MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sun Jan 31 12:57:35 2010
Length of input sequence	478 amino acids
Number of nanomers from input sequence	470
Number of nanomers with obligatory P1 anchor residue	148
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	47

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	FYIFDSVSF	135	2.1800	36.33
2	FRAAKTLNI	82	2.0000	33.33
3	YLAFSAMLM	376	1.2500	20.83
4	FFVHDPFTL	92	1.2000	20.00
5	YLTEGGVFT	435	0.8000	13.33
6	VRFCDLPGI	22	0.7700	12.83
7	YKYIIKNTA	244	0.5000	8.33
8	YQFNSLLHA	229	0.3400	5.67
9	YLISTGIAD	117	0.2000	3.33
10	WNTGAATEA	161	0.1900	3.17
11	WQNGKTVTF	253	0.1000	1.67
12	INYQFNSLL	227	-0.1000	0
13	LHHAPSLLA	309	-0.3000	0
14	YEFALYYDV	469	-0.3000	0

15	FILEKGHHE	210	-0.4000	0
16	LLHHAPSLL	308	-0.4000	0
17	IRGFQSIHE	57	-0.4200	0
18	YFGAEAEFY	128	-0.5000	0
19	YKRLVPGYE	326	-0.5000	0
20	FYEVDAISG	151	-0.5500	0
21	FQSIHESDM	60	-0.6200	0
22	YFPVAPNDQ	185	-0.6500	0
23	LLAFTNPTV	315	-0.6500	0
24	YVDLRDKML	194	-0.7000	0
25	LVYSQRNRS	339	-0.8000	0
26	FSAMLMAGL	379	-0.8000	0
27	MAGLDGIKN	384	-0.8000	0
28	VYSQRNRSA	340	-0.8100	0
29	YVDVRFCDL	19	-0.8500	0
30	INLVYSQRN	337	-0.8500	0
31	FKLAKDEKV	9	-0.9000	0
32	LPPEEAASI	407	-0.9000	0
33	MLLLPDPET	68	-0.9300	0
34	LVPGYEAPI	329	-1.0000	0
35	IIKNTAWQN	247	-1.1400	0
36	VEYVDVRFC	17	-1.1600	0
37	IMQHFTIPA	30	-1.2000	0
38	LYELPPEEA	404	-1.2000	0
39	FGAEAEFYI	129	-1.3000	0
40	LTNLINSGF	202	-1.3000	0
41	YIGGLLHHA	304	-1.3000	0
42	FRSPDSSGN	366	-1.5000	0
43	FKRENEIEP	453	-1.5000	0
44	VRHKGGYFP	179	-1.6000	0
45	MQHFTIPAS	31	-1.6500	0
46	FCDLPGIMQ	24	-1.7000	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	FYIFDSVSF	135	2.1800	36.33

2	FRAAKTLNI	82	2.0000	33.33
3	VRFCDLPGI	22	1.7700	29.50
4	FFVHDPFTL	92	1.2000	20.00
5	INYQFNSLL	227	0.9000	15.00
6	LHHAPSLLA	309	0.7000	11.67
7	LLHHAPSLL	308	0.6000	10.00
8	IRGFQSIHE	57	0.5800	9.67
9	LLAFTNPTV	315	0.3500	5.83
10	YLAFSAMLM	376	0.2500	4.17
11	LVYSQRNRS	339	0.2000	3.33
12	MAGLDGIKN	384	0.2000	3.33
13	VYSQRNRSA	340	0.1900	3.17
14	INLVYSQRN	337	0.1500	2.50
15	LPPEEAASI	407	0.1000	1.67
16	MLLLPDPET	68	0.0700	1.17
17	IIKNTAWQN	247	-0.1400	0
18	VEYVDVRFC	17	-0.1600	0
19	IMQHFTIPA	30	-0.2000	0
20	LYELPPEEA	404	-0.2000	0
21	YLTEGGVFT	435	-0.2000	0
22	LTNLINSGF	202	-0.3000	0
23	FILEKGHHE	210	-0.4000	0
24	YKYIIKNTA	244	-0.5000	0
25	FYEVDAISG	151	-0.5500	0
26	VRHKGGYFP	179	-0.6000	0
27	FQSIHESDM	60	-0.6200	0
28	MQHFTIPAS	31	-0.6500	0
29	YQFNSLLHA	229	-0.6600	0
30	LLLPDPETA	69	-0.7000	0
31	IEPQAPVDK	394	-0.7000	0
32	VTFMPKPLF	259	-0.7300	0
33	VFTNDLIET	441	-0.7600	0
34	YLISTGIAD	117	-0.8000	0
35	FSAMLMAGL	379	-0.8000	0
36	IRPHPYEFA	464	-0.8000	0
37	WNTGAATEA	161	-0.8100	0
38	FKLAKDEKV	9	-0.9000	0
39	WQNGKTVTF	253	-0.9000	0
40	MLMAGLDGI	382	-0.9000	0
41	LNINFFVHD	88	-0.9600	0
42	VGSGGQAEI	219	-1.1000	0

