MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Feb 23 23:31:07 2010
Length of input sequence	625 amino acids
Number of nanomers from input sequence	617
Number of nanomers with obligatory P1 anchor residue	170
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	62

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	IRIQEGSGL	472	2.8000	46.67
2	VLLLDVTPL	362	1.3900	23.17
3	FKGTSGIDL	215	1.1000	18.33
4	VVLVGGSTR	309	0.5500	9.17
5	MARAVGIDL	0	0.5000	8.33
6	LRIVNEPTA	141	0.3200	5.33
7	VVVANSEGS	24	0.1000	1.67
8	VRNQAETLV	508	-0.2100	0
9	LNKVDAAVA	540	-0.2500	0

10	LVYQTEKFV	515	-0.3000	0
11	LVGQPAKNQ	48	-0.4000	0
12	VVAVGAALQ	343	-0.5500	0
13	LEGGDPVVV	18	-0.6000	0
14	VLVGGSTRM	310	-0.6300	0
15	IVHVTAKDK	456	-0.6500	0
16	FARNGEVLV	41	-0.6600	0
17	VLRIVNEPT	140	-0.7000	0
18	LLDVTPLSL	364	-0.7500	0
19	YQGEREIAA	414	-0.8000	0
20	VVEVRATSG	186	-0.8600	0
21	FQRITQDLL	277	-0.9000	0
22	VAVGAALQA	344	-0.9000	0
23	IERNTTIPT	385	-0.9600	0
24	YLGEDITDA	105	-1.0100	0
25	VRSVKRHMG	65	-1.1500	0
26	IELSSSQST	242	-1.2000	0
27	MAMQRLREA	228	-1.4100	0
28	LGSFELTGI	427	-1.4300	0
29	FQSVIADTG	292	-1.4500	0
30	LTRAEFQRI	272	-1.5000	0
31	LTGIPPAPR	432	-1.5000	0
32	YEAAQAASQ	581	-1.5000	0
33	VLVGQPAKN	47	-1.6000	0
34	VITTPAYFN	114	-1.6000	0
35	LEIGEGVVE	180	-1.6000	0
36	LSSSQSTSI	244	-1.6100	0
37	LVGGSTRMP	311	-1.6100	0
38	LGTTNSVVS	8	-1.7000	0
39	VIADTGISV	295	-1.7000	0
40	VLKGEVKDV	354	-1.7000	0
41	FELTGIPPA	430	-1.7300	0
42	VKRHMGSDW	68	-1.8000	0
43	VANSEGSRT	26	-1.9000	0

44	LNVLRIVNE	138	-1.9000	0
45	VQIQVYQGE	409	-1.9000	0
46	MTRLIERNT	381	-1.9100	0
47	MGSDWSIEI	72	-2.0000	0
48	VGAALQAGV	346	-2.0000	0
49	VAFARNGEV	39	-2.1000	0
50	LVFDLGGGT	166	-2.1000	0
51	YITVDADKN	256	-2.1500	0
52	LGIETKGGV	372	-2.2000	0
53	FNDAQRQAT	121	-2.3000	0
54	VSVLEGGDP	15	-2.4000	0
55	VFDLGGGTF	167	-2.4000	0
56	VNPDEVVAV	338	-2.4000	0
57	LGGSDISAI	554	-2.4000	0
58	IVAFARNGE	38	-2.4200	0
59	MQRLREAAE	230	-2.5000	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	IRIQEGSGL	472	3.8000	63.33
2	VLLLDVTPL	362	2.3900	39.83
3	VVLVGGSTR	309	1.5500	25.83
4	MARAVGIDL	0	1.5000	25.00
5	LRIVNEPTA	141	1.3200	22.00
6	VVVANSEGS	24	1.1000	18.33
7	FKGTSGIDL	215	1.1000	18.33
8	IAGLNVLRI	135	1.0000	16.67
9	IVNEPTAAA	143	1.0000	16.67
10	VRNQAETLV	508	0.7900	13.17
11	LNKVDAAVA	540	0.7500	12.50
12	LVYQTEKFV	515	0.7000	11.67
13	LVGQPAKNQ	48	0.6000	10.00

14	VVAVGAALQ	343	0.4500	7.50
15	LEGGDPVVV	18	0.4000	6.67
16	VLVGGSTRM	310	0.3700	6.17
17	IVHVTAKDK	456	0.3500	5.83
18	VLRIVNEPT	140	0.3000	5.00
19	LLDVTPLSL	364	0.2500	4.17
20	VVEVRATSG	186	0.1400	2.33
21	VAVGAALQA	344	0.1000	1.67
22	IERNTTIPT	385	0.0400	0.67
23	VRSVKRHMG	65	-0.1500	0
24	IELSSSQST	242	-0.2000	0
25	MAMQRLREA	228	-0.4100	0
26	LGSFELTGI	427	-0.4300	0
27	LTRAEFQRI	272	-0.5000	0
28	LTGIPPAPR	432	-0.5000	0
29	VLVGQPAKN	47	-0.6000	0
30	VITTPAYFN	114	-0.6000	0
31	LEIGEGVVE	180	-0.6000	0
32	LSSSQSTSI	244	-0.6100	0
33	LVGGSTRMP	311	-0.6100	0
34	FARNGEVLV	41	-0.6600	0
35	LGTTNSVVS	8	-0.7000	0
36	VIADTGISV	295	-0.7000	0
37	VLKGEVKDV	354	-0.7000	0
38	VKRHMGSDW	68	-0.8000	0
39	VANSEGSRT	26	-0.9000	0
40	LNVLRIVNE	138	-0.9000	0
41	FQRITQDLL	277	-0.9000	0
42	VQIQVYQGE	409	-0.9000	0
43	MTRLIERNT	381	-0.9100	0
44	MGSDWSIEI	72	-1.0000	0
45	VGAALQAGV	346	-1.0000	0
46	VAFARNGEV	39	-1.1000	0
47	LVFDLGGGT	166	-1.1000	0

48	LGIETKGGV	372	-1.2000	0
49	VSVLEGGDP	15	-1.4000	0
50	VFDLGGGTF	167	-1.4000	0
51	VNPDEVVAV	338	-1.4000	0
52	LGGSDISAI	554	-1.4000	0
53	IVAFARNGE	38	-1.4200	0
54	FQSVIADTG	292	-1.4500	0
55	MQRLREAAE	230	-1.5000	0
56	VVDAEVVDD	611	-1.5000	0
57	ILMKLKRDA	94	-1.6100	0
58	VKDVLLLDV	359	-1.6500	0
59	VGGSTRMPA	312	-1.7100	0
60	FELTGIPPA	430	-1.7300	0
61	IDLGTTNSV	6	-1.8000	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	LLLDVTPLS	363	6.9000	72.63
2	VNPDEVVAV	338	5.1000	53.68
3	LFLDEQLTR	266	4.5000	47.37
4	LVFDLGGGT	166	4.1000	43.16
5	MGSDWSIEI	72	3.9000	41.05
6	IEIDGKKYT	78	3.8000	40.00
7	VVDDGREAK	616	3.7000	38.95
8	VGGSTRMPA	312	3.5000	36.84
9	VVVANSEGS	24	3.4000	35.79
10	VIADTGISV	295	3.4000	35.79
11	VLLLDVTPL	362	3.0600	32.21
12	IRIQEGSGL	472	3.0300	31.89
13	VRSVKRHMG	65	3.0000	31.58
14	LRIVNEPTA	141	3.0000	31.58
15	VVLVGGSTR	309	2.9700	31.26

16	VGIDLGTTN	4	2.9000	30.53
17	VLVGGSTRM	310	2.9000	30.53
18	LGGSDISAI	554	2.7700	29.16
19	LGIETKGGV	372	2.7000	28.42
20	LKRDAEAYL	98	2.6600	28.00
21	IVNEPTAAA	143	2.4000	25.26
22	LVGGSTRMP	311	2.4000	25.26
23	LVDKFKGTS	211	2.3000	24.21
24	IAGLNVLRI	135	2.2000	23.16
25	VYQGEREIA	413	2.2000	23.16
26	LGEDITDAV	106	2.1000	22.11
27	VLKGEVKDV	354	2.1000	22.11
28	VDADKNPLF	259	2.0000	21.05
29	MIKDAEAHA	488	2.0000	21.05
30	VLVGQPAKN	47	1.9000	20.00
31	VTNVDRTVR	58	1.9000	20.00
32	LNVLRIVNE	138	1.9000	20.00
33	VSLLEIGEG	177	1.9000	20.00
34	VVAVGAALQ	343	1.9000	20.00
35	IAAHNKLLG	420	1.9000	20.00
36	LEGGDPVVV	18	1.8000	18.95
37	ILMKLKRDA	94	1.8000	18.95
38	LVKELTGGK	324	1.8000	18.95
39	IVAFARNGE	38	1.7100	18.00
40	IERNTTIPT	385	1.7000	17.89
41	LTGIPPAPR	432	1.7000	17.89
42	YGLDKGEKE	154	1.6000	16.84
43	VVDAEVVDD	611	1.6000	16.84
44	VVANSEGSR	25	1.5000	15.79
45	LGGDDWDQR	198	1.5000	15.79
46	VRNQAETLV	508	1.5000	15.79
47	VYQTEKFVK	516	1.5000	15.79
48	YFNDAQRQA	120	1.4000	14.74
49	ITQDLLDRT	280	1.4000	14.74

50	VHVTAKDKG	457	1.4000	14.74
51	LEIGEGVVE	180	1.3000	13.68
52	IGEGVVEVR	182	1.3000	13.68
53	VVDWLVDKF	207	1.3000	13.68
54	ISVSEIDHV	301	1.3000	13.68
55	FDIDANGIV	449	1.3000	13.68
56	IDLGTTNSV	6	1.2100	12.74
57	LVGQPAKNQ	48	1.2000	12.63
58	LMKLKRDAE	95	1.2000	12.63
59	ILVFDLGGG	165	1.2000	12.63
60	VVEVRATSG	186	1.2000	12.63
61	LTKDKMAMQ	223	1.2000	12.63
62	VAVGAALQA	344	1.2000	12.63

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	LLLDVTPLS	363	5.5000	60.44
2	VNPDEVVAV	338	3.1000	34.07
3	VVDDGREAK	616	2.6000	28.57
4	VGGSTRMPA	312	2.5000	27.47
5	YFNDAQRQA	120	2.4000	26.37
6	LVFDLGGGT	166	2.4000	26.37
7	IEIDGKKYT	78	2.1000	23.08
8	VVVANSEGS	24	2.0000	21.98
9	MGSDWSIEI	72	2.0000	21.98
10	LRIVNEPTA	141	2.0000	21.98
11	LFLDEQLTR	266	2.0000	21.98
12	VVAVGAALQ	343	1.6000	17.58
13	FELTGIPPA	430	1.5000	16.48
14	IVNEPTAAA	143	1.4000	15.38
15	VIADTGISV	295	1.4000	15.38
16	FDIDANGIV	449	1.3000	14.29

17	YGLDKGEKE	154	1.2000	13.19
18	VYQGEREIA	413	1.2000	13.19
19	VGIDLGTTN	4	1.1000	12.09
20	VLLLDVTPL	362	1.1000	12.09
21	IRIQEGSGL	472	1.0700	11.76
22	MIKDAEAHA	488	1.0000	10.99
23	LVGQPAKNQ	48	0.9000	9.89
24	LVDKFKGTS	211	0.9000	9.89
25	LTKDKMAMQ	223	0.9000	9.89
26	LGGSDISAI	554	0.8700	9.56
27	ILMKLKRDA	94	0.8000	8.79
28	YLGEDITDA	105	0.8000	8.79
29	LKRDAEAYL	98	0.7000	7.69
30	LVKELTGGK	324	0.7000	7.69
31	LGIETKGGV	372	0.7000	7.69
32	VRSVKRHMG	65	0.6000	6.59
33	YEAAQAASQ	581	0.6000	6.59
34	FQRITQDLL	277	0.5000	5.49
35	VVLVGGSTR	309	0.4700	5.16
36	VLVGGSTRM	310	0.4000	4.40
37	LVGGSTRMP	311	0.4000	4.40
38	VYQTEKFVK	516	0.4000	4.40
39	IAGLNVLRI	135	0.3000	3.30
40	WLVDKFKGT	210	0.3000	3.30
41	VAVGAALQA	344	0.2000	2.20
42	FVKEQREAE	522	0.2000	2.20
43	VLVGQPAKN	47	0.1000	1.10
44	LGEDITDAV	106	0.1000	1.10
45	VLKGEVKDV	354	0.1000	1.10
46	IVHVTAKDK	456	0.1000	1.10
47	LDRTRKPFQ	285	-0.1000	0
48	LEGGDPVVV	18	-0.2000	0
49	FQSVIADTG	292	-0.2000	0
50	LNKVDAAVA	540	-0.2000	0

51	VGQPAKNQA	49	-0.2900	0
52	MAMQRLREA	228	-0.3000	0
53	ITQDLLDRT	280	-0.3000	0
54	LNVLRIVNE	138	-0.5000	0
55	VSLLEIGEG	177	-0.5000	0
56	IAAHNKLLG	420	-0.5000	0
57	VRNQAETLV	508	-0.5000	0
58	VVDAEVVDD	611	-0.5000	0
59	VTNVDRTVR	58	-0.6000	0
60	IELSSSQST	242	-0.6000	0

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	LLLDVTPLS	363	5.1000	57.95
2	VVDDGREAK	616	4.0000	45.45
3	VNPDEVVAV	338	3.9800	45.23
4	IEIDGKKYT	78	3.7000	42.05
5	LFLDEQLTR	266	3.5000	39.77
6	VVVANSEGS	24	3.4000	38.64
7	VGGSTRMPA	312	3.2000	36.36
8	MGSDWSIEI	72	2.6800	30.45
9	VVAVGAALQ	343	2.6000	29.55
10	VYQGEREIA	413	2.6000	29.55
11	LVGQPAKNQ	48	2.5000	28.41
12	VRSVKRHMG	65	2.4000	27.27
13	IVNEPTAAA	143	2.4000	27.27
14	VGIDLGTTN	4	2.1000	23.86
15	VLLLDVTPL	362	2.1000	23.86
16	VIADTGISV	295	2.0800	23.64
17	LVFDLGGGT	166	2.0000	22.73
18	MIKDAEAHA	488	2.0000	22.73
19	LTKDKMAMQ	223	1.9000	21.59

20	IAGLNVLRI	135	1.8000	20.45
21	IRIQEGSGL	472	1.8000	20.45
22	LKRDAEAYL	98	1.7000	19.32
23	VAVGAALQA	344	1.7000	19.32
24	VLKGEVKDV	354	1.7000	19.32
25	IVHVTAKDK	456	1.7000	19.32
26	LRIVNEPTA	141	1.6000	18.18
27	LGGSDISAI	554	1.6000	18.18
28	ILMKLKRDA	94	1.5000	17.05
29	VGQPAKNQA	49	1.4000	15.91
30	LGEDITDAV	106	1.4000	15.91
31	VLVGGSTRM	310	1.4000	15.91
32	VVLVGGSTR	309	1.2000	13.64
33	VLVGQPAKN	47	1.1000	12.50
34	YFNDAQRQA	120	1.1000	12.50
35	LVGGSTRMP	311	1.1000	12.50
36	IVAFARNGE	38	1.0000	11.36
37	ITQDLLDRT	280	1.0000	11.36
38	IAAHNKLLG	420	1.0000	11.36
39	IDLGTTNSV	6	0.9000	10.23
40	LNKVDAAVA	540	0.8000	9.09
41	VPEDTLNKV	535	0.7000	7.95
42	LEGGDPVVV	18	0.6800	7.73
43	IERNTTIPT	385	0.6800	7.73
44	VLRIVNEPT	140	0.6000	6.82
45	YGLDKGEKE	154	0.6000	6.82
46	ISVSEIDHV	301	0.6000	6.82
47	LVDKFKGTS	211	0.5000	5.68
48	IELSSSQST	242	0.5000	5.68
49	VRNQAETLV	508	0.5000	5.68
50	LVYQTEKFV	515	0.5000	5.68
51	MEKLGQESQ	566	0.5000	5.68
52	VTNVDRTVR	58	0.4000	4.55
53	MAMQRLREA	228	0.4000	4.55

54	LNVLRIVNE	138	0.3800	4.32
55	VVDAEVVDD	611	0.3800	4.32
56	LGGDDWDQR	198	0.3000	3.41
57	LVKELTGGK	324	0.3000	3.41
58	LKGEVKDVL	355	0.3000	3.41
59	LGIETKGGV	372	0.3000	3.41
60	VHVTAKDKG	457	0.3000	3.41
61	VRATSGDNH	189	0.2800	3.18
62	LGGGTFDVS	170	0.2000	2.27

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	LLLDVTPLS	363	5.1000	57.95
2	VVDDGREAK	616	4.0000	45.45
3	VNPDEVVAV	338	3.9800	45.23
4	IEIDGKKYT	78	3.7000	42.05
5	LFLDEQLTR	266	3.5000	39.77
6	VVVANSEGS	24	3.4000	38.64
7	VGGSTRMPA	312	3.2000	36.36
8	MGSDWSIEI	72	2.6800	30.45
9	VVAVGAALQ	343	2.6000	29.55
10	VYQGEREIA	413	2.6000	29.55
11	LVGQPAKNQ	48	2.5000	28.41
12	VRSVKRHMG	65	2.4000	27.27
13	IVNEPTAAA	143	2.4000	27.27
14	VGIDLGTTN	4	2.1000	23.86
15	VLLLDVTPL	362	2.1000	23.86
16	VIADTGISV	295	2.0800	23.64
17	LVFDLGGGT	166	2.0000	22.73
18	MIKDAEAHA	488	2.0000	22.73
19	LTKDKMAMQ	223	1.9000	21.59
20	IAGLNVLRI	135	1.8000	20.45

21	IRIQEGSGL	472	1.8000	20.45
22	LKRDAEAYL	98	1.7000	19.32
23	VAVGAALQA	344	1.7000	19.32
24	VLKGEVKDV	354	1.7000	19.32
25	IVHVTAKDK	456	1.7000	19.32
26	LRIVNEPTA	141	1.6000	18.18
27	LGGSDISAI	554	1.6000	18.18
28	ILMKLKRDA	94	1.5000	17.05
29	VGQPAKNQA	49	1.4000	15.91
30	LGEDITDAV	106	1.4000	15.91
31	VLVGGSTRM	310	1.4000	15.91
32	VVLVGGSTR	309	1.2000	13.64
33	VLVGQPAKN	47	1.1000	12.50
34	YFNDAQRQA	120	1.1000	12.50
35	LVGGSTRMP	311	1.1000	12.50
36	IVAFARNGE	38	1.0000	11.36
37	ITQDLLDRT	280	1.0000	11.36
38	IAAHNKLLG	420	1.0000	11.36
39	IDLGTTNSV	6	0.9000	10.23
40	LNKVDAAVA	540	0.8000	9.09
41	VPEDTLNKV	535	0.7000	7.95
42	LEGGDPVVV	18	0.6800	7.73
43	IERNTTIPT	385	0.6800	7.73
44	VLRIVNEPT	140	0.6000	6.82
45	YGLDKGEKE	154	0.6000	6.82
46	ISVSEIDHV	301	0.6000	6.82
47	LVDKFKGTS	211	0.5000	5.68
48	IELSSSQST	242	0.5000	5.68
49	VRNQAETLV	508	0.5000	5.68
50	LVYQTEKFV	515	0.5000	5.68
51	MEKLGQESQ	566	0.5000	5.68
52	VTNVDRTVR	58	0.4000	4.55
53	MAMQRLREA	228	0.4000	4.55
54	LNVLRIVNE	138	0.3800	4.32

55	VVDAEVVDD	611	0.3800	4.32
56	LGGDDWDQR	198	0.3000	3.41
57	LVKELTGGK	324	0.3000	3.41
58	LKGEVKDVL	355	0.3000	3.41
59	LGIETKGGV	372	0.3000	3.41
60	VHVTAKDKG	457	0.3000	3.41
61	VRATSGDNH	189	0.2800	3.18
62	LGGGTFDVS	170	0.2000	2.27

