MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Feb 3 20:03:57 2010
Length of input sequence	626 amino acids
Number of nanomers from input sequence	618
Number of nanomers with obligatory P1 anchor residue	179
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	WVAVVAVLA	331	2.7500	45.83
2	VVAVLAVLT	334	1.5500	25.83
3	VVYQNPPAG	602	1.0700	17.83
4	VVVTIAINT	343	1.0000	16.67
5	VRGQSSADA	364	0.9000	15.00
6	FRREAQNAA	55	0.8000	13.33
7	VYSLGCVLY	198	0.8000	13.33
8	MEYVDGVTL	91	0.7500	12.50
9	FGIARAIAD	156	0.7000	11.67

10	VKKLTAAGF	440	0.6000	10.00
11	VIIIVGSGP	483	0.5000	8.33
12	FKQANSPST	451	0.3700	6.17
13	FGGMSEVHL	18	0.3000	5.00
14	YIVMEYVDG	88	0.3000	5.00
15	IMISATNAV	143	0.1000	1.67
16	VVIIIVGSG	482	0.1000	1.67
17	VAVLAVLTV	335	-0.1000	0
18	IVHTEGPMT	102	-0.1300	0
19	IRTLQKPDS	383	-0.1300	0
20	LRALGWTGM	577	-0.1300	0
21	IIIVGSGPA	484	-0.1500	0
22	LRLHRDVAV	30	-0.2000	0
23	LAVLTVVVT	338	-0.2000	0
24	VLAVLTVVV	337	-0.2500	0
25	WVDAEPRLR	570	-0.3100	0
26	LTVVVTIAI	341	-0.4500	0
27	VYQNPPAGT	603	-0.4600	0
28	VKVLRADLA	38	-0.5000	0
29	YEVLTGEPP	206	-0.5000	0
30	FVMPDLSGM	560	-0.5200	0
31	VHNGEPPEA	275	-0.5300	0
32	IIVGSGPAT	485	-0.5300	0
33	VVTIAINTF	344	-0.6000	0
34	LQVSKGNQF	552	-0.6000	0
35	IVMEYVDGV	89	-0.7000	0
36	FSHQNGIIH	127	-0.8000	0
37	INTFGGITR	349	-0.8200	0
38	FGRFKQANS	448	-0.8200	0
39	LHRDVAVKV	32	-0.9000	0
40	VGRWVAVVA	328	-0.9000	0
41	VRVHNGEPP	273	-1.0000	0
42	VLTGEPPFT	208	-1.0300	0
43	VAVVAVLAV	332	-1.0500	0

44	VLTVVVTIA	340	-1.0600	0
45	VHLARDLRL	24	-1.1000	0
46	LNFSHQNGI	125	-1.1000	0
47	LLSSAAGNL	295	-1.1000	0
48	YQTAAEMRA	262	-1.1100	0
49	LTYAEAVKK	434	-1.2000	0
50	ISATNAVKV	145	-1.3000	0
51	VLKALAKNP	250	-1.3000	0
52	IVGSGPATK	486	-1.3000	0
53	VTIAINTFG	345	-1.3100	0
54	FTGDSPVSV	215	-1.4000	0
55	MDFGIARAI	154	-1.4100	0
56	FTKFSQASV	516	-1.4200	0
57	IATLQNRGF	373	-1.5100	0
58	LVRVHNGEP	272	-1.5500	0
59	ITNVVIIIV	479	-1.5500	0
60	YELGEILGF	10	-1.6000	0
61	VIADACQAL	117	-1.6000	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	VVAVLAVLT	334	2.5500	42.50
2	VVYQNPPAG	602	2.0700	34.50
3	VVVTIAINT	343	2.0000	33.33
4	VRGQSSADA	364	1.9000	31.67
5	VYSLGCVLY	198	1.8000	30.00
6	MEYVDGVTL	91	1.7500	29.17
7	WVAVVAVLA	331	1.7500	29.17
8	VKKLTAAGF	440	1.6000	26.67
9	VIIIVGSGP	483	1.5000	25.00
10	IMISATNAV	143	1.1000	18.33
11	VVIIIVGSG	482	1.1000	18.33
12	VAVLAVLTV	335	0.9000	15.00

13	IVHTEGPMT	102	0.8700	14.50
14	IRTLQKPDS	383	0.8700	14.50
15	LRALGWTGM	577	0.8700	14.50
16	IIIVGSGPA	484	0.8500	14.17
17	LRLHRDVAV	30	0.8000	13.33
18	FRREAQNAA	55	0.8000	13.33
19	LAVLTVVVT	338	0.8000	13.33
20	VLAVLTVVV	337	0.7500	12.50
21	FGIARAIAD	156	0.7000	11.67
22	LTVVVTIAI	341	0.5500	9.17
23	VYQNPPAGT	603	0.5400	9.00
24	VKVLRADLA	38	0.5000	8.33
25	VHNGEPPEA	275	0.4700	7.83
26	IIVGSGPAT	485	0.4700	7.83
27	VVTIAINTF	344	0.4000	6.67
28	LQVSKGNQF	552	0.4000	6.67
29	FKQANSPST	451	0.3700	6.17
30	FGGMSEVHL	18	0.3000	5.00
31	IVMEYVDGV	89	0.3000	5.00
32	INTFGGITR	349	0.1800	3.00
33	LHRDVAVKV	32	0.1000	1.67
34	VGRWVAVVA	328	0.1000	1.67
35	VLTGEPPFT	208	-0.0300	0
36	VAVVAVLAV	332	-0.0500	0
37	VLTVVVTIA	340	-0.0600	0
38	VHLARDLRL	24	-0.1000	0
39	LNFSHQNGI	125	-0.1000	0
40	LLSSAAGNL	295	-0.1000	0
41	LTYAEAVKK	434	-0.2000	0
42	ISATNAVKV	145	-0.3000	0
43	VLKALAKNP	250	-0.3000	0
44	IVGSGPATK	486	-0.3000	0
45	VTIAINTFG	345	-0.3100	0
46	MDFGIARAI	154	-0.4100	0

47	IATLQNRGF	373	-0.5100	0
48	FVMPDLSGM	560	-0.5200	0
49	LVRVHNGEP	272	-0.5500	0
50	ITNVVIIIV	479	-0.5500	0
51	VIADACQAL	117	-0.6000	0
52	LSSAAGNLS	296	-0.6000	0
53	YIVMEYVDG	88	-0.7000	0
54	VKPANIMIS	138	-0.7100	0
55	FSHQNGIIH	127	-0.8000	0
56	VKVMDFGIA	151	-0.8000	0
57	IELQVSKGN	550	-0.8000	0
58	VHTEGPMTP	103	-0.8100	0
59	FGRFKQANS	448	-0.8200	0
60	ILGFGGMSE	15	-0.8300	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	VREDPIPPS	228	5.8000	61.05
2	VVIIIVGSG	482	5.8000	61.05
3	IRTLQKPDS	383	5.3000	55.79
4	IHRDVKPAN	134	5.2000	54.74
5	VNRDGIITL	613	4.8600	51.16
6	LARDLRLHR	26	4.7000	49.47
7	VMPDLSGMF	561	4.6000	48.42
8	VVYQNPPAG	602	4.5000	47.37
9	IMISATNAV	143	4.3100	45.37
10	LHRDVAVKV	32	4.3000	45.26
11	VKPANIMIS	138	4.3000	45.26
12	MRADLVRVH	268	4.3000	45.26
13	VVTIAINTF	344	4.1100	43.26
14	VPVDSVIEL	544	3.8600	40.63
15	IVMEYVDGV	89	3.4000	35.79
16	LARDPSFYL	45	3.3600	35.37

17	LRADLARDP	41	3.3000	34.74
18	IVGSGPATK	486	3.3000	34.74
19	VIADACQAL	117	3.2600	34.32
20	IPPDHVIGT	393	3.2000	33.68
21	VHNGEPPEA	275	3.0000	31.58
22	FVMPDLSGM	560	2.8700	30.21
23	IIIVGSGPA	484	2.6000	27.37
24	LNFSHQNGI	125	2.5100	26.42
25	LQVSKGNQF	552	2.5100	26.42
26	FTGDSPVSV	215	2.5000	26.32
27	YELGEILGF	10	2.4000	25.26
28	VLAVLTVVV	337	2.3000	24.21
29	LTVVVTIAI	341	2.3000	24.21
30	ITRDVQVPD	355	2.3000	24.21
31	VRGQSSADA	364	2.3000	24.21
32	IGTDPAANT	399	2.3000	24.21
33	VLTGEPPFT	208	2.2000	23.16
34	VAVVAVLAV	332	2.2000	23.16
35	VAVLAVLTV	335	2.2000	23.16
36	VIIIVGSGP	483	2.1700	22.84
37	VLTDAERTS	286	2.1000	22.11
38	VLTVVVTIA	340	2.1000	22.11
39	LKALAKNPE	251	2.0100	21.16
40	LVRVHNGEP	272	2.0000	21.05
41	VKKLTAAGF	440	2.0000	21.05
42	LLSSAAGNL	295	1.9600	20.63
43	ITNVVIIIV	479	1.9000	20.00
44	VVAVLAVLT	334	1.8000	18.95
45	VNVSTGPEQ	417	1.8000	18.95
46	LRALGWTGM	577	1.8000	18.95
47	VVLKALAKN	249	1.7000	17.89
48	VYGFTKFSQ	513	1.7000	17.89
49	LRDIVHTEG	99	1.6000	16.84
50	VYSLGCVLY	198	1.6000	16.84

51	IIVGSGPAT	485	1.6000	16.84
52	VIELQVSKG	549	1.5700	16.53
53	VRVHNGEPP	273	1.5000	15.79
54	VVVTIAINT	343	1.5000	15.79
55	LVGKVIGTN	462	1.5000	15.79
56	VSKGNQFVM	554	1.5000	15.79
57	LAVLTVVVT	338	1.4000	14.74
58	LRLHRDVAV	30	1.3000	13.68
59	VLRADLARD	40	1.3000	13.68
60	YSLGCVLYE	199	1.3000	13.68
61	WVAVVAVLA	331	1.3000	13.68
62	LGFGGMSEV	16	1.2700	13.37

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	VREDPIPPS	228	4.4000	48.35
2	IRTLQKPDS	383	3.9000	42.86
3	MRADLVRVH	268	3.8800	42.64
4	IHRDVKPAN	134	3.4000	37.36
5	VVIIIVGSG	482	3.4000	37.36
6	VKPANIMIS	138	2.9000	31.87
7	VNRDGIITL	613	2.9000	31.87
8	FTGDSPVSV	215	2.5000	27.47
9	FVMPDLSGM	560	2.3700	26.04
10	IMISATNAV	143	2.3100	25.38
11	LHRDVAVKV	32	2.3000	25.27
12	WVAVVAVLA	331	2.3000	25.27
13	LARDLRLHR	26	2.2000	24.18
14	IVGSGPATK	486	2.2000	24.18
15	FGGITRDVQ	352	2.1000	23.08
16	VVYQNPPAG	602	2.1000	23.08
17	YLRFRREAQ	52	2.0000	21.98
18	VHNGEPPEA	275	2.0000	21.98

19	VPVDSVIEL	544	1.9000	20.88
20	VMPDLSGMF	561	1.7000	18.68
21	IIIVGSGPA	484	1.6000	17.58
22	FRREAQNAA	55	1.5100	16.59
23	YELGEILGF	10	1.5000	16.48
24	IPPDHVIGT	393	1.5000	16.48
25	VNVSTGPEQ	417	1.5000	16.48
26	LARDPSFYL	45	1.4000	15.38
27	IVMEYVDGV	89	1.4000	15.38
28	VYGFTKFSQ	513	1.4000	15.38
29	LRADLARDP	41	1.3000	14.29
30	VIADACQAL	117	1.3000	14.29
31	VRGQSSADA	364	1.3000	14.29
32	VVTIAINTF	344	1.2100	13.30
33	VLTVVVTIA	340	1.1000	12.09
34	FYLRFRREA	51	1.0000	10.99
35	FWVDAEPRL	569	1.0000	10.99
36	YSLGCVLYE	199	0.9000	9.89
37	YQTAAEMRA	262	0.9000	9.89
38	FGIARAIAD	156	0.7000	7.69
39	VLTDAERTS	286	0.7000	7.69
40	IGTNPPANQ	467	0.7000	7.69
41	LNFSHQNGI	125	0.6100	6.70
42	YVDGVTLRD	93	0.6000	6.59
43	IGTDPAANT	399	0.6000	6.59
44	FGRFKQANS	448	0.6000	6.59
45	VLTGEPPFT	208	0.5000	5.49
46	VQVPDVRGQ	359	0.5000	5.49
47	FKQANSPST	451	0.5000	5.49
48	LTVVVTIAI	341	0.4000	4.40
49	FKIRTLQKP	381	0.4000	4.40
50	VLAVLTVVV	337	0.3000	3.30
51	VAVVAVLAV	332	0.2000	2.20
52	VAVLAVLTV	335	0.2000	2.20

53	ITRDVQVPD	355	0.2000	2.20
54	VIIIVGSGP	483	0.1700	1.87
55	IGSVGRWVA	325	0.1000	1.10
56	VVAVLAVLT	334	0.1000	1.10
57	VVLKALAKN	249	-0.1000	0
58	ITNVVIIIV	479	-0.1000	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	MRADLVRVH	268	4.5800	52.05
2	IMISATNAV	143	4.0000	45.45
3	VREDPIPPS	228	4.0000	45.45
4	LARDLRLHR	26	3.7000	42.05
5	VKPANIMIS	138	3.6000	40.91
6	VNRDGIITL	613	3.5800	40.68
7	IRTLQKPDS	383	3.5000	39.77
8	IVGSGPATK	486	3.2000	36.36
9	LHRDVAVKV	32	3.1800	36.14
10	IHRDVKPAN	134	3.0000	34.09
11	VVIIIVGSG	482	3.0000	34.09
12	VVTIAINTF	344	2.9000	32.95
13	IVMEYVDGV	89	2.7000	30.68
14	VPVDSVIEL	544	2.5800	29.32
15	VIADACQAL	117	2.4000	27.27
16	LNFSHQNGI	125	2.3000	26.14
17	VRGQSSADA	364	2.3000	26.14
18	IPPDHVIGT	393	2.1800	24.77
19	VLTVVVTIA	340	2.1000	23.86
20	LRADLARDP	41	2.0000	22.73
21	VAVVAVLAV	332	1.7000	19.32
22	VAVLAVLTV	335	1.7000	19.32
23	IGTNPPANQ	467	1.7000	19.32
24	VVYQNPPAG	602	1.7000	19.32

25	VHNGEPPEA	275	1.6000	18.18
26	IGTDPAANT	399	1.6000	18.18
27	YLRFRREAQ	52	1.4000	15.91
28	VLTDAERTS	286	1.4000	15.91
29	FGGITRDVQ	352	1.4000	15.91
30	FTGDSPVSV	215	1.3800	15.68
31	VKVLRADLA	38	1.3000	14.77
32	LKALAKNPE	251	1.3000	14.77
33	LQVSKGNQF	552	1.3000	14.77
34	VMPDLSGMF	561	1.3000	14.77
35	FRREAQNAA	55	1.2000	13.64
36	IIHRDVKPA	133	1.2000	13.64
37	VQVPDVRGQ	359	1.2000	13.64
38	IIIVGSGPA	484	1.2000	13.64
39	WVAVVAVLA	331	1.1800	13.41
40	VLAVLTVVV	337	1.1800	13.41
41	VNVSTGPEQ	417	1.1000	12.50
42	VAGQTVDVA	499	1.1000	12.50
43	FVMPDLSGM	560	1.1000	12.50
44	LTVVVTIAI	341	1.0800	12.27
45	ITRDVQVPD	355	1.0800	12.27
46	YELGEILGF	10	1.0000	11.36
47	VVAVLAVLT	334	0.9800	11.14
48	LARDPSFYL	45	0.9000	10.23
49	VVLKALAKN	249	0.9000	10.23
50	VRVHNGEPP	273	0.9000	10.23
51	VIIIVGSGP	483	0.9000	10.23
52	VYGFTKFSQ	513	0.9000	10.23
53	LAVLTVVVT	338	0.5800	6.59
54	LTYAEAVKK	434	0.5800	6.59
55	ITNVVIIIV	479	0.5800	6.59
56	IPPSARHEG	233	0.5000	5.68
57	LSSAAGNLS	296	0.5000	5.68
58	VVVTIAINT	343	0.4800	5.45

59	MISATNAVK	144	0.4000	4.55
60	YSLGCVLYE	199	0.4000	4.55
61	VYQNPPAGT	603	0.4000	4.55
62	IGSVGRWVA	325	0.3000	3.41

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	MRADLVRVH	268	4.5800	52.05
2	IMISATNAV	143	4.0000	45.45
3	VREDPIPPS	228	4.0000	45.45
4	LARDLRLHR	26	3.7000	42.05
5	VKPANIMIS	138	3.6000	40.91
6	VNRDGIITL	613	3.5800	40.68
7	IRTLQKPDS	383	3.5000	39.77
8	IVGSGPATK	486	3.2000	36.36
9	LHRDVAVKV	32	3.1800	36.14
10	IHRDVKPAN	134	3.0000	34.09
11	VVIIIVGSG	482	3.0000	34.09
12	VVTIAINTF	344	2.9000	32.95
13	IVMEYVDGV	89	2.7000	30.68
14	VPVDSVIEL	544	2.5800	29.32
15	VIADACQAL	117	2.4000	27.27
16	LNFSHQNGI	125	2.3000	26.14
17	VRGQSSADA	364	2.3000	26.14
18	IPPDHVIGT	393	2.1800	24.77
19	VLTVVVTIA	340	2.1000	23.86
20	LRADLARDP	41	2.0000	22.73
21	VAVVAVLAV	332	1.7000	19.32
22	VAVLAVLTV	335	1.7000	19.32
23	IGTNPPANQ	467	1.7000	19.32
24	VVYQNPPAG	602	1.7000	19.32
25	VHNGEPPEA	275	1.6000	18.18
26	IGTDPAANT	399	1.6000	18.18

27	YLRFRREAQ	52	1.4000	15.91
28	VLTDAERTS	286	1.4000	15.91
29	FGGITRDVQ	352	1.4000	15.91
30	FTGDSPVSV	215	1.3800	15.68
31	VKVLRADLA	38	1.3000	14.77
32	LKALAKNPE	251	1.3000	14.77
33	LQVSKGNQF	552	1.3000	14.77
34	VMPDLSGMF	561	1.3000	14.77
35	FRREAQNAA	55	1.2000	13.64
36	IIHRDVKPA	133	1.2000	13.64
37	VQVPDVRGQ	359	1.2000	13.64
38	IIIVGSGPA	484	1.2000	13.64
39	WVAVVAVLA	331	1.1800	13.41
40	VLAVLTVVV	337	1.1800	13.41
41	VNVSTGPEQ	417	1.1000	12.50
42	VAGQTVDVA	499	1.1000	12.50
43	FVMPDLSGM	560	1.1000	12.50
44	LTVVVTIAI	341	1.0800	12.27
45	ITRDVQVPD	355	1.0800	12.27
46	YELGEILGF	10	1.0000	11.36
47	VVAVLAVLT	334	0.9800	11.14
48	LARDPSFYL	45	0.9000	10.23
49	VVLKALAKN	249	0.9000	10.23
50	VRVHNGEPP	273	0.9000	10.23
51	VIIIVGSGP	483	0.9000	10.23
52	VYGFTKFSQ	513	0.9000	10.23
53	LAVLTVVVT	338	0.5800	6.59
54	LTYAEAVKK	434	0.5800	6.59
55	ITNVVIIIV	479	0.5800	6.59
56	IPPSARHEG	233	0.5000	5.68
57	LSSAAGNLS	296	0.5000	5.68
58	VVVTIAINT	343	0.4800	5.45
59	MISATNAVK	144	0.4000	4.55
60	YSLGCVLYE	199	0.4000	4.55

61	VYQNPPAGT	603	0.4000	4.55
62	IGSVGRWVA	325	0.3000	3.41

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	MRADLVRVH	268	4.5800	52.05
2	IMISATNAV	143	4.0000	45.45
3	VREDPIPPS	228	4.0000	45.45
4	LARDLRLHR	26	3.7000	42.05
5	VKPANIMIS	138	3.6000	40.91
6	VNRDGIITL	613	3.5800	40.68
7	IRTLQKPDS	383	3.5000	39.77
8	IVGSGPATK	486	3.2000	36.36
9	LHRDVAVKV	32	3.1800	36.14
10	IHRDVKPAN	134	3.0000	34.09
11	VVIIIVGSG	482	3.0000	34.09
12	VVTIAINTF	344	2.9000	32.95
13	IVMEYVDGV	89	2.7000	30.68
14	VPVDSVIEL	544	2.5800	29.32
15	VIADACQAL	117	2.4000	27.27
16	LNFSHQNGI	125	2.3000	26.14
17	VRGQSSADA	364	2.3000	26.14
18	IPPDHVIGT	393	2.1800	24.77
19	VLTVVVTIA	340	2.1000	23.86
20	LRADLARDP	41	2.0000	22.73
21	VAVVAVLAV	332	1.7000	19.32
22	VAVLAVLTV	335	1.7000	19.32
23	IGTNPPANQ	467	1.7000	19.32
24	VVYQNPPAG	602	1.7000	19.32
25	VHNGEPPEA	275	1.6000	18.18
26	IGTDPAANT	399	1.6000	18.18
27	YLRFRREAQ	52	1.4000	15.91
28	VLTDAERTS	286	1.4000	15.91