43	IDPFRAAKT	79	-1.1200	0
44	FGAEAEFYI	129	-1.3000	0
45	YEFALYYDV	469	-1.3000	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	LVYSQRNRS	339	5.6100	59.05
2	LMYDETGYA	287	5.1000	53.68
3	VRFCDLPGI	22	4.5000	47.37
4	VSFDSRANG	141	4.2000	44.21
5	LAKDEKVEY	11	4.1000	43.16
6	LWKDGAPLM	280	4.0000	42.11
7	YIFDSVSFD	136	3.8700	40.74
8	LFGDNGSGM	266	3.7700	39.68
9	VTFMPKPLF	259	3.7000	38.95
10	LAFDGSSIR	50	3.5700	37.58
11	WQNGKTVTF	253	3.1000	32.63
12	VRIPITGSN	350	3.0000	31.58
13	MQHFTIPAS	31	2.9000	30.53
14	FRAAKTLNI	82	2.8000	29.47
15	YSRDPRNIA	103	2.6100	27.47
16	YKYIIKNTA	244	2.6100	27.47
17	LLPDPETAR	70	2.6000	27.37
18	MLMAGLDGI	382	2.6000	27.37
19	IMQHFTIPA	30	2.3000	24.21
20	MLTNLINSG	201	2.2100	23.26
21	INSGFILEK	206	2.2000	23.16
22	LVPGYEAPI	329	2.1000	22.11
23	FVHDPFTLE	93	1.8000	18.95
24	LLHHAPSLL	308	1.7300	18.21
25	IFDSVSFDS	137	1.7000	17.89
26	YEVDAISGW	152	1.6700	17.58
27	YQFNSLLHA	229	1.6000	16.84
28	VNIRPHPYE	462	1.6000	16.84
29	VGSGGQAEI	219	1.5000	15.79
30	VFDDGLAFD	45	1.4000	14.74

31	IRGFQSIHE	57	1.4000	14.74
32	FYIFDSVSF	135	1.4000	14.74
33	VFKLAKDEK	8	1.3000	13.68
34	LLLPDPETA	69	1.3000	13.68
35	YLISTGIAD	117	1.3000	13.68
36	YKVRHKGGY	177	1.3000	13.68
37	FTNDLIETW	442	1.3000	13.68
38	FFVHDPFTL	92	1.2600	13.26
39	VEYVDVRFC	17	1.2000	12.63
40	YIIKNTAWQ	246	1.2000	12.63
41	YLAFSAMLM	376	1.2000	12.63
42	LHHAPSLLA	309	1.1000	11.58
43	YKRLVPGYE	326	1.1000	11.58
44	VFTNDLIET	441	1.1000	11.58
45	INYQFNSLL	227	1.0300	10.84
46	LINSGFILE	205	1.0000	10.53
47	INLVYSQRN	337	1.0000	10.53

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	LVYSQRNRS	339	4.2100	46.26
2	LMYDETGYA	287	4.1000	45.05
3	YIFDSVSFD	136	3.7700	41.43
4	YSRDPRNIA	103	3.6100	39.67
5	YKYIIKNTA	244	3.6100	39.67
6	FRAAKTLNI	82	2.9000	31.87
7	YIIKNTAWQ	246	2.9000	31.87
8	YEVDAISGW	152	2.6700	29.34
9	VRFCDLPGI	22	2.6000	28.57
10	YQFNSLLHA	229	2.6000	28.57
11	FTNDLIETW	442	2.3000	25.27
12	WQNGKTVTF	253	2.2000	24.18
13	YFPVAPNDQ	185	2.0100	22.09
14	LAKDEKVEY	11	1.8000	19.78
15	VSFDSRANG	141	1.8000	19.78
16	MQHFTIPAS	31	1.5000	16.48

17	LWKDGAPLM	280	1.5000	16.48
18	FVHDPFTLE	93	1.4000	15.38
19	IMQHFTIPA	30	1.3000	14.29
20	FFVHDPFTL	92	1.3000	14.29
21	LFGDNGSGM	266	1.2700	13.96
22	YLISTGIAD	117	1.2000	13.19
23	WNTGAATEA	161	1.2000	13.19
24	YIGGLLHHA	304	1.2000	13.19
25	VRIPITGSN	350	1.2000	13.19
26	INSGFILEK	206	1.1000	12.09
27	LAFDGSSIR	50	1.0700	11.76
28	YKVRHKGGY	177	1.0000	10.99
29	VTFMPKPLF	259	0.8000	8.79
30	YKRLVPGYE	326	0.7000	7.69
31	YLAFSAMLM	376	0.7000	7.69
32	MLMAGLDGI	382	0.7000	7.69
33	FYIFDSVSF	135	0.5000	5.49
34	LLLPDPETA	69	0.3000	3.30
35	IFDSVSFDS	137	0.3000	3.30
36	VFKLAKDEK	8	0.2000	2.20
37	VEYVDVRFC	17	0.2000	2.20
38	LVPGYEAPI	329	0.2000	2.20
39	FQSIHESDM	60	0.1700	1.87
40	LLPDPETAR	70	0.1000	1.10
41	LHHAPSLLA	309	0.1000	1.10
42	FRSPDSSGN	366	-0.0300	0
43	IRPHPYEFA	464	-0.1000	0
44	MLTNLINSG	201	-0.1900	0
45	YFGAEAEFY	128	-0.2000	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	LVYSQRNRS	339	5.9000	67.05
2	LMYDETGYA	287	3.7000	42.05
3	YSRDPRNIA	103	3.3000	37.50
4	YKYIIKNTA	244	3.3000	37.50