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	LLLDVTPLS	363	5.1000	57.95
2	VVDDGREAK	616	4.0000	45.45
3	VNPDEVVAV	338	3.9800	45.23
4	IEIDGKKYT	78	3.7000	42.05
5	LFLDEQLTR	266	3.5000	39.77
6	VVVANSEGS	24	3.4000	38.64
7	VGGSTRMPA	312	3.2000	36.36
8	MGSDWSIEI	72	2.6800	30.45
9	VVAVGAALQ	343	2.6000	29.55
10	VYQGEREIA	413	2.6000	29.55
11	LVGQPAKNQ	48	2.5000	28.41
12	VRSVKRHMG	65	2.4000	27.27
13	IVNEPTAAA	143	2.4000	27.27
14	VGIDLGTTN	4	2.1000	23.86
15	VLLLDVTPL	362	2.1000	23.86
16	VIADTGISV	295	2.0800	23.64
17	LVFDLGGGT	166	2.0000	22.73
18	MIKDAEAHA	488	2.0000	22.73
19	LTKDKMAMQ	223	1.9000	21.59
20	IAGLNVLRI	135	1.8000	20.45
21	IRIQEGSGL	472	1.8000	20.45

22	LKRDAEAYL	98	1.7000	19.32
23	VAVGAALQA	344	1.7000	19.32
24	VLKGEVKDV	354	1.7000	19.32
25	IVHVTAKDK	456	1.7000	19.32
26	LRIVNEPTA	141	1.6000	18.18
27	LGGSDISAI	554	1.6000	18.18
28	ILMKLKRDA	94	1.5000	17.05
29	VGQPAKNQA	49	1.4000	15.91
30	LGEDITDAV	106	1.4000	15.91
31	VLVGGSTRM	310	1.4000	15.91
32	VVLVGGSTR	309	1.2000	13.64
33	VLVGQPAKN	47	1.1000	12.50
34	YFNDAQRQA	120	1.1000	12.50
35	LVGGSTRMP	311	1.1000	12.50
36	IVAFARNGE	38	1.0000	11.36
37	ITQDLLDRT	280	1.0000	11.36
38	IAAHNKLLG	420	1.0000	11.36
39	IDLGTTNSV	6	0.9000	10.23
40	LNKVDAAVA	540	0.8000	9.09
41	VPEDTLNKV	535	0.7000	7.95
42	LEGGDPVVV	18	0.6800	7.73
43	IERNTTIPT	385	0.6800	7.73
44	VLRIVNEPT	140	0.6000	6.82
45	YGLDKGEKE	154	0.6000	6.82
46	ISVSEIDHV	301	0.6000	6.82
47	LVDKFKGTS	211	0.5000	5.68
48	IELSSSQST	242	0.5000	5.68
49	VRNQAETLV	508	0.5000	5.68
50	LVYQTEKFV	515	0.5000	5.68
51	MEKLGQESQ	566	0.5000	5.68
52	VTNVDRTVR	58	0.4000	4.55
53	MAMQRLREA	228	0.4000	4.55
54	LNVLRIVNE	138	0.3800	4.32
55	VVDAEVVDD	611	0.3800	4.32

56	LGGDDWDQR	198	0.3000	3.41
57	LVKELTGGK	324	0.3000	3.41
58	LKGEVKDVL	355	0.3000	3.41
59	LGIETKGGV	372	0.3000	3.41
60	VHVTAKDKG	457	0.3000	3.41
61	VRATSGDNH	189	0.2800	3.18
62	LGGGTFDVS	170	0.2000	2.27

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	LLLDVTPLS	363	5.9000	62.11
2	VNPDEVVAV	338	4.1000	43.16
3	LFLDEQLTR	266	3.5000	36.84
4	LVFDLGGGT	166	3.1000	32.63
5	MGSDWSIEI	72	2.9000	30.53
6	IEIDGKKYT	78	2.8000	29.47
7	VVDDGREAK	616	2.7000	28.42
8	YGLDKGEKE	154	2.6000	27.37
9	VGGSTRMPA	312	2.5000	26.32
10	VVVANSEGS	24	2.4000	25.26
11	YFNDAQRQA	120	2.4000	25.26
12	VIADTGISV	295	2.4000	25.26
13	FDIDANGIV	449	2.3000	24.21
14	VLLLDVTPL	362	2.0600	21.68
15	IRIQEGSGL	472	2.0300	21.37
16	VRSVKRHMG	65	2.0000	21.05
17	LRIVNEPTA	141	2.0000	21.05
18	VVLVGGSTR	309	1.9700	20.74
19	VGIDLGTTN	4	1.9000	20.00
20	VLVGGSTRM	310	1.9000	20.00
21	LGGSDISAI	554	1.7700	18.63
22	LGIETKGGV	372	1.7000	17.89

23	LKRDAEAYL	98	1.6600	17.47
24	FVKEQREAE	522	1.6000	16.84
25	FELTGIPPA	430	1.5000	15.79
26	FQRITQDLL	277	1.4600	15.37
27	IVNEPTAAA	143	1.4000	14.74
28	LVGGSTRMP	311	1.4000	14.74
29	LVDKFKGTS	211	1.3000	13.68
30	IAGLNVLRI	135	1.2000	12.63
31	FQSVIADTG	292	1.2000	12.63
32	VYQGEREIA	413	1.2000	12.63
33	LGEDITDAV	106	1.1000	11.58
34	VLKGEVKDV	354	1.1000	11.58
35	WLVDKFKGT	210	1.0000	10.53
36	VDADKNPLF	259	1.0000	10.53
37	MIKDAEAHA	488	1.0000	10.53
38	VLVGQPAKN	47	0.9000	9.47
39	VTNVDRTVR	58	0.9000	9.47
40	LNVLRIVNE	138	0.9000	9.47
41	VSLLEIGEG	177	0.9000	9.47
42	VVAVGAALQ	343	0.9000	9.47
43	IAAHNKLLG	420	0.9000	9.47
44	LEGGDPVVV	18	0.8000	8.42
45	ILMKLKRDA	94	0.8000	8.42
46	YLGEDITDA	105	0.8000	8.42
47	LVKELTGGK	324	0.8000	8.42
48	IVAFARNGE	38	0.7100	7.47
49	IERNTTIPT	385	0.7000	7.37
50	LTGIPPAPR	432	0.7000	7.37
51	VVDAEVVDD	611	0.6000	6.32
52	VVANSEGSR	25	0.5000	5.26
53	LGGDDWDQR	198	0.5000	5.26
54	VRNQAETLV	508	0.5000	5.26
55	VYQTEKFVK	516	0.5000	5.26
56	ITQDLLDRT	280	0.4000	4.21

57	VHVTAKDKG	457	0.4000	4.21
58	FDVSLLEIG	175	0.3000	3.16
59	LEIGEGVVE	180	0.3000	3.16
60	IGEGVVEVR	182	0.3000	3.16
61	VVDWLVDKF	207	0.3000	3.16
62	ISVSEIDHV	301	0.3000	3.16

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	LLLDVTPLS	363	5.1000	57.95
2	VVDDGREAK	616	4.0000	45.45
3	VNPDEVVAV	338	3.9800	45.23
4	IEIDGKKYT	78	3.7000	42.05
5	LFLDEQLTR	266	3.5000	39.77
6	VVVANSEGS	24	3.4000	38.64
7	VGGSTRMPA	312	3.2000	36.36
8	MGSDWSIEI	72	2.6800	30.45
9	VVAVGAALQ	343	2.6000	29.55
10	VYQGEREIA	413	2.6000	29.55
11	LVGQPAKNQ	48	2.5000	28.41
12	VRSVKRHMG	65	2.4000	27.27
13	IVNEPTAAA	143	2.4000	27.27
14	VGIDLGTTN	4	2.1000	23.86
15	VLLLDVTPL	362	2.1000	23.86
16	VIADTGISV	295	2.0800	23.64
17	LVFDLGGGT	166	2.0000	22.73
18	MIKDAEAHA	488	2.0000	22.73
19	LTKDKMAMQ	223	1.9000	21.59
20	IAGLNVLRI	135	1.8000	20.45
21	IRIQEGSGL	472	1.8000	20.45
22	LKRDAEAYL	98	1.7000	19.32
23	VAVGAALQA	344	1.7000	19.32

24	VLKGEVKDV	354	1.7000	19.32
25	IVHVTAKDK	456	1.7000	19.32
26	LRIVNEPTA	141	1.6000	18.18
27	LGGSDISAI	554	1.6000	18.18
28	ILMKLKRDA	94	1.5000	17.05
29	VGQPAKNQA	49	1.4000	15.91
30	LGEDITDAV	106	1.4000	15.91
31	VLVGGSTRM	310	1.4000	15.91
32	VVLVGGSTR	309	1.2000	13.64
33	VLVGQPAKN	47	1.1000	12.50
34	YFNDAQRQA	120	1.1000	12.50
35	LVGGSTRMP	311	1.1000	12.50
36	IVAFARNGE	38	1.0000	11.36
37	ITQDLLDRT	280	1.0000	11.36
38	IAAHNKLLG	420	1.0000	11.36
39	IDLGTTNSV	6	0.9000	10.23
40	LNKVDAAVA	540	0.8000	9.09
41	VPEDTLNKV	535	0.7000	7.95
42	LEGGDPVVV	18	0.6800	7.73
43	IERNTTIPT	385	0.6800	7.73
44	VLRIVNEPT	140	0.6000	6.82
45	YGLDKGEKE	154	0.6000	6.82
46	ISVSEIDHV	301	0.6000	6.82
47	LVDKFKGTS	211	0.5000	5.68
48	IELSSSQST	242	0.5000	5.68
49	VRNQAETLV	508	0.5000	5.68
50	LVYQTEKFV	515	0.5000	5.68
51	MEKLGQESQ	566	0.5000	5.68
52	VTNVDRTVR	58	0.4000	4.55
53	MAMQRLREA	228	0.4000	4.55
54	LNVLRIVNE	138	0.3800	4.32
55	VVDAEVVDD	611	0.3800	4.32
56	LGGDDWDQR	198	0.3000	3.41
57	LVKELTGGK	324	0.3000	3.41

58	LKGEVKDVL	355	0.3000	3.41
59	LGIETKGGV	372	0.3000	3.41
60	VHVTAKDKG	457	0.3000	3.41
61	VRATSGDNH	189	0.2800	3.18
62	LGGGTFDVS	170	0.2000	2.27

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	IVNEPTAAA	143	5.0000	58.14
2	LLLDVTPLS	363	4.3000	50.00
3	VVVANSEGS	24	3.5000	40.70
4	LVKELTGGK	324	2.9000	33.72
5	YLGEDITDA	105	2.5000	29.07
6	LVGQPAKNQ	48	2.3000	26.74
7	LGTTNSVVS	8	1.9800	23.02
8	MGSDWSIEI	72	1.8800	21.86
9	VLRIVNEPT	140	1.8000	20.93
10	VNPDEVVAV	338	1.7800	20.70
11	VLLLDVTPL	362	1.6000	18.60
12	IERNTTIPT	385	1.4800	17.21
13	IAGLNVLRI	135	1.3000	15.12
14	FELTGIPPA	430	1.0000	11.63
15	FDIDANGIV	449	0.9000	10.47
16	IRIQEGSGL	472	0.8000	9.30
17	IELSSSQST	242	0.7000	8.14
18	VVAVGAALQ	343	0.7000	8.14
19	LGEDITDAV	106	0.6000	6.98
20	YEAAQAASQ	581	0.6000	6.98
21	YQGEREIAA	414	0.5800	6.74
22	LFLDEQLTR	266	0.4000	4.65
23	WLVDKFKGT	210	0.3000	3.49
24	LSSSQSTSI	244	0.3000	3.49

25	VRATSGDNH	189	0.1800	2.09
26	YQTEKFVKE	517	-0.0200	0
27	YGLDKGEKE	154	-0.1000	0
28	FQRITQDLL	277	-0.1000	0
29	LGGSDISAI	554	-0.1000	0
30	LTKDKMAMQ	223	-0.2000	0
31	IVHVTAKDK	456	-0.2000	0
32	FVKEQREAE	522	-0.3000	0
33	FKGTSGIDL	215	-0.4200	0
34	VGIDLGTTN	4	-0.6000	0
35	VLVGGSTRM	310	-0.6000	0
36	LSKEDIDRM	480	-0.6000	0
37	LNVLRIVNE	138	-0.6200	0
38	VIADTGISV	295	-0.6200	0
39	LVFDLGGGT	166	-0.7000	0
40	VQIQVYQGE	409	-0.7000	0
41	VRNQAETLV	508	-0.7000	0
42	LVYQTEKFV	515	-0.7000	0
43	IEVTFDIDA	445	-0.7200	0
44	VKRHMGSDW	68	-0.8000	0
45	FQSVIADTG	292	-0.8000	0
46	VAFARNGEV	39	-0.9000	0
47	LVGGSTRMP	311	-0.9000	0
48	VTFDIDANG	447	-0.9000	0
49	MIKDAEAHA	488	-0.9000	0
50	MEKLGQESQ	566	-0.9000	0
51	VVDAEVVDD	611	-0.9200	0
52	LPYITVDAD	254	-1.0000	0
53	LTGIPPAPR	432	-1.0000	0
54	IDLGTTNSV	6	-1.1000	0
55	MAMQRLREA	228	-1.1000	0
56	ISVSEIDHV	301	-1.1000	0
57	VGGSTRMPA	312	-1.1000	0
58	LNKVDAAVA	540	-1.1000	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	LVGGSTRMP	311	3.9000	40.62
2	VVVANSEGS	24	3.1000	32.29
3	LVGQPAKNQ	48	2.4000	25.00
4	IVNEPTAAA	143	2.2000	22.92
5	LGTTNSVVS	8	1.9000	19.79
6	VVAVGAALQ	343	1.9000	19.79
7	ILMKLKRDA	94	1.8000	18.75
8	MAMQRLREA	228	1.6000	16.67
9	LIERNTTIP	384	1.6000	16.67
10	IERNTTIPT	385	1.6000	16.67
11	VLVGGSTRM	310	1.5000	15.62
12	VEVRATSGD	187	1.4000	14.58
13	VLLLDVTPL	362	1.4000	14.58
14	LLLDVTPLS	363	1.3000	13.54
15	IVHVTAKDK	456	1.3000	13.54
16	IAGLNVLRI	135	1.2000	12.50
17	MKLKRDAEA	96	1.1000	11.46
18	IELSSSQST	242	1.0000	10.42
19	IDLGTTNSV	6	0.8000	8.33
20	VAVGAALQA	344	0.8000	8.33
21	VLRIVNEPT	140	0.6800	7.08
22	VLKGEVKDV	354	0.5000	5.21
23	LTRAEFQRI	272	0.4000	4.17
24	IRIQEGSGL	472	0.4000	4.17
25	VVDWLVDKF	207	0.2000	2.08
26	VQIQVYQGE	409	0.2000	2.08
27	VVDAEVVDD	611	0.2000	2.08
28	VKRHMGSDW	68	0.1000	1.04
29	VITTPAYFN	114	0.1000	1.04
30	LNKVDAAVA	540	0.1000	1.04

31	LSSSQSTSI	244	-0.3000	0
32	LGSFELTGI	427	-0.3000	0
33	MGSDWSIEI	72	-0.4000	0
34	LRIVNEPTA	141	-0.4000	0
35	YEAAQAASQ	581	-0.4000	0
36	VVLVGGSTR	309	-0.5000	0
37	IEVTFDIDA	445	-0.5000	0
38	VLVGQPAKN	47	-0.6000	0
39	ISARILMKL	90	-0.6000	0
40	VMTRLIERN	380	-0.6000	0
41	LVYQTEKFV	515	-0.6000	0
42	VAFARNGEV	39	-0.7000	0
43	VVEVRATSG	186	-0.7000	0
44	LVKELTGGK	324	-0.7000	0
45	VRNQAETLV	508	-0.7000	0
46	LTGIPPAPR	432	-0.7200	0
47	VNPDEVVAV	338	-0.8000	0
48	LEGGDPVVV	18	-0.9000	0
49	LNVLRIVNE	138	-0.9000	0
50	ISAIKSAME	559	-0.9200	0
51	LDEQLTRAE	268	-1.0000	0
52	LLDVTPLSL	364	-1.0000	0
53	IVAFARNGE	38	-1.1000	0
54	LGGSDISAI	554	-1.1000	0
55	IYEAAQAAS	580	-1.1000	0
56	IPQIEVTFD	442	-1.1200	0
57	VRSVKRHMG	65	-1.2000	0
58	INLPYITVD	252	-1.2000	0
59	IAAHNKLLG	420	-1.2000	0
60	MARAVGIDL	0	-1.3000	0
61	IKDAEAHAE	489	-1.4000	0

ALLELE: DRB1_0404	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	1.8	8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVVANSEGS	24	3.6000	40.91
2	IVNEPTAAA	143	3.4000	38.64
3	VLLLDVTPL	362	3.3000	37.50
4	VVAVGAALQ	343	3.1000	35.23
5	LLLDVTPLS	363	2.5000	28.41
6	VLRIVNEPT	140	2.2000	25.00
7	IAGLNVLRI	135	2.1000	23.86
8	IRIQEGSGL	472	1.7000	19.32
9	VVLVGGSTR	309	1.6000	18.18
10	LVGQPAKNQ	48	1.5000	17.05
11	LVKELTGGK	324	1.4000	15.91
12	LNKVDAAVA	540	1.3000	14.77
13	LGTTNSVVS	8	1.2000	13.64
14	IVHVTAKDK	456	1.2000	13.64
15	IERNTTIPT	385	0.8800	10.00
16	LRIVNEPTA	141	0.8000	9.09
17	VVEVRATSG	186	0.8000	9.09
18	LGSFELTGI	427	0.7000	7.95
19	LNVLRIVNE	138	0.4000	4.55
20	MGSDWSIEI	72	0.3800	4.32
21	LSSSQSTSI	244	0.3000	3.41
22	LTGIPPAPR	432	0.3000	3.41
23	VAFARNGEV	39	0.2000	2.27
24	IPQIEVTFD	442	0.2000	2.27
25	VLVGGSTRM	310	0.1000	1.14
26	VNPDEVVAV	338	0.1000	1.14
27	LGGSDISAI	554	0.1000	1.14
28	ISAIKSAME	559	0.1000	1.14
29	VVDAEVVDD	611	-0.1000	0
30	IVAFARNGE	38	-0.3000	0
31	LVGGSTRMP	311	-0.4000	0
32	YEAAQAASQ	581	-0.4000	0

33	MKLKRDAEA	96	-0.5000	0
34	LLDVTPLSL	364	-0.5000	0
35	VVDWLVDKF	207	-0.5500	0
36	YLGEDITDA	105	-0.6000	0
37	VSLLEIGEG	177	-0.6000	0
38	MAMQRLREA	228	-0.6000	0
39	LPYITVDAD	254	-0.6000	0
40	MEKLGQESQ	566	-0.6000	0
41	VQIQVYQGE	409	-0.7000	0
42	IDLGTTNSV	6	-0.8000	0
43	ILVFDLGGG	165	-0.8000	0
44	VRSVKRHMG	65	-0.9000	0
45	INLPYITVD	252	-0.9000	0
46	LTRAEFQRI	272	-0.9000	0
47	VEVRATSGD	187	-1.1000	0
48	IADTGISVS	296	-1.1000	0
49	MPAVTDLVK	318	-1.1000	0
50	IYEAAQAAS	580	-1.1000	0
51	VKRHMGSDW	68	-1.2000	0
52	MQRLREAAE	230	-1.2000	0
53	VKDVLLLDV	359	-1.2000	0
54	FQSVIADTG	292	-1.3000	0
55	VRATSGDNH	189	-1.3200	0
56	IEVTFDIDA	445	-1.3200	0
57	VITTPAYFN	114	-1.4000	0
58	LFLDEQLTR	266	-1.5000	0
59	LIERNTTIP	384	-1.5000	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	VLLLDVTPL	362	3.3000	35.11
2	VVAVGAALQ	343	2.9000	30.85

3	VVVANSEGS	24	2.6000	27.66
4	LNVLRIVNE	138	2.4000	25.53
5	IVNEPTAAA	143	2.4000	25.53
6	VLRIVNEPT	140	2.1000	22.34
7	ISAIKSAME	559	2.1000	22.34
8	IPQIEVTFD	442	1.9000	20.21
9	IVAFARNGE	38	1.7000	18.09
10	IRIQEGSGL	472	1.7000	18.09
11	VVDAEVVDD	611	1.6000	17.02
12	LLLDVTPLS	363	1.5000	15.96
13	YEAAQAASQ	581	1.4000	14.89
14	LVGQPAKNQ	48	1.3000	13.83
15	IAGLNVLRI	135	1.3000	13.83
16	VQIQVYQGE	409	1.3000	13.83
17	VVEVRATSG	186	1.1000	11.70
18	LPYITVDAD	254	1.1000	11.70
19	YITVDADKN	256	1.0000	10.64
20	FQSVIADTG	292	1.0000	10.64
21	MQRLREAAE	230	0.8000	8.51
22	INLPYITVD	252	0.8000	8.51
23	IERNTTIPT	385	0.7800	8.30
24	VEVRATSGD	187	0.6000	6.38
25	VVLVGGSTR	309	0.6000	6.38
26	YLGEDITDA	105	0.4000	4.26
27	FQRITQDLL	277	0.3000	3.19
28	LNKVDAAVA	540	0.3000	3.19
29	LGTTNSVVS	8	0.2000	2.13
30	VLVGGSTRM	310	0.2000	2.13
31	YQTEKFVKE	517	0.2000	2.13
32	IELSSSQST	242	-0.1000	0
33	LGSFELTGI	427	-0.1000	0
34	LRIVNEPTA	141	-0.2000	0
35	VSLLEIGEG	177	-0.3000	0
36	LVKELTGGK	324	-0.3000	0