29	FGGITRDVQ	352	1.4000	15.91
30	FTGDSPVSV	215	1.3800	15.68
31	VKVLRADLA	38	1.3000	14.77
32	LKALAKNPE	251	1.3000	14.77
33	LQVSKGNQF	552	1.3000	14.77
34	VMPDLSGMF	561	1.3000	14.77
35	FRREAQNAA	55	1.2000	13.64
36	IIHRDVKPA	133	1.2000	13.64
37	VQVPDVRGQ	359	1.2000	13.64
38	IIIVGSGPA	484	1.2000	13.64
39	WVAVVAVLA	331	1.1800	13.41
40	VLAVLTVVV	337	1.1800	13.41
41	VNVSTGPEQ	417	1.1000	12.50
42	VAGQTVDVA	499	1.1000	12.50
43	FVMPDLSGM	560	1.1000	12.50
44	LTVVVTIAI	341	1.0800	12.27
45	ITRDVQVPD	355	1.0800	12.27
46	YELGEILGF	10	1.0000	11.36
47	VVAVLAVLT	334	0.9800	11.14
48	LARDPSFYL	45	0.9000	10.23
49	VVLKALAKN	249	0.9000	10.23
50	VRVHNGEPP	273	0.9000	10.23
51	VIIIVGSGP	483	0.9000	10.23
52	VYGFTKFSQ	513	0.9000	10.23
53	LAVLTVVVT	338	0.5800	6.59
54	LTYAEAVKK	434	0.5800	6.59
55	ITNVVIIIV	479	0.5800	6.59
56	IPPSARHEG	233	0.5000	5.68
57	LSSAAGNLS	296	0.5000	5.68
58	VVVTIAINT	343	0.4800	5.45
59	MISATNAVK	144	0.4000	4.55
60	YSLGCVLYE	199	0.4000	4.55
61	VYQNPPAGT	603	0.4000	4.55
62	IGSVGRWVA	325	0.3000	3.41

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	VREDPIPPS	228	4.8000	50.53
2	VVIIIVGSG	482	4.8000	50.53
3	IRTLQKPDS	383	4.3000	45.26
4	IHRDVKPAN	134	4.2000	44.21
5	FVMPDLSGM	560	3.8700	40.74
6	VNRDGIITL	613	3.8600	40.63
7	LARDLRLHR	26	3.7000	38.95
8	VMPDLSGMF	561	3.6000	37.89
9	FTGDSPVSV	215	3.5000	36.84
10	VVYQNPPAG	602	3.5000	36.84
11	YELGEILGF	10	3.4000	35.79
12	IMISATNAV	143	3.3100	34.84
13	LHRDVAVKV	32	3.3000	34.74
14	VKPANIMIS	138	3.3000	34.74
15	MRADLVRVH	268	3.3000	34.74
16	VVTIAINTF	344	3.1100	32.74
17	VPVDSVIEL	544	2.8600	30.11
18	IVMEYVDGV	89	2.4000	25.26
19	LARDPSFYL	45	2.3600	24.84
20	LRADLARDP	41	2.3000	24.21
21	YSLGCVLYE	199	2.3000	24.21
22	WVAVVAVLA	331	2.3000	24.21
23	IVGSGPATK	486	2.3000	24.21
24	VIADACQAL	117	2.2600	23.79
25	IPPDHVIGT	393	2.2000	23.16
26	VHNGEPPEA	275	2.0000	21.05
27	FWVDAEPRL	569	1.9600	20.63
28	FGIARAIAD	156	1.8000	18.95
29	YVDGVTLRD	93	1.7000	17.89
30	IIIVGSGPA	484	1.6000	16.84

31	FRREAQNAA	55	1.5100	15.89
32	LNFSHQNGI	125	1.5100	15.89
33	LQVSKGNQF	552	1.5100	15.89
34	FGGITRDVQ	352	1.4000	14.74
35	FKIRTLQKP	381	1.4000	14.74
36	YLRFRREAQ	52	1.3000	13.68
37	VLAVLTVVV	337	1.3000	13.68
38	LTVVVTIAI	341	1.3000	13.68
39	ITRDVQVPD	355	1.3000	13.68
40	VRGQSSADA	364	1.3000	13.68
41	IGTDPAANT	399	1.3000	13.68
42	VLTGEPPFT	208	1.2000	12.63
43	VAVVAVLAV	332	1.2000	12.63
44	VAVLAVLTV	335	1.2000	12.63
45	FKQANSPST	451	1.2000	12.63
46	YQNPPAGTG	604	1.2000	12.63
47	VIIIVGSGP	483	1.1700	12.32
48	VLTDAERTS	286	1.1000	11.58
49	VLTVVVTIA	340	1.1000	11.58
50	LKALAKNPE	251	1.0100	10.63
51	FYLRFRREA	51	1.0000	10.53
52	LVRVHNGEP	272	1.0000	10.53
53	VKKLTAAGF	440	1.0000	10.53
54	FGRFKQANS	448	1.0000	10.53
55	LLSSAAGNL	295	0.9600	10.11
56	YQTAAEMRA	262	0.9000	9.47
57	ITNVVIIIV	479	0.9000	9.47
58	WVDAEPRLR	570	0.9000	9.47
59	YIVMEYVDG	88	0.8000	8.42
60	VVAVLAVLT	334	0.8000	8.42
61	VNVSTGPEQ	417	0.8000	8.42
62	LRALGWTGM	577	0.8000	8.42

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	MRADLVRVH	268	4.5800	52.05
2	IMISATNAV	143	4.0000	45.45
3	VREDPIPPS	228	4.0000	45.45
4	LARDLRLHR	26	3.7000	42.05
5	VKPANIMIS	138	3.6000	40.91
6	VNRDGIITL	613	3.5800	40.68
7	IRTLQKPDS	383	3.5000	39.77
8	IVGSGPATK	486	3.2000	36.36
9	LHRDVAVKV	32	3.1800	36.14
10	IHRDVKPAN	134	3.0000	34.09
11	VVIIIVGSG	482	3.0000	34.09
12	VVTIAINTF	344	2.9000	32.95
13	IVMEYVDGV	89	2.7000	30.68
14	VPVDSVIEL	544	2.5800	29.32
15	VIADACQAL	117	2.4000	27.27
16	LNFSHQNGI	125	2.3000	26.14
17	VRGQSSADA	364	2.3000	26.14
18	IPPDHVIGT	393	2.1800	24.77
19	VLTVVVTIA	340	2.1000	23.86
20	LRADLARDP	41	2.0000	22.73
21	VAVVAVLAV	332	1.7000	19.32
22	VAVLAVLTV	335	1.7000	19.32
23	IGTNPPANQ	467	1.7000	19.32
24	VVYQNPPAG	602	1.7000	19.32
25	VHNGEPPEA	275	1.6000	18.18
26	IGTDPAANT	399	1.6000	18.18
27	YLRFRREAQ	52	1.4000	15.91
28	VLTDAERTS	286	1.4000	15.91
29	FGGITRDVQ	352	1.4000	15.91
30	FTGDSPVSV	215	1.3800	15.68
31	VKVLRADLA	38	1.3000	14.77
32	LKALAKNPE	251	1.3000	14.77

33	LQVSKGNQF	552	1.3000	14.77
34	VMPDLSGMF	561	1.3000	14.77
35	FRREAQNAA	55	1.2000	13.64
36	IIHRDVKPA	133	1.2000	13.64
37	VQVPDVRGQ	359	1.2000	13.64
38	IIIVGSGPA	484	1.2000	13.64
39	WVAVVAVLA	331	1.1800	13.41
40	VLAVLTVVV	337	1.1800	13.41
41	VNVSTGPEQ	417	1.1000	12.50
42	VAGQTVDVA	499	1.1000	12.50
43	FVMPDLSGM	560	1.1000	12.50
44	LTVVVTIAI	341	1.0800	12.27
45	ITRDVQVPD	355	1.0800	12.27
46	YELGEILGF	10	1.0000	11.36
47	VVAVLAVLT	334	0.9800	11.14
48	LARDPSFYL	45	0.9000	10.23
49	VVLKALAKN	249	0.9000	10.23
50	VRVHNGEPP	273	0.9000	10.23
51	VIIIVGSGP	483	0.9000	10.23
52	VYGFTKFSQ	513	0.9000	10.23
53	LAVLTVVVT	338	0.5800	6.59
54	LTYAEAVKK	434	0.5800	6.59
55	ITNVVIIIV	479	0.5800	6.59
56	IPPSARHEG	233	0.5000	5.68
57	LSSAAGNLS	296	0.5000	5.68
58	VVVTIAINT	343	0.4800	5.45
59	MISATNAVK	144	0.4000	4.55
60	YSLGCVLYE	199	0.4000	4.55
61	VYQNPPAGT	603	0.4000	4.55
62	IGSVGRWVA	325	0.3000	3.41

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	IMISATNAV	143	4.2000	48.84
2	IVMEYVDGV	89	3.9000	45.35
3	FRREAQNAA	55	3.5000	40.70
4	VRGQSSADA	364	3.2000	37.21
5	MRADLVRVH	268	2.3800	27.67
6	VVIIIVGSG	482	2.0000	23.26
7	VKPANIMIS	138	1.8000	20.93
8	IVGSGPATK	486	1.8000	20.93
9	LRLHRDVAV	30	1.5800	18.37
10	VVTIAINTF	344	1.4000	16.28
11	MISATNAVK	144	1.3000	15.12
12	VREDPIPPS	228	1.3000	15.12
13	LHRDVAVKV	32	1.2800	14.88
14	WVAVVAVLA	331	1.2800	14.88
15	VAVLAVLTV	335	1.2000	13.95
16	VVVTIAINT	343	1.1800	13.72
17	VKVLRADLA	38	1.1000	12.79
18	VVYQNPPAG	602	1.0000	11.63
19	FTGDSPVSV	215	0.9800	11.40
20	IGTNPPANQ	467	0.9000	10.47
21	VNRDGIITL	613	0.8800	10.23
22	VHTEGPMTP	103	0.8000	9.30
23	VTIAINTFG	345	0.7000	8.14
24	YGFTKFSQA	514	0.7000	8.14
25	VAGQTVDVA	499	0.6000	6.98
26	VIADACQAL	117	0.5000	5.81
27	VMPDLSGMF	561	0.5000	5.81
28	LRALGWTGM	577	0.5000	5.81
29	IIIVGSGPA	484	0.4000	4.65
30	FGIARAIAD	156	0.3800	4.42
31	VLAVLTVVV	337	0.3800	4.42
32	VPVDSVIEL	544	0.3800	4.42
33	LTVVVTIAI	341	0.2800	3.26
34	LNFSHQNGI	125	0.2000	2.33

35	VRVHNGEPP	273	0.2000	2.33
36	FKQANSPST	451	0.2000	2.33
37	IELQVSKGN	550	0.2000	2.33
38	FVMPDLSGM	560	0.2000	2.33
39	LRADLARDP	41	0.1000	1.16
40	LARDPSFYL	45	0.1000	1.16
41	YVDGVTLRD	93	0.1000	1.16
42	YIVMEYVDG	88	0.0800	0.93
43	LAVLTVVVT	338	0.0800	0.93
44	VYSLGCVLY	198	-0.0200	0
45	IPPDHVIGT	393	-0.0200	0
46	VLTVVVTIA	340	-0.1000	0
47	VKKLTAAGF	440	-0.1000	0
48	IEVIADACQ	115	-0.2000	0
49	IGTDPAANT	399	-0.3000	0
50	WTGMLDKGA	582	-0.3000	0
51	YQTAAEMRA	262	-0.4000	0
52	LVRVHNGEP	272	-0.4000	0
53	IRTLQKPDS	383	-0.4000	0
54	VIGTDPAAN	398	-0.4000	0
55	LQVSKGNQF	552	-0.4000	0
56	VYQNPPAGT	603	-0.4000	0
57	LTYAEAVKK	434	-0.4200	0
58	VAVVAVLAV	332	-0.5000	0
59	FGRFKQANS	448	-0.5000	0
60	LGWTGMLDK	580	-0.5000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VQVPDVRGQ	359	3.5000	36.46
2	IMISATNAV	143	3.4000	35.42
3	IIHRDVKPA	133	3.2000	33.33
4	VGRWVAVVA	328	3.0000	31.25

5	VRGQSSADA	364	3.0000	31.25
6	LRLHRDVAV	30	2.8000	29.17
7	VKPANIMIS	138	2.8000	29.17
8	MRADLVRVH	268	2.5800	26.88
9	MISATNAVK	144	2.3000	23.96
10	LTVVVTIAI	341	1.9000	19.79
11	VTIAINTFG	345	1.9000	19.79
12	VLAVLTVVV	337	1.7000	17.71
13	VVTIAINTF	344	1.6800	17.50
14	VVIIIVGSG	482	1.4800	15.42
15	VVVTIAINT	343	1.4000	14.58
16	IATLQNRGF	373	1.4000	14.58
17	VAYQHVRED	223	1.3000	13.54
18	VLTVVVTIA	340	1.3000	13.54
19	FKIRTLQKP	381	1.3000	13.54
20	FYLRFRREA	51	1.2000	12.50
21	VAVLAVLTV	335	1.1000	11.46
22	VAVVAVLAV	332	1.0000	10.42
23	IVGSGPATK	486	1.0000	10.42
24	VTLRDIVHT	97	0.9000	9.38
25	VIGTAQYLS	175	0.9000	9.38
26	IIIVGSGPA	484	0.8000	8.33
27	VHLARDLRL	24	0.7000	7.29
28	VVLKALAKN	249	0.7000	7.29
29	LTYAEAVKK	434	0.7000	7.29
30	WVAVVAVLA	331	0.6000	6.25
31	LQNRGFKIR	376	0.6000	6.25
32	IGTNPPANQ	467	0.6000	6.25
33	WVDAEPRLR	570	0.5000	5.21
34	VVYQNPPAG	602	0.5000	5.21
35	VVAVLAVLT	334	0.4000	4.17
36	LRADLARDP	41	0.3000	3.12
37	YVDGVTLRD	93	0.3000	3.12
38	IELQVSKGN	550	0.3000	3.12

39	LRALGWTGM	577	0.3000	3.12
40	LRFRREAQN	53	0.2000	2.08
41	MTPKRAIEV	109	0.2000	2.08
42	MDFGIARAI	154	0.2000	2.08
43	IEVIADACQ	115	0.0800	0.83
44	VAVYDTGEA	71	-0.1000	0
45	VRVHNGEPP	273	-0.1000	0
46	ITVNVSTGP	415	-0.1000	0
47	FGIARAIAD	156	-0.2000	0
48	LAVLTVVVT	338	-0.2000	0
49	VYSLGCVLY	198	-0.3000	0
50	VLKALAKNP	250	-0.3000	0
51	LSSAAGNLS	296	-0.3000	0
52	LQKPDSTIP	386	-0.3000	0
53	FGRFKQANS	448	-0.3000	0
54	LSGMFWVDA	565	-0.3000	0
55	VHNGEPPEA	275	-0.4000	0
56	LGWTGMLDK	580	-0.4000	0
57	VAVKVLRAD	36	-0.5000	0
58	VDARSDVYS	192	-0.5000	0

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IMISATNAV	143	3.8000	43.18
2	VRGQSSADA	364	3.4000	38.64
3	VVIIIVGSG	482	3.4000	38.64
4	IIIVGSGPA	484	2.9000	32.95
5	VLTVVVTIA	340	2.8000	31.82
6	VVTIAINTF	344	2.8000	31.82
7	VKPANIMIS	138	2.7000	30.68
8	LTVVVTIAI	341	2.6800	30.45
9	VLAVLTVVV	337	2.6000	29.55
10	MISATNAVK	144	2.3000	26.14

11	VTIAINTFG	345	2.2000	25.00
12	LRALGWTGM	577	2.2000	25.00
13	LVRVHNGEP	272	2.1000	23.86
14	VAVLAVLTV	335	2.0000	22.73
15	WVAVVAVLA	331	1.5000	17.05
16	VAVVAVLAV	332	1.5000	17.05
17	VKVLRADLA	38	1.4000	15.91
18	IVMEYVDGV	89	1.4000	15.91
19	VIIIVGSGP	483	1.4000	15.91
20	VVAVLAVLT	334	1.3000	14.77
21	IVGSGPATK	486	1.3000	14.77
22	VIELQVSKG	549	1.3000	14.77
23	MRADLVRVH	268	1.1800	13.41
24	IEVIADACQ	115	1.1000	12.50
25	VKVMDFGIA	151	1.1000	12.50
26	LAVLTVVVT	338	1.1000	12.50
27	VKKLTAAGF	440	1.1000	12.50
28	VGRWVAVVA	328	1.0500	11.93
29	VYSLGCVLY	198	1.0000	11.36
30	VQVPDVRGQ	359	0.9000	10.23
31	VVYQNPPAG	602	0.9000	10.23
32	VAVYDTGEA	71	0.8000	9.09
33	VMDFGIARA	153	0.7000	7.95
34	LSGMFWVDA	565	0.6000	6.82
35	VVVTIAINT	343	0.5800	6.59
36	IRTLQKPDS	383	0.5000	5.68
37	IATLQNRGF	373	0.4000	4.55
38	LTYAEAVKK	434	0.4000	4.55
39	FGRFKQANS	448	0.4000	4.55
40	LRLHRDVAV	30	0.3000	3.41
41	IGTNPPANQ	467	0.3000	3.41
42	ITNVVIIIV	479	0.2800	3.18
43	IVAVYDTGE	70	0.2000	2.27
44	FVMPDLSGM	560	0.2000	2.27

45	VYGFTKFSQ	513	0.1500	1.70
46	ITVNVSTGP	415	-0.1000	0
47	IPDVSTLTY	428	-0.1000	0
48	VAGQTVDVA	499	-0.1000	0
49	YIVMEYVDG	88	-0.2000	0
50	LNFSHQNGI	125	-0.2000	0
51	LSSAAGNLS	296	-0.2000	0
52	ILGFGGMSE	15	-0.3000	0
53	LHRDVAVKV	32	-0.4000	0
54	LYEVLTGEP	205	-0.4000	0
55	MFWVDAEPR	568	-0.4000	0
56	LARDPSFYL	45	-0.4500	0
57	VREDPIPPS	228	-0.5000	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	VVIIIVGSG	482	3.7000	39.36
2	IMISATNAV	143	3.1000	32.98
3	FGIARAIAD	156	3.0800	32.77
4	VVTIAINTF	344	2.7000	28.72
5	WVAVVAVLA	331	2.5000	26.60
6	VTIAINTFG	345	2.5000	26.60
7	VRGQSSADA	364	2.4000	25.53
8	FVMPDLSGM	560	2.3000	24.47
9	LRALGWTGM	577	2.3000	24.47
10	IVAVYDTGE	70	2.2000	23.40
11	YIVMEYVDG	88	2.1000	22.34
12	VLAVLTVVV	337	1.9000	20.21
13	IIIVGSGPA	484	1.9000	20.21
14	LTVVVTIAI	341	1.8800	20.00
15	VLTVVVTIA	340	1.8000	19.15
16	ILGFGGMSE	15	1.7000	18.09
17	VKPANIMIS	138	1.7000	18.09

18	YVDGVTLRD	93	1.6000	17.02
19	VIELQVSKG	549	1.6000	17.02
20	LVRVHNGEP	272	1.5000	15.96
21	MRADLVRVH	268	1.4000	14.89
22	FGRFKQANS	448	1.4000	14.89
23	VAVLAVLTV	335	1.3000	13.83
24	VVAVLAVLT	334	1.2000	12.77
25	VVYQNPPAG	602	1.2000	12.77
26	VYSLGCVLY	198	1.1000	11.70
27	FRREAQNAA	55	1.0000	10.64
28	LAVLTVVVT	338	1.0000	10.64
29	VKKLTAAGF	440	1.0000	10.64
30	YLRFRREAQ	52	0.9000	9.57
31	IEVIADACQ	115	0.9000	9.57
32	YSLGCVLYE	199	0.8000	8.51
33	VAYQHVRED	223	0.8000	8.51
34	VAVVAVLAV	332	0.8000	8.51
35	FKQANSPST	451	0.8000	8.51
36	VIIIVGSGP	483	0.8000	8.51
37	IVMEYVDGV	89	0.7000	7.45
38	LKALAKNPE	251	0.7000	7.45
39	VQVPDVRGQ	359	0.7000	7.45
40	VLRADLARD	40	0.6000	6.38
41	MISATNAVK	144	0.6000	6.38
42	VVVTIAINT	343	0.4800	5.11
43	VKVLRADLA	38	0.4000	4.26
44	IELQVSKGN	550	0.4000	4.26
45	LRDIVHTEG	99	0.3000	3.19
46	VLYEVLTGE	204	0.3000	3.19
47	IATLQNRGF	373	0.3000	3.19
48	VKVMDFGIA	151	0.1000	1.06
49	VVLKALAKN	249	0.1000	1.06
50	IGTNPPANQ	467	0.1000	1.06
51	VGRWVAVVA	328	0.0500	0.53