5	VSFDSRANG	141	2.8000	31.82
6	LAKDEKVEY	11	2.6800	30.45
7	INSGFILEK	206	2.6000	29.55
8	YIFDSVSFD	136	2.5000	28.41
9	FRAAKTLNI	82	2.4000	27.27
10	VRFCDLPGI	22	2.2000	25.00
11	YQFNSLLHA	229	2.1000	23.86
12	LFGDNGSGM	266	2.0000	22.73
13	MLMAGLDGI	382	2.0000	22.73
14	IMQHFTIPA	30	1.9800	22.50
15	YIIKNTAWQ	246	1.9000	21.59
16	LAFDGSSIR	50	1.8000	20.45
17	LLLPDPETA	69	1.7000	19.32
18	YFPVAPNDQ	185	1.7000	19.32
19	FTNDLIETW	442	1.7000	19.32
20	LHHAPSLLA	309	1.6000	18.18
21	VFKLAKDEK	8	1.5000	17.05
22	MLTNLINSG	201	1.5000	17.05
23	YEVDAISGW	152	1.4000	15.91
24	LAFSAMLMA	377	1.3000	14.77
25	IRPHPYEFA	464	1.3000	14.77
26	LVPGYEAPI	329	1.2000	13.64
27	MQHFTIPAS	31	1.1000	12.50
28	LLPDPETAR	70	1.1000	12.50
29	MHCHQSLWK	274	1.1000	12.50
30	LWKDGAPLM	280	1.1000	12.50
31	WQNGKTVTF	253	1.0800	12.27
32	YIGGLLHHA	304	1.0000	11.36
33	VEYVDVRFC	17	0.9000	10.23
34	VRIPITGSN	350	0.8000	9.09
35	ITGSNPKAK	354	0.8000	9.09
36	LEFRSPDSS	364	0.8000	9.09
37	IEPQAPVDK	394	0.6800	7.73
38	VGSGGQAEI	219	0.6000	6.82
39	LLHHAPSLL	308	0.5000	5.68
40	FVHDPFTLE	93	0.4000	4.55
41	VTFMPKPLF	259	0.4000	4.55
42	VNSYKRLVP	323	0.4000	4.55
43	LYELPPEEA	404	0.4000	4.55
44	VFDDGLAFD	45	0.3000	3.41
45	INLVYSQRN	337	0.3000	3.41

46	WNTGAATEA	161	0.2000	2.27
47	IPITGSNPK	352	0.2000	2.27

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVYSQRNRS	339	5.9000	67.05
2	LMYDETGYA	287	3.7000	42.05
3	YSRDPRNIA	103	3.3000	37.50
4	YKYIIKNTA	244	3.3000	37.50
5	VSFDSRANG	141	2.8000	31.82
6	LAKDEKVEY	11	2.6800	30.45
7	INSGFILEK	206	2.6000	29.55
8	YIFDSVSFD	136	2.5000	28.41
9	FRAAKTLNI	82	2.4000	27.27
10	VRFCDLPGI	22	2.2000	25.00
11	YQFNSLLHA	229	2.1000	23.86
12	LFGDNGSGM	266	2.0000	22.73
13	MLMAGLDGI	382	2.0000	22.73
14	IMQHFTIPA	30	1.9800	22.50
15	YIIKNTAWQ	246	1.9000	21.59
16	LAFDGSSIR	50	1.8000	20.45
17	LLLPDPETA	69	1.7000	19.32
18	YFPVAPNDQ	185	1.7000	19.32
19	FTNDLIETW	442	1.7000	19.32
20	LHHAPSLLA	309	1.6000	18.18
21	VFKLAKDEK	8	1.5000	17.05
22	MLTNLINSG	201	1.5000	17.05
23	YEVDAISGW	152	1.4000	15.91
24	LAFSAMLMA	377	1.3000	14.77
25	IRPHPYEFA	464	1.3000	14.77
26	LVPGYEAPI	329	1.2000	13.64
27	MQHFTIPAS	31	1.1000	12.50
28	LLPDPETAR	70	1.1000	12.50
29	MHCHQSLWK	274	1.1000	12.50
30	LWKDGAPLM	280	1.1000	12.50
31	WQNGKTVTF	253	1.0800	12.27

32	YIGGLLHHA	304	1.0000	11.36
33	VEYVDVRFC	17	0.9000	10.23
34	VRIPITGSN	350	0.8000	9.09
35	ITGSNPKAK	354	0.8000	9.09
36	LEFRSPDSS	364	0.8000	9.09
37	IEPQAPVDK	394	0.6800	7.73
38	VGSGGQAEI	219	0.6000	6.82
39	LLHHAPSLL	308	0.5000	5.68
40	FVHDPFTLE	93	0.4000	4.55
41	VTFMPKPLF	259	0.4000	4.55
42	VNSYKRLVP	323	0.4000	4.55
43	LYELPPEEA	404	0.4000	4.55
44	VFDDGLAFD	45	0.3000	3.41
45	INLVYSQRN	337	0.3000	3.41
46	WNTGAATEA	161	0.2000	2.27
47	IPITGSNPK	352	0.2000	2.27

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVYSQRNRS	339	5.9000	67.05
2	LMYDETGYA	287	3.7000	42.05
3	YSRDPRNIA	103	3.3000	37.50
4	YKYIIKNTA	244	3.3000	37.50
5	VSFDSRANG	141	2.8000	31.82
6	LAKDEKVEY	11	2.6800	30.45
7	INSGFILEK	206	2.6000	29.55
8	YIFDSVSFD	136	2.5000	28.41
9	FRAAKTLNI	82	2.4000	27.27
10	VRFCDLPGI	22	2.2000	25.00
11	YQFNSLLHA	229	2.1000	23.86
12	LFGDNGSGM	266	2.0000	22.73
13	MLMAGLDGI	382	2.0000	22.73
14	IMQHFTIPA	30	1.9800	22.50
15	YIIKNTAWQ	246	1.9000	21.59
16	LAFDGSSIR	50	1.8000	20.45
17	LLLPDPETA	69	1.7000	19.32