37	IKDAEAHAE	489	-0.3000	0
38	VITTPAYFN	114	-0.4000	0
39	MGSDWSIEI	72	-0.4200	0
40	VAFARNGEV	39	-0.5000	0
41	YGLDKGEKE	154	-0.5000	0
42	ILVFDLGGG	165	-0.5000	0
43	LSSSQSTSI	244	-0.5000	0
44	LLDVTPLSL	364	-0.5000	0
45	IVHVTAKDK	456	-0.5000	0
46	VGIDLGTTN	4	-0.6000	0
47	VRSVKRHMG	65	-0.6000	0
48	VNPDEVVAV	338	-0.6000	0
49	IQVYQGERE	411	-0.6000	0
50	VVDWLVDKF	207	-0.6500	0
51	VTPLSLGIE	367	-0.7000	0
52	LTGIPPAPR	432	-0.7000	0
53	VRNQAETLV	508	-0.7000	0
54	LGGSDISAI	554	-0.7000	0
55	VVSVLEGGD	14	-0.8000	0
56	FVKEQREAE	522	-0.8000	0
57	MEKLGQESQ	566	-0.8000	0
58	FELTGIPPA	430	-0.9000	0
59	LVGGSTRMP	311	-1.0000	0
60	FKGTSGIDL	215	-1.0200	0
61	VRATSGDNH	189	-1.1000	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	VVVANSEGS	24	2.6000	29.55
2	IVNEPTAAA	143	2.4000	27.27
3	VLLLDVTPL	362	2.3000	26.14
4	VVAVGAALQ	343	2.1000	23.86

5	LLLDVTPLS	363	1.5000	17.05
6	VLRIVNEPT	140	1.2000	13.64
7	IAGLNVLRI	135	1.1000	12.50
8	IRIQEGSGL	472	0.7000	7.95
9	VVLVGGSTR	309	0.6000	6.82
10	YEAAQAASQ	581	0.6000	6.82
11	LVGQPAKNQ	48	0.5000	5.68
12	YLGEDITDA	105	0.4000	4.55
13	LVKELTGGK	324	0.4000	4.55
14	LNKVDAAVA	540	0.3000	3.41
15	LGTTNSVVS	8	0.2000	2.27
16	IVHVTAKDK	456	0.2000	2.27
17	IERNTTIPT	385	-0.1200	0
18	LRIVNEPTA	141	-0.2000	0
19	VVEVRATSG	186	-0.2000	0
20	FQSVIADTG	292	-0.3000	0
21	LGSFELTGI	427	-0.3000	0
22	LNVLRIVNE	138	-0.6000	0
23	MGSDWSIEI	72	-0.6200	0
24	LSSSQSTSI	244	-0.7000	0
25	FQRITQDLL	277	-0.7000	0
26	LTGIPPAPR	432	-0.7000	0
27	VAFARNGEV	39	-0.8000	0
28	IPQIEVTFD	442	-0.8000	0
29	VLVGGSTRM	310	-0.9000	0
30	VNPDEVVAV	338	-0.9000	0
31	FELTGIPPA	430	-0.9000	0
32	LGGSDISAI	554	-0.9000	0
33	ISAIKSAME	559	-0.9000	0
34	IELSSSQST	242	-1.0000	0
35	YITVDADKN	256	-1.0000	0
36	VRNQAETLV	508	-1.0000	0
37	VVDAEVVDD	611	-1.1000	0
38	IVAFARNGE	38	-1.3000	0

39	LVGGSTRMP	311	-1.4000	0
40	MKLKRDAEA	96	-1.5000	0
41	LLDVTPLSL	364	-1.5000	0
42	FDIDANGIV	449	-1.5000	0
43	VVDWLVDKF	207	-1.5500	0
44	VSLLEIGEG	177	-1.6000	0
45	MAMQRLREA	228	-1.6000	0
46	LPYITVDAD	254	-1.6000	0
47	MEKLGQESQ	566	-1.6000	0
48	FTTADDNQP	399	-1.7000	0
49	VQIQVYQGE	409	-1.7000	0
50	IDLGTTNSV	6	-1.8000	0
51	ILVFDLGGG	165	-1.8000	0
52	VRSVKRHMG	65	-1.9000	0
53	YTAPEISAR	85	-1.9000	0
54	INLPYITVD	252	-1.9000	0
55	LTRAEFQRI	272	-1.9000	0
56	FKGTSGIDL	215	-2.0200	0
57	YQGEREIAA	414	-2.0200	0
58	VEVRATSGD	187	-2.1000	0
59	FLDEQLTRA	267	-2.1000	0
60	IADTGISVS	296	-2.1000	0
61	MPAVTDLVK	318	-2.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VLLLDVTPL	362	4.3000	45.74
2	VVAVGAALQ	343	3.9000	41.49
3	VVVANSEGS	24	3.6000	38.30
4	LNVLRIVNE	138	3.4000	36.17
5	IVNEPTAAA	143	3.4000	36.17
6	VLRIVNEPT	140	3.1000	32.98

7	ISAIKSAME	559	3.1000	32.98
8	IPQIEVTFD	442	2.9000	30.85
9	IVAFARNGE	38	2.7000	28.72
10	IRIQEGSGL	472	2.7000	28.72
11	VVDAEVVDD	611	2.6000	27.66
12	LLLDVTPLS	363	2.5000	26.60
13	LVGQPAKNQ	48	2.3000	24.47
14	IAGLNVLRI	135	2.3000	24.47
15	VQIQVYQGE	409	2.3000	24.47
16	VVEVRATSG	186	2.1000	22.34
17	LPYITVDAD	254	2.1000	22.34
18	MQRLREAAE	230	1.8000	19.15
19	INLPYITVD	252	1.8000	19.15
20	IERNTTIPT	385	1.7800	18.94
21	VEVRATSGD	187	1.6000	17.02
22	VVLVGGSTR	309	1.6000	17.02
23	LNKVDAAVA	540	1.3000	13.83
24	LGTTNSVVS	8	1.2000	12.77
25	VLVGGSTRM	310	1.2000	12.77
26	IELSSSQST	242	0.9000	9.57
27	LGSFELTGI	427	0.9000	9.57
28	LRIVNEPTA	141	0.8000	8.51
29	VSLLEIGEG	177	0.7000	7.45
30	LVKELTGGK	324	0.7000	7.45
31	IKDAEAHAE	489	0.7000	7.45
32	VITTPAYFN	114	0.6000	6.38
33	MGSDWSIEI	72	0.5800	6.17
34	VAFARNGEV	39	0.5000	5.32
35	ILVFDLGGG	165	0.5000	5.32
36	LSSSQSTSI	244	0.5000	5.32
37	LLDVTPLSL	364	0.5000	5.32
38	IVHVTAKDK	456	0.5000	5.32
39	VGIDLGTTN	4	0.4000	4.26
40	VRSVKRHMG	65	0.4000	4.26

41	VNPDEVVAV	338	0.4000	4.26
42	IQVYQGERE	411	0.4000	4.26
43	YEAAQAASQ	581	0.4000	4.26
44	VVDWLVDKF	207	0.3500	3.72
45	VTPLSLGIE	367	0.3000	3.19
46	LTGIPPAPR	432	0.3000	3.19
47	VRNQAETLV	508	0.3000	3.19
48	LGGSDISAI	554	0.3000	3.19
49	VVSVLEGGD	14	0.2000	2.13
50	MEKLGQESQ	566	0.2000	2.13
51	VRATSGDNH	189	-0.1000	0
52	LMKLKRDAE	95	-0.2000	0
53	LDEQLTRAE	268	-0.2000	0
54	VLVGQPAKN	47	-0.3000	0
55	VKRHMGSDW	68	-0.3000	0
56	IDLGTTNSV	6	-0.5000	0
57	MKLKRDAEA	96	-0.5000	0
58	VKELTGGKE	325	-0.5000	0

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	IVNEPTAAA	143	5.0000	55.56
2	LLLDVTPLS	363	4.7000	52.22
3	VVVANSEGS	24	3.9000	43.33
4	LVKELTGGK	324	3.0000	33.33
5	MGSDWSIEI	72	2.7800	30.89
6	VNPDEVVAV	338	2.7800	30.89
7	VLLLDVTPL	362	2.5600	28.44
8	YLGEDITDA	105	2.5000	27.78
9	VLRIVNEPT	140	2.5000	27.78
10	LGTTNSVVS	8	2.3800	26.44
11	IAGLNVLRI	135	2.2000	24.44

12	IERNTTIPT	385	2.1800	24.22
13	LFLDEQLTR	266	1.9000	21.11
14	FDIDANGIV	449	1.9000	21.11
15	IRIQEGSGL	472	1.7600	19.56
16	LVGQPAKNQ	48	1.6000	17.78
17	LGEDITDAV	106	1.6000	17.78
18	IELSSSQST	242	1.4000	15.56
19	YQTEKFVKE	517	1.3800	15.33
20	YGLDKGEKE	154	1.3000	14.44
21	LSSSQSTSI	244	1.2000	13.33
22	FVKEQREAE	522	1.1000	12.22
23	WLVDKFKGT	210	1.0000	11.11
24	FELTGIPPA	430	1.0000	11.11
25	VLVGGSTRM	310	0.9000	10.00
26	LSKEDIDRM	480	0.9000	10.00
27	FQRITQDLL	277	0.8600	9.56
28	LGGSDISAI	554	0.8000	8.89
29	LNVLRIVNE	138	0.7800	8.67
30	VQIQVYQGE	409	0.7000	7.78
31	VDADKNPLF	259	0.6000	6.67
32	FQSVIADTG	292	0.6000	6.67
33	YQGEREIAA	414	0.5800	6.44
34	FKGTSGIDL	215	0.5400	6.00
35	LTGIPPAPR	432	0.5000	5.56
36	VTFDIDANG	447	0.5000	5.56
37	VIADTGISV	295	0.3800	4.22
38	LGGDDWDQR	198	0.3000	3.33
39	VRNQAETLV	508	0.3000	3.33
40	LVYQTEKFV	515	0.3000	3.33
41	VGIDLGTTN	4	0.2000	2.22
42	ISAIKSAME	559	0.2000	2.22
43	VDAEVVDDG	612	0.2000	2.22
44	VVDAEVVDD	611	0.1800	2.00
45	VAFARNGEV	39	0.1000	1.11

46	WSIEIDGKK	76	0.1000	1.11
47	VVDWLVDKF	207	0.1000	1.11
48	LPYITVDAD	254	0.1000	1.11
49	LVGGSTRMP	311	0.1000	1.11
50	IDLGTTNSV	6	-0.1000	0
51	ISVSEIDHV	301	-0.1000	0
52	IVHVTAKDK	456	-0.1000	0
53	LGQESQALG	569	-0.1000	0
54	YEAAQAASQ	581	-0.1000	0
55	LKRDAEAYL	98	-0.2400	0
56	LLGSFELTG	426	-0.3000	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	VVVANSEGS	24	3.6000	40.91
2	IVNEPTAAA	143	3.4000	38.64
3	VLLLDVTPL	362	3.3000	37.50
4	VVAVGAALQ	343	3.1000	35.23
5	LLLDVTPLS	363	2.5000	28.41
6	VLRIVNEPT	140	2.2000	25.00
7	IAGLNVLRI	135	2.1000	23.86
8	IRIQEGSGL	472	1.7000	19.32
9	VVLVGGSTR	309	1.6000	18.18
10	LVGQPAKNQ	48	1.5000	17.05
11	LVKELTGGK	324	1.4000	15.91
12	LNKVDAAVA	540	1.3000	14.77
13	LGTTNSVVS	8	1.2000	13.64
14	IVHVTAKDK	456	1.2000	13.64
15	IERNTTIPT	385	0.8800	10.00
16	LRIVNEPTA	141	0.8000	9.09
17	VVEVRATSG	186	0.8000	9.09
18	LGSFELTGI	427	0.7000	7.95

19	LNVLRIVNE	138	0.4000	4.55
20	MGSDWSIEI	72	0.3800	4.32
21	LSSSQSTSI	244	0.3000	3.41
22	LTGIPPAPR	432	0.3000	3.41
23	VAFARNGEV	39	0.2000	2.27
24	IPQIEVTFD	442	0.2000	2.27
25	VLVGGSTRM	310	0.1000	1.14
26	VNPDEVVAV	338	0.1000	1.14
27	LGGSDISAI	554	0.1000	1.14
28	ISAIKSAME	559	0.1000	1.14
29	VVDAEVVDD	611	-0.1000	0
30	IVAFARNGE	38	-0.3000	0
31	LVGGSTRMP	311	-0.4000	0
32	YEAAQAASQ	581	-0.4000	0
33	MKLKRDAEA	96	-0.5000	0
34	LLDVTPLSL	364	-0.5000	0
35	VVDWLVDKF	207	-0.5500	0
36	YLGEDITDA	105	-0.6000	0
37	VSLLEIGEG	177	-0.6000	0
38	MAMQRLREA	228	-0.6000	0
39	LPYITVDAD	254	-0.6000	0
40	MEKLGQESQ	566	-0.6000	0
41	VQIQVYQGE	409	-0.7000	0
42	IDLGTTNSV	6	-0.8000	0
43	ILVFDLGGG	165	-0.8000	0
44	VRSVKRHMG	65	-0.9000	0
45	INLPYITVD	252	-0.9000	0
46	LTRAEFQRI	272	-0.9000	0
47	VEVRATSGD	187	-1.1000	0
48	IADTGISVS	296	-1.1000	0
49	MPAVTDLVK	318	-1.1000	0
50	IYEAAQAAS	580	-1.1000	0
51	VKRHMGSDW	68	-1.2000	0
52	MQRLREAAE	230	-1.2000	0

53	VKDVLLLDV	359	-1.2000	0
54	FQSVIADTG	292	-1.3000	0
55	VRATSGDNH	189	-1.3200	0
56	IEVTFDIDA	445	-1.3200	0
57	VITTPAYFN	114	-1.4000	0
58	LFLDEQLTR	266	-1.5000	0
59	LIERNTTIP	384	-1.5000	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	IVNEPTAAA	143	5.0000	58.14
2	LLLDVTPLS	363	4.3000	50.00
3	VVVANSEGS	24	3.5000	40.70
4	LVKELTGGK	324	2.9000	33.72
5	YLGEDITDA	105	2.5000	29.07
6	LVGQPAKNQ	48	2.3000	26.74
7	LGTTNSVVS	8	1.9800	23.02
8	MGSDWSIEI	72	1.8800	21.86
9	VLRIVNEPT	140	1.8000	20.93
10	VNPDEVVAV	338	1.7800	20.70
11	VLLLDVTPL	362	1.6000	18.60
12	IERNTTIPT	385	1.4800	17.21
13	IAGLNVLRI	135	1.3000	15.12
14	FELTGIPPA	430	1.0000	11.63
15	FDIDANGIV	449	0.9000	10.47
16	IRIQEGSGL	472	0.8000	9.30
17	IELSSSQST	242	0.7000	8.14
18	VVAVGAALQ	343	0.7000	8.14
19	LGEDITDAV	106	0.6000	6.98
20	YEAAQAASQ	581	0.6000	6.98
21	YQGEREIAA	414	0.5800	6.74
22	LFLDEQLTR	266	0.4000	4.65

23	WLVDKFKGT	210	0.3000	3.49
24	LSSSQSTSI	244	0.3000	3.49
25	VRATSGDNH	189	0.1800	2.09
26	YQTEKFVKE	517	-0.0200	0
27	YGLDKGEKE	154	-0.1000	0
28	FQRITQDLL	277	-0.1000	0
29	LGGSDISAI	554	-0.1000	0
30	LTKDKMAMQ	223	-0.2000	0
31	IVHVTAKDK	456	-0.2000	0
32	FVKEQREAE	522	-0.3000	0
33	FKGTSGIDL	215	-0.4200	0
34	VGIDLGTTN	4	-0.6000	0
35	VLVGGSTRM	310	-0.6000	0
36	LSKEDIDRM	480	-0.6000	0
37	LNVLRIVNE	138	-0.6200	0
38	VIADTGISV	295	-0.6200	0
39	LVFDLGGGT	166	-0.7000	0
40	VQIQVYQGE	409	-0.7000	0
41	VRNQAETLV	508	-0.7000	0
42	LVYQTEKFV	515	-0.7000	0
43	IEVTFDIDA	445	-0.7200	0
44	VKRHMGSDW	68	-0.8000	0
45	FQSVIADTG	292	-0.8000	0
46	VAFARNGEV	39	-0.9000	0
47	LVGGSTRMP	311	-0.9000	0
48	VTFDIDANG	447	-0.9000	0
49	MIKDAEAHA	488	-0.9000	0
50	MEKLGQESQ	566	-0.9000	0
51	VVDAEVVDD	611	-0.9200	0
52	LPYITVDAD	254	-1.0000	0
53	LTGIPPAPR	432	-1.0000	0
54	IDLGTTNSV	6	-1.1000	0
55	MAMQRLREA	228	-1.1000	0
56	ISVSEIDHV	301	-1.1000	0

57	VGGSTRMPA	312	-1.1000	0
58	LNKVDAAVA	540	-1.1000	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	FKGTSGIDL	215	7.9000	68.10
2	LSSSQSTSI	244	5.3000	45.69
3	MARAVGIDL	0	4.9000	42.24
4	LLDVTPLSL	364	4.7000	40.52
5	VLLLDVTPL	362	4.6000	39.66
6	MGSDWSIEI	72	4.5000	38.79
7	LGGSDISAI	554	4.5000	38.79
8	IRIQEGSGL	472	4.4000	37.93
9	IAGLNVLRI	135	4.1000	35.34
10	FQRITQDLL	277	4.0000	34.48
11	IELSSSQST	242	3.7000	31.90
12	LTRAEFQRI	272	3.4000	29.31
13	LGSFELTGI	427	3.3000	28.45
14	VKDVLLLDV	359	3.0000	25.86
15	VLVGGSTRM	310	2.9000	25.00
16	LGTTNSVVS	8	2.8000	24.14
17	VVVANSEGS	24	2.8000	24.14
18	VSEIDHVVL	303	2.8000	24.14
19	VITTPAYFN	114	2.7000	23.28
20	VLRIVNEPT	140	2.5000	21.55
21	VIADTGISV	295	2.3000	19.83
22	VNPDEVVAV	338	2.2000	18.97
23	VVLVGGSTR	309	2.0000	17.24
24	ISARILMKL	90	1.9000	16.38
25	VGGSTRMPA	312	1.9000	16.38
26	FELTGIPPA	430	1.8000	15.52
27	IVHVTAKDK	456	1.6000	13.79

28	VRSVKRHMG	65	1.5000	12.93
29	VKRHMGSDW	68	1.5000	12.93
30	VLKGEVKDV	354	1.5000	12.93
31	IERNTTIPT	385	1.4200	12.24
32	LEGGDPVVV	18	1.3000	11.21
33	IVAFARNGE	38	1.3000	11.21
34	VANSEGSRT	26	1.2000	10.34
35	VAFARNGEV	39	1.2000	10.34
36	VYQTEKFVK	516	1.2000	10.34
37	VVEVRATSG	186	1.1000	9.48
38	VVAVGAALQ	343	1.1000	9.48
39	IDLGTTNSV	6	0.9200	7.93
40	LRIVNEPTA	141	0.9000	7.76
41	ISVSEIDHV	301	0.9000	7.76
42	IEVTFDIDA	445	0.9000	7.76
43	VNEPTAAAL	144	0.8000	6.90
44	IPTKRSETF	391	0.8000	6.90
45	LLGSFELTG	426	0.8000	6.90
46	FARNGEVLV	41	0.7000	6.03
47	LNKVDAAVA	540	0.7000	6.03
48	VAVGAALQA	344	0.6000	5.17
49	VRNQAETLV	508	0.6000	5.17
50	VRATSGDNH	189	0.5000	4.31
51	LGIETKGGV	372	0.5000	4.31
52	FQSVIADTG	292	0.4000	3.45
53	VGAALQAGV	346	0.4000	3.45
54	LVYQTEKFV	515	0.4000	3.45
55	LNVLRIVNE	138	0.3000	2.59
56	YQTEKFVKE	517	0.3000	2.59
57	VVDAEVVDD	611	0.3000	2.59
58	LVGGSTRMP	311	0.2200	1.90
59	YLGEDITDA	105	0.2000	1.72
60	LEIGEGVVE	180	0.2000	1.72
61	YITVDADKN	256	0.2000	1.72