52	VYGFTKFSQ	513	-0.0500	0
53	VAVYDTGEA	71	-0.2000	0
54	YGFTKFSQA	514	-0.2000	0
55	FSHQNGIIH	127	-0.2200	0
56	VMDFGIARA	153	-0.3000	0
57	LRLHRDVAV	30	-0.4000	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	IMISATNAV	143	2.8000	31.82
2	WVAVVAVLA	331	2.5000	28.41
3	VRGQSSADA	364	2.4000	27.27
4	VVIIIVGSG	482	2.4000	27.27
5	IIIVGSGPA	484	1.9000	21.59
6	VLTVVVTIA	340	1.8000	20.45
7	VVTIAINTF	344	1.8000	20.45
8	VKPANIMIS	138	1.7000	19.32
9	LTVVVTIAI	341	1.6800	19.09
10	VLAVLTVVV	337	1.6000	18.18
11	FGRFKQANS	448	1.4000	15.91
12	MISATNAVK	144	1.3000	14.77
13	VTIAINTFG	345	1.2000	13.64
14	FVMPDLSGM	560	1.2000	13.64
15	LRALGWTGM	577	1.2000	13.64
16	LVRVHNGEP	272	1.1000	12.50
17	FRREAQNAA	55	1.0000	11.36
18	VAVLAVLTV	335	1.0000	11.36
19	YIVMEYVDG	88	0.8000	9.09
20	VAVVAVLAV	332	0.5000	5.68
21	VKVLRADLA	38	0.4000	4.55
22	IVMEYVDGV	89	0.4000	4.55
23	VIIIVGSGP	483	0.4000	4.55
24	FGIARAIAD	156	0.3800	4.32

25	VVAVLAVLT	334	0.3000	3.41
26	IVGSGPATK	486	0.3000	3.41
27	VIELQVSKG	549	0.3000	3.41
28	MRADLVRVH	268	0.1800	2.05
29	YLRFRREAQ	52	0.1000	1.14
30	IEVIADACQ	115	0.1000	1.14
31	VKVMDFGIA	151	0.1000	1.14
32	LAVLTVVVT	338	0.1000	1.14
33	VKKLTAAGF	440	0.1000	1.14
34	VGRWVAVVA	328	0.0500	0.57
35	VQVPDVRGQ	359	-0.1000	0
36	FKQANSPST	451	-0.1000	0
37	VVYQNPPAG	602	-0.1000	0
38	VAVYDTGEA	71	-0.2000	0
39	YGFTKFSQA	514	-0.2000	0
40	VMDFGIARA	153	-0.3000	0
41	LSGMFWVDA	565	-0.4000	0
42	WTGMLDKGA	582	-0.4000	0
43	VVVTIAINT	343	-0.4200	0
44	YQTAAEMRA	262	-0.5000	0
45	IRTLQKPDS	383	-0.5000	0
46	IATLQNRGF	373	-0.6000	0
47	LTYAEAVKK	434	-0.6000	0
48	LRLHRDVAV	30	-0.7000	0
49	IGTNPPANQ	467	-0.7000	0
50	ITNVVIIIV	479	-0.7200	0
51	IVAVYDTGE	70	-0.8000	0
52	VYGFTKFSQ	513	-0.8500	0
53	FGGMSEVHL	18	-1.0000	0
54	VHLARDLRL	24	-1.0000	0
55	LRDIVHTEG	99	-1.0000	0
56	LQKPDSTIP	386	-1.0000	0
57	YVDGVTLRD	93	-1.1000	0
58	ITVNVSTGP	415	-1.1000	0

59	IPDVSTLTY	428	-1.1000	0
60	VAGQTVDVA	499	-1.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVIIIVGSG	482	4.7000	50.00
2	IMISATNAV	143	4.1000	43.62
3	VVTIAINTF	344	3.7000	39.36
4	VTIAINTFG	345	3.5000	37.23
5	VRGQSSADA	364	3.4000	36.17
6	LRALGWTGM	577	3.3000	35.11
7	IVAVYDTGE	70	3.2000	34.04
8	VLAVLTVVV	337	2.9000	30.85
9	IIIVGSGPA	484	2.9000	30.85
10	LTVVVTIAI	341	2.8800	30.64
11	VLTVVVTIA	340	2.8000	29.79
12	ILGFGGMSE	15	2.7000	28.72
13	VKPANIMIS	138	2.7000	28.72
14	VIELQVSKG	549	2.6000	27.66
15	LVRVHNGEP	272	2.5000	26.60
16	MRADLVRVH	268	2.4000	25.53
17	VAVLAVLTV	335	2.3000	24.47
18	VVAVLAVLT	334	2.2000	23.40
19	VVYQNPPAG	602	2.2000	23.40
20	VYSLGCVLY	198	2.1000	22.34
21	FGIARAIAD	156	2.0800	22.13
22	LAVLTVVVT	338	2.0000	21.28
23	VKKLTAAGF	440	2.0000	21.28
24	IEVIADACQ	115	1.9000	20.21
25	VAYQHVRED	223	1.8000	19.15
26	VAVVAVLAV	332	1.8000	19.15
27	VIIIVGSGP	483	1.8000	19.15
28	IVMEYVDGV	89	1.7000	18.09

29	LKALAKNPE	251	1.7000	18.09
30	VQVPDVRGQ	359	1.7000	18.09
31	VLRADLARD	40	1.6000	17.02
32	MISATNAVK	144	1.6000	17.02
33	WVAVVAVLA	331	1.5000	15.96
34	VVVTIAINT	343	1.4800	15.74
35	VKVLRADLA	38	1.4000	14.89
36	IELQVSKGN	550	1.4000	14.89
37	LRDIVHTEG	99	1.3000	13.83
38	VLYEVLTGE	204	1.3000	13.83
39	IATLQNRGF	373	1.3000	13.83
40	FVMPDLSGM	560	1.3000	13.83
41	YIVMEYVDG	88	1.1000	11.70
42	VKVMDFGIA	151	1.1000	11.70
43	VVLKALAKN	249	1.1000	11.70
44	IGTNPPANQ	467	1.1000	11.70
45	VGRWVAVVA	328	1.0500	11.17
46	VHLARDLRL	24	1.0000	10.64
47	VIGTDPAAN	398	1.0000	10.64
48	IPDVSTLTY	428	1.0000	10.64
49	VYGFTKFSQ	513	0.9500	10.11
50	VAVYDTGEA	71	0.8000	8.51
51	VMDFGIARA	153	0.7000	7.45
52	LRLHRDVAV	30	0.6000	6.38
53	YVDGVTLRD	93	0.6000	6.38
54	IVGSGPATK	486	0.6000	6.38
55	LSGMFWVDA	565	0.6000	6.38
56	ITNVVIIIV	479	0.5800	6.17
57	LARDPSFYL	45	0.5500	5.85
58	IRTLQKPDS	383	0.5000	5.32
59	LQKPDSTIP	386	0.4000	4.26
60	FGRFKQANS	448	0.4000	4.26
61	VNRDGIITL	613	0.3800	4.04
62	ITVNVSTGP	415	0.3000	3.19

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	IMISATNAV	143	5.2000	57.78
2	IVMEYVDGV	89	4.9000	54.44
3	FRREAQNAA	55	3.5000	38.89
4	VVIIIVGSG	482	3.4000	37.78
5	VVTIAINTF	344	3.3000	36.67
6	VRGQSSADA	364	3.2000	35.56
7	LRLHRDVAV	30	2.5800	28.67
8	VMPDLSGMF	561	2.4000	26.67
9	VVYQNPPAG	602	2.4000	26.67
10	LHRDVAVKV	32	2.2800	25.33
11	VKPANIMIS	138	2.2000	24.44
12	VAVLAVLTV	335	2.2000	24.44
13	VTIAINTFG	345	2.1000	23.33
14	LRALGWTGM	577	2.0000	22.22
15	FTGDSPVSV	215	1.9800	22.00
16	IVGSGPATK	486	1.9000	21.11
17	VVVTIAINT	343	1.8800	20.89
18	VNRDGIITL	613	1.8400	20.44
19	VHTEGPMTP	103	1.8000	20.00
20	MRADLVRVH	268	1.8000	20.00
21	VKKLTAAGF	440	1.8000	20.00
22	VREDPIPPS	228	1.7000	18.89
23	FVMPDLSGM	560	1.7000	18.89
24	LQVSKGNQF	552	1.5000	16.67
25	YIVMEYVDG	88	1.4800	16.44
26	FGIARAIAD	156	1.4800	16.44
27	VIADACQAL	117	1.4600	16.22
28	MISATNAVK	144	1.4000	15.56
29	VLAVLTVVV	337	1.3800	15.33
30	VPVDSVIEL	544	1.3400	14.89

31	VYSLGCVLY	198	1.2800	14.22
32	WVAVVAVLA	331	1.2800	14.22
33	YVDGVTLRD	93	1.2000	13.33
34	VRVHNGEPP	273	1.2000	13.33
35	LTVVVTIAI	341	1.1800	13.11
36	VKVLRADLA	38	1.1000	12.22
37	LRADLARDP	41	1.1000	12.22
38	LNFSHQNGI	125	1.1000	12.22
39	LARDPSFYL	45	1.0600	11.78
40	YELGEILGF	10	1.0000	11.11
41	ITVNVSTGP	415	1.0000	11.11
42	IELQVSKGN	550	1.0000	11.11
43	FKQANSPST	451	0.9000	10.00
44	VLYEVLTGE	204	0.8000	8.89
45	IATLQNRGF	373	0.8000	8.89
46	VIELQVSKG	549	0.8000	8.89
47	LAVLTVVVT	338	0.7800	8.67
48	YGFTKFSQA	514	0.7000	7.78
49	IPPDHVIGT	393	0.6800	7.56
50	LVRVHNGEP	272	0.6000	6.67
51	VAGQTVDVA	499	0.6000	6.67
52	VAVVAVLAV	332	0.5000	5.56
53	YSLGCVLYE	199	0.4000	4.44
54	VIGTDPAAN	398	0.4000	4.44
55	IGTDPAANT	399	0.4000	4.44
56	VIIIVGSGP	483	0.4000	4.44
57	IIIVGSGPA	484	0.4000	4.44
58	VHLARDLRL	24	0.3600	4.00
59	VYQNPPAGT	603	0.3000	3.33
60	IGTNPPANQ	467	0.2000	2.22
61	VTQTAAVIG	169	0.1800	2.00
62	LTGEPPFTG	209	0.1000	1.11

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	IMISATNAV	143	3.8000	43.18
2	VRGQSSADA	364	3.4000	38.64
3	VVIIIVGSG	482	3.4000	38.64
4	IIIVGSGPA	484	2.9000	32.95
5	VLTVVVTIA	340	2.8000	31.82
6	VVTIAINTF	344	2.8000	31.82
7	VKPANIMIS	138	2.7000	30.68
8	LTVVVTIAI	341	2.6800	30.45
9	VLAVLTVVV	337	2.6000	29.55
10	MISATNAVK	144	2.3000	26.14
11	VTIAINTFG	345	2.2000	25.00
12	LRALGWTGM	577	2.2000	25.00
13	LVRVHNGEP	272	2.1000	23.86
14	VAVLAVLTV	335	2.0000	22.73
15	WVAVVAVLA	331	1.5000	17.05
16	VAVVAVLAV	332	1.5000	17.05
17	VKVLRADLA	38	1.4000	15.91
18	IVMEYVDGV	89	1.4000	15.91
19	VIIIVGSGP	483	1.4000	15.91
20	VVAVLAVLT	334	1.3000	14.77
21	IVGSGPATK	486	1.3000	14.77
22	VIELQVSKG	549	1.3000	14.77
23	MRADLVRVH	268	1.1800	13.41
24	IEVIADACQ	115	1.1000	12.50
25	VKVMDFGIA	151	1.1000	12.50
26	LAVLTVVVT	338	1.1000	12.50
27	VKKLTAAGF	440	1.1000	12.50
28	VGRWVAVVA	328	1.0500	11.93
29	VYSLGCVLY	198	1.0000	11.36
30	VQVPDVRGQ	359	0.9000	10.23
31	VVYQNPPAG	602	0.9000	10.23
32	VAVYDTGEA	71	0.8000	9.09

33	VMDFGIARA	153	0.7000	7.95
34	LSGMFWVDA	565	0.6000	6.82
35	VVVTIAINT	343	0.5800	6.59
36	IRTLQKPDS	383	0.5000	5.68
37	IATLQNRGF	373	0.4000	4.55
38	LTYAEAVKK	434	0.4000	4.55
39	FGRFKQANS	448	0.4000	4.55
40	LRLHRDVAV	30	0.3000	3.41
41	IGTNPPANQ	467	0.3000	3.41
42	ITNVVIIIV	479	0.2800	3.18
43	IVAVYDTGE	70	0.2000	2.27
44	FVMPDLSGM	560	0.2000	2.27
45	VYGFTKFSQ	513	0.1500	1.70
46	ITVNVSTGP	415	-0.1000	0
47	IPDVSTLTY	428	-0.1000	0
48	VAGQTVDVA	499	-0.1000	0
49	YIVMEYVDG	88	-0.2000	0
50	LNFSHQNGI	125	-0.2000	0
51	LSSAAGNLS	296	-0.2000	0
52	ILGFGGMSE	15	-0.3000	0
53	LHRDVAVKV	32	-0.4000	0
54	LYEVLTGEP	205	-0.4000	0
55	MFWVDAEPR	568	-0.4000	0
56	LARDPSFYL	45	-0.4500	0
57	VREDPIPPS	228	-0.5000	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	IMISATNAV	143	4.2000	48.84
2	IVMEYVDGV	89	3.9000	45.35
3	FRREAQNAA	55	3.5000	40.70
4	VRGQSSADA	364	3.2000	37.21
5	MRADLVRVH	268	2.3800	27.67

6	VVIIIVGSG	482	2.0000	23.26
7	VKPANIMIS	138	1.8000	20.93
8	IVGSGPATK	486	1.8000	20.93
9	LRLHRDVAV	30	1.5800	18.37
10	VVTIAINTF	344	1.4000	16.28
11	MISATNAVK	144	1.3000	15.12
12	VREDPIPPS	228	1.3000	15.12
13	LHRDVAVKV	32	1.2800	14.88
14	WVAVVAVLA	331	1.2800	14.88
15	VAVLAVLTV	335	1.2000	13.95
16	VVVTIAINT	343	1.1800	13.72
17	VKVLRADLA	38	1.1000	12.79
18	VVYQNPPAG	602	1.0000	11.63
19	FTGDSPVSV	215	0.9800	11.40
20	IGTNPPANQ	467	0.9000	10.47
21	VNRDGIITL	613	0.8800	10.23
22	VHTEGPMTP	103	0.8000	9.30
23	VTIAINTFG	345	0.7000	8.14
24	YGFTKFSQA	514	0.7000	8.14
25	VAGQTVDVA	499	0.6000	6.98
26	VIADACQAL	117	0.5000	5.81
27	VMPDLSGMF	561	0.5000	5.81
28	LRALGWTGM	577	0.5000	5.81
29	IIIVGSGPA	484	0.4000	4.65
30	FGIARAIAD	156	0.3800	4.42
31	VLAVLTVVV	337	0.3800	4.42
32	VPVDSVIEL	544	0.3800	4.42
33	LTVVVTIAI	341	0.2800	3.26
34	LNFSHQNGI	125	0.2000	2.33
35	VRVHNGEPP	273	0.2000	2.33
36	FKQANSPST	451	0.2000	2.33
37	IELQVSKGN	550	0.2000	2.33
38	FVMPDLSGM	560	0.2000	2.33
39	LRADLARDP	41	0.1000	1.16

40	LARDPSFYL	45	0.1000	1.16
41	YVDGVTLRD	93	0.1000	1.16
42	YIVMEYVDG	88	0.0800	0.93
43	LAVLTVVVT	338	0.0800	0.93
44	VYSLGCVLY	198	-0.0200	0
45	IPPDHVIGT	393	-0.0200	0
46	VLTVVVTIA	340	-0.1000	0
47	VKKLTAAGF	440	-0.1000	0
48	IEVIADACQ	115	-0.2000	0
49	IGTDPAANT	399	-0.3000	0
50	WTGMLDKGA	582	-0.3000	0
51	YQTAAEMRA	262	-0.4000	0
52	LVRVHNGEP	272	-0.4000	0
53	IRTLQKPDS	383	-0.4000	0
54	VIGTDPAAN	398	-0.4000	0
55	LQVSKGNQF	552	-0.4000	0
56	VYQNPPAGT	603	-0.4000	0
57	LTYAEAVKK	434	-0.4200	0
58	VAVVAVLAV	332	-0.5000	0
59	FGRFKQANS	448	-0.5000	0
60	LGWTGMLDK	580	-0.5000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	IMISATNAV	143	6.4200	55.34
2	LTVVVTIAI	341	6.1200	52.76
3	LNFSHQNGI	125	5.8000	50.00
4	VVVTIAINT	343	5.8000	50.00
5	MEYVDGVTL	91	5.2000	44.83
6	VVTIAINTF	344	5.2000	44.83
7	LLSSAAGNL	295	5.1000	43.97
8	LQVSKGNQF	552	5.1000	43.97
9	VAVVAVLAV	332	4.7000	40.52

10	WVAVVAVLA	331	4.6000	39.66
11	VLAVLTVVV	337	4.4200	38.10
12	ITNVVIIIV	479	4.3000	37.07
13	LARDPSFYL	45	4.2000	36.21
14	VNRDGIITL	613	4.2000	36.21
15	VVAVLAVLT	334	4.0000	34.48
16	VHLARDLRL	24	3.9000	33.62
17	YELGEILGF	10	3.8000	32.76
18	FVMPDLSGM	560	3.8000	32.76
19	ISATNAVKV	145	3.7000	31.90
20	LGCVLYEVL	201	3.7000	31.90
21	LRLHRDVAV	30	3.4000	29.31
22	VPVDSVIEL	544	3.3000	28.45
23	FGIARAIAD	156	3.2000	27.59
24	VVIIIVGSG	482	3.2000	27.59
25	IIIVGSGPA	484	3.1000	26.72
26	VIADACQAL	117	3.0000	25.86
27	VAVLAVLTV	335	3.0000	25.86
28	FGGMSEVHL	18	2.8000	24.14
29	LHRDVAVKV	32	2.5000	21.55
30	LPYIVMEYV	86	2.5000	21.55
31	MTPKRAIEV	109	2.4000	20.69
32	LRALGWTGM	577	2.4000	20.69
33	IVHTEGPMT	102	2.3000	19.83
34	YGFTKFSQA	514	2.3000	19.83
35	VDGVTLRDI	94	2.0000	17.24
36	VIGTAQYLS	175	2.0000	17.24
37	VYSLGCVLY	198	2.0000	17.24
38	IAINTFGGI	347	2.0000	17.24
39	LNHPAIVAV	65	1.9000	16.38
40	IVMEYVDGV	89	1.9000	16.38
41	YQHVREDPI	225	1.9000	16.38
42	VLTVVVTIA	340	1.9000	16.38
43	FKQANSPST	451	1.9000	16.38

44	VIIIVGSGP	483	1.9000	16.38
45	FRREAQNAA	55	1.8000	15.52
46	FTGDSPVSV	215	1.7000	14.66
47	YSLGCVLYE	199	1.6000	13.79
48	LDAVVLKAL	246	1.6000	13.79
49	LNVYGFTKF	511	1.6000	13.79
50	MDFGIARAI	154	1.5000	12.93
51	LVRVHNGEP	272	1.5000	12.93
52	VRVHNGEPP	273	1.5000	12.93
53	VMPDLSGMF	561	1.5000	12.93
54	VKPANIMIS	138	1.4000	12.07
55	VTQTAAVIG	169	1.4000	12.07
56	VKKLTAAGF	440	1.4000	12.07
57	IPDVSTLTY	428	1.3200	11.38
58	ILGFGGMSE	15	1.3000	11.21
59	YIVMEYVDG	88	1.2000	10.34
60	IVGSGPATK	486	1.2000	10.34
61	LGWTGMLDK	580	1.2000	10.34
62	FKIRTLQKP	381	1.1000	9.48