18	YFPVAPNDQ	185	1.7000	19.32
19	FTNDLIETW	442	1.7000	19.32
20	LHHAPSLLA	309	1.6000	18.18
21	VFKLAKDEK	8	1.5000	17.05
22	MLTNLINSG	201	1.5000	17.05
23	YEVDAISGW	152	1.4000	15.91
24	LAFSAMLMA	377	1.3000	14.77
25	IRPHPYEFA	464	1.3000	14.77
26	LVPGYEAPI	329	1.2000	13.64
27	MQHFTIPAS	31	1.1000	12.50
28	LLPDPETAR	70	1.1000	12.50
29	MHCHQSLWK	274	1.1000	12.50
30	LWKDGAPLM	280	1.1000	12.50
31	WQNGKTVTF	253	1.0800	12.27
32	YIGGLLHHA	304	1.0000	11.36
33	VEYVDVRFC	17	0.9000	10.23
34	VRIPITGSN	350	0.8000	9.09
35	ITGSNPKAK	354	0.8000	9.09
36	LEFRSPDSS	364	0.8000	9.09
37	IEPQAPVDK	394	0.6800	7.73
38	VGSGGQAEI	219	0.6000	6.82
39	LLHHAPSLL	308	0.5000	5.68
40	FVHDPFTLE	93	0.4000	4.55
41	VTFMPKPLF	259	0.4000	4.55
42	VNSYKRLVP	323	0.4000	4.55
43	LYELPPEEA	404	0.4000	4.55
44	VFDDGLAFD	45	0.3000	3.41
45	INLVYSQRN	337	0.3000	3.41
46	WNTGAATEA	161	0.2000	2.27
47	IPITGSNPK	352	0.2000	2.27

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	YIFDSVSFD	136	4.8700	51.26
2	LVYSQRNRS	339	4.6100	48.53
3	WQNGKTVTF	253	4.1000	43.16

4	LMYDETGYA	287	4.1000	43.16
5	FRAAKTLNI	82	3.8000	40.00
6	YSRDPRNIA	103	3.6100	38.00
7	YKYIIKNTA	244	3.6100	38.00
8	VRFCDLPGI	22	3.5000	36.84
9	VSFDSRANG	141	3.2000	33.68
10	LAKDEKVEY	11	3.1000	32.63
11	LWKDGAPLM	280	3.0000	31.58
12	FVHDPFTLE	93	2.8000	29.47
13	LFGDNGSGM	266	2.7700	29.16
14	VTFMPKPLF	259	2.7000	28.42
15	YEVDAISGW	152	2.6700	28.11
16	YQFNSLLHA	229	2.6000	27.37
17	LAFDGSSIR	50	2.5700	27.05
18	FYIFDSVSF	135	2.4000	25.26
19	YLISTGIAD	117	2.3000	24.21
20	YKVRHKGGY	177	2.3000	24.21
21	FTNDLIETW	442	2.3000	24.21
22	FFVHDPFTL	92	2.2600	23.79
23	YIIKNTAWQ	246	2.2000	23.16
24	YLAFSAMLM	376	2.2000	23.16
25	YKRLVPGYE	326	2.1000	22.11
26	VRIPITGSN	350	2.0000	21.05
27	MQHFTIPAS	31	1.9000	20.00
28	FQSIHESDM	60	1.6700	17.58
29	LLPDPETAR	70	1.6000	16.84
30	MLMAGLDGI	382	1.6000	16.84
31	YFPVAPNDQ	185	1.3100	13.79
32	IMQHFTIPA	30	1.3000	13.68
33	WKDGAPLMY	281	1.3000	13.68
34	MLTNLINSG	201	1.2100	12.74
35	WNTGAATEA	161	1.2000	12.63
36	INSGFILEK	206	1.2000	12.63
37	YIGGLLHHA	304	1.2000	12.63
38	YFGAEAEFY	128	1.1000	11.58
39	LVPGYEAPI	329	1.1000	11.58
40	FTNPTVNSY	318	0.9100	9.58
41	WISFKRENE	450	0.8000	8.42
42	FRSPDSSGN	366	0.7700	8.11
43	LLHHAPSLL	308	0.7300	7.68
44	IFDSVSFDS	137	0.7000	7.37

45	VNIRPHPYE	462	0.6000	6.32
46	FYEVDAISG	151	0.5000	5.26
47	VGSGGQAEI	219	0.5000	5.26

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	LVYSQRNRS	339	5.9000	67.05
2	LMYDETGYA	287	3.7000	42.05
3	YSRDPRNIA	103	3.3000	37.50
4	YKYIIKNTA	244	3.3000	37.50
5	VSFDSRANG	141	2.8000	31.82
6	LAKDEKVEY	11	2.6800	30.45
7	INSGFILEK	206	2.6000	29.55
8	YIFDSVSFD	136	2.5000	28.41
9	FRAAKTLNI	82	2.4000	27.27
10	VRFCDLPGI	22	2.2000	25.00
11	YQFNSLLHA	229	2.1000	23.86
12	LFGDNGSGM	266	2.0000	22.73
13	MLMAGLDGI	382	2.0000	22.73
14	IMQHFTIPA	30	1.9800	22.50
15	YIIKNTAWQ	246	1.9000	21.59
16	LAFDGSSIR	50	1.8000	20.45
17	LLLPDPETA	69	1.7000	19.32
18	YFPVAPNDQ	185	1.7000	19.32
19	FTNDLIETW	442	1.7000	19.32
20	LHHAPSLLA	309	1.6000	18.18
21	VFKLAKDEK	8	1.5000	17.05
22	MLTNLINSG	201	1.5000	17.05
23	YEVDAISGW	152	1.4000	15.91
24	LAFSAMLMA	377	1.3000	14.77
25	IRPHPYEFA	464	1.3000	14.77
26	LVPGYEAPI	329	1.2000	13.64
27	MQHFTIPAS	31	1.1000	12.50
28	LLPDPETAR	70	1.1000	12.50
29	MHCHQSLWK	274	1.1000	12.50
30	LWKDGAPLM	280	1.1000	12.50

