1.5600	15.92
34	YTPHVAVIT	180	1.5000	15.31
35	YSRTKAFAA	386	1.5000	15.31
36	VHMVGIGGA	12	1.4500	14.80
37	ILLDRGGLV	28	1.4000	14.29
38	LAGFEGVRR	322	1.4000	14.29
39	ILTALRVRA	473	1.3000	13.27
40	VGAVAHIRL	267	1.2000	12.24
41	VFVLDVYGA	406	1.2000	12.24
42	LVEARRRGI	90	1.1000	11.22
43	LLDRGGLVS	29	1.0000	10.20
44	LVSWQQQGV	259	0.9000	9.18

45	IGGAGMSGI	17	0.8000	8.16
46	LLPGGATAV	68	0.8000	8.16
47	IPVVLRPAV	98	0.8000	8.16
48	LQYTPHVAV	178	0.8000	8.16
49	VRANRSAPG	479	0.8000	8.16

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	IVPGGALVV	215	4.6000	46.94
2	MVVFQPHLY	378	4.5000	45.92
3	VLRYGSVPG	244	4.3000	43.88
4	VRVFDDYAH	345	4.3000	43.88
5	LRRVHMVGI	9	4.2000	42.86
6	MRYVPDFSA	435	4.2000	42.86
7	LLQYTPHVA	177	3.9000	39.80
8	IRVLRYGSV	242	3.9000	39.80
9	IRLASELAT	273	3.9000	39.80
10	VVLRPAVLA	100	3.6000	36.73
11	MSGIARILL	22	3.5000	35.71
12	MVGIGGAGM	14	3.4800	35.51
13	IVTMGAGDV	458	3.4000	34.69
14	LRARGALIR	50	3.3000	33.67
15	LRPAVLAKL	102	3.2000	32.65
16	LNALGALLA	299	3.2000	32.65
17	VRRRFELVG	328	3.2000	32.65
18	VVFQPHLYS	379	3.2000	32.65
19	LRVRANRSA	477	3.1000	31.63
20	IRIGHDASS	57	3.0000	30.61
21	VAVITNIES	184	3.0000	30.61
22	VAVFDSFVE	205	3.0000	30.61
23	LDFYGSVEA	195	2.9000	29.59
24	LLGPEILTA	468	2.8500	29.08

25	MLIVALQHC	131	2.6000	26.53
26	IVALQHCGL	133	2.6000	26.53
27	MAGRTTLMV	111	2.5600	26.12
28	VHMVGIGGA	12	2.4500	25.00
29	ILLDRGGLV	28	2.4000	24.49
30	LAGFEGVRR	322	2.4000	24.49
31	ILTALRVRA	473	2.3000	23.47
32	VGAVAHIRL	267	2.2000	22.45
33	VFVLDVYGA	406	2.2000	22.45
34	LVEARRRGI	90	2.1000	21.43
35	FQPHLYSRT	381	2.1000	21.43
36	LLDRGGLVS	29	2.0000	20.41
37	LVSWQQQGV	259	1.9000	19.39
38	IGGAGMSGI	17	1.8000	18.37
39	LLPGGATAV	68	1.8000	18.37
40	IPVVLRPAV	98	1.8000	18.37
41	LQYTPHVAV	178	1.8000	18.37
42	VRANRSAPG	479	1.8000	18.37
43	VGIGGAGMS	15	1.7000	17.35
44	LLAAVQIGA	305	1.7000	17.35
45	MRLSVPGRH	288	1.6000	16.33
46	YVPDFSAVA	437	1.6000	16.33
47	ITNIESDHL	187	1.5000	15.31
48	YVAVFDSFV	204	1.5000	15.31
49	LSVPGRHMA	290	1.5000	15.31

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	LMVTGTHGK	117	4.0000	40.82
2	LVGTCGVGK	334	3.7000	37.76
3	MVVFQPHLY	378	3.7000	37.76
4	MRLSVPGRH	288	3.5000	35.71