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	IMISATNAV	143	6.4200	55.34
2	LTVVVTIAI	341	6.1200	52.76
3	LNFSHQNGI	125	5.8000	50.00
4	VVVTIAINT	343	5.8000	50.00
5	MEYVDGVTL	91	5.2000	44.83
6	VVTIAINTF	344	5.2000	44.83
7	LLSSAAGNL	295	5.1000	43.97
8	LQVSKGNQF	552	5.1000	43.97
9	VAVVAVLAV	332	4.7000	40.52
10	WVAVVAVLA	331	4.6000	39.66
11	VLAVLTVVV	337	4.4200	38.10

12	ITNVVIIIV	479	4.3000	37.07
13	LARDPSFYL	45	4.2000	36.21
14	VNRDGIITL	613	4.2000	36.21
15	VVAVLAVLT	334	4.0000	34.48
16	VHLARDLRL	24	3.9000	33.62
17	YELGEILGF	10	3.8000	32.76
18	FVMPDLSGM	560	3.8000	32.76
19	ISATNAVKV	145	3.7000	31.90
20	LGCVLYEVL	201	3.7000	31.90
21	LRLHRDVAV	30	3.4000	29.31
22	VPVDSVIEL	544	3.3000	28.45
23	FGIARAIAD	156	3.2000	27.59
24	VVIIIVGSG	482	3.2000	27.59
25	IIIVGSGPA	484	3.1000	26.72
26	VIADACQAL	117	3.0000	25.86
27	VAVLAVLTV	335	3.0000	25.86
28	FGGMSEVHL	18	2.8000	24.14
29	LHRDVAVKV	32	2.5000	21.55
30	LPYIVMEYV	86	2.5000	21.55
31	MTPKRAIEV	109	2.4000	20.69
32	LRALGWTGM	577	2.4000	20.69
33	IVHTEGPMT	102	2.3000	19.83
34	YGFTKFSQA	514	2.3000	19.83
35	VDGVTLRDI	94	2.0000	17.24
36	VIGTAQYLS	175	2.0000	17.24
37	VYSLGCVLY	198	2.0000	17.24
38	IAINTFGGI	347	2.0000	17.24
39	LNHPAIVAV	65	1.9000	16.38
40	IVMEYVDGV	89	1.9000	16.38
41	YQHVREDPI	225	1.9000	16.38
42	VLTVVVTIA	340	1.9000	16.38
43	FKQANSPST	451	1.9000	16.38
44	VIIIVGSGP	483	1.9000	16.38
45	FRREAQNAA	55	1.8000	15.52

46	FTGDSPVSV	215	1.7000	14.66
47	YSLGCVLYE	199	1.6000	13.79
48	LDAVVLKAL	246	1.6000	13.79
49	LNVYGFTKF	511	1.6000	13.79
50	MDFGIARAI	154	1.5000	12.93
51	LVRVHNGEP	272	1.5000	12.93
52	VRVHNGEPP	273	1.5000	12.93
53	VMPDLSGMF	561	1.5000	12.93
54	VKPANIMIS	138	1.4000	12.07
55	VTQTAAVIG	169	1.4000	12.07
56	VKKLTAAGF	440	1.4000	12.07
57	IPDVSTLTY	428	1.3200	11.38
58	ILGFGGMSE	15	1.3000	11.21
59	YIVMEYVDG	88	1.2000	10.34
60	IVGSGPATK	486	1.2000	10.34
61	LGWTGMLDK	580	1.2000	10.34
62	FKIRTLQKP	381	1.1000	9.48

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	VVLKALAKN	249	5.2000	60.47
2	FYLRFRREA	51	4.6000	53.49
3	LVGKVIGTN	462	4.4000	51.16
4	VVIIIVGSG	482	3.9000	45.35
5	LRFRREAQN	53	3.5000	40.70
6	IIHRDVKPA	133	3.0000	34.88
7	FKIRTLQKP	381	3.0000	34.88
8	IRTLQKPDS	383	2.7000	31.40
9	VAVKVLRAD	36	2.4000	27.91
10	VYGFTKFSQ	513	2.3000	26.74
11	FGIARAIAD	156	2.2000	25.58
12	YLRFRREAQ	52	2.1000	24.42
13	LKALAKNPE	251	2.1000	24.42

14	MRADLVRVH	268	2.1000	24.42
15	FGRFKQANS	448	2.1000	24.42
16	FVMPDLSGM	560	2.1000	24.42
17	VAVYDTGEA	71	2.0000	23.26
18	VLRADLARD	40	1.9000	22.09
19	YSLGCVLYE	199	1.9000	22.09
20	VTLRDIVHT	97	1.6000	18.60
21	VQVPDVRGQ	359	1.6000	18.60
22	VKPANIMIS	138	1.5000	17.44
23	YVDGVTLRD	93	1.3000	15.12
24	WVAVVAVLA	331	1.3000	15.12
25	IGTNPPANQ	467	1.3000	15.12
26	IIIVGSGPA	484	1.3000	15.12
27	ILGFGGMSE	15	1.0000	11.63
28	FGGITRDVQ	352	0.9000	10.47
29	YIVMEYVDG	88	0.8000	9.30
30	VAVLAVLTV	335	0.7000	8.14
31	VVTIAINTF	344	0.7000	8.14
32	VKKLTAAGF	440	0.7000	8.14
33	VVYQNPPAG	602	0.5000	5.81
34	YQNPPAGTG	604	0.5000	5.81
35	YELGEILGF	10	0.4000	4.65
36	MTPKRAIEV	109	0.4000	4.65
37	VAYQHVRED	223	0.4000	4.65
38	VIGTDPAAN	398	0.4000	4.65
39	FRREAQNAA	55	0.3000	3.49
40	VAVVAVLAV	332	0.3000	3.49
41	VRGQSSADA	364	0.3000	3.49
42	VAQKNLNVY	506	0.3000	3.49
43	IHRDVKPAN	134	0.2000	2.33
44	YLSPEQARG	181	0.2000	2.33
45	VKVMDFGIA	151	0.1000	1.16
46	LVRVHNGEP	272	0.1000	1.16
47	VYQNPPAGT	603	0.1000	1.16

48	IVMEYVDGV	89	-0.1000	0
49	VYSLGCVLY	198	-0.2000	0
50	IGSVGRWVA	325	-0.2000	0
51	LQNRGFKIR	376	-0.2000	0
52	IVGSGPATK	486	-0.2000	0
53	FTKFSQASV	516	-0.2000	0
54	VIELQVSKG	549	-0.2000	0
55	IMISATNAV	143	-0.3000	0
56	LTVVVTIAI	341	-0.3000	0
57	WVDAEPRLR	570	-0.3000	0
58	FGGMSEVHL	18	-0.4000	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	FYLRFRREA	51	4.6000	57.50
2	VVLKALAKN	249	3.2000	40.00
3	IIHRDVKPA	133	3.0000	37.50
4	IRTLQKPDS	383	2.7000	33.75
5	FKIRTLQKP	381	2.6000	32.50
6	VVIIIVGSG	482	2.6000	32.50
7	LVGKVIGTN	462	2.4000	30.00
8	FGRFKQANS	448	2.1000	26.25
9	VAVYDTGEA	71	2.0000	25.00
10	LRFRREAQN	53	1.5000	18.75
11	VKPANIMIS	138	1.5000	18.75
12	VYGFTKFSQ	513	1.5000	18.75
13	YLRFRREAQ	52	1.3000	16.25
14	WVAVVAVLA	331	1.3000	16.25
15	IIIVGSGPA	484	1.3000	16.25
16	FVMPDLSGM	560	1.0000	12.50
17	MRADLVRVH	268	0.8800	11.00
18	VQVPDVRGQ	359	0.8000	10.00
19	VTLRDIVHT	97	0.7000	8.75

20	IGTNPPANQ	467	0.5000	6.25
21	IVGSGPATK	486	0.5000	6.25
22	VAVLAVLTV	335	0.4000	5.00
23	FRREAQNAA	55	0.3000	3.75
24	VRGQSSADA	364	0.3000	3.75
25	MTPKRAIEV	109	0.1000	1.25
26	VKVMDFGIA	151	0.1000	1.25
27	FGGITRDVQ	352	0.1000	1.25
28	IGSVGRWVA	325	-0.2000	0
29	VVTIAINTF	344	-0.2000	0
30	LQNRGFKIR	376	-0.2000	0
31	VKKLTAAGF	440	-0.2000	0
32	VAVKVLRAD	36	-0.3000	0
33	LVRVHNGEP	272	-0.3000	0
34	WVDAEPRLR	570	-0.3000	0
35	IVMEYVDGV	89	-0.4000	0
36	YELGEILGF	10	-0.5000	0
37	YIVMEYVDG	88	-0.5000	0
38	FGIARAIAD	156	-0.5000	0
39	YQTAAEMRA	262	-0.5000	0
40	LTVVVTIAI	341	-0.5000	0
41	FTKFSQASV	516	-0.5000	0
42	IMISATNAV	143	-0.6000	0
43	MISATNAVK	144	-0.6000	0
44	VLAVLTVVV	337	-0.7000	0
45	VLRADLARD	40	-0.8000	0
46	VREDPIPPS	228	-0.8000	0
47	VAQKNLNVY	506	-0.8000	0
48	VVYQNPPAG	602	-0.8000	0
49	VYQNPPAGT	603	-0.8000	0
50	YQNPPAGTG	604	-0.8000	0
51	LKALAKNPE	251	-0.9000	0
52	VGRWVAVVA	328	-0.9000	0
53	VVAVLAVLT	334	-0.9000	0

54	LAVLTVVVT	338	-0.9000	0
55	VLTVVVTIA	340	-0.9000	0
56	ITNVVIIIV	479	-1.0000	0
57	VKVLRADLA	38	-1.1000	0
58	YLSPEQARG	181	-1.1000	0
59	YSLGCVLYE	199	-1.1000	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	VVLKALAKN	249	4.2000	52.50
2	IIHRDVKPA	133	4.0000	50.00
3	IRTLQKPDS	383	3.7000	46.25
4	FYLRFRREA	51	3.6000	45.00
5	VVIIIVGSG	482	3.6000	45.00
6	LVGKVIGTN	462	3.4000	42.50
7	VAVYDTGEA	71	3.0000	37.50
8	LRFRREAQN	53	2.5000	31.25
9	VKPANIMIS	138	2.5000	31.25
10	VYGFTKFSQ	513	2.5000	31.25
11	IIIVGSGPA	484	2.3000	28.75
12	MRADLVRVH	268	1.8800	23.50
13	VQVPDVRGQ	359	1.8000	22.50
14	VTLRDIVHT	97	1.7000	21.25
15	FKIRTLQKP	381	1.6000	20.00
16	IGTNPPANQ	467	1.5000	18.75
17	IVGSGPATK	486	1.5000	18.75
18	VAVLAVLTV	335	1.4000	17.50
19	VRGQSSADA	364	1.3000	16.25
20	MTPKRAIEV	109	1.1000	13.75
21	VKVMDFGIA	151	1.1000	13.75
22	FGRFKQANS	448	1.1000	13.75
23	VMDFGIARA	153	1.0000	12.50
24	VAVVAVLAV	332	1.0000	12.50

25	IGSVGRWVA	325	0.8000	10.00
26	VVTIAINTF	344	0.8000	10.00
27	LQNRGFKIR	376	0.8000	10.00
28	VKKLTAAGF	440	0.8000	10.00
29	VAVKVLRAD	36	0.7000	8.75
30	LVRVHNGEP	272	0.7000	8.75
31	IVMEYVDGV	89	0.6000	7.50
32	LTVVVTIAI	341	0.5000	6.25
33	IMISATNAV	143	0.4000	5.00
34	MISATNAVK	144	0.4000	5.00
35	YLRFRREAQ	52	0.3000	3.75
36	WVAVVAVLA	331	0.3000	3.75
37	VLAVLTVVV	337	0.3000	3.75
38	VLRADLARD	40	0.2000	2.50
39	VREDPIPPS	228	0.2000	2.50
40	VAQKNLNVY	506	0.2000	2.50
41	VVYQNPPAG	602	0.2000	2.50
42	VYQNPPAGT	603	0.2000	2.50
43	LKALAKNPE	251	0.1000	1.25
44	VGRWVAVVA	328	0.1000	1.25
45	VVAVLAVLT	334	0.1000	1.25
46	LAVLTVVVT	338	0.1000	1.25
47	VLTVVVTIA	340	0.1000	1.25
48	VKVLRADLA	38	-0.1000	0
49	VYSLGCVLY	198	-0.3000	0
50	VIGTAQYLS	175	-0.4000	0
51	VHNGEPPEA	275	-0.4000	0
52	VVVTIAINT	343	-0.4000	0
53	VIIIVGSGP	483	-0.4000	0
54	VIELQVSKG	549	-0.5000	0
55	LARDLRLHR	26	-0.6000	0
56	VIGTDPAAN	398	-0.6000	0
57	LTYAEAVKK	434	-0.6000	0
58	VNRDGIITL	613	-0.6000	0

59	LRADLARDP	41	-0.7000	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	VVLKALAKN	249	6.2000	72.09
2	LVGKVIGTN	462	5.4000	62.79
3	VVIIIVGSG	482	4.9000	56.98
4	LRFRREAQN	53	4.5000	52.33
5	IIHRDVKPA	133	4.0000	46.51
6	IRTLQKPDS	383	3.7000	43.02
7	FYLRFRREA	51	3.6000	41.86
8	VAVKVLRAD	36	3.4000	39.53
9	VYGFTKFSQ	513	3.3000	38.37
10	LKALAKNPE	251	3.1000	36.05
11	MRADLVRVH	268	3.1000	36.05
12	VAVYDTGEA	71	3.0000	34.88
13	VLRADLARD	40	2.9000	33.72
14	VTLRDIVHT	97	2.6000	30.23
15	VQVPDVRGQ	359	2.6000	30.23
16	VKPANIMIS	138	2.5000	29.07
17	IGTNPPANQ	467	2.3000	26.74
18	IIIVGSGPA	484	2.3000	26.74
19	ILGFGGMSE	15	2.0000	23.26
20	FKIRTLQKP	381	2.0000	23.26
21	VAVLAVLTV	335	1.7000	19.77
22	VVTIAINTF	344	1.7000	19.77
23	VKKLTAAGF	440	1.7000	19.77
24	VVYQNPPAG	602	1.5000	17.44
25	MTPKRAIEV	109	1.4000	16.28
26	VAYQHVRED	223	1.4000	16.28
27	VIGTDPAAN	398	1.4000	16.28
28	VAVVAVLAV	332	1.3000	15.12
29	VRGQSSADA	364	1.3000	15.12

30	VAQKNLNVY	506	1.3000	15.12
31	IHRDVKPAN	134	1.2000	13.95
32	FGIARAIAD	156	1.2000	13.95
33	YLRFRREAQ	52	1.1000	12.79
34	VKVMDFGIA	151	1.1000	12.79
35	LVRVHNGEP	272	1.1000	12.79
36	FGRFKQANS	448	1.1000	12.79
37	FVMPDLSGM	560	1.1000	12.79
38	VYQNPPAGT	603	1.1000	12.79
39	VMDFGIARA	153	1.0000	11.63
40	VVAVLAVLT	334	1.0000	11.63
41	LAVLTVVVT	338	1.0000	11.63
42	IVMEYVDGV	89	0.9000	10.47
43	YSLGCVLYE	199	0.9000	10.47
44	VYSLGCVLY	198	0.8000	9.30
45	IGSVGRWVA	325	0.8000	9.30
46	LQNRGFKIR	376	0.8000	9.30
47	IVGSGPATK	486	0.8000	9.30
48	VIELQVSKG	549	0.8000	9.30
49	IMISATNAV	143	0.7000	8.14
50	LTVVVTIAI	341	0.7000	8.14
51	VLAVLTVVV	337	0.6000	6.98
52	MLDKGADVD	585	0.6000	6.98
53	VVVTIAINT	343	0.5000	5.81
54	VNRDGIITL	613	0.4000	4.65
55	LSDRYELGE	6	0.3000	3.49
56	YVDGVTLRD	93	0.3000	3.49
57	WVAVVAVLA	331	0.3000	3.49
58	ITNVVIIIV	479	0.3000	3.49
59	VREDPIPPS	228	0.2000	2.33
60	VIGTNPPAN	466	0.2000	2.33
61	VGRWVAVVA	328	0.1000	1.16
62	VLTVVVTIA	340	0.1000	1.16

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	FYLRFRREA	51	4.3000	49.43
2	FKIRTLQKP	381	3.6000	41.38
3	VVLKALAKN	249	3.2000	36.78
4	YLRFRREAQ	52	3.0000	34.48
5	IRTLQKPDS	383	2.9000	33.33
6	FVMPDLSGM	560	2.8000	32.18
7	IIHRDVKPA	133	2.5000	28.74
8	VKPANIMIS	138	2.5000	28.74
9	VYGFTKFSQ	513	2.3500	27.01
10	FRREAQNAA	55	2.3000	26.44
11	WVAVVAVLA	331	2.3000	26.44
12	FGRFKQANS	448	2.1000	24.14
13	VLTVVVTIA	340	1.9000	21.84
14	VVIIIVGSG	482	1.9000	21.84
15	VVTIAINTF	344	1.8000	20.69
16	VTLRDIVHT	97	1.7000	19.54
17	LVGKVIGTN	462	1.7000	19.54
18	LRFRREAQN	53	1.5000	17.24
19	IMISATNAV	143	1.4000	16.09
20	VAVYDTGEA	71	1.3000	14.94
21	FGGITRDVQ	352	1.3000	14.94
22	VAQKNLNVY	506	1.2000	13.79
23	LKALAKNPE	251	1.1000	12.64
24	VAVLAVLTV	335	1.0000	11.49
25	MTPKRAIEV	109	0.9800	11.26
26	IVMEYVDGV	89	0.8000	9.20
27	VAVVAVLAV	332	0.6000	6.90
28	IIIVGSGPA	484	0.6000	6.90
29	MRADLVRVH	268	0.5800	6.67
30	YIVMEYVDG	88	0.5000	5.75
31	YQTAAEMRA	262	0.5000	5.75

32	VQVPDVRGQ	359	0.5000	5.75
33	IGTNPPANQ	467	0.5000	5.75
34	IVGSGPATK	486	0.5000	5.75
35	LNVYGFTKF	511	0.5000	5.75
36	LRALGWTGM	577	0.5000	5.75
37	VIIIVGSGP	483	0.4000	4.60
38	FGIARAIAD	156	0.3800	4.37
39	LTVVVTIAI	341	0.3800	4.37
40	IGSVGRWVA	325	0.3000	3.45
41	VLAVLTVVV	337	0.3000	3.45
42	VRGQSSADA	364	0.3000	3.45
43	VIELQVSKG	549	0.3000	3.45
44	YELGEILGF	10	0.1000	1.15
45	VKVLRADLA	38	0.1000	1.15
46	VGRWVAVVA	328	0.1000	1.15
47	VVAVLAVLT	334	0.1000	1.15
48	LAVLTVVVT	338	0.1000	1.15
49	ITNVVIIIV	479	-0.1200	0
50	VKKLTAAGF	440	-0.2000	0
51	LNFSHQNGI	125	-0.3000	0
52	VYSLGCVLY	198	-0.3000	0
53	FGGMSEVHL	18	-0.4000	0
54	LSSAAGNLS	296	-0.4000	0
55	LRDIVHTEG	99	-0.5000	0
56	VIGTAQYLS	175	-0.5000	0
57	YSLGCVLYE	199	-0.5000	0
58	FTKFSQASV	516	-0.5000	0
59	VVVTIAINT	343	-0.5200	0
60	VAVKVLRAD	36	-0.6000	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	VVLKALAKN	249	5.2000	51.49

2	FYLRFRREA	51	4.8000	47.52
3	LVGKVIGTN	462	4.5000	44.55
4	VVIIIVGSG	482	4.0000	39.60
5	IRTLQKPDS	383	3.8500	38.12
6	FGIARAIAD	156	3.8000	37.62
7	YSLGCVLYE	199	3.7000	36.63
8	IIHRDVKPA	133	3.6000	35.64
9	LRFRREAQN	53	3.5000	34.65
10	YLRFRREAQ	52	3.2000	31.68
11	YVDGVTLRD	93	3.1000	30.69
12	VKPANIMIS	138	3.1000	30.69
13	FKIRTLQKP	381	3.1000	30.69
14	VYGFTKFSQ	513	2.8000	27.72
15	ILGFGGMSE	15	2.6000	25.74
16	VAVKVLRAD	36	2.6000	25.74
17	VAVLAVLTV	335	2.5000	24.75
18	LKALAKNPE	251	2.4000	23.76
19	MRADLVRVH	268	2.3000	22.77
20	YELGEILGF	10	2.2000	21.78
21	VAVYDTGEA	71	2.1000	20.79
22	VTLRDIVHT	97	2.1000	20.79
23	VAVVAVLAV	332	2.1000	20.79
24	FGRFKQANS	448	2.1000	20.79
25	FVMPDLSGM	560	2.1000	20.79
26	MTPKRAIEV	109	2.0000	19.80
27	VLRADLARD	40	1.9000	18.81
28	WVAVVAVLA	331	1.8000	17.82
29	VQVPDVRGQ	359	1.8000	17.82
30	VVYQNPPAG	602	1.6500	16.34
31	IIIVGSGPA	484	1.4000	13.86
32	IHRDVKPAN	134	1.3500	13.37
33	YIVMEYVDG	88	1.3000	12.87
34	LTVVVTIAI	341	1.3000	12.87
35	IGTNPPANQ	467	1.3000	12.87