62	FVKEQREAE	522	0.2000	1.72

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	FKGTSGIDL	215	7.9000	68.10
2	LSSSQSTSI	244	5.3000	45.69
3	MARAVGIDL	0	4.9000	42.24
4	LLDVTPLSL	364	4.7000	40.52
5	VLLLDVTPL	362	4.6000	39.66
6	MGSDWSIEI	72	4.5000	38.79
7	LGGSDISAI	554	4.5000	38.79
8	IRIQEGSGL	472	4.4000	37.93
9	IAGLNVLRI	135	4.1000	35.34
10	FQRITQDLL	277	4.0000	34.48
11	IELSSSQST	242	3.7000	31.90
12	LTRAEFQRI	272	3.4000	29.31
13	LGSFELTGI	427	3.3000	28.45
14	VKDVLLLDV	359	3.0000	25.86
15	VLVGGSTRM	310	2.9000	25.00
16	LGTTNSVVS	8	2.8000	24.14
17	VVVANSEGS	24	2.8000	24.14
18	VSEIDHVVL	303	2.8000	24.14
19	VITTPAYFN	114	2.7000	23.28
20	VLRIVNEPT	140	2.5000	21.55
21	VIADTGISV	295	2.3000	19.83
22	VNPDEVVAV	338	2.2000	18.97
23	VVLVGGSTR	309	2.0000	17.24
24	ISARILMKL	90	1.9000	16.38
25	VGGSTRMPA	312	1.9000	16.38
26	FELTGIPPA	430	1.8000	15.52
27	IVHVTAKDK	456	1.6000	13.79
28	VRSVKRHMG	65	1.5000	12.93

29	VKRHMGSDW	68	1.5000	12.93
30	VLKGEVKDV	354	1.5000	12.93
31	IERNTTIPT	385	1.4200	12.24
32	LEGGDPVVV	18	1.3000	11.21
33	IVAFARNGE	38	1.3000	11.21
34	VANSEGSRT	26	1.2000	10.34
35	VAFARNGEV	39	1.2000	10.34
36	VYQTEKFVK	516	1.2000	10.34
37	VVEVRATSG	186	1.1000	9.48
38	VVAVGAALQ	343	1.1000	9.48
39	IDLGTTNSV	6	0.9200	7.93
40	LRIVNEPTA	141	0.9000	7.76
41	ISVSEIDHV	301	0.9000	7.76
42	IEVTFDIDA	445	0.9000	7.76
43	VNEPTAAAL	144	0.8000	6.90
44	IPTKRSETF	391	0.8000	6.90
45	LLGSFELTG	426	0.8000	6.90
46	FARNGEVLV	41	0.7000	6.03
47	LNKVDAAVA	540	0.7000	6.03
48	VAVGAALQA	344	0.6000	5.17
49	VRNQAETLV	508	0.6000	5.17
50	VRATSGDNH	189	0.5000	4.31
51	LGIETKGGV	372	0.5000	4.31
52	FQSVIADTG	292	0.4000	3.45
53	VGAALQAGV	346	0.4000	3.45
54	LVYQTEKFV	515	0.4000	3.45
55	LNVLRIVNE	138	0.3000	2.59
56	YQTEKFVKE	517	0.3000	2.59
57	VVDAEVVDD	611	0.3000	2.59
58	LVGGSTRMP	311	0.2200	1.90
59	YLGEDITDA	105	0.2000	1.72
60	LEIGEGVVE	180	0.2000	1.72
61	YITVDADKN	256	0.2000	1.72
62	FVKEQREAE	522	0.2000	1.72

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	ILMKLKRDA	94	4.4000	51.16
2	LVDKFKGTS	211	3.6000	41.86
3	VVAVGAALQ	343	2.7000	31.40
4	IVAFARNGE	38	2.6000	30.23
5	VEVRATSGD	187	2.4000	27.91
6	VTAKDKGTG	459	2.4000	27.91
7	VRSVKRHMG	65	2.1000	24.42
8	LNVLRIVNE	138	1.9000	22.09
9	MQRLREAAE	230	1.5000	17.44
10	IVNEPTAAA	143	1.4000	16.28
11	YEAAQAASQ	581	1.4000	16.28
12	VMTRLIERN	380	1.3000	15.12
13	LLDRTRKPF	284	1.1000	12.79
14	IQVYQGERE	411	1.1000	12.79
15	MKLKRDAEA	96	1.0000	11.63
16	ILVFDLGGG	165	1.0000	11.63
17	VTPLSLGIE	367	1.0000	11.63
18	FVKEQREAE	522	1.0000	11.63
19	ISARILMKL	90	0.9000	10.47
20	VSLLEIGEG	177	0.9000	10.47
21	VVDAEVVDD	611	0.9000	10.47
22	LVGQPAKNQ	48	0.8000	9.30
23	VVSVLEGGD	14	0.7000	8.14
24	LMKLKRDAE	95	0.7000	8.14
25	IAGLNVLRI	135	0.7000	8.14
26	VLVGQPAKN	47	0.6000	6.98
27	VLLLDVTPL	362	0.5000	5.81
28	LRIVNEPTA	141	0.4000	4.65
29	LGIETKGGV	372	0.4000	4.65
30	LLLDVTPLS	363	0.3000	3.49

31	ISAIKSAME	559	0.2000	2.33
32	LNKVDAAVA	540	0.1000	1.16
33	LQAGVLKGE	350	-0.1000	0
34	VVVANSEGS	24	-0.2000	0
35	IEIDGKKYT	78	-0.2000	0
36	WDQRVVDWL	203	-0.2000	0
37	IVHVTAKDK	456	-0.2000	0
38	VKELTGGKE	325	-0.3000	0
39	IRIQEGSGL	472	-0.3000	0
40	YITVDADKN	256	-0.4000	0
41	FQSVIADTG	292	-0.4000	0
42	LVGGSTRMP	311	-0.4000	0
43	FELTGIPPA	430	-0.4000	0
44	FQRITQDLL	277	-0.5000	0
45	IERNTTIPT	385	-0.5000	0
46	YFNDAQRQA	120	-0.6000	0
47	LVFDLGGGT	166	-0.6000	0
48	LPYITVDAD	254	-0.6000	0
49	VVLVGGSTR	309	-0.6000	0
50	VGGSTRMPA	312	-0.6000	0
51	LVKELTGGK	324	-0.6000	0
52	VQIQVYQGE	409	-0.6000	0
53	IETKGGVMT	374	-0.7000	0
54	IAAHNKLLG	420	-0.7000	0
55	LLDVTPLSL	364	-0.8000	0
56	IKDAEAHAE	489	-0.8000	0
57	LEIGEGVVE	180	-0.9000	0
58	INLPYITVD	252	-0.9000	0
59	IYEAAQAAS	580	-0.9000	0
60	FNDAQRQAT	121	-1.0000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	ILMKLKRDA	94	4.4000	55.00
2	LVDKFKGTS	211	3.6000	45.00
3	VVAVGAALQ	343	1.9000	23.75
4	IVNEPTAAA	143	1.4000	17.50
5	VTAKDKGTG	459	1.1000	13.75
6	MKLKRDAEA	96	1.0000	12.50
7	VRSVKRHMG	65	0.8000	10.00
8	YEAAQAASQ	581	0.6000	7.50
9	IAGLNVLRI	135	0.5000	6.25
10	IVHVTAKDK	456	0.5000	6.25
11	LRIVNEPTA	141	0.4000	5.00
12	LLLDVTPLS	363	0.3000	3.75
13	LLDRTRKPF	284	0.2000	2.50
14	LVKELTGGK	324	0.1000	1.25
15	LGIETKGGV	372	0.1000	1.25
16	LNKVDAAVA	540	0.1000	1.25
17	ISARILMKL	90	-0.1000	0
18	VVVANSEGS	24	-0.2000	0
19	ILVFDLGGG	165	-0.3000	0
20	VEVRATSGD	187	-0.3000	0
21	IVAFARNGE	38	-0.4000	0
22	VSLLEIGEG	177	-0.4000	0
23	FELTGIPPA	430	-0.4000	0
24	VLLLDVTPL	362	-0.5000	0
25	YFNDAQRQA	120	-0.6000	0
26	VVLVGGSTR	309	-0.6000	0
27	VGGSTRMPA	312	-0.6000	0
28	VMTRLIERN	380	-0.7000	0
29	LVGGSTRMP	311	-0.8000	0
30	IYEAAQAAS	580	-0.9000	0
31	MAMQRLREA	228	-1.0000	0
32	LTGIPPAPR	432	-1.0000	0
33	VYQTEKFVK	516	-1.0000	0

34	IEIDGKKYT	78	-1.1000	0
35	LNVLRIVNE	138	-1.1000	0
36	WDQRVVDWL	203	-1.2000	0
37	VLKGEVKDV	354	-1.3000	0
38	IRIQEGSGL	472	-1.3000	0
39	VLVGQPAKN	47	-1.4000	0
40	IERNTTIPT	385	-1.4000	0
41	VGQPAKNQA	49	-1.5000	0
42	YLGEDITDA	105	-1.5000	0
43	LVFDLGGGT	166	-1.5000	0
44	MQRLREAAE	230	-1.5000	0
45	FQRITQDLL	277	-1.5000	0
46	VNPDEVVAV	338	-1.5000	0
47	VGAALQAGV	346	-1.5000	0
48	IETKGGVMT	374	-1.6000	0
49	FQSVIADTG	292	-1.7000	0
50	VKDVLLLDV	359	-1.7000	0
51	LIERNTTIP	384	-1.7000	0
52	VVANSEGSR	25	-1.8000	0
53	LFLDEQLTR	266	-1.8000	0
54	VAVGAALQA	344	-1.8000	0
55	LLDVTPLSL	364	-1.8000	0
56	YQGEREIAA	414	-1.8000	0
57	VVDAEVVDD	611	-1.8000	0
58	FNDAQRQAT	121	-1.9000	0
59	IQVYQGERE	411	-1.9000	0
60	LGTTNSVVS	8	-2.0000	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	ILMKLKRDA	94	5.4000	67.50
2	LVDKFKGTS	211	4.6000	57.50

3	VVAVGAALQ	343	2.9000	36.25
4	IVNEPTAAA	143	2.4000	30.00
5	VTAKDKGTG	459	2.1000	26.25
6	MKLKRDAEA	96	2.0000	25.00
7	VRSVKRHMG	65	1.8000	22.50
8	IAGLNVLRI	135	1.5000	18.75
9	IVHVTAKDK	456	1.5000	18.75
10	LRIVNEPTA	141	1.4000	17.50
11	LLLDVTPLS	363	1.3000	16.25
12	LLDRTRKPF	284	1.2000	15.00
13	LVKELTGGK	324	1.1000	13.75
14	LGIETKGGV	372	1.1000	13.75
15	LNKVDAAVA	540	1.1000	13.75
16	LVGQPAKNQ	48	1.0000	12.50
17	ISARILMKL	90	0.9000	11.25
18	VVVANSEGS	24	0.8000	10.00
19	ILVFDLGGG	165	0.7000	8.75
20	VEVRATSGD	187	0.7000	8.75
21	IVAFARNGE	38	0.6000	7.50
22	VSLLEIGEG	177	0.6000	7.50
23	VLLLDVTPL	362	0.5000	6.25
24	VVLVGGSTR	309	0.4000	5.00
25	VGGSTRMPA	312	0.4000	5.00
26	VMTRLIERN	380	0.3000	3.75
27	LVGGSTRMP	311	0.2000	2.50
28	IYEAAQAAS	580	0.1000	1.25
29	IEIDGKKYT	78	-0.1000	0
30	LNVLRIVNE	138	-0.1000	0
31	VLKGEVKDV	354	-0.3000	0
32	IRIQEGSGL	472	-0.3000	0
33	VLVGQPAKN	47	-0.4000	0
34	IERNTTIPT	385	-0.4000	0
35	YEAAQAASQ	581	-0.4000	0
36	VGQPAKNQA	49	-0.5000	0

37	LVFDLGGGT	166	-0.5000	0
38	MQRLREAAE	230	-0.5000	0
39	VNPDEVVAV	338	-0.5000	0
40	VGAALQAGV	346	-0.5000	0
41	IETKGGVMT	374	-0.6000	0
42	VKDVLLLDV	359	-0.7000	0
43	LIERNTTIP	384	-0.7000	0
44	VVANSEGSR	25	-0.8000	0
45	LFLDEQLTR	266	-0.8000	0
46	VAVGAALQA	344	-0.8000	0
47	LLDVTPLSL	364	-0.8000	0
48	VVDAEVVDD	611	-0.8000	0
49	IQVYQGERE	411	-0.9000	0
50	LGTTNSVVS	8	-1.0000	0
51	VVSVLEGGD	14	-1.0000	0
52	VAFARNGEV	39	-1.0000	0
53	LDRTRKPFQ	285	-1.0000	0
54	VTPLSLGIE	367	-1.0000	0
55	IAAHNKLLG	420	-1.0000	0
56	IPPAPRGIP	435	-1.0000	0
57	LVYQTEKFV	515	-1.0000	0
58	LGGSDISAI	554	-1.2000	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	ILMKLKRDA	94	5.4000	62.79
2	LVDKFKGTS	211	4.6000	53.49
3	VVAVGAALQ	343	3.7000	43.02
4	IVAFARNGE	38	3.6000	41.86
5	VEVRATSGD	187	3.4000	39.53
6	VTAKDKGTG	459	3.4000	39.53
7	VRSVKRHMG	65	3.1000	36.05

8	LNVLRIVNE	138	2.9000	33.72
9	MQRLREAAE	230	2.5000	29.07
10	IVNEPTAAA	143	2.4000	27.91
11	VMTRLIERN	380	2.3000	26.74
12	LLDRTRKPF	284	2.1000	24.42
13	IQVYQGERE	411	2.1000	24.42
14	MKLKRDAEA	96	2.0000	23.26
15	ILVFDLGGG	165	2.0000	23.26
16	VTPLSLGIE	367	2.0000	23.26
17	ISARILMKL	90	1.9000	22.09
18	VSLLEIGEG	177	1.9000	22.09
19	VVDAEVVDD	611	1.9000	22.09
20	LVGQPAKNQ	48	1.8000	20.93
21	VVSVLEGGD	14	1.7000	19.77
22	LMKLKRDAE	95	1.7000	19.77
23	IAGLNVLRI	135	1.7000	19.77
24	VLVGQPAKN	47	1.6000	18.60
25	VLLLDVTPL	362	1.5000	17.44
26	LRIVNEPTA	141	1.4000	16.28
27	LGIETKGGV	372	1.4000	16.28
28	LLLDVTPLS	363	1.3000	15.12
29	ISAIKSAME	559	1.2000	13.95
30	LNKVDAAVA	540	1.1000	12.79
31	IDRMIKDAE	485	1.0000	11.63
32	LQAGVLKGE	350	0.9000	10.47
33	VVVANSEGS	24	0.8000	9.30
34	IEIDGKKYT	78	0.8000	9.30
35	IVHVTAKDK	456	0.8000	9.30
36	VKELTGGKE	325	0.7000	8.14
37	IRIQEGSGL	472	0.7000	8.14
38	LVGGSTRMP	311	0.6000	6.98
39	IERNTTIPT	385	0.5000	5.81
40	LVFDLGGGT	166	0.4000	4.65
41	LPYITVDAD	254	0.4000	4.65

42	VVLVGGSTR	309	0.4000	4.65
43	VGGSTRMPA	312	0.4000	4.65
44	LVKELTGGK	324	0.4000	4.65
45	VQIQVYQGE	409	0.4000	4.65
46	YEAAQAASQ	581	0.4000	4.65
47	IETKGGVMT	374	0.3000	3.49
48	IAAHNKLLG	420	0.3000	3.49
49	LLDVTPLSL	364	0.2000	2.33
50	IKDAEAHAE	489	0.2000	2.33
51	LEIGEGVVE	180	0.1000	1.16
52	INLPYITVD	252	0.1000	1.16
53	IYEAAQAAS	580	0.1000	1.16
54	LDRTRKPFQ	285	-0.2000	0
55	VNPDEVVAV	338	-0.2000	0
56	VGAALQAGV	346	-0.2000	0
57	LIERNTTIP	384	-0.3000	0

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	ILMKLKRDA	94	4.1000	47.13
2	LVDKFKGTS	211	2.9000	33.33
3	VLLLDVTPL	362	2.3000	26.44
4	VVAVGAALQ	343	1.9000	21.84
5	IVAFARNGE	38	1.6000	18.39
6	VVVANSEGS	24	1.5000	17.24
7	VEVRATSGD	187	1.5000	17.24
8	IVNEPTAAA	143	1.4000	16.09
9	VRSVKRHMG	65	1.3000	14.94
10	YLGEDITDA	105	1.3000	14.94
11	VVLVGGSTR	309	1.2000	13.79
12	IAGLNVLRI	135	1.1000	12.64
13	LIERNTTIP	384	1.1000	12.64

14	MKLKRDAEA	96	1.0000	11.49
15	VMTRLIERN	380	1.0000	11.49
16	ISARILMKL	90	0.9000	10.34
17	LRIVNEPTA	141	0.6000	6.90
18	YEAAQAASQ	581	0.6000	6.90
19	VGQPAKNQA	49	0.5000	5.75
20	LLLDVTPLS	363	0.5000	5.75
21	LGSFELTGI	427	0.5000	5.75
22	IRIQEGSGL	472	0.5000	5.75
23	VGGSTRMPA	312	0.4000	4.60
24	VTAKDKGTG	459	0.4000	4.60
25	VTNVDRTVR	58	0.2000	2.30
26	LNKVDAAVA	540	0.1000	1.15
27	LNVLRIVNE	138	-0.1000	0
28	VYQTEKFVK	516	-0.1500	0
29	IQVYQGERE	411	-0.2000	0
30	FELTGIPPA	430	-0.2000	0
31	FQRITQDLL	277	-0.3000	0
32	LLDRTRKPF	284	-0.3000	0
33	FVKEQREAE	522	-0.3000	0
34	VVEVRATSG	186	-0.4000	0
35	LGGSDISAI	554	-0.4000	0
36	LVGQPAKNQ	48	-0.5000	0
37	FQSVIADTG	292	-0.5000	0
38	VNPDEVVAV	338	-0.5000	0
39	IERNTTIPT	385	-0.5200	0
40	VLVGGSTRM	310	-0.6000	0
41	LVKELTGGK	324	-0.6000	0
42	LGIETKGGV	372	-0.6000	0
43	IETKGGVMT	374	-0.6000	0
44	FLDEQLTRA	267	-0.7000	0
45	MEKLGQESQ	566	-0.7000	0
46	YTAPEISAR	85	-0.8000	0
47	INLPYITVD	252	-0.8000	0

48	VYQGEREIA	413	-0.8000	0
49	VVDAEVVDD	611	-0.8000	0
50	YFNDAQRQA	120	-0.9000	0
51	FNDAQRQAT	121	-0.9000	0
52	IYEAAQAAS	580	-0.9000	0
53	YQGEREIAA	414	-0.9200	0
54	LGTTNSVVS	8	-1.0000	0
55	ILVFDLGGG	165	-1.0000	0
56	IPTKRSETF	391	-1.0000	0
57	LTGIPPAPR	432	-1.0000	0
58	VRNQAETLV	508	-1.0000	0
59	LMKLKRDAE	95	-1.1000	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	ILMKLKRDA	94	4.6000	45.54
2	LVDKFKGTS	211	3.7000	36.63
3	IVAFARNGE	38	2.9000	28.71
4	VRSVKRHMG	65	2.8000	27.72
5	VVAVGAALQ	343	2.7000	26.73
6	ISARILMKL	90	2.5000	24.75
7	IAGLNVLRI	135	2.5000	24.75
8	VTAKDKGTG	459	2.5000	24.75
9	LNVLRIVNE	138	2.4000	23.76
10	VEVRATSGD	187	2.4000	23.76
11	VMTRLIERN	380	2.4000	23.76
12	IQVYQGERE	411	2.2000	21.78
13	FVKEQREAE	522	2.1000	20.79
14	LLDRTRKPF	284	1.7000	16.83
15	VLLLDVTPL	362	1.6000	15.84
16	LRIVNEPTA	141	1.5500	15.35
17	MQRLREAAE	230	1.5000	14.85