31	WQNGKTVTF	253	1.0800	12.27
32	YIGGLLHHA	304	1.0000	11.36
33	VEYVDVRFC	17	0.9000	10.23
34	VRIPITGSN	350	0.8000	9.09
35	ITGSNPKAK	354	0.8000	9.09
36	LEFRSPDSS	364	0.8000	9.09
37	IEPQAPVDK	394	0.6800	7.73
38	VGSGGQAEI	219	0.6000	6.82
39	LLHHAPSLL	308	0.5000	5.68
40	FVHDPFTLE	93	0.4000	4.55
41	VTFMPKPLF	259	0.4000	4.55
42	VNSYKRLVP	323	0.4000	4.55
43	LYELPPEEA	404	0.4000	4.55
44	VFDDGLAFD	45	0.3000	3.41
45	INLVYSQRN	337	0.3000	3.41
46	WNTGAATEA	161	0.2000	2.27
47	IPITGSNPK	352	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FRAAKTLNI	82	4.5000	52.33
2	YIIKNTAWQ	246	3.3000	38.37
3	IMQHFTIPA	30	3.1800	36.98
4	LMYDETGYA	287	2.9000	33.72
5	YQFNSLLHA	229	2.5000	29.07
6	YIFDSVSFD	136	2.3000	26.74
7	MHCHQSLWK	274	2.3000	26.74
8	IPITGSNPK	352	2.0000	23.26
9	IPQTPTQLS	415	1.8000	20.93
10	LHHAPSLLA	309	1.7000	19.77
11	LVYSQRNRS	339	1.6000	18.60
12	FYIFDSVSF	135	1.5800	18.37
13	INYQFNSLL	227	1.5000	17.44
14	YFPVAPNDQ	185	1.3000	15.12
15	IRPHPYEFA	464	1.3000	15.12
16	WQNGKTVTF	253	1.0800	12.56

17	LAFDGSSIR	50	1.0000	11.63
18	VYSQRNRSA	340	1.0000	11.63
19	FTNDLIETW	442	1.0000	11.63
20	YKYIIKNTA	244	0.9000	10.47
21	FVHDPFTLE	93	0.8000	9.30
22	YEVDAISGW	152	0.7000	8.14
23	FKLAKDEKV	9	0.5000	5.81
24	YLAFSAMLM	376	0.5000	5.81
25	FFVHDPFTL	92	0.4000	4.65
26	MLTNLINSG	201	0.4000	4.65
27	LTNLINSGF	202	0.4000	4.65
28	FILEKGHHE	210	0.4000	4.65
29	VRIPITGSN	350	0.3000	3.49
30	YFGAEAEFY	128	0.2000	2.33
31	FRSPDSSGN	366	0.2000	2.33
32	LAFSAMLMA	377	0.2000	2.33
33	YLISTGIAD	117	0.1800	2.09
34	LLHHAPSLL	308	0.1000	1.16
35	IEPQAPVDK	394	-0.0200	0
36	VRFCDLPGI	22	-0.1000	0
37	IRGFQSIHE	57	-0.1200	0
38	FGDNGSGMH	267	-0.1200	0
39	YLTEGGVFT	435	-0.1200	0
40	LISTGIADT	118	-0.3000	0
41	MLMAGLDGI	382	-0.3000	0
42	LYELPPEEA	404	-0.3000	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	IMQHFTIPA	30	4.7000	48.96
2	YIIKNTAWQ	246	4.1000	42.71
3	FRAAKTLNI	82	3.8000	39.58
4	MHCHQSLWK	274	3.7000	38.54
5	VYSQRNRSA	340	3.7000	38.54
6	LHHAPSLLA	309	3.0000	31.25
7	ISGWWNTGA	157	2.9000	30.21