36	LSDRYELGE	6	1.1000	10.89
37	YQTAAEMRA	262	1.1000	10.89
38	VVVTIAINT	343	1.1000	10.89
39	VVTIAINTF	344	1.0000	9.90
40	VNRDGIITL	613	1.0000	9.90
41	ITNVVIIIV	479	0.9000	8.91
42	VKKLTAAGF	440	0.7000	6.93
43	FKQANSPST	451	0.6500	6.44
44	FRREAQNAA	55	0.6000	5.94
45	VAYQHVRED	223	0.6000	5.94
46	IGSVGRWVA	325	0.6000	5.94
47	FGGITRDVQ	352	0.6000	5.94
48	VAQKNLNVY	506	0.6000	5.94
49	YQNPPAGTG	604	0.6000	5.94
50	VVAVLAVLT	334	0.5000	4.95
51	LAVLTVVVT	338	0.5000	4.95
52	MTTPSHLSD	0	0.4000	3.96
53	LQNRGFKIR	376	0.4000	3.96
54	VIGTDPAAN	398	0.4000	3.96
55	VREDPIPPS	228	0.3500	3.47
56	VIGTNPPAN	466	0.3500	3.47
57	FSHQNGIIH	127	0.3000	2.97
58	VYSLGCVLY	198	0.3000	2.97
59	VRGQSSADA	364	0.3000	2.97
60	LARDLRLHR	26	0.2000	1.98
61	VKVMDFGIA	151	0.2000	1.98
62	YLSPEQARG	181	0.2000	1.98

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	IRTLQKPDS	383	4.2500	51.20
2	VVIIIVGSG	482	3.3000	39.76
3	VKPANIMIS	138	3.1000	37.35

4	VAVLAVLTV	335	2.6000	31.33
5	YLRFRREAQ	52	2.3000	27.71
6	FGRFKQANS	448	2.0000	24.10
7	WVAVVAVLA	331	1.9000	22.89
8	VAVVAVLAV	332	1.9000	22.89
9	VYGFTKFSQ	513	1.9000	22.89
10	FYLRFRREA	51	1.8000	21.69
11	IIIVGSGPA	484	1.5000	18.07
12	LTVVVTIAI	341	1.2000	14.46
13	FGIARAIAD	156	1.1000	13.25
14	YQTAAEMRA	262	1.1000	13.25
15	VVYQNPPAG	602	0.9500	11.45
16	VRGQSSADA	364	0.9000	10.84
17	IVGSGPATK	486	0.8000	9.64
18	IGSVGRWVA	325	0.7000	8.43
19	VVTIAINTF	344	0.7000	8.43
20	ITNVVIIIV	479	0.7000	8.43
21	YELGEILGF	10	0.6000	7.23
22	IIHRDVKPA	133	0.6000	7.23
23	VVVTIAINT	343	0.6000	7.23
24	IGTNPPANQ	467	0.5000	6.02
25	VVLKALAKN	249	0.4000	4.82
26	FGGITRDVQ	352	0.4000	4.82
27	MRADLVRVH	268	0.3800	4.58
28	VLTVVVTIA	340	0.3000	3.61
29	VQVPDVRGQ	359	0.3000	3.61
30	FVMPDLSGM	560	0.3000	3.61
31	VKKLTAAGF	440	0.2000	2.41
32	FRREAQNAA	55	-0.1000	0
33	VMDFGIARA	153	-0.1000	0
34	LVRVHNGEP	272	-0.1000	0
35	VLAVLTVVV	337	-0.1000	0
36	WVDAEPRLR	570	-0.1000	0
37	VKVMDFGIA	151	-0.2000	0

38	LKALAKNPE	251	-0.2000	0
39	FKQANSPST	451	-0.2500	0
40	YVDGVTLRD	93	-0.3000	0
41	VIGTAQYLS	175	-0.3000	0
42	VVAVLAVLT	334	-0.3000	0
43	FKIRTLQKP	381	-0.3000	0
44	LVGKVIGTN	462	-0.3000	0
45	FSHQNGIIH	127	-0.3200	0
46	VREDPIPPS	228	-0.3500	0
47	YIVMEYVDG	88	-0.4000	0
48	VYSLGCVLY	198	-0.4000	0
49	ILGFGGMSE	15	-0.5000	0
50	LARDLRLHR	26	-0.5000	0
51	VGRWVAVVA	328	-0.5000	0
52	MISATNAVK	144	-0.6000	0
53	FTKFSQASV	516	-0.6000	0
54	VNVSTGPEQ	417	-0.6500	0
55	INTFGGITR	349	-0.7000	0
56	VNRDGIITL	613	-0.7000	0
57	VLRADLARD	40	-0.8000	0
58	VAVYDTGEA	71	-0.8000	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	VYGFTKFSQ	513	4.3000	51.19
2	IRTLQKPDS	383	4.1000	48.81
3	FYLRFRREA	51	3.3000	39.29
4	MRADLVRVH	268	3.2800	39.05
5	VQVPDVRGQ	359	3.1000	36.90
6	VRGQSSADA	364	2.9000	34.52
7	VKPANIMIS	138	2.8000	33.33
8	IIHRDVKPA	133	2.7000	32.14
9	VVLKALAKN	249	2.7000	32.14

10	VVYQNPPAG	602	2.5000	29.76
11	IMISATNAV	143	2.2000	26.19
12	VAYQHVRED	223	2.1000	25.00
13	YLRFRREAQ	52	2.0000	23.81
14	IVGSGPATK	486	1.9000	22.62
15	VGRWVAVVA	328	1.8000	21.43
16	VAVLAVLTV	335	1.8000	21.43
17	VVIIIVGSG	482	1.7000	20.24
18	IGTNPPANQ	467	1.6000	19.05
19	LRLHRDVAV	30	1.5000	17.86
20	IVMEYVDGV	89	1.4000	16.67
21	FGRFKQANS	448	1.4000	16.67
22	VMDFGIARA	153	1.3000	15.48
23	VVTIAINTF	344	1.3000	15.48
24	LKALAKNPE	251	1.2000	14.29
25	VRVHNGEPP	273	1.2000	14.29
26	IGSVGRWVA	325	1.2000	14.29
27	VAVKVLRAD	36	1.0000	11.90
28	LVGKVIGTN	462	0.9000	10.71
29	LAVLTVVVT	338	0.8000	9.52
30	LRADLARDP	41	0.7000	8.33
31	FRREAQNAA	55	0.6000	7.14
32	VTLRDIVHT	97	0.6000	7.14
33	VKVLRADLA	38	0.5000	5.95
34	LNFSHQNGI	125	0.5000	5.95
35	VREDPIPPS	228	0.5000	5.95
36	VAVVAVLAV	332	0.5000	5.95
37	VKKLTAAGF	440	0.5000	5.95
38	VAGQTVDVA	499	0.5000	5.95
39	WVDAEPRLR	570	0.5000	5.95
40	LRFRREAQN	53	0.4000	4.76
41	MISATNAVK	144	0.4000	4.76
42	VIGTAQYLS	175	0.4000	4.76
43	VYSLGCVLY	198	0.4000	4.76

44	VLTVVVTIA	340	0.4000	4.76
45	LTYAEAVKK	434	0.4000	4.76
46	FKIRTLQKP	381	0.3000	3.57
47	VYQNPPAGT	603	0.3000	3.57
48	VLRADLARD	40	0.2000	2.38
49	VAVYDTGEA	71	0.2000	2.38
50	IELQVSKGN	550	0.2000	2.38
51	VLTDAERTS	286	0.1000	1.19
52	WVAVVAVLA	331	0.1000	1.19
53	VLAVLTVVV	337	0.1000	1.19
54	IIIVGSGPA	484	0.1000	1.19
55	VAQKNLNVY	506	0.1000	1.19
56	MTPKRAIEV	109	-0.1000	0
57	VVAVLAVLT	334	-0.1000	0
58	FVMPDLSGM	560	-0.1000	0

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	IRTLQKPDS	383	5.2500	63.25
2	VVIIIVGSG	482	4.3000	51.81
3	VKPANIMIS	138	4.1000	49.40
4	VAVLAVLTV	335	3.6000	43.37
5	VAVVAVLAV	332	2.9000	34.94
6	VYGFTKFSQ	513	2.9000	34.94
7	IIIVGSGPA	484	2.5000	30.12
8	LTVVVTIAI	341	2.2000	26.51
9	VVYQNPPAG	602	1.9500	23.49
10	VRGQSSADA	364	1.9000	22.89
11	IVGSGPATK	486	1.8000	21.69
12	IGSVGRWVA	325	1.7000	20.48
13	VVTIAINTF	344	1.7000	20.48
14	ITNVVIIIV	479	1.7000	20.48
15	IIHRDVKPA	133	1.6000	19.28

16	VVVTIAINT	343	1.6000	19.28
17	IGTNPPANQ	467	1.5000	18.07
18	VVLKALAKN	249	1.4000	16.87
19	MRADLVRVH	268	1.3800	16.63
20	YLRFRREAQ	52	1.3000	15.66
21	VLTVVVTIA	340	1.3000	15.66
22	VQVPDVRGQ	359	1.3000	15.66
23	VKKLTAAGF	440	1.2000	14.46
24	IMISATNAV	143	1.0000	12.05
25	LAVLTVVVT	338	1.0000	12.05
26	FGRFKQANS	448	1.0000	12.05
27	VMDFGIARA	153	0.9000	10.84
28	LVRVHNGEP	272	0.9000	10.84
29	WVAVVAVLA	331	0.9000	10.84
30	VLAVLTVVV	337	0.9000	10.84
31	FYLRFRREA	51	0.8000	9.64
32	VKVMDFGIA	151	0.8000	9.64
33	LKALAKNPE	251	0.8000	9.64
34	VIGTAQYLS	175	0.7000	8.43
35	VVAVLAVLT	334	0.7000	8.43
36	LVGKVIGTN	462	0.7000	8.43
37	VREDPIPPS	228	0.6500	7.83
38	VYSLGCVLY	198	0.6000	7.23
39	ILGFGGMSE	15	0.5000	6.02
40	LARDLRLHR	26	0.5000	6.02
41	VGRWVAVVA	328	0.5000	6.02
42	MISATNAVK	144	0.4000	4.82
43	VNVSTGPEQ	417	0.3500	4.22
44	INTFGGITR	349	0.3000	3.61
45	VNRDGIITL	613	0.3000	3.61
46	VLRADLARD	40	0.2000	2.41
47	VAVYDTGEA	71	0.2000	2.41
48	VIIIVGSGP	483	0.2000	2.41
49	LRALGWTGM	577	0.2000	2.41

50	LGWTGMLDK	580	0.2000	2.41
51	VYQNPPAGT	603	0.2000	2.41
52	FGIARAIAD	156	0.1000	1.20
53	YQTAAEMRA	262	0.1000	1.20
54	VHNGEPPEA	275	0.0500	0.60
55	VHLARDLRL	24	-0.1000	0
56	MTPKRAIEV	109	-0.1000	0
57	IPDVSTLTY	428	-0.1000	0
58	LTYAEAVKK	434	-0.1000	0
59	VIELQVSKG	549	-0.1000	0
60	VIGTDPAAN	398	-0.2000	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	IRTLQKPDS	383	5.2500	63.25
2	VVIIIVGSG	482	4.3000	51.81
3	VKPANIMIS	138	4.1000	49.40
4	VAVLAVLTV	335	3.6000	43.37
5	VAVVAVLAV	332	2.9000	34.94
6	VYGFTKFSQ	513	2.9000	34.94
7	IIIVGSGPA	484	2.5000	30.12
8	LTVVVTIAI	341	2.2000	26.51
9	VVYQNPPAG	602	1.9500	23.49
10	VRGQSSADA	364	1.9000	22.89
11	IVGSGPATK	486	1.8000	21.69
12	IGSVGRWVA	325	1.7000	20.48
13	VVTIAINTF	344	1.7000	20.48
14	ITNVVIIIV	479	1.7000	20.48
15	IIHRDVKPA	133	1.6000	19.28
16	VVVTIAINT	343	1.6000	19.28
17	IGTNPPANQ	467	1.5000	18.07
18	VVLKALAKN	249	1.4000	16.87
19	MRADLVRVH	268	1.3800	16.63

20	YLRFRREAQ	52	1.3000	15.66
21	VLTVVVTIA	340	1.3000	15.66
22	VQVPDVRGQ	359	1.3000	15.66
23	VKKLTAAGF	440	1.2000	14.46
24	IMISATNAV	143	1.0000	12.05
25	LAVLTVVVT	338	1.0000	12.05
26	FGRFKQANS	448	1.0000	12.05
27	VMDFGIARA	153	0.9000	10.84
28	LVRVHNGEP	272	0.9000	10.84
29	WVAVVAVLA	331	0.9000	10.84
30	VLAVLTVVV	337	0.9000	10.84
31	FYLRFRREA	51	0.8000	9.64
32	VKVMDFGIA	151	0.8000	9.64
33	LKALAKNPE	251	0.8000	9.64
34	VIGTAQYLS	175	0.7000	8.43
35	VVAVLAVLT	334	0.7000	8.43
36	LVGKVIGTN	462	0.7000	8.43
37	VREDPIPPS	228	0.6500	7.83
38	VYSLGCVLY	198	0.6000	7.23
39	ILGFGGMSE	15	0.5000	6.02
40	LARDLRLHR	26	0.5000	6.02
41	VGRWVAVVA	328	0.5000	6.02
42	MISATNAVK	144	0.4000	4.82
43	VNVSTGPEQ	417	0.3500	4.22
44	INTFGGITR	349	0.3000	3.61
45	VNRDGIITL	613	0.3000	3.61
46	VLRADLARD	40	0.2000	2.41
47	VAVYDTGEA	71	0.2000	2.41
48	VIIIVGSGP	483	0.2000	2.41
49	LRALGWTGM	577	0.2000	2.41
50	LGWTGMLDK	580	0.2000	2.41
51	VYQNPPAGT	603	0.2000	2.41
52	FGIARAIAD	156	0.1000	1.20
53	YQTAAEMRA	262	0.1000	1.20

54	VHNGEPPEA	275	0.0500	0.60
55	VHLARDLRL	24	-0.1000	0
56	MTPKRAIEV	109	-0.1000	0
57	IPDVSTLTY	428	-0.1000	0
58	LTYAEAVKK	434	-0.1000	0
59	VIELQVSKG	549	-0.1000	0
60	VIGTDPAAN	398	-0.2000	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	VREDPIPPS	228	5.4000	59.34
2	IRTLQKPDS	383	4.9000	53.85
3	MRADLVRVH	268	4.8800	53.63
4	IHRDVKPAN	134	4.4000	48.35
5	VVIIIVGSG	482	4.4000	48.35
6	VKPANIMIS	138	3.9000	42.86
7	VNRDGIITL	613	3.9000	42.86
8	IMISATNAV	143	3.3100	36.37
9	LHRDVAVKV	32	3.3000	36.26
10	LARDLRLHR	26	3.2000	35.16
11	IVGSGPATK	486	3.2000	35.16
12	VVYQNPPAG	602	3.1000	34.07
13	VHNGEPPEA	275	3.0000	32.97
14	VPVDSVIEL	544	2.9000	31.87
15	VMPDLSGMF	561	2.7000	29.67
16	IIIVGSGPA	484	2.6000	28.57
17	IPPDHVIGT	393	2.5000	27.47
18	VNVSTGPEQ	417	2.5000	27.47
19	LARDPSFYL	45	2.4000	26.37
20	IVMEYVDGV	89	2.4000	26.37
21	VYGFTKFSQ	513	2.4000	26.37
22	LRADLARDP	41	2.3000	25.27
23	VIADACQAL	117	2.3000	25.27

24	VRGQSSADA	364	2.3000	25.27
25	VVTIAINTF	344	2.2100	24.29
26	VLTVVVTIA	340	2.1000	23.08
27	VLTDAERTS	286	1.7000	18.68
28	IGTNPPANQ	467	1.7000	18.68
29	LNFSHQNGI	125	1.6100	17.69
30	IGTDPAANT	399	1.6000	17.58
31	VLTGEPPFT	208	1.5000	16.48
32	FTGDSPVSV	215	1.5000	16.48
33	VQVPDVRGQ	359	1.5000	16.48
34	LTVVVTIAI	341	1.4000	15.38
35	FVMPDLSGM	560	1.3700	15.05
36	WVAVVAVLA	331	1.3000	14.29
37	VLAVLTVVV	337	1.3000	14.29
38	VAVVAVLAV	332	1.2000	13.19
39	VAVLAVLTV	335	1.2000	13.19
40	ITRDVQVPD	355	1.2000	13.19
41	VIIIVGSGP	483	1.1700	12.86
42	IGSVGRWVA	325	1.1000	12.09
43	VVAVLAVLT	334	1.1000	12.09
44	FGGITRDVQ	352	1.1000	12.09
45	VKVLRADLA	38	1.0000	10.99
46	YLRFRREAQ	52	1.0000	10.99
47	LVRVHNGEP	272	1.0000	10.99
48	LLSSAAGNL	295	1.0000	10.99
49	VVLKALAKN	249	0.9000	9.89
50	ITNVVIIIV	479	0.9000	9.89
51	IIVGSGPAT	485	0.9000	9.89
52	VVVTIAINT	343	0.8000	8.79
53	VAGQTVDVA	499	0.8000	8.79
54	LAVLTVVVT	338	0.7000	7.69
55	LTYAEAVKK	434	0.7000	7.69
56	LVGKVIGTN	462	0.7000	7.69
57	VIGTAQYLS	175	0.6500	7.14

58	LKALAKNPE	251	0.6100	6.70
59	LQVSKGNQF	552	0.6100	6.70
60	IIHRDVKPA	133	0.6000	6.59
61	FRREAQNAA	55	0.5100	5.60
62	YELGEILGF	10	0.5000	5.49

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	FYLRFRREA	51	4.3000	51.19
2	VYGFTKFSQ	513	3.3000	39.29
3	IRTLQKPDS	383	3.1000	36.90
4	YLRFRREAQ	52	3.0000	35.71
5	FGRFKQANS	448	2.4000	28.57
6	MRADLVRVH	268	2.2800	27.14
7	VQVPDVRGQ	359	2.1000	25.00
8	VRGQSSADA	364	1.9000	22.62
9	VKPANIMIS	138	1.8000	21.43
10	IIHRDVKPA	133	1.7000	20.24
11	VVLKALAKN	249	1.7000	20.24
12	FRREAQNAA	55	1.6000	19.05
13	WVDAEPRLR	570	1.5000	17.86
14	VVYQNPPAG	602	1.5000	17.86
15	FKIRTLQKP	381	1.3000	15.48
16	IMISATNAV	143	1.2000	14.29
17	VAYQHVRED	223	1.1000	13.10
18	WVAVVAVLA	331	1.1000	13.10
19	IVGSGPATK	486	0.9000	10.71
20	FVMPDLSGM	560	0.9000	10.71
21	VGRWVAVVA	328	0.8000	9.52
22	VAVLAVLTV	335	0.8000	9.52
23	VVIIIVGSG	482	0.7000	8.33
24	IGTNPPANQ	467	0.6000	7.14
25	LRLHRDVAV	30	0.5000	5.95

26	IVMEYVDGV	89	0.4000	4.76
27	VMDFGIARA	153	0.3000	3.57
28	VVTIAINTF	344	0.3000	3.57
29	LKALAKNPE	251	0.2000	2.38
30	VRVHNGEPP	273	0.2000	2.38
31	IGSVGRWVA	325	0.2000	2.38
32	FGGITRDVQ	352	0.1000	1.19
33	YIVMEYVDG	88	-0.1000	0
34	LVGKVIGTN	462	-0.1000	0
35	FGIARAIAD	156	-0.2000	0
36	YQTAAEMRA	262	-0.2000	0
37	LAVLTVVVT	338	-0.2000	0
38	FTKFSQASV	516	-0.2000	0
39	YELGEILGF	10	-0.3000	0
40	LRADLARDP	41	-0.3000	0
41	VTLRDIVHT	97	-0.4000	0
42	VKVLRADLA	38	-0.5000	0
43	LNFSHQNGI	125	-0.5000	0
44	VREDPIPPS	228	-0.5000	0
45	VAVVAVLAV	332	-0.5000	0
46	VKKLTAAGF	440	-0.5000	0
47	VAGQTVDVA	499	-0.5000	0
48	LRFRREAQN	53	-0.6000	0
49	MISATNAVK	144	-0.6000	0
50	VIGTAQYLS	175	-0.6000	0
51	VYSLGCVLY	198	-0.6000	0
52	VLTVVVTIA	340	-0.6000	0
53	LTYAEAVKK	434	-0.6000	0
54	FSHQNGIIH	127	-0.6200	0
55	FKQANSPST	451	-0.7000	0
56	VYQNPPAGT	603	-0.7000	0
57	VLRADLARD	40	-0.8000	0
58	VAVYDTGEA	71	-0.8000	0
59	IELQVSKGN	550	-0.8000	0