18	LLLDVTPLS	363	1.4500	14.36
19	LVGQPAKNQ	48	1.4000	13.86
20	IVNEPTAAA	143	1.4000	13.86
21	YEAAQAASQ	581	1.4000	13.86
22	VVDAEVVDD	611	1.4000	13.86
23	ILVFDLGGG	165	1.1000	10.89
24	VTPLSLGIE	367	1.1000	10.89
25	IERNTTIPT	385	1.1000	10.89
26	IAAHNKLLG	420	1.1000	10.89
27	MKLKRDAEA	96	1.0000	9.90
28	VSLLEIGEG	177	1.0000	9.90
29	VGGSTRMPA	312	1.0000	9.90
30	LLDVTPLSL	364	1.0000	9.90
31	VVVANSEGS	24	0.9000	8.91
32	VVSVLEGGD	14	0.8000	7.92
33	FELTGIPPA	430	0.7500	7.43
34	VLVGQPAKN	47	0.6000	5.94
35	LQAGVLKGE	350	0.5000	4.95
36	LGIETKGGV	372	0.5000	4.95
37	IEIDGKKYT	78	0.4000	3.96
38	LMKLKRDAE	95	0.4000	3.96
39	FKGTSGIDL	215	0.4000	3.96
40	VKDVLLLDV	359	0.4000	3.96
41	IVHVTAKDK	456	0.4000	3.96
42	INLPYITVD	252	0.2000	1.98
43	ISAIKSAME	559	0.2000	1.98
44	LNKVDAAVA	540	0.1000	0.99
45	LDRTRKPFQ	285	-0.0500	0
46	IKDAEAHAE	489	-0.1000	0
47	MARAVGIDL	0	-0.2000	0
48	YGLDKGEKE	154	-0.2000	0
49	LVGGSTRMP	311	-0.2000	0
50	VKELTGGKE	325	-0.2000	0
51	IETKGGVMT	374	-0.2000	0

52	LIERNTTIP	384	-0.2000	0
53	YQGEREIAA	414	-0.2000	0
54	IPQIEVTFD	442	-0.3000	0
55	IRIQEGSGL	472	-0.3000	0
56	IDRMIKDAE	485	-0.3000	0
57	YLGEDITDA	105	-0.4000	0
58	YFNDAQRQA	120	-0.4000	0
59	LEIGEGVVE	180	-0.4000	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	IAGLNVLRI	135	2.7000	32.53
2	VVAVGAALQ	343	2.0000	24.10
3	ILMKLKRDA	94	1.8000	21.69
4	LRIVNEPTA	141	1.6500	19.88
5	VRSVKRHMG	65	1.6000	19.28
6	VGGSTRMPA	312	1.3000	15.66
7	LVGQPAKNQ	48	1.2000	14.46
8	IVHVTAKDK	456	1.2000	14.46
9	FELTGIPPA	430	1.1500	13.86
10	VLLLDVTPL	362	1.0000	12.05
11	VVVANSEGS	24	0.9000	10.84
12	LVDKFKGTS	211	0.9000	10.84
13	LLLDVTPLS	363	0.7500	9.04
14	IVNEPTAAA	143	0.7000	8.43
15	YEAAQAASQ	581	0.6000	7.23
16	VKDVLLLDV	359	0.2000	2.41
17	IERNTTIPT	385	0.2000	2.41
18	IAAHNKLLG	420	0.2000	2.41
19	LNKVDAAVA	540	0.2000	2.41
20	VSLLEIGEG	177	0.1000	1.20
21	LLDVTPLSL	364	0.1000	1.20

22	VYQTEKFVK	516	-0.1000	0
23	IVAFARNGE	38	-0.2000	0
24	LNVLRIVNE	138	-0.2000	0
25	FKGTSGIDL	215	-0.2000	0
26	MAMQRLREA	228	-0.2000	0
27	ILVFDLGGG	165	-0.3000	0
28	LTGIPPAPR	432	-0.4000	0
29	LDRTRKPFQ	285	-0.4500	0
30	VVLVGGSTR	309	-0.5000	0
31	LVKELTGGK	324	-0.5000	0
32	LGIETKGGV	372	-0.5000	0
33	LFLDEQLTR	266	-0.7000	0
34	VAVGAALQA	344	-0.7000	0
35	IRIQEGSGL	472	-0.7000	0
36	LVYQTEKFV	515	-0.8000	0
37	YQGEREIAA	414	-0.9000	0
38	MEKLGQESQ	566	-0.9000	0
39	IYEAAQAAS	580	-0.9000	0
40	LGTTNSVVS	8	-1.1000	0
41	YLGEDITDA	105	-1.1000	0
42	YFNDAQRQA	120	-1.1000	0
43	MQRLREAAE	230	-1.1000	0
44	MARAVGIDL	0	-1.2000	0
45	IEIDGKKYT	78	-1.2000	0
46	FQRITQDLL	277	-1.2000	0
47	LVGGSTRMP	311	-1.3000	0
48	LGSFELTGI	427	-1.3000	0
49	VVDAEVVDD	611	-1.3000	0
50	VTNVDRTVR	58	-1.4000	0
51	VLKGEVKDV	354	-1.4000	0
52	LLGSFELTG	426	-1.4000	0
53	ISARILMKL	90	-1.5000	0
54	VLRIVNEPT	140	-1.5000	0
55	VGAALQAGV	346	-1.5000	0

56	VTPLSLGIE	367	-1.5000	0
57	MGSDWSIEI	72	-1.6000	0
58	VTAKDKGTG	459	-1.6000	0
59	FVKEQREAE	522	-1.6000	0
60	VVANSEGSR	25	-1.7000	0
61	VNPDEVVAV	338	-1.7000	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	ILMKLKRDA	94	5.7000	67.86
2	LVGQPAKNQ	48	3.4000	40.48
3	MAMQRLREA	228	3.4000	40.48
4	IVAFARNGE	38	2.3000	27.38
5	IVNEPTAAA	143	2.3000	27.38
6	VVVANSEGS	24	2.2000	26.19
7	IAAHNKLLG	420	2.2000	26.19
8	LVDKFKGTS	211	2.1000	25.00
9	IAGLNVLRI	135	1.9000	22.62
10	VRSVKRHMG	65	1.8000	21.43
11	VVAVGAALQ	343	1.7000	20.24
12	VLLLDVTPL	362	1.7000	20.24
13	IRIQEGSGL	472	1.7000	20.24
14	LLLDVTPLS	363	1.6000	19.05
15	LVGGSTRMP	311	1.5000	17.86
16	LVYQTEKFV	515	1.4000	16.67
17	VYQTEKFVK	516	1.4000	16.67
18	VGGSTRMPA	312	1.1000	13.10
19	IVHVTAKDK	456	1.1000	13.10
20	LRIVNEPTA	141	0.9000	10.71
21	VKRHMGSDW	68	0.7000	8.33
22	LNVLRIVNE	138	0.6000	7.14
23	MKLKRDAEA	96	0.5000	5.95

24	LGSFELTGI	427	0.5000	5.95
25	VGQPAKNQA	49	0.4000	4.76
26	IEIDGKKYT	78	0.3000	3.57
27	VRNQAETLV	508	0.3000	3.57
28	VVDWLVDKF	207	0.2000	2.38
29	VVDAEVVDD	611	0.2000	2.38
30	VNPDEVVAV	338	0.1000	1.19
31	IYEAAQAAS	580	0.1000	1.19
32	LGTTNSVVS	8	-0.1000	0
33	LLDRTRKPF	284	-0.1000	0
34	LNKVDAAVA	540	-0.1000	0
35	YFNDAQRQA	120	-0.2000	0
36	VQIQVYQGE	409	-0.2000	0
37	MTRLIERNT	381	-0.3000	0
38	MEKLGQESQ	566	-0.3000	0
39	LDRTRKPFQ	285	-0.4000	0
40	VVLVGGSTR	309	-0.4000	0
41	VMTRLIERN	380	-0.4000	0
42	VTAKDKGTG	459	-0.4000	0
43	LGGSDISAI	554	-0.4000	0
44	YEAAQAASQ	581	-0.4000	0
45	LFLDEQLTR	266	-0.5000	0
46	VGAALQAGV	346	-0.5000	0
47	VAVGAALQA	344	-0.6000	0
48	VYQGEREIA	413	-0.6000	0
49	LMKLKRDAE	95	-0.7000	0
50	VSLLEIGEG	177	-0.7000	0
51	LREAAEKAK	233	-0.7000	0
52	MQRLREAAE	230	-0.8000	0
53	FELTGIPPA	430	-0.8000	0
54	VLVGQPAKN	47	-0.9000	0
55	ISARILMKL	90	-0.9000	0
56	LTGIPPAPR	432	-0.9000	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	IAGLNVLRI	135	3.7000	44.58
2	VVAVGAALQ	343	3.0000	36.14
3	ILMKLKRDA	94	2.8000	33.73
4	LRIVNEPTA	141	2.6500	31.93
5	VRSVKRHMG	65	2.6000	31.33
6	VGGSTRMPA	312	2.3000	27.71
7	LVGQPAKNQ	48	2.2000	26.51
8	IVHVTAKDK	456	2.2000	26.51
9	VLLLDVTPL	362	2.0000	24.10
10	VVVANSEGS	24	1.9000	22.89
11	LVDKFKGTS	211	1.9000	22.89
12	LLLDVTPLS	363	1.7500	21.08
13	IVNEPTAAA	143	1.7000	20.48
14	VKDVLLLDV	359	1.2000	14.46
15	IERNTTIPT	385	1.2000	14.46
16	IAAHNKLLG	420	1.2000	14.46
17	LNKVDAAVA	540	1.2000	14.46
18	VSLLEIGEG	177	1.1000	13.25
19	LLDVTPLSL	364	1.1000	13.25
20	VYQTEKFVK	516	0.9000	10.84
21	IVAFARNGE	38	0.8000	9.64
22	LNVLRIVNE	138	0.8000	9.64
23	MAMQRLREA	228	0.8000	9.64
24	ILVFDLGGG	165	0.7000	8.43
25	LTGIPPAPR	432	0.6000	7.23
26	LDRTRKPFQ	285	0.5500	6.63
27	VVLVGGSTR	309	0.5000	6.02
28	LVKELTGGK	324	0.5000	6.02
29	LGIETKGGV	372	0.5000	6.02
30	LFLDEQLTR	266	0.3000	3.61

31	VAVGAALQA	344	0.3000	3.61
32	IRIQEGSGL	472	0.3000	3.61
33	LVYQTEKFV	515	0.2000	2.41
34	FELTGIPPA	430	0.1500	1.81
35	MEKLGQESQ	566	0.1000	1.20
36	IYEAAQAAS	580	0.1000	1.20
37	LGTTNSVVS	8	-0.1000	0
38	MQRLREAAE	230	-0.1000	0
39	MARAVGIDL	0	-0.2000	0
40	IEIDGKKYT	78	-0.2000	0
41	LVGGSTRMP	311	-0.3000	0
42	LGSFELTGI	427	-0.3000	0
43	VVDAEVVDD	611	-0.3000	0
44	VTNVDRTVR	58	-0.4000	0
45	VLKGEVKDV	354	-0.4000	0
46	LLGSFELTG	426	-0.4000	0
47	YEAAQAASQ	581	-0.4000	0
48	ISARILMKL	90	-0.5000	0
49	VLRIVNEPT	140	-0.5000	0
50	VGAALQAGV	346	-0.5000	0
51	VTPLSLGIE	367	-0.5000	0
52	MGSDWSIEI	72	-0.6000	0
53	VTAKDKGTG	459	-0.6000	0
54	VVANSEGSR	25	-0.7000	0
55	VNPDEVVAV	338	-0.7000	0
56	VVSVLEGGD	14	-0.8000	0
57	MKLKRDAEA	96	-0.8000	0
58	VAFARNGEV	39	-0.9000	0
59	VGQPAKNQA	49	-0.9000	0
60	LREAAEKAK	233	-0.9000	0
61	IPPAPRGIP	435	-0.9000	0

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

	2.0	

Rank	Sequence	At Position	Score	% of Highest Score
1	IAGLNVLRI	135	3.7000	44.58
2	VVAVGAALQ	343	3.0000	36.14
3	ILMKLKRDA	94	2.8000	33.73
4	LRIVNEPTA	141	2.6500	31.93
5	VRSVKRHMG	65	2.6000	31.33
6	VGGSTRMPA	312	2.3000	27.71
7	LVGQPAKNQ	48	2.2000	26.51
8	IVHVTAKDK	456	2.2000	26.51
9	VLLLDVTPL	362	2.0000	24.10
10	VVVANSEGS	24	1.9000	22.89
11	LVDKFKGTS	211	1.9000	22.89
12	LLLDVTPLS	363	1.7500	21.08
13	IVNEPTAAA	143	1.7000	20.48
14	VKDVLLLDV	359	1.2000	14.46
15	IERNTTIPT	385	1.2000	14.46
16	IAAHNKLLG	420	1.2000	14.46
17	LNKVDAAVA	540	1.2000	14.46
18	VSLLEIGEG	177	1.1000	13.25
19	LLDVTPLSL	364	1.1000	13.25
20	VYQTEKFVK	516	0.9000	10.84
21	IVAFARNGE	38	0.8000	9.64
22	LNVLRIVNE	138	0.8000	9.64
23	MAMQRLREA	228	0.8000	9.64
24	ILVFDLGGG	165	0.7000	8.43
25	LTGIPPAPR	432	0.6000	7.23
26	LDRTRKPFQ	285	0.5500	6.63
27	VVLVGGSTR	309	0.5000	6.02
28	LVKELTGGK	324	0.5000	6.02
29	LGIETKGGV	372	0.5000	6.02
30	LFLDEQLTR	266	0.3000	3.61
31	VAVGAALQA	344	0.3000	3.61
32	IRIQEGSGL	472	0.3000	3.61

33	LVYQTEKFV	515	0.2000	2.41
34	FELTGIPPA	430	0.1500	1.81
35	MEKLGQESQ	566	0.1000	1.20
36	IYEAAQAAS	580	0.1000	1.20
37	LGTTNSVVS	8	-0.1000	0
38	MQRLREAAE	230	-0.1000	0
39	MARAVGIDL	0	-0.2000	0
40	IEIDGKKYT	78	-0.2000	0
41	LVGGSTRMP	311	-0.3000	0
42	LGSFELTGI	427	-0.3000	0
43	VVDAEVVDD	611	-0.3000	0
44	VTNVDRTVR	58	-0.4000	0
45	VLKGEVKDV	354	-0.4000	0
46	LLGSFELTG	426	-0.4000	0
47	YEAAQAASQ	581	-0.4000	0
48	ISARILMKL	90	-0.5000	0
49	VLRIVNEPT	140	-0.5000	0
50	VGAALQAGV	346	-0.5000	0
51	VTPLSLGIE	367	-0.5000	0
52	MGSDWSIEI	72	-0.6000	0
53	VTAKDKGTG	459	-0.6000	0
54	VVANSEGSR	25	-0.7000	0
55	VNPDEVVAV	338	-0.7000	0
56	VVSVLEGGD	14	-0.8000	0
57	MKLKRDAEA	96	-0.8000	0
58	VAFARNGEV	39	-0.9000	0
59	VGQPAKNQA	49	-0.9000	0
60	LREAAEKAK	233	-0.9000	0
61	IPPAPRGIP	435	-0.9000	0

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	LLLDVTPLS	363	6.5000	71.43
2	VNPDEVVAV	338	4.1000	45.05
3	VVDDGREAK	616	3.6000	39.56
4	VGGSTRMPA	312	3.5000	38.46
5	LVFDLGGGT	166	3.4000	37.36
6	IEIDGKKYT	78	3.1000	34.07
7	VVVANSEGS	24	3.0000	32.97
8	MGSDWSIEI	72	3.0000	32.97
9	LRIVNEPTA	141	3.0000	32.97
10	LFLDEQLTR	266	3.0000	32.97
11	VVAVGAALQ	343	2.6000	28.57
12	IVNEPTAAA	143	2.4000	26.37
13	VIADTGISV	295	2.4000	26.37
14	VYQGEREIA	413	2.2000	24.18
15	VGIDLGTTN	4	2.1000	23.08
16	VLLLDVTPL	362	2.1000	23.08
17	IRIQEGSGL	472	2.0700	22.75
18	MIKDAEAHA	488	2.0000	21.98
19	LVGQPAKNQ	48	1.9000	20.88
20	LVDKFKGTS	211	1.9000	20.88
21	LTKDKMAMQ	223	1.9000	20.88
22	LGGSDISAI	554	1.8700	20.55
23	ILMKLKRDA	94	1.8000	19.78
24	LKRDAEAYL	98	1.7000	18.68
25	LVKELTGGK	324	1.7000	18.68
26	LGIETKGGV	372	1.7000	18.68
27	VRSVKRHMG	65	1.6000	17.58
28	VVLVGGSTR	309	1.4700	16.15
29	YFNDAQRQA	120	1.4000	15.38
30	VLVGGSTRM	310	1.4000	15.38
31	LVGGSTRMP	311	1.4000	15.38
32	VYQTEKFVK	516	1.4000	15.38
33	IAGLNVLRI	135	1.3000	14.29
34	VAVGAALQA	344	1.2000	13.19

35	VLVGQPAKN	47	1.1000	12.09
36	LGEDITDAV	106	1.1000	12.09
37	VLKGEVKDV	354	1.1000	12.09
38	IVHVTAKDK	456	1.1000	12.09
39	IERNTTIPT	385	1.0000	10.99
40	LDRTRKPFQ	285	0.9000	9.89
41	LEGGDPVVV	18	0.8000	8.79
42	LNKVDAAVA	540	0.8000	8.79
43	VGQPAKNQA	49	0.7100	7.80
44	MAMQRLREA	228	0.7000	7.69
45	ITQDLLDRT	280	0.7000	7.69
46	LNVLRIVNE	138	0.5000	5.49
47	VSLLEIGEG	177	0.5000	5.49
48	IAAHNKLLG	420	0.5000	5.49
49	FELTGIPPA	430	0.5000	5.49
50	VRNQAETLV	508	0.5000	5.49
51	VVDAEVVDD	611	0.5000	5.49
52	VTNVDRTVR	58	0.4000	4.40
53	IELSSSQST	242	0.4000	4.40
54	IVAFARNGE	38	0.3100	3.41
55	LGTTNSVVS	8	0.3000	3.30
56	ISVSEIDHV	301	0.3000	3.30
57	FDIDANGIV	449	0.3000	3.30
58	IDLGTTNSV	6	0.2100	2.31
59	VLRIVNEPT	140	0.2000	2.20
60	YGLDKGEKE	154	0.2000	2.20
61	LTGIPPAPR	432	0.2000	2.20
62	VKRHMGSDW	68	0.1700	1.87

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	ILMKLKRDA	94	4.7000	55.95

2	LVGQPAKNQ	48	2.4000	28.57
3	MAMQRLREA	228	2.4000	28.57
4	IVAFARNGE	38	1.3000	15.48
5	IVNEPTAAA	143	1.3000	15.48
6	VVVANSEGS	24	1.2000	14.29
7	IAAHNKLLG	420	1.2000	14.29
8	LVDKFKGTS	211	1.1000	13.10
9	IAGLNVLRI	135	0.9000	10.71
10	VRSVKRHMG	65	0.8000	9.52
11	YFNDAQRQA	120	0.8000	9.52
12	VVAVGAALQ	343	0.7000	8.33
13	VLLLDVTPL	362	0.7000	8.33
14	IRIQEGSGL	472	0.7000	8.33
15	LLLDVTPLS	363	0.6000	7.14
16	YEAAQAASQ	581	0.6000	7.14
17	LVGGSTRMP	311	0.5000	5.95
18	LVYQTEKFV	515	0.4000	4.76
19	VYQTEKFVK	516	0.4000	4.76
20	FELTGIPPA	430	0.2000	2.38
21	VGGSTRMPA	312	0.1000	1.19
22	IVHVTAKDK	456	0.1000	1.19
23	YLGEDITDA	105	-0.1000	0
24	LRIVNEPTA	141	-0.1000	0
25	VKRHMGSDW	68	-0.3000	0
26	LNVLRIVNE	138	-0.4000	0
27	MKLKRDAEA	96	-0.5000	0
28	LGSFELTGI	427	-0.5000	0
29	VGQPAKNQA	49	-0.6000	0
30	IEIDGKKYT	78	-0.7000	0
31	VRNQAETLV	508	-0.7000	0
32	FVKEQREAE	522	-0.7000	0
33	VVDWLVDKF	207	-0.8000	0
34	VVDAEVVDD	611	-0.8000	0
35	VNPDEVVAV	338	-0.9000	0