8	VEYVDVRFC	17	2.8000	29.17
9	IPQTPTQLS	415	2.7000	28.13
10	IRGFQSIHE	57	2.5000	26.04
11	IETWISFKR	447	2.2000	22.92
12	FYIFDSVSF	135	1.9000	19.79
13	INLVYSQRN	337	1.8000	18.75
14	IPITGSNPK	352	1.8000	18.75
15	IEPVNIRPH	459	1.3800	14.37
16	MQHFTIPAS	31	1.3000	13.54
17	INYQFNSLL	227	1.1000	11.46
18	WQNGKTVTF	253	1.1000	11.46
19	FFVHDPFTL	92	1.0000	10.42
20	LLHHAPSLL	308	1.0000	10.42
21	IRPHPYEFA	464	1.0000	10.42
22	INSGFILEK	206	0.9000	9.38
23	LLAFTNPTV	315	0.9000	9.38
24	LVYSQRNRS	339	0.8000	8.33
25	VRIPITGSN	350	0.8000	8.33
26	IFDSVSFDS	137	0.7000	7.29
27	IIKNTAWQN	247	0.7000	7.29
28	YLAFSAMLM	376	0.7000	7.29
29	VRFCDLPGI	22	0.6000	6.25
30	VRHKGGYFP	179	0.6000	6.25
31	YFPVAPNDQ	185	0.5000	5.21
32	YQFNSLLHA	229	0.5000	5.21
33	MQLYKYIIK	241	0.5000	5.21
34	LEFRSPDSS	364	0.5000	5.21
35	IKNTAWQNG	248	0.2000	2.08
36	MLTNLINSG	201	0.1000	1.04
37	IEPQAPVDK	394	-0.1000	0
38	VHDPFTLEP	94	-0.2000	0
39	LTNLINSGF	202	-0.2000	0
40	LAFSAMLMA	377	-0.3000	0
41	LLLPDPETA	69	-0.5000	0
42	LISTGIADT	118	-0.5000	0
43	LHAADDMQL	235	-0.5000	0
44	LMYDETGYA	287	-0.6000	0
45	LNINFFVHD	88	-0.7000	0
46	FRSPDSSGN	366	-0.7000	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	FRAAKTLNI	82	3.1000	35.23
2	IRGFQSIHE	57	2.7800	31.59
3	YIIKNTAWQ	246	2.5000	28.41
4	INYQFNSLL	227	2.4000	27.27
5	FYIFDSVSF	135	2.3000	26.14
6	LTNLINSGF	202	2.3000	26.14
7	LHHAPSLLA	309	2.3000	26.14
8	IMQHFTIPA	30	2.0800	23.64
9	MQHFTIPAS	31	2.0000	22.73
10	YFPVAPNDQ	185	1.8000	20.45
11	INLVYSQRN	337	1.7000	19.32
12	VRIPITGSN	350	1.7000	19.32
13	LLAFTNPTV	315	1.6000	18.18
14	ISGWWNTGA	157	1.5500	17.61
15	LMYDETGYA	287	1.5000	17.05
16	VYSQRNRSA	340	1.5000	17.05
17	IPITGSNPK	352	1.5000	17.05
18	VEYVDVRFC	17	1.4000	15.91
19	YLAFSAMLM	376	1.3000	14.77
20	LVYSQRNRS	339	1.2000	13.64
21	IPQTPTQLS	415	1.0000	11.36
22	MHCHQSLWK	274	0.8000	9.09
23	VRFCDLPGI	22	0.6000	6.82
24	IFDSVSFDS	137	0.4500	5.11
25	YKYIIKNTA	244	0.3000	3.41
26	LAFDGSSIR	50	0.2000	2.27
27	FRSPDSSGN	366	0.2000	2.27
28	MQLYKYIIK	241	0.0800	0.91
29	IEPVNIRPH	459	-0.0200	0
30	MLTNLINSG	201	-0.1000	0
31	MLMAGLDGI	382	-0.2000	0
32	MLLLPDPET	68	-0.3000	0
33	LLHHAPSLL	308	-0.3000	0
34	YIFDSVSFD	136	-0.5000	0
35	YQFNSLLHA	229	-0.5000	0
36	LLHAADDMQ	234	-0.6000	0

37	LHAADDMQL	235	-0.6000	0
38	LAFSAMLMA	377	-0.7000	0
39	IRPHPYEFA	464	-0.7000	0
40	FQSIHESDM	60	-0.8000	0
41	VHDPFTLEP	94	-0.9000	0
42	LISTGIADT	118	-0.9000	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	IRGFQSIHE	57	4.7800	50.85
2	FRAAKTLNI	82	4.3000	45.74
3	YIIKNTAWQ	246	4.3000	45.74
4	FYIFDSVSF	135	4.2000	44.68
5	YFPVAPNDQ	185	3.6000	38.30
6	YLAFSAMLM	376	3.4000	36.17
7	YIFDSVSFD	136	3.2000	34.04
8	FRSPDSSGN	366	3.2000	34.04
9	YKRLVPGYE	326	2.9000	30.85
10	INLVYSQRN	337	2.7000	28.72
11	VRIPITGSN	350	2.7000	28.72
12	INYQFNSLL	227	2.4000	25.53
13	FTIPASAFD	34	2.2000	23.40
14	LTNLINSGF	202	2.2000	23.40
15	FVHDPFTLE	93	1.8000	19.15
16	FNSLLHAAD	231	1.6000	17.02
17	YLISTGIAD	117	1.3800	14.68
18	FQSIHESDM	60	1.3000	13.83
19	YKYIIKNTA	244	1.3000	13.83
20	LHHAPSLLA	309	1.3000	13.83
21	IMQHFTIPA	30	1.0800	11.49
22	MQHFTIPAS	31	1.0000	10.64
23	WQNGKTVTF	253	1.0000	10.64
24	LLAFTNPTV	315	0.9000	9.57
25	FTNPTVNSY	318	0.9000	9.57
26	WWNTGAATE	160	0.8000	8.51
27	FYEVDAISG	151	0.5800	6.17

28	ISGWWNTGA	157	0.5500	5.85
29	YQFNSLLHA	229	0.5000	5.32
30	LMYDETGYA	287	0.5000	5.32
31	YEAPINLVY	333	0.5000	5.32
32	VYSQRNRSA	340	0.5000	5.32
33	WISFKRENE	450	0.5000	5.32
34	VEYVDVRFC	17	0.4000	4.26
35	LNINFFVHD	88	0.4000	4.26
36	YFGAEAEFY	128	0.4000	4.26
37	FILEKGHHE	210	0.4000	4.26
38	FSAMLMAGL	379	0.4000	4.26
39	LDGIKNKIE	387	0.3000	3.19
40	FFVHDPFTL	92	0.2500	2.66
41	YVDVRFCDL	19	0.2000	2.13
42	FPVAPNDQY	186	0.2000	2.13
43	MLTNLINSG	201	0.2000	2.13
44	LVYSQRNRS	339	0.2000	2.13
45	IEPVNIRPH	459	0.2000	2.13
46	LINSGFILE	205	0.1800	1.91