60	YSLGCVLYE	199	-0.9000	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	FYLRFRREA	51	4.3000	48.86
2	IRTLQKPDS	383	3.5000	39.77
3	WVDAEPRLR	570	3.0000	34.09
4	VVYQNPPAG	602	2.9000	32.95
5	FGRFKQANS	448	2.8000	31.82
6	VYGFTKFSQ	513	2.6000	29.55
7	VVLKALAKN	249	2.5000	28.41
8	FVMPDLSGM	560	2.4000	27.27
9	YLRFRREAQ	52	2.3000	26.14
10	FKIRTLQKP	381	2.3000	26.14
11	VKPANIMIS	138	2.2000	25.00
12	IMISATNAV	143	2.2000	25.00
13	VAYQHVRED	223	2.2000	25.00
14	VVTIAINTF	344	2.2000	25.00
15	VVIIIVGSG	482	2.1000	23.86
16	VRGQSSADA	364	1.9000	21.59
17	VAVLAVLTV	335	1.8000	20.45
18	IIHRDVKPA	133	1.7000	19.32
19	MRADLVRVH	268	1.7000	19.32
20	YELGEILGF	10	1.6000	18.18
21	FRREAQNAA	55	1.6000	18.18
22	LKALAKNPE	251	1.6000	18.18
23	LRLHRDVAV	30	1.5000	17.05
24	IVMEYVDGV	89	1.4000	15.91
25	VQVPDVRGQ	359	1.4000	15.91
26	VKKLTAAGF	440	1.4000	15.91
27	YIVMEYVDG	88	1.3000	14.77
28	VRVHNGEPP	273	1.2000	13.64
29	VAVKVLRAD	36	1.1000	12.50

30	WVAVVAVLA	331	1.1000	12.50
31	IVGSGPATK	486	1.0000	11.36
32	FGIARAIAD	156	0.9000	10.23
33	IATLQNRGF	373	0.9000	10.23
34	VGRWVAVVA	328	0.8000	9.09
35	FTKFSQASV	516	0.8000	9.09
36	LRADLARDP	41	0.7000	7.95
37	VYSLGCVLY	198	0.7000	7.95
38	LVGKVIGTN	462	0.7000	7.95
39	YSLGCVLYE	199	0.5000	5.68
40	VAVVAVLAV	332	0.5000	5.68
41	LAVLTVVVT	338	0.5000	5.68
42	LNFSHQNGI	125	0.4000	4.55
43	VAQKNLNVY	506	0.4000	4.55
44	LQVSKGNQF	552	0.4000	4.55
45	LRALGWTGM	577	0.4000	4.55
46	VLRADLARD	40	0.3000	3.41
47	VTLRDIVHT	97	0.3000	3.41
48	VMDFGIARA	153	0.3000	3.41
49	LARDLRLHR	26	0.2000	2.27
50	LRFRREAQN	53	0.2000	2.27
51	IGSVGRWVA	325	0.2000	2.27
52	VLAVLTVVV	337	0.1000	1.14
53	FGGMSEVHL	18	-0.0400	0
54	YVDGVTLRD	93	-0.1000	0
55	MTPKRAIEV	109	-0.1000	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	VYGFTKFSQ	513	4.3000	51.19
2	IRTLQKPDS	383	4.1000	48.81
3	FYLRFRREA	51	3.3000	39.29
4	MRADLVRVH	268	3.2800	39.05

5	VQVPDVRGQ	359	3.1000	36.90
6	VRGQSSADA	364	2.9000	34.52
7	VKPANIMIS	138	2.8000	33.33
8	IIHRDVKPA	133	2.7000	32.14
9	VVLKALAKN	249	2.7000	32.14
10	VVYQNPPAG	602	2.5000	29.76
11	IMISATNAV	143	2.2000	26.19
12	VAYQHVRED	223	2.1000	25.00
13	YLRFRREAQ	52	2.0000	23.81
14	IVGSGPATK	486	1.9000	22.62
15	VGRWVAVVA	328	1.8000	21.43
16	VAVLAVLTV	335	1.8000	21.43
17	VVIIIVGSG	482	1.7000	20.24
18	IGTNPPANQ	467	1.6000	19.05
19	LRLHRDVAV	30	1.5000	17.86
20	IVMEYVDGV	89	1.4000	16.67
21	FGRFKQANS	448	1.4000	16.67
22	VMDFGIARA	153	1.3000	15.48
23	VVTIAINTF	344	1.3000	15.48
24	LKALAKNPE	251	1.2000	14.29
25	VRVHNGEPP	273	1.2000	14.29
26	IGSVGRWVA	325	1.2000	14.29
27	VAVKVLRAD	36	1.0000	11.90
28	LVGKVIGTN	462	0.9000	10.71
29	LAVLTVVVT	338	0.8000	9.52
30	LRADLARDP	41	0.7000	8.33
31	FRREAQNAA	55	0.6000	7.14
32	VTLRDIVHT	97	0.6000	7.14
33	VKVLRADLA	38	0.5000	5.95
34	LNFSHQNGI	125	0.5000	5.95
35	VREDPIPPS	228	0.5000	5.95
36	VAVVAVLAV	332	0.5000	5.95
37	VKKLTAAGF	440	0.5000	5.95
38	VAGQTVDVA	499	0.5000	5.95

39	WVDAEPRLR	570	0.5000	5.95
40	LRFRREAQN	53	0.4000	4.76
41	MISATNAVK	144	0.4000	4.76
42	VIGTAQYLS	175	0.4000	4.76
43	VYSLGCVLY	198	0.4000	4.76
44	VLTVVVTIA	340	0.4000	4.76
45	LTYAEAVKK	434	0.4000	4.76
46	FKIRTLQKP	381	0.3000	3.57
47	VYQNPPAGT	603	0.3000	3.57
48	VLRADLARD	40	0.2000	2.38
49	VAVYDTGEA	71	0.2000	2.38
50	IELQVSKGN	550	0.2000	2.38
51	VLTDAERTS	286	0.1000	1.19
52	WVAVVAVLA	331	0.1000	1.19
53	VLAVLTVVV	337	0.1000	1.19
54	IIIVGSGPA	484	0.1000	1.19
55	VAQKNLNVY	506	0.1000	1.19
56	MTPKRAIEV	109	-0.1000	0
57	VVAVLAVLT	334	-0.1000	0
58	FVMPDLSGM	560	-0.1000	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	VVIIIVGSG	482	4.7000	54.02
2	IRTLQKPDS	383	4.6500	53.45
3	VAVLAVLTV	335	3.6000	41.38
4	VKPANIMIS	138	3.5000	40.23
5	VAVVAVLAV	332	2.9000	33.33
6	VVTIAINTF	344	2.6000	29.89
7	YELGEILGF	10	2.5000	28.74
8	FGRFKQANS	448	2.4000	27.59
9	VVYQNPPAG	602	2.3500	27.01
10	FGIARAIAD	156	2.2000	25.29

11	LTVVVTIAI	341	2.1000	24.14
12	VKKLTAAGF	440	2.1000	24.14
13	WVAVVAVLA	331	1.9000	21.84
14	FYLRFRREA	51	1.8000	20.69
15	FVMPDLSGM	560	1.8000	20.69
16	ITNVVIIIV	479	1.7000	19.54
17	YLRFRREAQ	52	1.6000	18.39
18	IIIVGSGPA	484	1.5000	17.24
19	YSLGCVLYE	199	1.4000	16.09
20	WVDAEPRLR	570	1.4000	16.09
21	VVVTIAINT	343	1.3000	14.94
22	VVLKALAKN	249	1.2000	13.79
23	LKALAKNPE	251	1.2000	13.79
24	VYGFTKFSQ	513	1.2000	13.79
25	YQTAAEMRA	262	1.1000	12.64
26	LARDLRLHR	26	1.0000	11.49
27	YIVMEYVDG	88	1.0000	11.49
28	IMISATNAV	143	1.0000	11.49
29	ILGFGGMSE	15	0.9000	10.34
30	VYSLGCVLY	198	0.9000	10.34
31	LVRVHNGEP	272	0.9000	10.34
32	VLAVLTVVV	337	0.9000	10.34
33	VRGQSSADA	364	0.9000	10.34
34	IVGSGPATK	486	0.9000	10.34
35	YVDGVTLRD	93	0.8000	9.20
36	INTFGGITR	349	0.8000	9.20
37	IGSVGRWVA	325	0.7000	8.05
38	LAVLTVVVT	338	0.7000	8.05
39	FKIRTLQKP	381	0.7000	8.05
40	LRALGWTGM	577	0.7000	8.05
41	IIHRDVKPA	133	0.6000	6.90
42	LVGKVIGTN	462	0.5000	5.75
43	FKQANSPST	451	0.4500	5.17
44	VVAVLAVLT	334	0.4000	4.60

45	FTKFSQASV	516	0.4000	4.60
46	VLRADLARD	40	0.3000	3.45
47	VLTVVVTIA	340	0.3000	3.45
48	VIELQVSKG	549	0.3000	3.45
49	VNRDGIITL	613	0.2600	2.99
50	IPDVSTLTY	428	0.2000	2.30
51	VIIIVGSGP	483	0.2000	2.30
52	VIGTAQYLS	175	0.1000	1.15
53	VREDPIPPS	228	0.0500	0.57
54	FRREAQNAA	55	-0.1000	0
55	MTPKRAIEV	109	-0.1000	0
56	VMDFGIARA	153	-0.1000	0
57	VYQNPPAGT	603	-0.1000	0
58	VHLARDLRL	24	-0.1400	0
59	LRDIVHTEG	99	-0.2000	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	IRTLQKPDS	383	4.5000	51.14
2	VVYQNPPAG	602	3.9000	44.32
3	VYGFTKFSQ	513	3.6000	40.91
4	VVLKALAKN	249	3.5000	39.77
5	FYLRFRREA	51	3.3000	37.50
6	VKPANIMIS	138	3.2000	36.36
7	IMISATNAV	143	3.2000	36.36
8	VAYQHVRED	223	3.2000	36.36
9	VVTIAINTF	344	3.2000	36.36
10	VVIIIVGSG	482	3.1000	35.23
11	VRGQSSADA	364	2.9000	32.95
12	VAVLAVLTV	335	2.8000	31.82
13	IIHRDVKPA	133	2.7000	30.68
14	MRADLVRVH	268	2.7000	30.68
15	LKALAKNPE	251	2.6000	29.55

16	LRLHRDVAV	30	2.5000	28.41
17	IVMEYVDGV	89	2.4000	27.27
18	VQVPDVRGQ	359	2.4000	27.27
19	VKKLTAAGF	440	2.4000	27.27
20	VRVHNGEPP	273	2.2000	25.00
21	VAVKVLRAD	36	2.1000	23.86
22	IVGSGPATK	486	2.0000	22.73
23	WVDAEPRLR	570	2.0000	22.73
24	IATLQNRGF	373	1.9000	21.59
25	VGRWVAVVA	328	1.8000	20.45
26	FGRFKQANS	448	1.8000	20.45
27	LRADLARDP	41	1.7000	19.32
28	VYSLGCVLY	198	1.7000	19.32
29	LVGKVIGTN	462	1.7000	19.32
30	VAVVAVLAV	332	1.5000	17.05
31	LAVLTVVVT	338	1.5000	17.05
32	LNFSHQNGI	125	1.4000	15.91
33	VAQKNLNVY	506	1.4000	15.91
34	LQVSKGNQF	552	1.4000	15.91
35	FVMPDLSGM	560	1.4000	15.91
36	LRALGWTGM	577	1.4000	15.91
37	VLRADLARD	40	1.3000	14.77
38	YLRFRREAQ	52	1.3000	14.77
39	VTLRDIVHT	97	1.3000	14.77
40	VMDFGIARA	153	1.3000	14.77
41	FKIRTLQKP	381	1.3000	14.77
42	LARDLRLHR	26	1.2000	13.64
43	LRFRREAQN	53	1.2000	13.64
44	IGSVGRWVA	325	1.2000	13.64
45	VLAVLTVVV	337	1.1000	12.50
46	ILGFGGMSE	15	1.0000	11.36
47	LQNRGFKIR	376	1.0000	11.36
48	VIELQVSKG	549	1.0000	11.36
49	IELQVSKGN	550	1.0000	11.36

50	VYQNPPAGT	603	1.0000	11.36
51	MTPKRAIEV	109	0.9000	10.23
52	VREDPIPPS	228	0.9000	10.23
53	IPPSARHEG	233	0.9000	10.23
54	INTFGGITR	349	0.9000	10.23
55	IGTNPPANQ	467	0.9000	10.23
56	VIGTAQYLS	175	0.8000	9.09
57	VSVAYQHVR	221	0.7000	7.95
58	VLKALAKNP	250	0.7000	7.95
59	YELGEILGF	10	0.6000	6.82
60	FRREAQNAA	55	0.6000	6.82
61	LTGEPPFTG	209	0.6000	6.82
62	VVAVLAVLT	334	0.6000	6.82

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	FYLRFRREA	51	4.3000	48.86
2	IRTLQKPDS	383	3.5000	39.77
3	WVDAEPRLR	570	3.0000	34.09
4	VVYQNPPAG	602	2.9000	32.95
5	FGRFKQANS	448	2.8000	31.82
6	VYGFTKFSQ	513	2.6000	29.55
7	VVLKALAKN	249	2.5000	28.41
8	FVMPDLSGM	560	2.4000	27.27
9	YLRFRREAQ	52	2.3000	26.14
10	FKIRTLQKP	381	2.3000	26.14
11	VKPANIMIS	138	2.2000	25.00
12	IMISATNAV	143	2.2000	25.00
13	VAYQHVRED	223	2.2000	25.00
14	VVTIAINTF	344	2.2000	25.00
15	VVIIIVGSG	482	2.1000	23.86
16	VRGQSSADA	364	1.9000	21.59
17	VAVLAVLTV	335	1.8000	20.45

18	IIHRDVKPA	133	1.7000	19.32
19	MRADLVRVH	268	1.7000	19.32
20	YELGEILGF	10	1.6000	18.18
21	FRREAQNAA	55	1.6000	18.18
22	LKALAKNPE	251	1.6000	18.18
23	LRLHRDVAV	30	1.5000	17.05
24	IVMEYVDGV	89	1.4000	15.91
25	VQVPDVRGQ	359	1.4000	15.91
26	VKKLTAAGF	440	1.4000	15.91
27	YIVMEYVDG	88	1.3000	14.77
28	VRVHNGEPP	273	1.2000	13.64
29	VAVKVLRAD	36	1.1000	12.50
30	WVAVVAVLA	331	1.1000	12.50
31	IVGSGPATK	486	1.0000	11.36
32	FGIARAIAD	156	0.9000	10.23
33	IATLQNRGF	373	0.9000	10.23
34	VGRWVAVVA	328	0.8000	9.09
35	FTKFSQASV	516	0.8000	9.09
36	LRADLARDP	41	0.7000	7.95
37	VYSLGCVLY	198	0.7000	7.95
38	LVGKVIGTN	462	0.7000	7.95
39	YSLGCVLYE	199	0.5000	5.68
40	VAVVAVLAV	332	0.5000	5.68
41	LAVLTVVVT	338	0.5000	5.68
42	LNFSHQNGI	125	0.4000	4.55
43	VAQKNLNVY	506	0.4000	4.55
44	LQVSKGNQF	552	0.4000	4.55
45	LRALGWTGM	577	0.4000	4.55
46	VLRADLARD	40	0.3000	3.41
47	VTLRDIVHT	97	0.3000	3.41
48	VMDFGIARA	153	0.3000	3.41
49	LARDLRLHR	26	0.2000	2.27
50	LRFRREAQN	53	0.2000	2.27
51	IGSVGRWVA	325	0.2000	2.27

52	VLAVLTVVV	337	0.1000	1.14
53	FGGMSEVHL	18	-0.0400	0
54	YVDGVTLRD	93	-0.1000	0
55	MTPKRAIEV	109	-0.1000	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	VYGFTKFSQ	513	5.1000	56.67
2	VAYQHVRED	223	4.8000	53.33
3	VVLKALAKN	249	4.7000	52.22
4	MRADLVRVH	268	4.5000	50.00
5	LKALAKNPE	251	4.2000	46.67
6	IRTLQKPDS	383	4.1000	45.56
7	VQVPDVRGQ	359	3.9000	43.33
8	VVYQNPPAG	602	3.8000	42.22
9	VAVKVLRAD	36	3.7000	41.11
10	FYLRFRREA	51	3.3000	36.67
11	VVIIIVGSG	482	3.0000	33.33
12	VLRADLARD	40	2.9000	32.22
13	VRGQSSADA	364	2.9000	32.22
14	LVGKVIGTN	462	2.9000	32.22
15	YLRFRREAQ	52	2.8000	31.11
16	VKPANIMIS	138	2.8000	31.11
17	IIHRDVKPA	133	2.7000	30.00
18	ILGFGGMSE	15	2.6000	28.89
19	IMISATNAV	143	2.5000	27.78
20	LRFRREAQN	53	2.4000	26.67
21	IGTNPPANQ	467	2.4000	26.67
22	VVTIAINTF	344	2.2000	24.44
23	IELQVSKGN	550	2.2000	24.44
24	VAVLAVLTV	335	2.1000	23.33
25	LRLHRDVAV	30	1.8000	20.00
26	VGRWVAVVA	328	1.8000	20.00

27	IVMEYVDGV	89	1.7000	18.89
28	LAVLTVVVT	338	1.7000	18.89
29	VRVHNGEPP	273	1.6000	17.78
30	VTLRDIVHT	97	1.5000	16.67
31	IHRDVKPAN	134	1.5000	16.67
32	FGIARAIAD	156	1.5000	16.67
33	VYSLGCVLY	198	1.5000	16.67
34	VKKLTAAGF	440	1.4000	15.56
35	FGRFKQANS	448	1.4000	15.56
36	VMDFGIARA	153	1.3000	14.44
37	VLYEVLTGE	204	1.3000	14.44
38	VIGTDPAAN	398	1.3000	14.44
39	IGSVGRWVA	325	1.2000	13.33
40	IVGSGPATK	486	1.2000	13.33
41	VDVAQKNLN	504	1.2000	13.33
42	VAQKNLNVY	506	1.2000	13.33
43	VYQNPPAGT	603	1.2000	13.33
44	LRADLARDP	41	1.1000	12.22
45	LSPEQARGD	182	1.1000	12.22
46	YSLGCVLYE	199	1.1000	12.22
47	FVMPDLSGM	560	1.0000	11.11
48	LRALGWTGM	577	1.0000	11.11
49	IATLQNRGF	373	0.9000	10.00
50	VIELQVSKG	549	0.9000	10.00
51	IPPSARHEG	233	0.8000	8.89
52	VAVVAVLAV	332	0.8000	8.89
53	VVAVLAVLT	334	0.8000	8.89
54	VNVSTGPEQ	417	0.8000	8.89
55	VIGTNPPAN	466	0.8000	8.89
56	LNFSHQNGI	125	0.7000	7.78
57	VVVTIAINT	343	0.7000	7.78
58	FKIRTLQKP	381	0.7000	7.78
59	FRREAQNAA	55	0.6000	6.67
60	VKVLRADLA	38	0.5000	5.56

61	YVDGVTLRD	93	0.5000	5.56
62	LTGEPPFTG	209	0.5000	5.56

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	VVIIIVGSG	482	4.7000	54.02
2	IRTLQKPDS	383	4.6500	53.45
3	VAVLAVLTV	335	3.6000	41.38
4	VKPANIMIS	138	3.5000	40.23
5	VAVVAVLAV	332	2.9000	33.33
6	VVTIAINTF	344	2.6000	29.89
7	YELGEILGF	10	2.5000	28.74
8	FGRFKQANS	448	2.4000	27.59
9	VVYQNPPAG	602	2.3500	27.01
10	FGIARAIAD	156	2.2000	25.29
11	LTVVVTIAI	341	2.1000	24.14
12	VKKLTAAGF	440	2.1000	24.14
13	WVAVVAVLA	331	1.9000	21.84
14	FYLRFRREA	51	1.8000	20.69
15	FVMPDLSGM	560	1.8000	20.69
16	ITNVVIIIV	479	1.7000	19.54
17	YLRFRREAQ	52	1.6000	18.39
18	IIIVGSGPA	484	1.5000	17.24
19	YSLGCVLYE	199	1.4000	16.09
20	WVDAEPRLR	570	1.4000	16.09
21	VVVTIAINT	343	1.3000	14.94
22	VVLKALAKN	249	1.2000	13.79
23	LKALAKNPE	251	1.2000	13.79
24	VYGFTKFSQ	513	1.2000	13.79
25	YQTAAEMRA	262	1.1000	12.64
26	LARDLRLHR	26	1.0000	11.49
27	YIVMEYVDG	88	1.0000	11.49
28	IMISATNAV	143	1.0000	11.49