36	IYEAAQAAS	580	-0.9000	0
37	ILVFDLGGG	165	-1.0000	0
38	LVKELTGGK	324	-1.0000	0
39	VLKGEVKDV	354	-1.0000	0
40	LGIETKGGV	372	-1.0000	0
41	IERNTTIPT	385	-1.0000	0
42	LGTTNSVVS	8	-1.1000	0
43	FNDAQRQAT	121	-1.1000	0
44	LLDRTRKPF	284	-1.1000	0
45	LNKVDAAVA	540	-1.1000	0
46	VQIQVYQGE	409	-1.2000	0
47	MTRLIERNT	381	-1.3000	0
48	MEKLGQESQ	566	-1.3000	0
49	FARNGEVLV	41	-1.4000	0
50	LDRTRKPFQ	285	-1.4000	0
51	VVLVGGSTR	309	-1.4000	0
52	VMTRLIERN	380	-1.4000	0
53	VTAKDKGTG	459	-1.4000	0
54	LGGSDISAI	554	-1.4000	0
55	LFLDEQLTR	266	-1.5000	0
56	FQRITQDLL	277	-1.5000	0
57	VGAALQAGV	346	-1.5000	0
58	VAVGAALQA	344	-1.6000	0
59	VYQGEREIA	413	-1.6000	0
60	YQGEREIAA	414	-1.6000	0
61	LMKLKRDAE	95	-1.7000	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	ILMKLKRDA	94	4.7000	53.41
2	IVAFARNGE	38	2.7000	30.68
3	IAAHNKLLG	420	2.6000	29.55

4	MAMQRLREA	228	2.4000	27.27
5	VRSVKRHMG	65	2.2000	25.00
6	IAGLNVLRI	135	1.8000	20.45
7	LVGQPAKNQ	48	1.7000	19.32
8	VLLLDVTPL	362	1.6600	18.86
9	IRIQEGSGL	472	1.6600	18.86
10	VVVANSEGS	24	1.6000	18.18
11	LVDKFKGTS	211	1.5000	17.05
12	LVGGSTRMP	311	1.5000	17.05
13	LVYQTEKFV	515	1.4000	15.91
14	IVNEPTAAA	143	1.3000	14.77
15	VVDWLVDKF	207	1.1000	12.50
16	LNVLRIVNE	138	1.0000	11.36
17	LLLDVTPLS	363	1.0000	11.36
18	YFNDAQRQA	120	0.8000	9.09
19	LLDRTRKPF	284	0.8000	9.09
20	FVKEQREAE	522	0.7000	7.95
21	VYQTEKFVK	516	0.5000	5.68
22	ILVFDLGGG	165	0.4000	4.55
23	LGSFELTGI	427	0.4000	4.55
24	VRNQAETLV	508	0.3000	3.41
25	VVDAEVVDD	611	0.3000	3.41
26	VQIQVYQGE	409	0.2000	2.27
27	FELTGIPPA	430	0.2000	2.27
28	IVHVTAKDK	456	0.2000	2.27
29	VVLVGGSTR	309	0.1000	1.14
30	VGGSTRMPA	312	0.1000	1.14
31	VNPDEVVAV	338	0.1000	1.14
32	YLGEDITDA	105	-0.1000	0
33	LRIVNEPTA	141	-0.1000	0
34	YEAAQAASQ	581	-0.1000	0
35	VKRHMGSDW	68	-0.3000	0
36	LMKLKRDAE	95	-0.3000	0
37	VSLLEIGEG	177	-0.3000	0

38	IERNTTIPT	385	-0.3000	0
39	FARNGEVLV	41	-0.4000	0
40	FNDAQRQAT	121	-0.4000	0
41	MQRLREAAE	230	-0.4000	0
42	LTGIPPAPR	432	-0.4000	0
43	MKLKRDAEA	96	-0.5000	0
44	VGAALQAGV	346	-0.5000	0
45	LGGSDISAI	554	-0.5000	0
46	IYEAAQAAS	580	-0.5000	0
47	FQRITQDLL	277	-0.5400	0
48	VGQPAKNQA	49	-0.6000	0
49	FQSVIADTG	292	-0.6000	0
50	VMTRLIERN	380	-0.6000	0
51	MTRLIERNT	381	-0.6000	0
52	VHVTAKDKG	457	-0.6000	0
53	LGTTNSVVS	8	-0.7000	0
54	IKSAMEKLG	562	-0.7000	0
55	VTNVDRTVR	58	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	ILMKLKRDA	94	5.7000	67.86
2	LVGQPAKNQ	48	3.4000	40.48
3	MAMQRLREA	228	3.4000	40.48
4	IVAFARNGE	38	2.3000	27.38
5	IVNEPTAAA	143	2.3000	27.38
6	VVVANSEGS	24	2.2000	26.19
7	IAAHNKLLG	420	2.2000	26.19
8	LVDKFKGTS	211	2.1000	25.00
9	IAGLNVLRI	135	1.9000	22.62
10	VRSVKRHMG	65	1.8000	21.43
11	VVAVGAALQ	343	1.7000	20.24

12	VLLLDVTPL	362	1.7000	20.24
13	IRIQEGSGL	472	1.7000	20.24
14	LLLDVTPLS	363	1.6000	19.05
15	LVGGSTRMP	311	1.5000	17.86
16	LVYQTEKFV	515	1.4000	16.67
17	VYQTEKFVK	516	1.4000	16.67
18	VGGSTRMPA	312	1.1000	13.10
19	IVHVTAKDK	456	1.1000	13.10
20	LRIVNEPTA	141	0.9000	10.71
21	VKRHMGSDW	68	0.7000	8.33
22	LNVLRIVNE	138	0.6000	7.14
23	MKLKRDAEA	96	0.5000	5.95
24	LGSFELTGI	427	0.5000	5.95
25	VGQPAKNQA	49	0.4000	4.76
26	IEIDGKKYT	78	0.3000	3.57
27	VRNQAETLV	508	0.3000	3.57
28	VVDWLVDKF	207	0.2000	2.38
29	VVDAEVVDD	611	0.2000	2.38
30	VNPDEVVAV	338	0.1000	1.19
31	IYEAAQAAS	580	0.1000	1.19
32	LGTTNSVVS	8	-0.1000	0
33	LLDRTRKPF	284	-0.1000	0
34	LNKVDAAVA	540	-0.1000	0
35	YFNDAQRQA	120	-0.2000	0
36	VQIQVYQGE	409	-0.2000	0
37	MTRLIERNT	381	-0.3000	0
38	MEKLGQESQ	566	-0.3000	0
39	LDRTRKPFQ	285	-0.4000	0
40	VVLVGGSTR	309	-0.4000	0
41	VMTRLIERN	380	-0.4000	0
42	VTAKDKGTG	459	-0.4000	0
43	LGGSDISAI	554	-0.4000	0
44	YEAAQAASQ	581	-0.4000	0
45	LFLDEQLTR	266	-0.5000	0

46	VGAALQAGV	346	-0.5000	0
47	VAVGAALQA	344	-0.6000	0
48	VYQGEREIA	413	-0.6000	0
49	LMKLKRDAE	95	-0.7000	0
50	VSLLEIGEG	177	-0.7000	0
51	LREAAEKAK	233	-0.7000	0
52	MQRLREAAE	230	-0.8000	0
53	FELTGIPPA	430	-0.8000	0
54	VLVGQPAKN	47	-0.9000	0
55	ISARILMKL	90	-0.9000	0
56	LTGIPPAPR	432	-0.9000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IAGLNVLRI	135	3.6000	41.38
2	VRSVKRHMG	65	3.0000	34.48
3	VLLLDVTPL	362	1.9600	22.53
4	ILMKLKRDA	94	1.8000	20.69
5	LRIVNEPTA	141	1.6500	18.97
6	IAAHNKLLG	420	1.6000	18.39
7	VSLLEIGEG	177	1.5000	17.24
8	VVVANSEGS	24	1.3000	14.94
9	LVDKFKGTS	211	1.3000	14.94
10	VGGSTRMPA	312	1.3000	14.94
11	VVAVGAALQ	343	1.3000	14.94
12	IVHVTAKDK	456	1.3000	14.94
13	IVAFARNGE	38	1.2000	13.79
14	LNVLRIVNE	138	1.2000	13.79
15	VKDVLLLDV	359	1.2000	13.79
16	LLLDVTPLS	363	1.1500	13.22
17	FELTGIPPA	430	1.1500	13.22
18	ILVFDLGGG	165	1.1000	12.64

19	LTGIPPAPR	432	1.1000	12.64
20	LLDVTPLSL	364	1.0600	12.18
21	VVLVGGSTR	309	1.0000	11.49
22	IERNTTIPT	385	0.9000	10.34
23	LFLDEQLTR	266	0.8000	9.20
24	FKGTSGIDL	215	0.7600	8.74
25	IVNEPTAAA	143	0.7000	8.05
26	LVGQPAKNQ	48	0.5000	5.75
27	LGIETKGGV	372	0.5000	5.75
28	MQRLREAAE	230	0.3000	3.45
29	IRIQEGSGL	472	0.2600	2.99
30	LVYQTEKFV	515	0.2000	2.30
31	LNKVDAAVA	540	0.2000	2.30
32	VTNVDRTVR	58	0.1000	1.15
33	VTPLSLGIE	367	-0.1000	0
34	YEAAQAASQ	581	-0.1000	0
35	VVANSEGSR	25	-0.2000	0
36	MAMQRLREA	228	-0.2000	0
37	VTAKDKGTG	459	-0.2000	0
38	FVKEQREAE	522	-0.2000	0
39	VVDAEVVDD	611	-0.2000	0
40	MARAVGIDL	0	-0.2400	0
41	FQRITQDLL	277	-0.2400	0
42	LLDRTRKPF	284	-0.3000	0
43	LVGGSTRMP	311	-0.3000	0
44	LVKELTGGK	324	-0.4000	0
45	VLKGEVKDV	354	-0.4000	0
46	LGSFELTGI	427	-0.4000	0
47	IEIDGKKYT	78	-0.5000	0
48	FQSVIADTG	292	-0.5000	0
49	VGAALQAGV	346	-0.5000	0
50	IYEAAQAAS	580	-0.5000	0
51	ISARILMKL	90	-0.5400	0
52	VFDLGGGTF	167	-0.6000	0

53	VVEVRATSG	186	-0.6000	0
54	LGTTNSVVS	8	-0.7000	0
55	VVSVLEGGD	14	-0.7000	0
56	MGSDWSIEI	72	-0.7000	0
57	VNPDEVVAV	338	-0.7000	0
58	VAVGAALQA	344	-0.7000	0
59	LMKLKRDAE	95	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	ILMKLKRDA	94	5.7000	64.77
2	IVAFARNGE	38	3.7000	42.05
3	IAAHNKLLG	420	3.6000	40.91
4	MAMQRLREA	228	3.4000	38.64
5	VRSVKRHMG	65	3.2000	36.36
6	IAGLNVLRI	135	2.8000	31.82
7	LVGQPAKNQ	48	2.7000	30.68
8	VLLLDVTPL	362	2.6600	30.23
9	IRIQEGSGL	472	2.6600	30.23
10	VVVANSEGS	24	2.6000	29.55
11	LVDKFKGTS	211	2.5000	28.41
12	LVGGSTRMP	311	2.5000	28.41
13	LVYQTEKFV	515	2.4000	27.27
14	IVNEPTAAA	143	2.3000	26.14
15	VVDWLVDKF	207	2.1000	23.86
16	LNVLRIVNE	138	2.0000	22.73
17	LLLDVTPLS	363	2.0000	22.73
18	LLDRTRKPF	284	1.8000	20.45
19	VYQTEKFVK	516	1.5000	17.05
20	ILVFDLGGG	165	1.4000	15.91
21	LGSFELTGI	427	1.4000	15.91
22	VRNQAETLV	508	1.3000	14.77

23	VVDAEVVDD	611	1.3000	14.77
24	VQIQVYQGE	409	1.2000	13.64
25	IVHVTAKDK	456	1.2000	13.64
26	VVLVGGSTR	309	1.1000	12.50
27	VGGSTRMPA	312	1.1000	12.50
28	VNPDEVVAV	338	1.1000	12.50
29	IEIDGKKYT	78	1.0000	11.36
30	LFLDEQLTR	266	1.0000	11.36
31	VVAVGAALQ	343	1.0000	11.36
32	VLKGEVKDV	354	1.0000	11.36
33	LGIETKGGV	372	1.0000	11.36
34	VTAKDKGTG	459	1.0000	11.36
35	LRIVNEPTA	141	0.9000	10.23
36	VKRHMGSDW	68	0.7000	7.95
37	LMKLKRDAE	95	0.7000	7.95
38	VSLLEIGEG	177	0.7000	7.95
39	IERNTTIPT	385	0.7000	7.95
40	MQRLREAAE	230	0.6000	6.82
41	LTGIPPAPR	432	0.6000	6.82
42	MKLKRDAEA	96	0.5000	5.68
43	VGAALQAGV	346	0.5000	5.68
44	LGGSDISAI	554	0.5000	5.68
45	IYEAAQAAS	580	0.5000	5.68
46	VGQPAKNQA	49	0.4000	4.55
47	VMTRLIERN	380	0.4000	4.55
48	MTRLIERNT	381	0.4000	4.55
49	VHVTAKDKG	457	0.4000	4.55
50	LGTTNSVVS	8	0.3000	3.41
51	IKSAMEKLG	562	0.3000	3.41
52	VTNVDRTVR	58	0.2000	2.27
53	VEVRATSGD	187	0.1000	1.14
54	VLVGGSTRM	310	0.1000	1.14
55	LVKELTGGK	324	0.1000	1.14
56	IPTKRSETF	391	0.1000	1.14

57	IQVYQGERE	411	0.1000	1.14
58	ISARILMKL	90	0.0600	0.68
59	LKGEVKDVL	355	-0.0400	0
60	VLVGQPAKN	47	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	ILMKLKRDA	94	4.7000	53.41
2	IVAFARNGE	38	2.7000	30.68
3	IAAHNKLLG	420	2.6000	29.55
4	MAMQRLREA	228	2.4000	27.27
5	VRSVKRHMG	65	2.2000	25.00
6	IAGLNVLRI	135	1.8000	20.45
7	LVGQPAKNQ	48	1.7000	19.32
8	VLLLDVTPL	362	1.6600	18.86
9	IRIQEGSGL	472	1.6600	18.86
10	VVVANSEGS	24	1.6000	18.18
11	LVDKFKGTS	211	1.5000	17.05
12	LVGGSTRMP	311	1.5000	17.05
13	LVYQTEKFV	515	1.4000	15.91
14	IVNEPTAAA	143	1.3000	14.77
15	VVDWLVDKF	207	1.1000	12.50
16	LNVLRIVNE	138	1.0000	11.36
17	LLLDVTPLS	363	1.0000	11.36
18	YFNDAQRQA	120	0.8000	9.09
19	LLDRTRKPF	284	0.8000	9.09
20	FVKEQREAE	522	0.7000	7.95
21	VYQTEKFVK	516	0.5000	5.68
22	ILVFDLGGG	165	0.4000	4.55
23	LGSFELTGI	427	0.4000	4.55
24	VRNQAETLV	508	0.3000	3.41
25	VVDAEVVDD	611	0.3000	3.41

26	VQIQVYQGE	409	0.2000	2.27
27	FELTGIPPA	430	0.2000	2.27
28	IVHVTAKDK	456	0.2000	2.27
29	VVLVGGSTR	309	0.1000	1.14
30	VGGSTRMPA	312	0.1000	1.14
31	VNPDEVVAV	338	0.1000	1.14
32	YLGEDITDA	105	-0.1000	0
33	LRIVNEPTA	141	-0.1000	0
34	YEAAQAASQ	581	-0.1000	0
35	VKRHMGSDW	68	-0.3000	0
36	LMKLKRDAE	95	-0.3000	0
37	VSLLEIGEG	177	-0.3000	0
38	IERNTTIPT	385	-0.3000	0
39	FARNGEVLV	41	-0.4000	0
40	FNDAQRQAT	121	-0.4000	0
41	MQRLREAAE	230	-0.4000	0
42	LTGIPPAPR	432	-0.4000	0
43	MKLKRDAEA	96	-0.5000	0
44	VGAALQAGV	346	-0.5000	0
45	LGGSDISAI	554	-0.5000	0
46	IYEAAQAAS	580	-0.5000	0
47	FQRITQDLL	277	-0.5400	0
48	VGQPAKNQA	49	-0.6000	0
49	FQSVIADTG	292	-0.6000	0
50	VMTRLIERN	380	-0.6000	0
51	MTRLIERNT	381	-0.6000	0
52	VHVTAKDKG	457	-0.6000	0
53	LGTTNSVVS	8	-0.7000	0
54	IKSAMEKLG	562	-0.7000	0
55	VTNVDRTVR	58	-0.8000	0

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	ILMKLKRDA	94	5.7000	63.33
2	IVAFARNGE	38	5.3000	58.89
3	LVGQPAKNQ	48	4.2000	46.67
4	LNVLRIVNE	138	3.6000	40.00
5	IAAHNKLLG	420	3.5000	38.89
6	MAMQRLREA	228	3.4000	37.78
7	VRSVKRHMG	65	3.1000	34.44
8	VVDAEVVDD	611	2.9000	32.22
9	VQIQVYQGE	409	2.8000	31.11
10	VLLLDVTPL	362	2.7000	30.00
11	IRIQEGSGL	472	2.7000	30.00
12	VVAVGAALQ	343	2.5000	27.78
13	LMKLKRDAE	95	2.3000	25.56
14	IVNEPTAAA	143	2.3000	25.56
15	VVVANSEGS	24	2.2000	24.44
16	MQRLREAAE	230	2.2000	24.44
17	IAGLNVLRI	135	2.1000	23.33
18	LVDKFKGTS	211	2.1000	23.33
19	LVGGSTRMP	311	1.9000	21.11
20	VEVRATSGD	187	1.7000	18.89
21	IQVYQGERE	411	1.7000	18.89
22	LVYQTEKFV	515	1.7000	18.89
23	VKRHMGSDW	68	1.6000	17.78
24	LLLDVTPLS	363	1.6000	17.78
25	VMTRLIERN	380	1.6000	17.78
26	LDEQLTRAE	268	1.4000	15.56
27	IKDAEAHAE	489	1.4000	15.56
28	ILVFDLGGG	165	1.3000	14.44
29	IDRMIKDAE	485	1.3000	14.44
30	FVKEQREAE	522	1.3000	14.44
31	IEIDGKKYT	78	1.2000	13.33
32	LQAGVLKGE	350	1.2000	13.33
33	VLVGQPAKN	47	1.1000	12.22

34	VVDWLVDKF	207	1.1000	12.22
35	INLPYITVD	252	1.1000	12.22
36	VGGSTRMPA	312	1.1000	12.22
37	LRIVNEPTA	141	0.9000	10.00
38	IERNTTIPT	385	0.9000	10.00
39	VTAKDKGTG	459	0.9000	10.00
40	LLDRTRKPF	284	0.8000	8.89
41	VTPLSLGIE	367	0.7000	7.78
42	LGSFELTGI	427	0.7000	7.78
43	VYQTEKFVK	516	0.7000	7.78
44	VSLLEIGEG	177	0.6000	6.67
45	LEIGEGVVE	180	0.6000	6.67
46	MTRLIERNT	381	0.6000	6.67
47	VRNQAETLV	508	0.6000	6.67
48	MKLKRDAEA	96	0.5000	5.56
49	MEKLGQESQ	566	0.5000	5.56
50	VGQPAKNQA	49	0.4000	4.44
51	VITTPAYFN	114	0.4000	4.44
52	LPYITVDAD	254	0.4000	4.44
53	LDRTRKPFQ	285	0.4000	4.44
54	VNPDEVVAV	338	0.4000	4.44
55	IVHVTAKDK	456	0.4000	4.44
56	YEAAQAASQ	581	0.4000	4.44
57	VLKGEVKDV	354	0.3000	3.33
58	LGIETKGGV	372	0.3000	3.33
59	VHVTAKDKG	457	0.3000	3.33
60	ISAIKSAME	559	0.3000	3.33
61	VRATSGDNH	189	0.2000	2.22
62	IPQIEVTFD	442	0.2000	2.22