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	FRAAKTLNI	82	4.1000	46.59
2	YIIKNTAWQ	246	3.5000	39.77
3	FYIFDSVSF	135	3.3000	37.50
4	YFPVAPNDQ	185	2.8000	31.82
5	YLAFSAMLM	376	2.3000	26.14
6	IRGFQSIHE	57	1.7800	20.23
7	INYQFNSLL	227	1.4000	15.91
8	LTNLINSGF	202	1.3000	14.77
9	YKYIIKNTA	244	1.3000	14.77
10	LHHAPSLLA	309	1.3000	14.77
11	FRSPDSSGN	366	1.2000	13.64
12	IMQHFTIPA	30	1.0800	12.27
13	MQHFTIPAS	31	1.0000	11.36
14	INLVYSQRN	337	0.7000	7.95

15	VRIPITGSN	350	0.7000	7.95
16	LLAFTNPTV	315	0.6000	6.82
17	ISGWWNTGA	157	0.5500	6.25
18	YIFDSVSFD	136	0.5000	5.68
19	YQFNSLLHA	229	0.5000	5.68
20	LMYDETGYA	287	0.5000	5.68
21	VYSQRNRSA	340	0.5000	5.68
22	IPITGSNPK	352	0.5000	5.68
23	VEYVDVRFC	17	0.4000	4.55
24	FQSIHESDM	60	0.2000	2.27
25	LVYSQRNRS	339	0.2000	2.27
26	WQNGKTVTF	253	0.1000	1.14
27	YKRLVPGYE	326	-0.1000	0
28	MHCHQSLWK	274	-0.2000	0
29	FTNPTVNSY	318	-0.2000	0
30	FKLAKDEKV	9	-0.4000	0
31	VRFCDLPGI	22	-0.4000	0
32	FTIPASAFD	34	-0.5000	0
33	YAGLSDTAR	294	-0.5000	0
34	IFDSVSFDS	137	-0.5500	0
35	YEAPINLVY	333	-0.6000	0
36	FSAMLMAGL	379	-0.6000	0
37	YFGAEAEFY	128	-0.7000	0
38	FYEVDAISG	151	-0.7200	0
39	FFVHDPFTL	92	-0.7500	0
40	YVDVRFCDL	19	-0.8000	0
41	LAFDGSSIR	50	-0.8000	0
42	FPVAPNDQY	186	-0.9000	0
43	MQLYKYIIK	241	-0.9200	0
44	LLLPDPETA	69	-1.0000	0
45	IEPQAPVDK	394	-1.0000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRGFQSIHE	57	5.7800	61.49
2	INLVYSQRN	337	3.7000	39.36

3	VRIPITGSN	350	3.7000	39.36
4	INYQFNSLL	227	3.4000	36.17
5	FRAAKTLNI	82	3.3000	35.11
6	YIIKNTAWQ	246	3.3000	35.11
7	FYIFDSVSF	135	3.2000	34.04
8	LTNLINSGF	202	3.2000	34.04
9	YFPVAPNDQ	185	2.6000	27.66
10	YLAFSAMLM	376	2.4000	25.53
11	LHHAPSLLA	309	2.3000	24.47
12	YIFDSVSFD	136	2.2000	23.40
13	FRSPDSSGN	366	2.2000	23.40
14	IMQHFTIPA	30	2.0800	22.13
15	MQHFTIPAS	31	2.0000	21.28
16	LLAFTNPTV	315	1.9000	20.21
17	YKRLVPGYE	326	1.9000	20.21
18	ISGWWNTGA	157	1.5500	16.49
19	LMYDETGYA	287	1.5000	15.96
20	VYSQRNRSA	340	1.5000	15.96
21	VEYVDVRFC	17	1.4000	14.89
22	LNINFFVHD	88	1.4000	14.89
23	LDGIKNKIE	387	1.3000	13.83
24	FTIPASAFD	34	1.2000	12.77
25	MLTNLINSG	201	1.2000	12.77
26	LVYSQRNRS	339	1.2000	12.77
27	IEPVNIRPH	459	1.2000	12.77
28	LINSGFILE	205	1.1800	12.55
29	IPQTPTQLS	415	1.0000	10.64
30	LAFTNPTVN	316	0.9000	9.57
31	VRFCDLPGI	22	0.8000	8.51
32	FVHDPFTLE	93	0.8000	8.51
33	IPITGSNPK	352	0.8000	8.51
34	LLHHAPSLL	308	0.7000	7.45
35	MLLLPDPET	68	0.6000	6.38
36	FNSLLHAAD	231	0.6000	6.38
37	IDRLEADHE	426	0.5000	5.32
38	IFDSVSFDS	137	0.4500	4.79
39	LHAADDMQL	235	0.4000	4.26
40	YLISTGIAD	117	0.3800	4.04
41	MAGLDGIKN	384	0.3800	4.04
42	FQSIHESDM	60	0.3000	3.19
43	YKYIIKNTA	244	0.3000	3.19