29	ILGFGGMSE	15	0.9000	10.34
30	VYSLGCVLY	198	0.9000	10.34
31	LVRVHNGEP	272	0.9000	10.34
32	VLAVLTVVV	337	0.9000	10.34
33	VRGQSSADA	364	0.9000	10.34
34	IVGSGPATK	486	0.9000	10.34
35	YVDGVTLRD	93	0.8000	9.20
36	INTFGGITR	349	0.8000	9.20
37	IGSVGRWVA	325	0.7000	8.05
38	LAVLTVVVT	338	0.7000	8.05
39	FKIRTLQKP	381	0.7000	8.05
40	LRALGWTGM	577	0.7000	8.05
41	IIHRDVKPA	133	0.6000	6.90
42	LVGKVIGTN	462	0.5000	5.75
43	FKQANSPST	451	0.4500	5.17
44	VVAVLAVLT	334	0.4000	4.60
45	FTKFSQASV	516	0.4000	4.60
46	VLRADLARD	40	0.3000	3.45
47	VLTVVVTIA	340	0.3000	3.45
48	VIELQVSKG	549	0.3000	3.45
49	VNRDGIITL	613	0.2600	2.99
50	IPDVSTLTY	428	0.2000	2.30
51	VIIIVGSGP	483	0.2000	2.30
52	VIGTAQYLS	175	0.1000	1.15
53	VREDPIPPS	228	0.0500	0.57
54	FRREAQNAA	55	-0.1000	0
55	MTPKRAIEV	109	-0.1000	0
56	VMDFGIARA	153	-0.1000	0
57	VYQNPPAGT	603	-0.1000	0
58	VHLARDLRL	24	-0.1400	0
59	LRDIVHTEG	99	-0.2000	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	VVIIIVGSG	482	3.2000	47.06
2	IRTLQKPDS	383	3.1000	45.59
3	FGRFKQANS	448	2.0000	29.41
4	FYLRFRREA	51	1.6000	23.53
5	VKPANIMIS	138	1.5000	22.06
6	WVAVVAVLA	331	1.4000	20.59
7	IIIVGSGPA	484	1.4000	20.59
8	VYGFTKFSQ	513	1.4000	20.59
9	YLRFRREAQ	52	1.2000	17.65
10	VRGQSSADA	364	0.9000	13.24
11	VAVLAVLTV	335	0.8000	11.76
12	IVGSGPATK	486	0.8000	11.76
13	FGGITRDVQ	352	0.7000	10.29
14	IGTNPPANQ	467	0.5000	7.35
15	VVLKALAKN	249	0.4000	5.88
16	VVTIAINTF	344	0.4000	5.88
17	FVMPDLSGM	560	0.3000	4.41
18	VKKLTAAGF	440	0.2000	2.94
19	MRADLVRVH	268	0.1800	2.65
20	VAVVAVLAV	332	0.1000	1.47
21	VQVPDVRGQ	359	0.1000	1.47
22	VMDFGIARA	153	-0.1000	0
23	IGSVGRWVA	325	-0.1000	0
24	LVRVHNGEP	272	-0.2000	0
25	VVYQNPPAG	602	-0.2000	0
26	IMISATNAV	143	-0.3000	0
27	VKVMDFGIA	151	-0.3000	0
28	WVDAEPRLR	570	-0.3000	0
29	FRREAQNAA	55	-0.4000	0
30	LTVVVTIAI	341	-0.4000	0
31	FKIRTLQKP	381	-0.4000	0
32	LVGKVIGTN	462	-0.4000	0
33	FGIARAIAD	156	-0.5000	0

34	LKALAKNPE	251	-0.5000	0
35	YQTAAEMRA	262	-0.5000	0
36	LAVLTVVVT	338	-0.5000	0
37	MISATNAVK	144	-0.6000	0
38	VLAVLTVVV	337	-0.6000	0
39	FTKFSQASV	516	-0.6000	0
40	VKVLRADLA	38	-0.7000	0
41	VLRADLARD	40	-0.8000	0
42	VVAVLAVLT	334	-0.8000	0
43	VLTVVVTIA	340	-0.8000	0
44	VIIIVGSGP	483	-0.8000	0
45	VYQNPPAGT	603	-0.8000	0
46	VAVYDTGEA	71	-0.9000	0
47	YIVMEYVDG	88	-0.9000	0
48	VYSLGCVLY	198	-0.9000	0
49	ITNVVIIIV	479	-0.9000	0
50	VIGTAQYLS	175	-1.0000	0
51	VGRWVAVVA	328	-1.0000	0
52	VVVTIAINT	343	-1.0000	0
53	IVMEYVDGV	89	-1.1000	0
54	VIELQVSKG	549	-1.1000	0
55	YELGEILGF	10	-1.2000	0
56	VIGTDPAAN	398	-1.2000	0
57	IEVIADACQ	115	-1.4000	0
58	FKQANSPST	451	-1.4000	0
59	LRFRREAQN	53	-1.5000	0
60	VREDPIPPS	228	-1.5000	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	IRTLQKPDS	383	5.2500	63.25
2	VVIIIVGSG	482	4.3000	51.81
3	VKPANIMIS	138	4.1000	49.40

4	VAVLAVLTV	335	3.6000	43.37
5	VAVVAVLAV	332	2.9000	34.94
6	VYGFTKFSQ	513	2.9000	34.94
7	IIIVGSGPA	484	2.5000	30.12
8	LTVVVTIAI	341	2.2000	26.51
9	VVYQNPPAG	602	1.9500	23.49
10	VRGQSSADA	364	1.9000	22.89
11	IVGSGPATK	486	1.8000	21.69
12	IGSVGRWVA	325	1.7000	20.48
13	VVTIAINTF	344	1.7000	20.48
14	ITNVVIIIV	479	1.7000	20.48
15	IIHRDVKPA	133	1.6000	19.28
16	VVVTIAINT	343	1.6000	19.28
17	IGTNPPANQ	467	1.5000	18.07
18	VVLKALAKN	249	1.4000	16.87
19	MRADLVRVH	268	1.3800	16.63
20	YLRFRREAQ	52	1.3000	15.66
21	VLTVVVTIA	340	1.3000	15.66
22	VQVPDVRGQ	359	1.3000	15.66
23	VKKLTAAGF	440	1.2000	14.46
24	IMISATNAV	143	1.0000	12.05
25	LAVLTVVVT	338	1.0000	12.05
26	FGRFKQANS	448	1.0000	12.05
27	VMDFGIARA	153	0.9000	10.84
28	LVRVHNGEP	272	0.9000	10.84
29	WVAVVAVLA	331	0.9000	10.84
30	VLAVLTVVV	337	0.9000	10.84
31	FYLRFRREA	51	0.8000	9.64
32	VKVMDFGIA	151	0.8000	9.64
33	LKALAKNPE	251	0.8000	9.64
34	VIGTAQYLS	175	0.7000	8.43
35	VVAVLAVLT	334	0.7000	8.43
36	LVGKVIGTN	462	0.7000	8.43
37	VREDPIPPS	228	0.6500	7.83

38	VYSLGCVLY	198	0.6000	7.23
39	ILGFGGMSE	15	0.5000	6.02
40	LARDLRLHR	26	0.5000	6.02
41	VGRWVAVVA	328	0.5000	6.02
42	MISATNAVK	144	0.4000	4.82
43	VNVSTGPEQ	417	0.3500	4.22
44	INTFGGITR	349	0.3000	3.61
45	VNRDGIITL	613	0.3000	3.61
46	VLRADLARD	40	0.2000	2.41
47	VAVYDTGEA	71	0.2000	2.41
48	VIIIVGSGP	483	0.2000	2.41
49	LRALGWTGM	577	0.2000	2.41
50	LGWTGMLDK	580	0.2000	2.41
51	VYQNPPAGT	603	0.2000	2.41
52	FGIARAIAD	156	0.1000	1.20
53	YQTAAEMRA	262	0.1000	1.20
54	VHNGEPPEA	275	0.0500	0.60
55	VHLARDLRL	24	-0.1000	0
56	MTPKRAIEV	109	-0.1000	0
57	IPDVSTLTY	428	-0.1000	0
58	LTYAEAVKK	434	-0.1000	0
59	VIELQVSKG	549	-0.1000	0
60	VIGTDPAAN	398	-0.2000	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	VVIIIVGSG	482	4.6000	51.69
2	IRTLQKPDS	383	4.2500	47.75
3	FGIARAIAD	156	3.8000	42.70
4	YLRFRREAQ	52	3.1000	34.83
5	VKPANIMIS	138	3.1000	34.83
6	YSLGCVLYE	199	3.0000	33.71
7	VAVLAVLTV	335	2.9000	32.58

8	LKALAKNPE	251	2.8000	31.46
9	VYGFTKFSQ	513	2.7000	30.34
10	ILGFGGMSE	15	2.5000	28.09
11	YVDGVTLRD	93	2.4000	26.97
12	VVLKALAKN	249	2.4000	26.97
13	VVYQNPPAG	602	2.2500	25.28
14	VAVVAVLAV	332	2.2000	24.72
15	FGRFKQANS	448	2.0000	22.47
16	VLRADLARD	40	1.9000	21.35
17	WVAVVAVLA	331	1.9000	21.35
18	FYLRFRREA	51	1.8000	20.22
19	LVGKVIGTN	462	1.7000	19.10
20	MRADLVRVH	268	1.6000	17.98
21	VVTIAINTF	344	1.6000	17.98
22	YELGEILGF	10	1.5000	16.85
23	VVVTIAINT	343	1.5000	16.85
24	IIIVGSGPA	484	1.5000	16.85
25	LTVVVTIAI	341	1.4000	15.73
26	FVMPDLSGM	560	1.4000	15.73
27	IGTNPPANQ	467	1.3000	14.61
28	VAYQHVRED	223	1.2000	13.48
29	FGGITRDVQ	352	1.2000	13.48
30	YQTAAEMRA	262	1.1000	12.36
31	VQVPDVRGQ	359	1.1000	12.36
32	VKKLTAAGF	440	1.1000	12.36
33	ITNVVIIIV	479	1.0000	11.24
34	YIVMEYVDG	88	0.9000	10.11
35	FSHQNGIIH	127	0.9000	10.11
36	LAVLTVVVT	338	0.9000	10.11
37	VRGQSSADA	364	0.9000	10.11
38	VIGTDPAAN	398	0.8000	8.99
39	VIGTNPPAN	466	0.7500	8.43
40	VYSLGCVLY	198	0.7000	7.87
41	IGSVGRWVA	325	0.7000	7.87

42	IHRDVKPAN	134	0.6500	7.30
43	FKQANSPST	451	0.6500	7.30
44	IIHRDVKPA	133	0.6000	6.74
45	VVAVLAVLT	334	0.6000	6.74
46	LRFRREAQN	53	0.5000	5.62
47	IMISATNAV	143	0.3000	3.37
48	LVRVHNGEP	272	0.3000	3.37
49	VLTVVVTIA	340	0.3000	3.37
50	LRALGWTGM	577	0.3000	3.37
51	VNRDGIITL	613	0.3000	3.37
52	VLAVLTVVV	337	0.2000	2.25
53	VIELQVSKG	549	0.2000	2.25
54	VNVSTGPEQ	417	0.1500	1.69
55	FKIRTLQKP	381	0.1000	1.12
56	IVGSGPATK	486	0.1000	1.12
57	VYQNPPAGT	603	0.1000	1.12
58	VHLARDLRL	24	-0.1000	0
59	FRREAQNAA	55	-0.1000	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	VYGFTKFSQ	513	4.3000	51.19
2	IRTLQKPDS	383	4.1000	48.81
3	FYLRFRREA	51	3.3000	39.29
4	MRADLVRVH	268	3.2800	39.05
5	VQVPDVRGQ	359	3.1000	36.90
6	VRGQSSADA	364	2.9000	34.52
7	VKPANIMIS	138	2.8000	33.33
8	IIHRDVKPA	133	2.7000	32.14
9	VVLKALAKN	249	2.7000	32.14
10	VVYQNPPAG	602	2.5000	29.76
11	IMISATNAV	143	2.2000	26.19
12	VAYQHVRED	223	2.1000	25.00

13	YLRFRREAQ	52	2.0000	23.81
14	IVGSGPATK	486	1.9000	22.62
15	VGRWVAVVA	328	1.8000	21.43
16	VAVLAVLTV	335	1.8000	21.43
17	VVIIIVGSG	482	1.7000	20.24
18	IGTNPPANQ	467	1.6000	19.05
19	LRLHRDVAV	30	1.5000	17.86
20	IVMEYVDGV	89	1.4000	16.67
21	FGRFKQANS	448	1.4000	16.67
22	VMDFGIARA	153	1.3000	15.48
23	VVTIAINTF	344	1.3000	15.48
24	LKALAKNPE	251	1.2000	14.29
25	VRVHNGEPP	273	1.2000	14.29
26	IGSVGRWVA	325	1.2000	14.29
27	VAVKVLRAD	36	1.0000	11.90
28	LVGKVIGTN	462	0.9000	10.71
29	LAVLTVVVT	338	0.8000	9.52
30	LRADLARDP	41	0.7000	8.33
31	FRREAQNAA	55	0.6000	7.14
32	VTLRDIVHT	97	0.6000	7.14
33	VKVLRADLA	38	0.5000	5.95
34	LNFSHQNGI	125	0.5000	5.95
35	VREDPIPPS	228	0.5000	5.95
36	VAVVAVLAV	332	0.5000	5.95
37	VKKLTAAGF	440	0.5000	5.95
38	VAGQTVDVA	499	0.5000	5.95
39	WVDAEPRLR	570	0.5000	5.95
40	LRFRREAQN	53	0.4000	4.76
41	MISATNAVK	144	0.4000	4.76
42	VIGTAQYLS	175	0.4000	4.76
43	VYSLGCVLY	198	0.4000	4.76
44	VLTVVVTIA	340	0.4000	4.76
45	LTYAEAVKK	434	0.4000	4.76
46	FKIRTLQKP	381	0.3000	3.57

47	VYQNPPAGT	603	0.3000	3.57
48	VLRADLARD	40	0.2000	2.38
49	VAVYDTGEA	71	0.2000	2.38
50	IELQVSKGN	550	0.2000	2.38
51	VLTDAERTS	286	0.1000	1.19
52	WVAVVAVLA	331	0.1000	1.19
53	VLAVLTVVV	337	0.1000	1.19
54	IIIVGSGPA	484	0.1000	1.19
55	VAQKNLNVY	506	0.1000	1.19
56	MTPKRAIEV	109	-0.1000	0
57	VVAVLAVLT	334	-0.1000	0
58	FVMPDLSGM	560	-0.1000	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	FYLRFRREA	51	4.3000	51.19
2	VYGFTKFSQ	513	3.3000	39.29
3	IRTLQKPDS	383	3.1000	36.90
4	YLRFRREAQ	52	3.0000	35.71
5	FGRFKQANS	448	2.4000	28.57
6	MRADLVRVH	268	2.2800	27.14
7	VQVPDVRGQ	359	2.1000	25.00
8	VRGQSSADA	364	1.9000	22.62
9	VKPANIMIS	138	1.8000	21.43
10	IIHRDVKPA	133	1.7000	20.24
11	VVLKALAKN	249	1.7000	20.24
12	FRREAQNAA	55	1.6000	19.05
13	WVDAEPRLR	570	1.5000	17.86
14	VVYQNPPAG	602	1.5000	17.86
15	FKIRTLQKP	381	1.3000	15.48
16	IMISATNAV	143	1.2000	14.29
17	VAYQHVRED	223	1.1000	13.10
18	WVAVVAVLA	331	1.1000	13.10

19	IVGSGPATK	486	0.9000	10.71
20	FVMPDLSGM	560	0.9000	10.71
21	VGRWVAVVA	328	0.8000	9.52
22	VAVLAVLTV	335	0.8000	9.52
23	VVIIIVGSG	482	0.7000	8.33
24	IGTNPPANQ	467	0.6000	7.14
25	LRLHRDVAV	30	0.5000	5.95
26	IVMEYVDGV	89	0.4000	4.76
27	VMDFGIARA	153	0.3000	3.57
28	VVTIAINTF	344	0.3000	3.57
29	LKALAKNPE	251	0.2000	2.38
30	VRVHNGEPP	273	0.2000	2.38
31	IGSVGRWVA	325	0.2000	2.38
32	FGGITRDVQ	352	0.1000	1.19
33	YIVMEYVDG	88	-0.1000	0
34	LVGKVIGTN	462	-0.1000	0
35	FGIARAIAD	156	-0.2000	0
36	YQTAAEMRA	262	-0.2000	0
37	LAVLTVVVT	338	-0.2000	0
38	FTKFSQASV	516	-0.2000	0
39	YELGEILGF	10	-0.3000	0
40	LRADLARDP	41	-0.3000	0
41	VTLRDIVHT	97	-0.4000	0
42	VKVLRADLA	38	-0.5000	0
43	LNFSHQNGI	125	-0.5000	0
44	VREDPIPPS	228	-0.5000	0
45	VAVVAVLAV	332	-0.5000	0
46	VKKLTAAGF	440	-0.5000	0
47	VAGQTVDVA	499	-0.5000	0
48	LRFRREAQN	53	-0.6000	0
49	MISATNAVK	144	-0.6000	0
50	VIGTAQYLS	175	-0.6000	0
51	VYSLGCVLY	198	-0.6000	0
52	VLTVVVTIA	340	-0.6000	0

53	LTYAEAVKK	434	-0.6000	0
54	FSHQNGIIH	127	-0.6200	0
55	FKQANSPST	451	-0.7000	0
56	VYQNPPAGT	603	-0.7000	0
57	VLRADLARD	40	-0.8000	0
58	VAVYDTGEA	71	-0.8000	0
59	IELQVSKGN	550	-0.8000	0
60	YSLGCVLYE	199	-0.9000	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	IRTLQKPDS	383	4.5000	51.14
2	VVYQNPPAG	602	3.9000	44.32
3	VYGFTKFSQ	513	3.6000	40.91
4	VVLKALAKN	249	3.5000	39.77
5	FYLRFRREA	51	3.3000	37.50
6	VKPANIMIS	138	3.2000	36.36
7	IMISATNAV	143	3.2000	36.36
8	VAYQHVRED	223	3.2000	36.36
9	VVTIAINTF	344	3.2000	36.36
10	VVIIIVGSG	482	3.1000	35.23
11	VRGQSSADA	364	2.9000	32.95
12	VAVLAVLTV	335	2.8000	31.82
13	IIHRDVKPA	133	2.7000	30.68
14	MRADLVRVH	268	2.7000	30.68
15	LKALAKNPE	251	2.6000	29.55
16	LRLHRDVAV	30	2.5000	28.41
17	IVMEYVDGV	89	2.4000	27.27
18	VQVPDVRGQ	359	2.4000	27.27
19	VKKLTAAGF	440	2.4000	27.27
20	VRVHNGEPP	273	2.2000	25.00
21	VAVKVLRAD	36	2.1000	23.86
22	IVGSGPATK	486	2.0000	22.73

23	WVDAEPRLR	570	2.0000	22.73
24	IATLQNRGF	373	1.9000	21.59
25	VGRWVAVVA	328	1.8000	20.45
26	FGRFKQANS	448	1.8000	20.45
27	LRADLARDP	41	1.7000	19.32
28	VYSLGCVLY	198	1.7000	19.32
29	LVGKVIGTN	462	1.7000	19.32
30	VAVVAVLAV	332	1.5000	17.05
31	LAVLTVVVT	338	1.5000	17.05
32	LNFSHQNGI	125	1.4000	15.91
33	VAQKNLNVY	506	1.4000	15.91
34	LQVSKGNQF	552	1.4000	15.91
35	FVMPDLSGM	560	1.4000	15.91
36	LRALGWTGM	577	1.4000	15.91
37	VLRADLARD	40	1.3000	14.77
38	YLRFRREAQ	52	1.3000	14.77
39	VTLRDIVHT	97	1.3000	14.77
40	VMDFGIARA	153	1.3000	14.77
41	FKIRTLQKP	381	1.3000	14.77
42	LARDLRLHR	26	1.2000	13.64
43	LRFRREAQN	53	1.2000	13.64
44	IGSVGRWVA	325	1.2000	13.64
45	VLAVLTVVV	337	1.1000	12.50
46	ILGFGGMSE	15	1.0000	11.36
47	LQNRGFKIR	376	1.0000	11.36
48	VIELQVSKG	549	1.0000	11.36
49	IELQVSKGN	550	1.0000	11.36
50	VYQNPPAGT	603	1.0000	11.36
51	MTPKRAIEV	109	0.9000	10.23
52	VREDPIPPS	228	0.9000	10.23
53	IPPSARHEG	233	0.9000	10.23
54	INTFGGITR	349	0.9000	10.23
55	IGTNPPANQ	467	0.9000	10.23
56	VIGTAQYLS	175	0.8000	9.09