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	IAGLNVLRI	135	3.6000	41.38
2	VRSVKRHMG	65	3.0000	34.48
3	VLLLDVTPL	362	1.9600	22.53
4	ILMKLKRDA	94	1.8000	20.69
5	LRIVNEPTA	141	1.6500	18.97
6	IAAHNKLLG	420	1.6000	18.39
7	VSLLEIGEG	177	1.5000	17.24
8	VVVANSEGS	24	1.3000	14.94
9	LVDKFKGTS	211	1.3000	14.94
10	VGGSTRMPA	312	1.3000	14.94
11	VVAVGAALQ	343	1.3000	14.94
12	IVHVTAKDK	456	1.3000	14.94
13	IVAFARNGE	38	1.2000	13.79
14	LNVLRIVNE	138	1.2000	13.79
15	VKDVLLLDV	359	1.2000	13.79
16	LLLDVTPLS	363	1.1500	13.22
17	FELTGIPPA	430	1.1500	13.22
18	ILVFDLGGG	165	1.1000	12.64
19	LTGIPPAPR	432	1.1000	12.64
20	LLDVTPLSL	364	1.0600	12.18
21	VVLVGGSTR	309	1.0000	11.49
22	IERNTTIPT	385	0.9000	10.34
23	LFLDEQLTR	266	0.8000	9.20
24	FKGTSGIDL	215	0.7600	8.74
25	IVNEPTAAA	143	0.7000	8.05
26	LVGQPAKNQ	48	0.5000	5.75
27	LGIETKGGV	372	0.5000	5.75
28	MQRLREAAE	230	0.3000	3.45
29	IRIQEGSGL	472	0.2600	2.99
30	LVYQTEKFV	515	0.2000	2.30
31	LNKVDAAVA	540	0.2000	2.30
32	VTNVDRTVR	58	0.1000	1.15
33	VTPLSLGIE	367	-0.1000	0
34	YEAAQAASQ	581	-0.1000	0

35	VVANSEGSR	25	-0.2000	0
36	MAMQRLREA	228	-0.2000	0
37	VTAKDKGTG	459	-0.2000	0
38	FVKEQREAE	522	-0.2000	0
39	VVDAEVVDD	611	-0.2000	0
40	MARAVGIDL	0	-0.2400	0
41	FQRITQDLL	277	-0.2400	0
42	LLDRTRKPF	284	-0.3000	0
43	LVGGSTRMP	311	-0.3000	0
44	LVKELTGGK	324	-0.4000	0
45	VLKGEVKDV	354	-0.4000	0
46	LGSFELTGI	427	-0.4000	0
47	IEIDGKKYT	78	-0.5000	0
48	FQSVIADTG	292	-0.5000	0
49	VGAALQAGV	346	-0.5000	0
50	IYEAAQAAS	580	-0.5000	0
51	ISARILMKL	90	-0.5400	0
52	VFDLGGGTF	167	-0.6000	0
53	VVEVRATSG	186	-0.6000	0
54	LGTTNSVVS	8	-0.7000	0
55	VVSVLEGGD	14	-0.7000	0
56	MGSDWSIEI	72	-0.7000	0
57	VNPDEVVAV	338	-0.7000	0
58	VAVGAALQA	344	-0.7000	0
59	LMKLKRDAE	95	-0.8000	0

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	VVAVGAALQ	343	2.0000	29.41
2	ILMKLKRDA	94	1.6000	23.53
3	VRSVKRHMG	65	0.9000	13.24
4	IAGLNVLRI	135	0.9000	13.24

5	LVDKFKGTS	211	0.8000	11.76
6	IVNEPTAAA	143	0.7000	10.29
7	LVGQPAKNQ	48	0.6000	8.82
8	IVHVTAKDK	456	0.6000	8.82
9	YEAAQAASQ	581	0.6000	8.82
10	LRIVNEPTA	141	0.5000	7.35
11	LNKVDAAVA	540	0.2000	2.94
12	VLLLDVTPL	362	-0.1000	0
13	VVVANSEGS	24	-0.2000	0
14	VGGSTRMPA	312	-0.3000	0
15	ILVFDLGGG	165	-0.4000	0
16	MAMQRLREA	228	-0.4000	0
17	LLLDVTPLS	363	-0.4000	0
18	LTGIPPAPR	432	-0.4000	0
19	IVAFARNGE	38	-0.5000	0
20	VVLVGGSTR	309	-0.5000	0
21	LVKELTGGK	324	-0.6000	0
22	LGIETKGGV	372	-0.6000	0
23	VYQTEKFVK	516	-0.6000	0
24	LNVLRIVNE	138	-0.7000	0
25	IRIQEGSGL	472	-0.7000	0
26	FQRITQDLL	277	-0.9000	0
27	IYEAAQAAS	580	-0.9000	0
28	MQRLREAAE	230	-1.1000	0
29	YFNDAQRQA	120	-1.3000	0
30	IERNTTIPT	385	-1.4000	0
31	LVYQTEKFV	515	-1.4000	0
32	LVGGSTRMP	311	-1.5000	0
33	VGAALQAGV	346	-1.5000	0
34	LGTTNSVVS	8	-1.6000	0
35	LDRTRKPFQ	285	-1.6000	0
36	FQSVIADTG	292	-1.6000	0
37	VKDVLLLDV	359	-1.6000	0
38	VTPLSLGIE	367	-1.6000	0

39	IAAHNKLLG	420	-1.6000	0
40	LLDVTPLSL	364	-1.7000	0
41	VTAKDKGTG	459	-1.7000	0
42	VVANSEGSR	25	-1.8000	0
43	IEIDGKKYT	78	-1.8000	0
44	MKLKRDAEA	96	-1.8000	0
45	FKGTSGIDL	215	-1.8000	0
46	VVDAEVVDD	611	-1.8000	0
47	VVSVLEGGD	14	-1.9000	0
48	LMKLKRDAE	95	-1.9000	0
49	FNDAQRQAT	121	-1.9000	0
50	LGGSDISAI	554	-1.9000	0
51	VAFARNGEV	39	-2.0000	0
52	VLKGEVKDV	354	-2.0000	0
53	IPPAPRGIP	435	-2.0000	0
54	MEKLGQESQ	566	-2.0000	0
55	VLVGQPAKN	47	-2.1000	0
56	VSVLEGGDP	15	-2.2000	0
57	VGQPAKNQA	49	-2.2000	0
58	YLGEDITDA	105	-2.2000	0
59	LVFDLGGGT	166	-2.2000	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	IAGLNVLRI	135	3.7000	44.58
2	VVAVGAALQ	343	3.0000	36.14
3	ILMKLKRDA	94	2.8000	33.73
4	LRIVNEPTA	141	2.6500	31.93
5	VRSVKRHMG	65	2.6000	31.33
6	VGGSTRMPA	312	2.3000	27.71
7	LVGQPAKNQ	48	2.2000	26.51
8	IVHVTAKDK	456	2.2000	26.51

9	VLLLDVTPL	362	2.0000	24.10
10	VVVANSEGS	24	1.9000	22.89
11	LVDKFKGTS	211	1.9000	22.89
12	LLLDVTPLS	363	1.7500	21.08
13	IVNEPTAAA	143	1.7000	20.48
14	VKDVLLLDV	359	1.2000	14.46
15	IERNTTIPT	385	1.2000	14.46
16	IAAHNKLLG	420	1.2000	14.46
17	LNKVDAAVA	540	1.2000	14.46
18	VSLLEIGEG	177	1.1000	13.25
19	LLDVTPLSL	364	1.1000	13.25
20	VYQTEKFVK	516	0.9000	10.84
21	IVAFARNGE	38	0.8000	9.64
22	LNVLRIVNE	138	0.8000	9.64
23	MAMQRLREA	228	0.8000	9.64
24	ILVFDLGGG	165	0.7000	8.43
25	LTGIPPAPR	432	0.6000	7.23
26	LDRTRKPFQ	285	0.5500	6.63
27	VVLVGGSTR	309	0.5000	6.02
28	LVKELTGGK	324	0.5000	6.02
29	LGIETKGGV	372	0.5000	6.02
30	LFLDEQLTR	266	0.3000	3.61
31	VAVGAALQA	344	0.3000	3.61
32	IRIQEGSGL	472	0.3000	3.61
33	LVYQTEKFV	515	0.2000	2.41
34	FELTGIPPA	430	0.1500	1.81
35	MEKLGQESQ	566	0.1000	1.20
36	IYEAAQAAS	580	0.1000	1.20
37	LGTTNSVVS	8	-0.1000	0
38	MQRLREAAE	230	-0.1000	0
39	MARAVGIDL	0	-0.2000	0
40	IEIDGKKYT	78	-0.2000	0
41	LVGGSTRMP	311	-0.3000	0
42	LGSFELTGI	427	-0.3000	0

43	VVDAEVVDD	611	-0.3000	0
44	VTNVDRTVR	58	-0.4000	0
45	VLKGEVKDV	354	-0.4000	0
46	LLGSFELTG	426	-0.4000	0
47	YEAAQAASQ	581	-0.4000	0
48	ISARILMKL	90	-0.5000	0
49	VLRIVNEPT	140	-0.5000	0
50	VGAALQAGV	346	-0.5000	0
51	VTPLSLGIE	367	-0.5000	0
52	MGSDWSIEI	72	-0.6000	0
53	VTAKDKGTG	459	-0.6000	0
54	VVANSEGSR	25	-0.7000	0
55	VNPDEVVAV	338	-0.7000	0
56	VVSVLEGGD	14	-0.8000	0
57	MKLKRDAEA	96	-0.8000	0
58	VAFARNGEV	39	-0.9000	0
59	VGQPAKNQA	49	-0.9000	0
60	LREAAEKAK	233	-0.9000	0
61	IPPAPRGIP	435	-0.9000	0

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	VRSVKRHMG	65	2.9000	32.58
2	IAGLNVLRI	135	2.9000	32.58
3	IVAFARNGE	38	2.8000	31.46
4	LNVLRIVNE	138	2.8000	31.46
5	VVAVGAALQ	343	2.8000	31.46
6	LVGQPAKNQ	48	2.0000	22.47
7	VLLLDVTPL	362	2.0000	22.47
8	MQRLREAAE	230	1.9000	21.35
9	ILMKLKRDA	94	1.8000	20.22
10	LRIVNEPTA	141	1.6500	18.54

11	VTPLSLGIE	367	1.5000	16.85
12	IAAHNKLLG	420	1.5000	16.85
13	VSLLEIGEG	177	1.4000	15.73
14	FVKEQREAE	522	1.4000	15.73
15	YEAAQAASQ	581	1.4000	15.73
16	VVDAEVVDD	611	1.4000	15.73
17	VGGSTRMPA	312	1.3000	14.61
18	FELTGIPPA	430	1.1500	12.92
19	LLDVTPLSL	364	1.1000	12.36
20	IERNTTIPT	385	1.1000	12.36
21	ILVFDLGGG	165	1.0000	11.24
22	VVSVLEGGD	14	0.9000	10.11
23	VVVANSEGS	24	0.9000	10.11
24	LVDKFKGTS	211	0.9000	10.11
25	LMKLKRDAE	95	0.8000	8.99
26	FKGTSGIDL	215	0.8000	8.99
27	ISAIKSAME	559	0.8000	8.99
28	LLLDVTPLS	363	0.7500	8.43
29	IVNEPTAAA	143	0.7000	7.87
30	VKDVLLLDV	359	0.5000	5.62
31	IVHVTAKDK	456	0.5000	5.62
32	LDRTRKPFQ	285	0.3500	3.93
33	IPQIEVTFD	442	0.3000	3.37
34	IRIQEGSGL	472	0.3000	3.37
35	VKELTGGKE	325	0.2000	2.25
36	LNKVDAAVA	540	0.2000	2.25
37	VQIQVYQGE	409	0.1000	1.12
38	VLVGQPAKN	47	-0.1000	0
39	LLGSFELTG	426	-0.1000	0
40	IKDAEAHAE	489	-0.1000	0
41	MEKLGQESQ	566	-0.1000	0
42	MARAVGIDL	0	-0.2000	0
43	MAMQRLREA	228	-0.2000	0
44	FQRITQDLL	277	-0.2000	0

45	LQAGVLKGE	350	-0.2000	0
46	LGIETKGGV	372	-0.2000	0
47	IEIDGKKYT	78	-0.3000	0
48	VITTPAYFN	114	-0.3000	0
49	LPYITVDAD	254	-0.3000	0
50	VTAKDKGTG	459	-0.3000	0
51	LTGIPPAPR	432	-0.4000	0
52	ISARILMKL	90	-0.5000	0
53	INLPYITVD	252	-0.5000	0
54	VVLVGGSTR	309	-0.5000	0
55	LVYQTEKFV	515	-0.5000	0
56	VLRIVNEPT	140	-0.6000	0
57	VEVRATSGD	187	-0.6000	0
58	YITVDADKN	256	-0.6000	0
59	FQSVIADTG	292	-0.6000	0
60	VMTRLIERN	380	-0.6000	0
61	VVEVRATSG	186	-0.7000	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	ILMKLKRDA	94	5.7000	67.86
2	LVGQPAKNQ	48	3.4000	40.48
3	MAMQRLREA	228	3.4000	40.48
4	IVAFARNGE	38	2.3000	27.38
5	IVNEPTAAA	143	2.3000	27.38
6	VVVANSEGS	24	2.2000	26.19
7	IAAHNKLLG	420	2.2000	26.19
8	LVDKFKGTS	211	2.1000	25.00
9	IAGLNVLRI	135	1.9000	22.62
10	VRSVKRHMG	65	1.8000	21.43
11	VVAVGAALQ	343	1.7000	20.24
12	VLLLDVTPL	362	1.7000	20.24

13	IRIQEGSGL	472	1.7000	20.24
14	LLLDVTPLS	363	1.6000	19.05
15	LVGGSTRMP	311	1.5000	17.86
16	LVYQTEKFV	515	1.4000	16.67
17	VYQTEKFVK	516	1.4000	16.67
18	VGGSTRMPA	312	1.1000	13.10
19	IVHVTAKDK	456	1.1000	13.10
20	LRIVNEPTA	141	0.9000	10.71
21	VKRHMGSDW	68	0.7000	8.33
22	LNVLRIVNE	138	0.6000	7.14
23	MKLKRDAEA	96	0.5000	5.95
24	LGSFELTGI	427	0.5000	5.95
25	VGQPAKNQA	49	0.4000	4.76
26	IEIDGKKYT	78	0.3000	3.57
27	VRNQAETLV	508	0.3000	3.57
28	VVDWLVDKF	207	0.2000	2.38
29	VVDAEVVDD	611	0.2000	2.38
30	VNPDEVVAV	338	0.1000	1.19
31	IYEAAQAAS	580	0.1000	1.19
32	LGTTNSVVS	8	-0.1000	0
33	LLDRTRKPF	284	-0.1000	0
34	LNKVDAAVA	540	-0.1000	0
35	YFNDAQRQA	120	-0.2000	0
36	VQIQVYQGE	409	-0.2000	0
37	MTRLIERNT	381	-0.3000	0
38	MEKLGQESQ	566	-0.3000	0
39	LDRTRKPFQ	285	-0.4000	0
40	VVLVGGSTR	309	-0.4000	0
41	VMTRLIERN	380	-0.4000	0
42	VTAKDKGTG	459	-0.4000	0
43	LGGSDISAI	554	-0.4000	0
44	YEAAQAASQ	581	-0.4000	0
45	LFLDEQLTR	266	-0.5000	0
46	VGAALQAGV	346	-0.5000	0

47	VAVGAALQA	344	-0.6000	0
48	VYQGEREIA	413	-0.6000	0
49	LMKLKRDAE	95	-0.7000	0
50	VSLLEIGEG	177	-0.7000	0
51	LREAAEKAK	233	-0.7000	0
52	MQRLREAAE	230	-0.8000	0
53	FELTGIPPA	430	-0.8000	0
54	VLVGQPAKN	47	-0.9000	0
55	ISARILMKL	90	-0.9000	0
56	LTGIPPAPR	432	-0.9000	0

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	ILMKLKRDA	94	4.7000	55.95
2	LVGQPAKNQ	48	2.4000	28.57
3	MAMQRLREA	228	2.4000	28.57
4	IVAFARNGE	38	1.3000	15.48
5	IVNEPTAAA	143	1.3000	15.48
6	VVVANSEGS	24	1.2000	14.29
7	IAAHNKLLG	420	1.2000	14.29
8	LVDKFKGTS	211	1.1000	13.10
9	IAGLNVLRI	135	0.9000	10.71
10	VRSVKRHMG	65	0.8000	9.52
11	YFNDAQRQA	120	0.8000	9.52
12	VVAVGAALQ	343	0.7000	8.33
13	VLLLDVTPL	362	0.7000	8.33
14	IRIQEGSGL	472	0.7000	8.33
15	LLLDVTPLS	363	0.6000	7.14
16	YEAAQAASQ	581	0.6000	7.14
17	LVGGSTRMP	311	0.5000	5.95
18	LVYQTEKFV	515	0.4000	4.76
19	VYQTEKFVK	516	0.4000	4.76

20	FELTGIPPA	430	0.2000	2.38
21	VGGSTRMPA	312	0.1000	1.19
22	IVHVTAKDK	456	0.1000	1.19
23	YLGEDITDA	105	-0.1000	0
24	LRIVNEPTA	141	-0.1000	0
25	VKRHMGSDW	68	-0.3000	0
26	LNVLRIVNE	138	-0.4000	0
27	MKLKRDAEA	96	-0.5000	0
28	LGSFELTGI	427	-0.5000	0
29	VGQPAKNQA	49	-0.6000	0
30	IEIDGKKYT	78	-0.7000	0
31	VRNQAETLV	508	-0.7000	0
32	FVKEQREAE	522	-0.7000	0
33	VVDWLVDKF	207	-0.8000	0
34	VVDAEVVDD	611	-0.8000	0
35	VNPDEVVAV	338	-0.9000	0
36	IYEAAQAAS	580	-0.9000	0
37	ILVFDLGGG	165	-1.0000	0
38	LVKELTGGK	324	-1.0000	0
39	VLKGEVKDV	354	-1.0000	0
40	LGIETKGGV	372	-1.0000	0
41	IERNTTIPT	385	-1.0000	0
42	LGTTNSVVS	8	-1.1000	0
43	FNDAQRQAT	121	-1.1000	0
44	LLDRTRKPF	284	-1.1000	0
45	LNKVDAAVA	540	-1.1000	0
46	VQIQVYQGE	409	-1.2000	0
47	MTRLIERNT	381	-1.3000	0
48	MEKLGQESQ	566	-1.3000	0
49	FARNGEVLV	41	-1.4000	0
50	LDRTRKPFQ	285	-1.4000	0
51	VVLVGGSTR	309	-1.4000	0
52	VMTRLIERN	380	-1.4000	0
53	VTAKDKGTG	459	-1.4000	0

54	LGGSDISAI	554	-1.4000	0
55	LFLDEQLTR	266	-1.5000	0
56	FQRITQDLL	277	-1.5000	0
57	VGAALQAGV	346	-1.5000	0
58	VAVGAALQA	344	-1.6000	0
59	VYQGEREIA	413	-1.6000	0
60	YQGEREIAA	414	-1.6000	0
61	LMKLKRDAE	95	-1.7000	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	ILMKLKRDA	94	5.7000	64.77
2	IVAFARNGE	38	3.7000	42.05
3	IAAHNKLLG	420	3.6000	40.91
4	MAMQRLREA	228	3.4000	38.64
5	VRSVKRHMG	65	3.2000	36.36
6	IAGLNVLRI	135	2.8000	31.82
7	LVGQPAKNQ	48	2.7000	30.68
8	VLLLDVTPL	362	2.6600	30.23
9	IRIQEGSGL	472	2.6600	30.23
10	VVVANSEGS	24	2.6000	29.55
11	LVDKFKGTS	211	2.5000	28.41
12	LVGGSTRMP	311	2.5000	28.41
13	LVYQTEKFV	515	2.4000	27.27
14	IVNEPTAAA	143	2.3000	26.14
15	VVDWLVDKF	207	2.1000	23.86
16	LNVLRIVNE	138	2.0000	22.73
17	LLLDVTPLS	363	2.0000	22.73
18	LLDRTRKPF	284	1.8000	20.45
19	VYQTEKFVK	516	1.5000	17.05
20	ILVFDLGGG	165	1.4000	15.91
21	LGSFELTGI	427	1.4000	15.91

22	VRNQAETLV	508	1.3000	14.77
23	VVDAEVVDD	611	1.3000	14.77
24	VQIQVYQGE	409	1.2000	13.64
25	IVHVTAKDK	456	1.2000	13.64
26	VVLVGGSTR	309	1.1000	12.50
27	VGGSTRMPA	312	1.1000	12.50
28	VNPDEVVAV	338	1.1000	12.50
29	IEIDGKKYT	78	1.0000	11.36
30	LFLDEQLTR	266	1.0000	11.36
31	VVAVGAALQ	343	1.0000	11.36
32	VLKGEVKDV	354	1.0000	11.36
33	LGIETKGGV	372	1.0000	11.36
34	VTAKDKGTG	459	1.0000	11.36
35	LRIVNEPTA	141	0.9000	10.23
36	VKRHMGSDW	68	0.7000	7.95
37	LMKLKRDAE	95	0.7000	7.95
38	VSLLEIGEG	177	0.7000	7.95
39	IERNTTIPT	385	0.7000	7.95
40	MQRLREAAE	230	0.6000	6.82
41	LTGIPPAPR	432	0.6000	6.82
42	MKLKRDAEA	96	0.5000	5.68
43	VGAALQAGV	346	0.5000	5.68
44	LGGSDISAI	554	0.5000	5.68
45	IYEAAQAAS	580	0.5000	5.68
46	VGQPAKNQA	49	0.4000	4.55
47	VMTRLIERN	380	0.4000	4.55
48	MTRLIERNT	381	0.4000	4.55
49	VHVTAKDKG	457	0.4000	4.55
50	LGTTNSVVS	8	0.3000	3.41
51	IKSAMEKLG	562	0.3000	3.41
52	VTNVDRTVR	58	0.2000	2.27
53	VEVRATSGD	187	0.1000	1.14
54	VLVGGSTRM	310	0.1000	1.14
55	LVKELTGGK	324	0.1000	1.14