5	FVLDVYGAR	407	3.3000	33.67
6	IVTMGAGDV	458	3.2000	32.65
7	YGSVEAYVA	198	3.0000	30.61
8	MVGIGGAGM	14	2.8000	28.57
9	LRARGALIR	50	2.6000	26.53
10	MRYVPDFSA	435	2.6000	26.53
11	LRRVHMVGI	9	2.4000	24.49
12	MLIVALQHC	131	2.3000	23.47
13	YSRTKAFAA	386	2.2000	22.45
14	VMRLSVPGR	287	2.0000	20.41
15	VERIVPGGA	212	1.9000	19.39
16	VGAVAHIRL	267	1.9000	19.39
17	LRPAVLAKL	102	1.8000	18.37
18	IVALQHCGL	133	1.8000	18.37
19	VHALRARGA	47	1.7000	17.35
20	IRVLRYGSV	242	1.7000	17.35
21	VHMVGIGGA	12	1.5000	15.31
22	VTTHAAIPK	77	1.5000	15.31
23	ISATLAAAR	358	1.5000	15.31
24	MSGIARILL	22	1.4000	14.29
25	VAVITNIES	184	1.4000	14.29
26	VRVFDDYAH	345	1.3000	13.27
27	VVFQPHLYS	379	1.3000	13.27
28	VLRPAVLAK	101	1.2000	12.24
29	FELVGTCGV	332	1.2000	12.24
30	VTLLGPEIL	466	1.2000	12.24
31	LVEARRRGI	90	1.1000	11.22
32	YGSVPGETM	247	1.1000	11.22
33	LNALGALLA	299	1.0000	10.20
34	VFQPHLYSR	380	1.0000	10.20
35	FAAEFGRAL	392	1.0000	10.20
36	LIVALQHCG	132	0.8000	8.16
37	LLQYTPHVA	177	0.8000	8.16
38	YVAVFDSFV	204	0.8000	8.16

39	LGALLAAVQ	302	0.8000	8.16
40	FEGVRRRFE	325	0.8000	8.16
41	VFVLDVYGA	406	0.8000	8.16
42	VGIGGAGMS	15	0.7000	7.14
43	VGKASVRVF	340	0.7000	7.14
44	VVTTHAAIP	76	0.6000	6.12
45	IRLASELAT	273	0.6000	6.12
46	LAGFEGVRR	322	0.5000	5.10
47	IVPGGALVV	215	0.2000	2.04
48	LIRIGHDAS	56	0.1000	1.02
49	VVLRPAVLA	100	0.1000	1.02

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	LMVTGTHGK	117	4.0000	40.82
2	LVGTCGVGK	334	3.7000	37.76
3	MVVFQPHLY	378	3.7000	37.76
4	MRLSVPGRH	288	3.5000	35.71
5	FVLDVYGAR	407	3.3000	33.67
6	IVTMGAGDV	458	3.2000	32.65
7	YGSVEAYVA	198	3.0000	30.61
8	MVGIGGAGM	14	2.8000	28.57
9	LRARGALIR	50	2.6000	26.53
10	MRYVPDFSA	435	2.6000	26.53
11	LRRVHMVGI	9	2.4000	24.49
12	MLIVALQHC	131	2.3000	23.47
13	YSRTKAFAA	386	2.2000	22.45
14	VMRLSVPGR	287	2.0000	20.41
15	VERIVPGGA	212	1.9000	19.39
16	VGAVAHIRL	267	1.9000	19.39
17	LRPAVLAKL	102	1.8000	18.37
18	IVALQHCGL	133	1.8000	18.37

19	VHALRARGA	47	1.7000	17.35
20	IRVLRYGSV	242	1.7000	17.35
21	VHMVGIGGA	12	1.5000	15.31
22	VTTHAAIPK	77	1.5000	15.31
23	ISATLAAAR	358	1.5000	15.31
24	MSGIARILL	22	1.4000	14.29
25	VAVITNIES	184	1.4000	14.29
26	VRVFDDYAH	345	1.3000	13.27
27	VVFQPHLYS	379	1.3000	13.27
28	VLRPAVLAK	101	1.2000	12.24
29	FELVGTCGV	332	1.2000	12.24
30	VTLLGPEIL	466	1.2000	12.24
31	LVEARRRGI	90	1.1000	11.22
32	YGSVPGETM	247	1.1000	11.22
33	LNALGALLA	299	1.0000	10.20
34	VFQPHLYSR	380	1.0000	10.20
35	FAAEFGRAL	392	1.0000	10.20
36	LIVALQHCG	132	0.8000	8.16
37	LLQYTPHVA	177	0.8000	8.16
38	YVAVFDSFV	204	0.8000	8.16
39	LGALLAAVQ	302	0.8000	8.16
40	FEGVRRRFE	325	0.8000	8.16
41	VFVLDVYGA	406	0.8000	8.16
42	VGIGGAGMS	15	0.7000	7.14
43	VGKASVRVF	340	0.7000	7.14
44	VVTTHAAIP	76	0.6000	6.12
45	IRLASELAT	273	0.6000	6.12
46	LAGFEGVRR	322	0.5000	5.10
47	IVPGGALVV	215	0.2000	2.04
48	LIRIGHDAS	56	0.1000	1.02
49	VVLRPAVLA	100	0.1000	1.02