57	VSVAYQHVR	221	0.7000	7.95
58	VLKALAKNP	250	0.7000	7.95
59	YELGEILGF	10	0.6000	6.82
60	FRREAQNAA	55	0.6000	6.82
61	LTGEPPFTG	209	0.6000	6.82
62	VVAVLAVLT	334	0.6000	6.82

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	IRTLQKPDS	383	4.5000	51.14
2	VVYQNPPAG	602	3.9000	44.32
3	VYGFTKFSQ	513	3.6000	40.91
4	VVLKALAKN	249	3.5000	39.77
5	FYLRFRREA	51	3.3000	37.50
6	VKPANIMIS	138	3.2000	36.36
7	IMISATNAV	143	3.2000	36.36
8	VAYQHVRED	223	3.2000	36.36
9	VVTIAINTF	344	3.2000	36.36
10	VVIIIVGSG	482	3.1000	35.23
11	VRGQSSADA	364	2.9000	32.95
12	VAVLAVLTV	335	2.8000	31.82
13	IIHRDVKPA	133	2.7000	30.68
14	MRADLVRVH	268	2.7000	30.68
15	LKALAKNPE	251	2.6000	29.55
16	LRLHRDVAV	30	2.5000	28.41
17	IVMEYVDGV	89	2.4000	27.27
18	VQVPDVRGQ	359	2.4000	27.27
19	VKKLTAAGF	440	2.4000	27.27
20	VRVHNGEPP	273	2.2000	25.00
21	VAVKVLRAD	36	2.1000	23.86
22	IVGSGPATK	486	2.0000	22.73
23	WVDAEPRLR	570	2.0000	22.73
24	IATLQNRGF	373	1.9000	21.59

25	VGRWVAVVA	328	1.8000	20.45
26	FGRFKQANS	448	1.8000	20.45
27	LRADLARDP	41	1.7000	19.32
28	VYSLGCVLY	198	1.7000	19.32
29	LVGKVIGTN	462	1.7000	19.32
30	VAVVAVLAV	332	1.5000	17.05
31	LAVLTVVVT	338	1.5000	17.05
32	LNFSHQNGI	125	1.4000	15.91
33	VAQKNLNVY	506	1.4000	15.91
34	LQVSKGNQF	552	1.4000	15.91
35	FVMPDLSGM	560	1.4000	15.91
36	LRALGWTGM	577	1.4000	15.91
37	VLRADLARD	40	1.3000	14.77
38	YLRFRREAQ	52	1.3000	14.77
39	VTLRDIVHT	97	1.3000	14.77
40	VMDFGIARA	153	1.3000	14.77
41	FKIRTLQKP	381	1.3000	14.77
42	LARDLRLHR	26	1.2000	13.64
43	LRFRREAQN	53	1.2000	13.64
44	IGSVGRWVA	325	1.2000	13.64
45	VLAVLTVVV	337	1.1000	12.50
46	ILGFGGMSE	15	1.0000	11.36
47	LQNRGFKIR	376	1.0000	11.36
48	VIELQVSKG	549	1.0000	11.36
49	IELQVSKGN	550	1.0000	11.36
50	VYQNPPAGT	603	1.0000	11.36
51	MTPKRAIEV	109	0.9000	10.23
52	VREDPIPPS	228	0.9000	10.23
53	IPPSARHEG	233	0.9000	10.23
54	INTFGGITR	349	0.9000	10.23
55	IGTNPPANQ	467	0.9000	10.23
56	VIGTAQYLS	175	0.8000	9.09
57	VSVAYQHVR	221	0.7000	7.95
58	VLKALAKNP	250	0.7000	7.95

59	YELGEILGF	10	0.6000	6.82
60	FRREAQNAA	55	0.6000	6.82
61	LTGEPPFTG	209	0.6000	6.82
62	VVAVLAVLT	334	0.6000	6.82

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	LRLHRDVAV	30	4.5000	45.92
2	INTFGGITR	349	4.2000	42.86
3	ILGFGGMSE	15	3.9000	39.80
4	VHLARDLRL	24	3.8000	38.78
5	VVVTIAINT	343	3.6000	36.73
6	IIIVGSGPA	484	3.4000	34.69
7	LNVYGFTKF	511	3.3000	33.67
8	IMISATNAV	143	3.2600	33.27
9	VNRDGIITL	613	3.1500	32.14
10	VVIIIVGSG	482	3.1000	31.63
11	VVTIAINTF	344	3.0500	31.12
12	VYGFTKFSQ	513	3.0000	30.61
13	VAVYDTGEA	71	2.9600	30.20
14	VAVLAVLTV	335	2.9000	29.59
15	VIIIVGSGP	483	2.9000	29.59
16	LTVVVTIAI	341	2.8600	29.18
17	VKPANIMIS	138	2.8500	29.08
18	LARDPSFYL	45	2.8000	28.57
19	FVMPDLSGM	560	2.7800	28.37
20	IVHTEGPMT	102	2.6000	26.53
21	LVRVHNGEP	272	2.6000	26.53
22	VAVVAVLAV	332	2.6000	26.53
23	LRALGWTGM	577	2.5800	26.33
24	ITNVVIIIV	479	2.5500	26.02
25	VRVHNGEPP	273	2.5000	25.51
26	IGSVGRWVA	325	2.5000	25.51

27	MEYVDGVTL	91	2.4000	24.49
28	VVAVLAVLT	334	2.4000	24.49
29	IRTLQKPDS	383	2.4000	24.49
30	VKVMDFGIA	151	2.3000	23.47
31	VMDFGIARA	153	2.2500	22.96
32	LARDLRLHR	26	2.2000	22.45
33	IVMEYVDGV	89	2.2000	22.45
34	VRGQSSADA	364	2.2000	22.45
35	IIVGSGPAT	485	2.2000	22.45
36	LQVSKGNQF	552	2.2000	22.45
37	LGFGGMSEV	16	2.0000	20.41
38	LNFSHQNGI	125	1.9000	19.39
39	VGRWVAVVA	328	1.9000	19.39
40	YLRFRREAQ	52	1.8000	18.37
41	VMEYVDGVT	90	1.8000	18.37
42	VLAVLTVVV	337	1.7600	17.96
43	LHRDVAVKV	32	1.7000	17.35
44	IGTAQYLSP	176	1.7000	17.35
45	IAINTFGGI	347	1.7000	17.35
46	YELGEILGF	10	1.6500	16.84
47	FYLRFRREA	51	1.6000	16.33
48	WVAVVAVLA	331	1.6000	16.33
49	VTIAINTFG	345	1.6000	16.33
50	YIVMEYVDG	88	1.5000	15.31
51	FGRFKQANS	448	1.5000	15.31
52	VKVLRADLA	38	1.4000	14.29
53	MTPKRAIEV	109	1.4000	14.29
54	VVLKALAKN	249	1.4000	14.29
55	VHNGEPPEA	275	1.4000	14.29
56	LLSSAAGNL	295	1.4000	14.29
57	VVYQNPPAG	602	1.4000	14.29
58	LNHPAIVAV	65	1.3500	13.78
59	VTLRDIVHT	97	1.3500	13.78
60	VPVDSVIEL	544	1.3000	13.27

61	FRREAQNAA	55	1.2000	12.24
62	VKKLTAAGF	440	1.2000	12.24

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	FVMPDLSGM	560	3.7800	38.57
2	LRLHRDVAV	30	3.5000	35.71
3	INTFGGITR	349	3.2000	32.65
4	ILGFGGMSE	15	2.9000	29.59
5	VHLARDLRL	24	2.8000	28.57
6	YLRFRREAQ	52	2.8000	28.57
7	YELGEILGF	10	2.6500	27.04
8	FYLRFRREA	51	2.6000	26.53
9	WVAVVAVLA	331	2.6000	26.53
10	VVVTIAINT	343	2.6000	26.53
11	YIVMEYVDG	88	2.5000	25.51
12	FGRFKQANS	448	2.5000	25.51
13	IIIVGSGPA	484	2.4000	24.49
14	LNVYGFTKF	511	2.3000	23.47
15	IMISATNAV	143	2.2600	23.06
16	FRREAQNAA	55	2.2000	22.45
17	VNRDGIITL	613	2.1500	21.94
18	VVIIIVGSG	482	2.1000	21.43
19	VVTIAINTF	344	2.0500	20.92
20	VYGFTKFSQ	513	2.0000	20.41
21	VAVYDTGEA	71	1.9600	20.00
22	YQTAAEMRA	262	1.9000	19.39
23	VAVLAVLTV	335	1.9000	19.39
24	VIIIVGSGP	483	1.9000	19.39
25	FTKFSQASV	516	1.9000	19.39
26	LTVVVTIAI	341	1.8600	18.98
27	VKPANIMIS	138	1.8500	18.88
28	LARDPSFYL	45	1.8000	18.37

29	FKQANSPST	451	1.8000	18.37
30	IVHTEGPMT	102	1.6000	16.33
31	FGIARAIAD	156	1.6000	16.33
32	LVRVHNGEP	272	1.6000	16.33
33	VAVVAVLAV	332	1.6000	16.33
34	FKIRTLQKP	381	1.6000	16.33
35	LRALGWTGM	577	1.5800	16.12
36	ITNVVIIIV	479	1.5500	15.82
37	FGGMSEVHL	18	1.5000	15.31
38	VRVHNGEPP	273	1.5000	15.31
39	IGSVGRWVA	325	1.5000	15.31
40	MEYVDGVTL	91	1.4000	14.29
41	VVAVLAVLT	334	1.4000	14.29
42	IRTLQKPDS	383	1.4000	14.29
43	VKVMDFGIA	151	1.3000	13.27
44	VMDFGIARA	153	1.2500	12.76
45	LARDLRLHR	26	1.2000	12.24
46	IVMEYVDGV	89	1.2000	12.24
47	VRGQSSADA	364	1.2000	12.24
48	IIVGSGPAT	485	1.2000	12.24
49	LQVSKGNQF	552	1.2000	12.24
50	LGFGGMSEV	16	1.0000	10.20
51	YGFTKFSQA	514	1.0000	10.20
52	LNFSHQNGI	125	0.9000	9.18
53	VGRWVAVVA	328	0.9000	9.18
54	VMEYVDGVT	90	0.8000	8.16
55	YVDGVTLRD	93	0.7600	7.76
56	VLAVLTVVV	337	0.7600	7.76
57	LHRDVAVKV	32	0.7000	7.14
58	IGTAQYLSP	176	0.7000	7.14
59	IAINTFGGI	347	0.7000	7.14
60	YQHVREDPI	225	0.6000	6.12
61	VTIAINTFG	345	0.6000	6.12
62	YQNPPAGTG	604	0.6000	6.12

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	LRLHRDVAV	30	4.5000	45.92
2	INTFGGITR	349	4.2000	42.86
3	ILGFGGMSE	15	3.9000	39.80
4	VHLARDLRL	24	3.8000	38.78
5	VVVTIAINT	343	3.6000	36.73
6	IIIVGSGPA	484	3.4000	34.69
7	LNVYGFTKF	511	3.3000	33.67
8	IMISATNAV	143	3.2600	33.27
9	VNRDGIITL	613	3.1500	32.14
10	VVIIIVGSG	482	3.1000	31.63
11	VVTIAINTF	344	3.0500	31.12
12	VYGFTKFSQ	513	3.0000	30.61
13	VAVYDTGEA	71	2.9600	30.20
14	VAVLAVLTV	335	2.9000	29.59
15	VIIIVGSGP	483	2.9000	29.59
16	LTVVVTIAI	341	2.8600	29.18
17	VKPANIMIS	138	2.8500	29.08
18	LARDPSFYL	45	2.8000	28.57
19	FVMPDLSGM	560	2.7800	28.37
20	IVHTEGPMT	102	2.6000	26.53
21	LVRVHNGEP	272	2.6000	26.53
22	VAVVAVLAV	332	2.6000	26.53
23	LRALGWTGM	577	2.5800	26.33
24	ITNVVIIIV	479	2.5500	26.02
25	VRVHNGEPP	273	2.5000	25.51
26	IGSVGRWVA	325	2.5000	25.51
27	MEYVDGVTL	91	2.4000	24.49
28	VVAVLAVLT	334	2.4000	24.49
29	IRTLQKPDS	383	2.4000	24.49
30	VKVMDFGIA	151	2.3000	23.47

31	VMDFGIARA	153	2.2500	22.96
32	LARDLRLHR	26	2.2000	22.45
33	IVMEYVDGV	89	2.2000	22.45
34	VRGQSSADA	364	2.2000	22.45
35	IIVGSGPAT	485	2.2000	22.45
36	LQVSKGNQF	552	2.2000	22.45
37	LGFGGMSEV	16	2.0000	20.41
38	LNFSHQNGI	125	1.9000	19.39
39	VGRWVAVVA	328	1.9000	19.39
40	YLRFRREAQ	52	1.8000	18.37
41	VMEYVDGVT	90	1.8000	18.37
42	VLAVLTVVV	337	1.7600	17.96
43	LHRDVAVKV	32	1.7000	17.35
44	IGTAQYLSP	176	1.7000	17.35
45	IAINTFGGI	347	1.7000	17.35
46	YELGEILGF	10	1.6500	16.84
47	FYLRFRREA	51	1.6000	16.33
48	WVAVVAVLA	331	1.6000	16.33
49	VTIAINTFG	345	1.6000	16.33
50	YIVMEYVDG	88	1.5000	15.31
51	FGRFKQANS	448	1.5000	15.31
52	VKVLRADLA	38	1.4000	14.29
53	MTPKRAIEV	109	1.4000	14.29
54	VVLKALAKN	249	1.4000	14.29
55	VHNGEPPEA	275	1.4000	14.29
56	LLSSAAGNL	295	1.4000	14.29
57	VVYQNPPAG	602	1.4000	14.29
58	LNHPAIVAV	65	1.3500	13.78
59	VTLRDIVHT	97	1.3500	13.78
60	VPVDSVIEL	544	1.3000	13.27
61	FRREAQNAA	55	1.2000	12.24
62	VKKLTAAGF	440	1.2000	12.24

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	WVDAEPRLR	570	4.8000	48.98
2	IVGSGPATK	486	3.7000	37.76
3	VVIIIVGSG	482	3.6000	36.73
4	WVAVVAVLA	331	2.9000	29.59
5	VVVTIAINT	343	2.9000	29.59
6	IIIVGSGPA	484	2.8000	28.57
7	VVTIAINTF	344	2.7000	27.55
8	INTFGGITR	349	2.6000	26.53
9	MFWVDAEPR	568	2.5000	25.51
10	YIVMEYVDG	88	2.4000	24.49
11	LTVVVTIAI	341	2.2000	22.45
12	LTYAEAVKK	434	2.2000	22.45
13	VKKLTAAGF	440	1.9000	19.39
14	MEYVDGVTL	91	1.7000	17.35
15	MISATNAVK	144	1.7000	17.35
16	FGIARAIAD	156	1.7000	17.35
17	VYSLGCVLY	198	1.7000	17.35
18	VVAVLAVLT	334	1.7000	17.35
19	LLSSAAGNL	295	1.6000	16.33
20	VIIIVGSGP	483	1.6000	16.33
21	LQVSKGNQF	552	1.6000	16.33
22	LGWTGMLDK	580	1.6000	16.33
23	VSVAYQHVR	221	1.5000	15.31
24	FGGMSEVHL	18	1.4000	14.29
25	LVRVHNGEP	272	1.4000	14.29
26	FVMPDLSGM	560	1.3000	13.27
27	LGEILGFGG	12	1.2000	12.24
28	VKVMDFGIA	151	1.2000	12.24
29	VVYQNPPAG	602	1.2000	12.24
30	YQNPPAGTG	604	1.2000	12.24
31	FSHQNGIIH	127	1.1000	11.22
32	VIGTAQYLS	175	1.1000	11.22

33	LRALGWTGM	577	0.9000	9.18
34	IATLQNRGF	373	0.8000	8.16
35	VIGTDPAAN	398	0.8000	8.16
36	WTGMLDKGA	582	0.8000	8.16
37	VHLARDLRL	24	0.7000	7.14
38	FRREAQNAA	55	0.7000	7.14
39	LRDIVHTEG	99	0.7000	7.14
40	LQNRGFKIR	376	0.7000	7.14
41	IMISATNAV	143	0.6000	6.12
42	VDGVTLRDI	94	0.5000	5.10
43	IVHTEGPMT	102	0.5000	5.10
44	LNFSHQNGI	125	0.4000	4.08
45	IRTLQKPDS	383	0.4000	4.08
46	MRADLVRVH	268	0.3000	3.06
47	FYLRFRREA	51	0.2000	2.04
48	VIADACQAL	117	0.2000	2.04
49	YQHVREDPI	225	0.2000	2.04
50	VRGQSSADA	364	0.2000	2.04
51	VIGTNPPAN	466	0.2000	2.04
52	ITNVVIIIV	479	0.2000	2.04
53	VYGFTKFSQ	513	0.2000	2.04
54	LARDPSFYL	45	0.1000	1.02
55	VKPANIMIS	138	0.1000	1.02
56	VLKALAKNP	250	0.1000	1.02
57	VLTVVVTIA	340	0.1000	1.02
58	YELGEILGF	10	-0.1000	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	WVDAEPRLR	570	4.8000	48.98
2	IVGSGPATK	486	3.7000	37.76
3	VVIIIVGSG	482	3.6000	36.73
4	WVAVVAVLA	331	2.9000	29.59

5	VVVTIAINT	343	2.9000	29.59
6	IIIVGSGPA	484	2.8000	28.57
7	VVTIAINTF	344	2.7000	27.55
8	INTFGGITR	349	2.6000	26.53
9	MFWVDAEPR	568	2.5000	25.51
10	YIVMEYVDG	88	2.4000	24.49
11	LTVVVTIAI	341	2.2000	22.45
12	LTYAEAVKK	434	2.2000	22.45
13	VKKLTAAGF	440	1.9000	19.39
14	MEYVDGVTL	91	1.7000	17.35
15	MISATNAVK	144	1.7000	17.35
16	FGIARAIAD	156	1.7000	17.35
17	VYSLGCVLY	198	1.7000	17.35
18	VVAVLAVLT	334	1.7000	17.35
19	LLSSAAGNL	295	1.6000	16.33
20	VIIIVGSGP	483	1.6000	16.33
21	LQVSKGNQF	552	1.6000	16.33
22	LGWTGMLDK	580	1.6000	16.33
23	VSVAYQHVR	221	1.5000	15.31
24	FGGMSEVHL	18	1.4000	14.29
25	LVRVHNGEP	272	1.4000	14.29
26	FVMPDLSGM	560	1.3000	13.27
27	LGEILGFGG	12	1.2000	12.24
28	VKVMDFGIA	151	1.2000	12.24
29	VVYQNPPAG	602	1.2000	12.24
30	YQNPPAGTG	604	1.2000	12.24
31	FSHQNGIIH	127	1.1000	11.22
32	VIGTAQYLS	175	1.1000	11.22
33	LRALGWTGM	577	0.9000	9.18
34	IATLQNRGF	373	0.8000	8.16
35	VIGTDPAAN	398	0.8000	8.16
36	WTGMLDKGA	582	0.8000	8.16
37	VHLARDLRL	24	0.7000	7.14
38	FRREAQNAA	55	0.7000	7.14

39	LRDIVHTEG	99	0.7000	7.14
40	LQNRGFKIR	376	0.7000	7.14
41	IMISATNAV	143	0.6000	6.12
42	VDGVTLRDI	94	0.5000	5.10
43	IVHTEGPMT	102	0.5000	5.10
44	LNFSHQNGI	125	0.4000	4.08
45	IRTLQKPDS	383	0.4000	4.08
46	MRADLVRVH	268	0.3000	3.06
47	FYLRFRREA	51	0.2000	2.04
48	VIADACQAL	117	0.2000	2.04
49	YQHVREDPI	225	0.2000	2.04
50	VRGQSSADA	364	0.2000	2.04
51	VIGTNPPAN	466	0.2000	2.04
52	ITNVVIIIV	479	0.2000	2.04
53	VYGFTKFSQ	513	0.2000	2.04
54	LARDPSFYL	45	0.1000	1.02
55	VKPANIMIS	138	0.1000	1.02
56	VLKALAKNP	250	0.1000	1.02
57	VLTVVVTIA	340	0.1000	1.02
58	YELGEILGF	10	-0.1000	0