56	IPTKRSETF	391	0.1000	1.14
57	IQVYQGERE	411	0.1000	1.14
58	ISARILMKL	90	0.0600	0.68
59	LKGEVKDVL	355	-0.0400	0
60	VLVGQPAKN	47	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	ILMKLKRDA	94	5.7000	64.77
2	IVAFARNGE	38	3.7000	42.05
3	IAAHNKLLG	420	3.6000	40.91
4	MAMQRLREA	228	3.4000	38.64
5	VRSVKRHMG	65	3.2000	36.36
6	IAGLNVLRI	135	2.8000	31.82
7	LVGQPAKNQ	48	2.7000	30.68
8	VLLLDVTPL	362	2.6600	30.23
9	IRIQEGSGL	472	2.6600	30.23
10	VVVANSEGS	24	2.6000	29.55
11	LVDKFKGTS	211	2.5000	28.41
12	LVGGSTRMP	311	2.5000	28.41
13	LVYQTEKFV	515	2.4000	27.27
14	IVNEPTAAA	143	2.3000	26.14
15	VVDWLVDKF	207	2.1000	23.86
16	LNVLRIVNE	138	2.0000	22.73
17	LLLDVTPLS	363	2.0000	22.73
18	LLDRTRKPF	284	1.8000	20.45
19	VYQTEKFVK	516	1.5000	17.05
20	ILVFDLGGG	165	1.4000	15.91
21	LGSFELTGI	427	1.4000	15.91
22	VRNQAETLV	508	1.3000	14.77
23	VVDAEVVDD	611	1.3000	14.77
24	VQIQVYQGE	409	1.2000	13.64

25	IVHVTAKDK	456	1.2000	13.64
26	VVLVGGSTR	309	1.1000	12.50
27	VGGSTRMPA	312	1.1000	12.50
28	VNPDEVVAV	338	1.1000	12.50
29	IEIDGKKYT	78	1.0000	11.36
30	LFLDEQLTR	266	1.0000	11.36
31	VVAVGAALQ	343	1.0000	11.36
32	VLKGEVKDV	354	1.0000	11.36
33	LGIETKGGV	372	1.0000	11.36
34	VTAKDKGTG	459	1.0000	11.36
35	LRIVNEPTA	141	0.9000	10.23
36	VKRHMGSDW	68	0.7000	7.95
37	LMKLKRDAE	95	0.7000	7.95
38	VSLLEIGEG	177	0.7000	7.95
39	IERNTTIPT	385	0.7000	7.95
40	MQRLREAAE	230	0.6000	6.82
41	LTGIPPAPR	432	0.6000	6.82
42	MKLKRDAEA	96	0.5000	5.68
43	VGAALQAGV	346	0.5000	5.68
44	LGGSDISAI	554	0.5000	5.68
45	IYEAAQAAS	580	0.5000	5.68
46	VGQPAKNQA	49	0.4000	4.55
47	VMTRLIERN	380	0.4000	4.55
48	MTRLIERNT	381	0.4000	4.55
49	VHVTAKDKG	457	0.4000	4.55
50	LGTTNSVVS	8	0.3000	3.41
51	IKSAMEKLG	562	0.3000	3.41
52	VTNVDRTVR	58	0.2000	2.27
53	VEVRATSGD	187	0.1000	1.14
54	VLVGGSTRM	310	0.1000	1.14
55	LVKELTGGK	324	0.1000	1.14
56	IPTKRSETF	391	0.1000	1.14
57	IQVYQGERE	411	0.1000	1.14
58	ISARILMKL	90	0.0600	0.68

59	LKGEVKDVL	355	-0.0400	0
60	VLVGQPAKN	47	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IVAFARNGE	38	4.3000	43.88
2	LGSFELTGI	427	4.2000	42.86
3	IRIQEGSGL	472	4.2000	42.86
4	VRSVKRHMG	65	3.4000	34.69
5	ILVFDLGGG	165	3.3000	33.67
6	MARAVGIDL	0	3.2000	32.65
7	LRIVNEPTA	141	3.2000	32.65
8	MGSDWSIEI	72	3.1000	31.63
9	VVLVGGSTR	309	3.1000	31.63
10	VGGSTRMPA	312	3.1000	31.63
11	IAGLNVLRI	135	3.0000	30.61
12	VIADTGISV	295	3.0000	30.61
13	VLLLDVTPL	362	2.9000	29.59
14	LVFDLGGGT	166	2.8000	28.57
15	FKGTSGIDL	215	2.5000	25.51
16	VAVGAALQA	344	2.4000	24.49
17	VKDVLLLDV	359	2.4000	24.49
18	VLVGGSTRM	310	2.3800	24.29
19	VKRHMGSDW	68	2.3000	23.47
20	ISARILMKL	90	2.3000	23.47
21	VVVANSEGS	24	2.2000	22.45
22	VLRIVNEPT	140	2.1000	21.43
23	LLDVTPLSL	364	2.1000	21.43
24	IQVYQGERE	411	2.1000	21.43
25	IVNEPTAAA	143	1.9600	20.00
26	IAAHNKLLG	420	1.9000	19.39
27	IERNTTIPT	385	1.8600	18.98

28	VAFARNGEV	39	1.8000	18.37
29	LLLDVTPLS	363	1.5600	15.92
30	LFLDEQLTR	266	1.5000	15.31
31	LGGSDISAI	554	1.4500	14.80
32	LGIETKGGV	372	1.4000	14.29
33	IEVTFDIDA	445	1.4000	14.29
34	VRNQAETLV	508	1.4000	14.29
35	VYQGEREIA	413	1.2000	12.24
36	VGIDLGTTN	4	1.1000	11.22
37	LSSSQSTSI	244	1.1000	11.22
38	LVYQTEKFV	515	1.1000	11.22
39	MKLKRDAEA	96	1.0000	10.20
40	VDKFKGTSG	212	1.0000	10.20
41	VNPDEVVAV	338	1.0000	10.20
42	LLGSFELTG	426	1.0000	10.20
43	LNKVDAAVA	540	1.0000	10.20
44	VTNVDRTVR	58	0.9000	9.18
45	ILMKLKRDA	94	0.9000	9.18
46	LKRDAEAYL	98	0.9000	9.18
47	IELSSSQST	242	0.9000	9.18
48	LGTTNSVVS	8	0.8000	8.16
49	VANSEGSRT	26	0.8000	8.16
50	LTRAEFQRI	272	0.8000	8.16
51	LEGGDPVVV	18	0.7000	7.14
52	VVAVGAALQ	343	0.7000	7.14
53	VLKGEVKDV	354	0.7000	7.14
54	IQEGSGLSK	474	0.7000	7.14
55	IDLGTTNSV	6	0.6600	6.73
56	LVGGSTRMP	311	0.6600	6.73
57	VGQPAKNQA	49	0.6000	6.12
58	VRATSGDNH	189	0.6000	6.12
59	LEIGEGVVE	180	0.5000	5.10
60	VVEVRATSG	186	0.5000	5.10
61	FQRITQDLL	277	0.5000	5.10

62	IVHVTAKDK	456	0.5000	5.10

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	FKGTSGIDL	215	3.5000	35.71
2	IVAFARNGE	38	3.3000	33.67
3	LGSFELTGI	427	3.2000	32.65
4	IRIQEGSGL	472	3.2000	32.65
5	VRSVKRHMG	65	2.4000	24.49
6	ILVFDLGGG	165	2.3000	23.47
7	MARAVGIDL	0	2.2000	22.45
8	LRIVNEPTA	141	2.2000	22.45
9	MGSDWSIEI	72	2.1000	21.43
10	VVLVGGSTR	309	2.1000	21.43
11	VGGSTRMPA	312	2.1000	21.43
12	IAGLNVLRI	135	2.0000	20.41
13	VIADTGISV	295	2.0000	20.41
14	VLLLDVTPL	362	1.9000	19.39
15	LVFDLGGGT	166	1.8000	18.37
16	FQRITQDLL	277	1.5000	15.31
17	VAVGAALQA	344	1.4000	14.29
18	VKDVLLLDV	359	1.4000	14.29
19	VLVGGSTRM	310	1.3800	14.08
20	VKRHMGSDW	68	1.3000	13.27
21	ISARILMKL	90	1.3000	13.27
22	YQGEREIAA	414	1.3000	13.27
23	VVVANSEGS	24	1.2000	12.24
24	FELTGIPPA	430	1.1500	11.73
25	VLRIVNEPT	140	1.1000	11.22
26	LLDVTPLSL	364	1.1000	11.22
27	IQVYQGERE	411	1.1000	11.22
28	IVNEPTAAA	143	0.9600	9.80

29	IAAHNKLLG	420	0.9000	9.18
30	IERNTTIPT	385	0.8600	8.78
31	YLGEDITDA	105	0.8500	8.67
32	VAFARNGEV	39	0.8000	8.16
33	FDIDANGIV	449	0.8000	8.16
34	LLLDVTPLS	363	0.5600	5.71
35	LFLDEQLTR	266	0.5000	5.10
36	LGGSDISAI	554	0.4500	4.59
37	LGIETKGGV	372	0.4000	4.08
38	IEVTFDIDA	445	0.4000	4.08
39	VRNQAETLV	508	0.4000	4.08
40	WLVDKFKGT	210	0.3000	3.06
41	VYQGEREIA	413	0.2000	2.04
42	VGIDLGTTN	4	0.1000	1.02
43	FARNGEVLV	41	0.1000	1.02
44	LSSSQSTSI	244	0.1000	1.02
45	FQSVIADTG	292	0.1000	1.02
46	LVYQTEKFV	515	0.1000	1.02
47	VTNVDRTVR	58	-0.1000	0
48	ILMKLKRDA	94	-0.1000	0
49	LKRDAEAYL	98	-0.1000	0
50	IELSSSQST	242	-0.1000	0
51	FVKEQREAE	522	-0.1000	0
52	LGTTNSVVS	8	-0.2000	0
53	VANSEGSRT	26	-0.2000	0
54	LTRAEFQRI	272	-0.2000	0
55	LEGGDPVVV	18	-0.3000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IVAFARNGE	38	4.3000	43.88
2	LGSFELTGI	427	4.2000	42.86

3	IRIQEGSGL	472	4.2000	42.86
4	VRSVKRHMG	65	3.4000	34.69
5	ILVFDLGGG	165	3.3000	33.67
6	MARAVGIDL	0	3.2000	32.65
7	LRIVNEPTA	141	3.2000	32.65
8	MGSDWSIEI	72	3.1000	31.63
9	VVLVGGSTR	309	3.1000	31.63
10	VGGSTRMPA	312	3.1000	31.63
11	IAGLNVLRI	135	3.0000	30.61
12	VIADTGISV	295	3.0000	30.61
13	VLLLDVTPL	362	2.9000	29.59
14	LVFDLGGGT	166	2.8000	28.57
15	FKGTSGIDL	215	2.5000	25.51
16	VAVGAALQA	344	2.4000	24.49
17	VKDVLLLDV	359	2.4000	24.49
18	VLVGGSTRM	310	2.3800	24.29
19	VKRHMGSDW	68	2.3000	23.47
20	ISARILMKL	90	2.3000	23.47
21	VVVANSEGS	24	2.2000	22.45
22	VLRIVNEPT	140	2.1000	21.43
23	LLDVTPLSL	364	2.1000	21.43
24	IQVYQGERE	411	2.1000	21.43
25	IVNEPTAAA	143	1.9600	20.00
26	IAAHNKLLG	420	1.9000	19.39
27	IERNTTIPT	385	1.8600	18.98
28	VAFARNGEV	39	1.8000	18.37
29	LLLDVTPLS	363	1.5600	15.92
30	LFLDEQLTR	266	1.5000	15.31
31	LGGSDISAI	554	1.4500	14.80
32	LGIETKGGV	372	1.4000	14.29
33	IEVTFDIDA	445	1.4000	14.29
34	VRNQAETLV	508	1.4000	14.29
35	VYQGEREIA	413	1.2000	12.24
36	VGIDLGTTN	4	1.1000	11.22

37	LSSSQSTSI	244	1.1000	11.22
38	LVYQTEKFV	515	1.1000	11.22
39	MKLKRDAEA	96	1.0000	10.20
40	VDKFKGTSG	212	1.0000	10.20
41	VNPDEVVAV	338	1.0000	10.20
42	LLGSFELTG	426	1.0000	10.20
43	LNKVDAAVA	540	1.0000	10.20
44	VTNVDRTVR	58	0.9000	9.18
45	ILMKLKRDA	94	0.9000	9.18
46	LKRDAEAYL	98	0.9000	9.18
47	IELSSSQST	242	0.9000	9.18
48	LGTTNSVVS	8	0.8000	8.16
49	VANSEGSRT	26	0.8000	8.16
50	LTRAEFQRI	272	0.8000	8.16
51	LEGGDPVVV	18	0.7000	7.14
52	VVAVGAALQ	343	0.7000	7.14
53	VLKGEVKDV	354	0.7000	7.14
54	IQEGSGLSK	474	0.7000	7.14
55	IDLGTTNSV	6	0.6600	6.73
56	LVGGSTRMP	311	0.6600	6.73
57	VGQPAKNQA	49	0.6000	6.12
58	VRATSGDNH	189	0.6000	6.12
59	LEIGEGVVE	180	0.5000	5.10
60	VVEVRATSG	186	0.5000	5.10
61	FQRITQDLL	277	0.5000	5.10
62	IVHVTAKDK	456	0.5000	5.10

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	IVHVTAKDK	456	6.0000	61.22
2	VVLVGGSTR	309	5.2000	53.06
3	FKGTSGIDL	215	3.8000	38.78

4	LTGIPPAPR	432	3.2000	32.65
5	VVAVGAALQ	343	2.9000	29.59
6	VYQTEKFVK	516	2.9000	29.59
7	VRSVKRHMG	65	2.8000	28.57
8	IRIQEGSGL	472	2.8000	28.57
9	LVKELTGGK	324	2.3000	23.47
10	LVGQPAKNQ	48	2.2000	22.45
11	VTNVDRTVR	58	2.1000	21.43
12	MARAVGIDL	0	1.9000	19.39
13	VLLLDVTPL	362	1.9000	19.39
14	LLDVTPLSL	364	1.9000	19.39
15	VVEVRATSG	186	1.7000	17.35
16	VITTPAYFN	114	1.6000	16.33
17	LREAAEKAK	233	1.6000	16.33
18	FQRITQDLL	277	1.6000	16.33
19	FQSVIADTG	292	1.4000	14.29
20	WSIEIDGKK	76	1.2000	12.24
21	LRIVNEPTA	141	1.2000	12.24
22	VVVANSEGS	24	0.9000	9.18
23	MPAVTDLVK	318	0.9000	9.18
24	LNKVDAAVA	540	0.9000	9.18
25	YEAAQAASQ	581	0.8000	8.16
26	VRATSGDNH	189	0.7000	7.14
27	YITVDADKN	256	0.7000	7.14
28	VFDLGGGTF	167	0.6000	6.12
29	LFLDEQLTR	266	0.6000	6.12
30	VVANSEGSR	25	0.5000	5.10
31	IQEGSGLSK	474	0.4000	4.08
32	IAGLNVLRI	135	0.3000	3.06
33	LVFDLGGGT	166	0.1000	1.02
34	VQIQVYQGE	409	0.1000	1.02
35	VDRTVRSVK	61	-0.1000	0
36	ILVFDLGGG	165	-0.1000	0
37	VSLLEIGEG	177	-0.1000	0

38	VDWLVDKFK	208	-0.1000	0
39	LTRAEFQRI	272	-0.1000	0
40	LVYQTEKFV	515	-0.1000	0
41	LGTTNSVVS	8	-0.3000	0
42	MGSDWSIEI	72	-0.3000	0
43	VLRIVNEPT	140	-0.4000	0
44	IELSSSQST	242	-0.4000	0
45	LGSFELTGI	427	-0.4000	0
46	IKSAMEKLG	562	-0.4000	0
47	VVSVLEGGD	14	-0.5000	0
48	ILMKLKRDA	94	-0.5000	0
49	IVNEPTAAA	143	-0.5000	0
50	VDAAVAEAK	543	-0.5000	0
51	YTAPEISAR	85	-0.6000	0
52	LSSSQSTSI	244	-0.6000	0
53	LVGGSTRMP	311	-0.6000	0
54	MTRLIERNT	381	-0.6000	0
55	FELTGIPPA	430	-0.6000	0
56	IKDAEAHAE	489	-0.6000	0
57	VSVLEGGDP	15	-0.7000	0
58	YFNDAQRQA	120	-0.7000	0
59	VKDVLLLDV	359	-0.7000	0
60	YQGEREIAA	414	-0.7000	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	IVHVTAKDK	456	6.0000	61.22
2	VVLVGGSTR	309	5.2000	53.06
3	FKGTSGIDL	215	3.8000	38.78
4	LTGIPPAPR	432	3.2000	32.65
5	VVAVGAALQ	343	2.9000	29.59
6	VYQTEKFVK	516	2.9000	29.59

7	VRSVKRHMG	65	2.8000	28.57
8	IRIQEGSGL	472	2.8000	28.57
9	LVKELTGGK	324	2.3000	23.47
10	LVGQPAKNQ	48	2.2000	22.45
11	VTNVDRTVR	58	2.1000	21.43
12	MARAVGIDL	0	1.9000	19.39
13	VLLLDVTPL	362	1.9000	19.39
14	LLDVTPLSL	364	1.9000	19.39
15	VVEVRATSG	186	1.7000	17.35
16	VITTPAYFN	114	1.6000	16.33
17	LREAAEKAK	233	1.6000	16.33
18	FQRITQDLL	277	1.6000	16.33
19	FQSVIADTG	292	1.4000	14.29
20	WSIEIDGKK	76	1.2000	12.24
21	LRIVNEPTA	141	1.2000	12.24
22	VVVANSEGS	24	0.9000	9.18
23	MPAVTDLVK	318	0.9000	9.18
24	LNKVDAAVA	540	0.9000	9.18
25	YEAAQAASQ	581	0.8000	8.16
26	VRATSGDNH	189	0.7000	7.14
27	YITVDADKN	256	0.7000	7.14
28	VFDLGGGTF	167	0.6000	6.12
29	LFLDEQLTR	266	0.6000	6.12
30	VVANSEGSR	25	0.5000	5.10
31	IQEGSGLSK	474	0.4000	4.08
32	IAGLNVLRI	135	0.3000	3.06
33	LVFDLGGGT	166	0.1000	1.02
34	VQIQVYQGE	409	0.1000	1.02
35	VDRTVRSVK	61	-0.1000	0
36	ILVFDLGGG	165	-0.1000	0
37	VSLLEIGEG	177	-0.1000	0
38	VDWLVDKFK	208	-0.1000	0
39	LTRAEFQRI	272	-0.1000	0
40	LVYQTEKFV	515	-0.1000	0

41	LGTTNSVVS	8	-0.3000	0
42	MGSDWSIEI	72	-0.3000	0
43	VLRIVNEPT	140	-0.4000	0
44	IELSSSQST	242	-0.4000	0
45	LGSFELTGI	427	-0.4000	0
46	IKSAMEKLG	562	-0.4000	0
47	VVSVLEGGD	14	-0.5000	0
48	ILMKLKRDA	94	-0.5000	0
49	IVNEPTAAA	143	-0.5000	0
50	VDAAVAEAK	543	-0.5000	0
51	YTAPEISAR	85	-0.6000	0
52	LSSSQSTSI	244	-0.6000	0
53	LVGGSTRMP	311	-0.6000	0
54	MTRLIERNT	381	-0.6000	0
55	FELTGIPPA	430	-0.6000	0
56	IKDAEAHAE	489	-0.6000	0
57	VSVLEGGDP	15	-0.7000	0
58	YFNDAQRQA	120	-0.7000	0
59	VKDVLLLDV	359	-0.7000	0
60	YQGEREIAA	414	-0.7000	0