44	IIKNTAWQN	247	0.3000	3.19
45	LAFDGSSIR	50	0.2000	2.13
46	LLHAADDMQ	234	0.2000	2.13
47	MHCHQSLWK	274	0.1000	1.06

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	FRAAKTLNI	82	5.4000	60.00
2	FYIFDSVSF	135	3.4800	38.67
3	YIFDSVSFD	136	3.4000	37.78
4	IMQHFTIPA	30	3.1800	35.33
5	WQNGKTVTF	253	2.9800	33.11
6	LMYDETGYA	287	2.9000	32.22
7	YIIKNTAWQ	246	2.6000	28.89
8	LAFDGSSIR	50	2.5000	27.78
9	YQFNSLLHA	229	2.5000	27.78
10	INYQFNSLL	227	2.4600	27.33
11	MHCHQSLWK	274	2.4000	26.67
12	LTNLINSGF	202	2.3000	25.56
13	FVHDPFTLE	93	2.2000	24.44
14	IPQTPTQLS	415	2.2000	24.44
15	IPITGSNPK	352	2.1000	23.33
16	LVYSQRNRS	339	2.0000	22.22
17	YLAFSAMLM	376	2.0000	22.22
18	MLTNLINSG	201	1.8000	20.00
19	FILEKGHHE	210	1.8000	20.00
20	LHHAPSLLA	309	1.7000	18.89
21	FKLAKDEKV	9	1.5000	16.67
22	YFGAEAEFY	128	1.5000	16.67
23	FFVHDPFTL	92	1.3600	15.11
24	FPVAPNDQY	186	1.3000	14.44
25	IRPHPYEFA	464	1.3000	14.44
26	IRGFQSIHE	57	1.2800	14.22
27	YLISTGIAD	117	1.2800	14.22
28	VRIPITGSN	350	1.1000	12.22
29	LLHHAPSLL	308	1.0600	11.78

30	YKRLVPGYE	326	1.0000	11.11
31	VYSQRNRSA	340	1.0000	11.11
32	FRSPDSSGN	366	1.0000	11.11
33	FTNDLIETW	442	1.0000	11.11
34	YKYIIKNTA	244	0.9000	10.00
35	LPPEEAASI	407	0.9000	10.00
36	VRFCDLPGI	22	0.8000	8.89
37	WWNTGAATE	160	0.8000	8.89
38	LFGDNGSGM	266	0.8000	8.89
39	YEAPINLVY	333	0.8000	8.89
40	FQSIHESDM	60	0.7000	7.78
41	YEVDAISGW	152	0.7000	7.78
42	IKNTAWQNG	248	0.7000	7.78
43	LWKDGAPLM	280	0.7000	7.78
44	FTNPTVNSY	318	0.7000	7.78
45	FKRENEIEP	453	0.6800	7.56
46	YFPVAPNDQ	185	0.6000	6.67
47	MLMAGLDGI	382	0.6000	6.67

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	FRAAKTLNI	82	3.1000	35.23
2	IRGFQSIHE	57	2.7800	31.59
3	YIIKNTAWQ	246	2.5000	28.41
4	INYQFNSLL	227	2.4000	27.27
5	FYIFDSVSF	135	2.3000	26.14
6	LTNLINSGF	202	2.3000	26.14
7	LHHAPSLLA	309	2.3000	26.14
8	IMQHFTIPA	30	2.0800	23.64
9	MQHFTIPAS	31	2.0000	22.73
10	YFPVAPNDQ	185	1.8000	20.45
11	INLVYSQRN	337	1.7000	19.32
12	VRIPITGSN	350	1.7000	19.32
13	LLAFTNPTV	315	1.6000	18.18
14	ISGWWNTGA	157	1.5500	17.61
15	LMYDETGYA	287	1.5000	17.05

16	VYSQRNRSA	340	1.5000	17.05
17	IPITGSNPK	352	1.5000	17.05
18	VEYVDVRFC	17	1.4000	15.91
19	YLAFSAMLM	376	1.3000	14.77
20	LVYSQRNRS	339	1.2000	13.64
21	IPQTPTQLS	415	1.0000	11.36
22	MHCHQSLWK	274	0.8000	9.09
23	VRFCDLPGI	22	0.6000	6.82
24	IFDSVSFDS	137	0.4500	5.11
25	YKYIIKNTA	244	0.3000	3.41
26	LAFDGSSIR	50	0.2000	2.27
27	FRSPDSSGN	366	0.2000	2.27
28	MQLYKYIIK	241	0.0800	0.91
29	IEPVNIRPH	459	-0.0200	0
30	MLTNLINSG	201	-0.1000	0
31	MLMAGLDGI	382	-0.2000	0
32	MLLLPDPET	68	-0.3000	0
33	LLHHAPSLL	308	-0.3000	0
34	YIFDSVSFD	136	-0.5000	0
35	YQFNSLLHA	229	-0.5000	0
36	LLHAADDMQ	234	-0.6000	0
37	LHAADDMQL	235	-0.6000	0
38	LAFSAMLMA	377	-0.7000	0
39	IRPHPYEFA	464	-0.7000	0
40	FQSIHESDM	60	-0.8000	0
41	VHDPFTLEP	94	-0.9000	0
42	LISTGIADT	118	-0.9000	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	FRAAKTLNI	82	4.5000	52.33
2	YIIKNTAWQ	246	3.3000	38.37
3	IMQHFTIPA	30	3.1800	36.98
4	LMYDETGYA	287	2.9000	33.72
5	YQFNSLLHA	229	2.5000	29.07
6	YIFDSVSFD	136	2.3000	26.74

7	MHCHQSLWK	274	2.3000	26.74
8	IPITGSNPK	352	2.0000	23.26
9	IPQTPTQLS	415	1.8000	20.93
10	LHHAPSLLA	309	1.7000	19.77
11	LVYSQRNRS	339	1.6000	18.60
12	FYIFDSVSF	135	1.5800	18.37
13	INYQFNSLL	227	1.5000	17.44
14	YFPVAPNDQ	185	1.3000	15.12
15	IRPHPYEFA	464	1.3000	15.12
16	WQNGKTVTF	253	1.0800	12.56
17	LAFDGSSIR	50	1.0000	11.63
18	VYSQRNRSA	340	1.0000	11.63
19	FTNDLIETW	442	1.0000	11.63
20	YKYIIKNTA	244	0.9000	10.47
21	FVHDPFTLE	93	0.8000	9.30
22	YEVDAISGW	152	0.7000	8.14
23	FKLAKDEKV	9	0.5000	5.81
24	YLAFSAMLM	376	0.5000	5.81
25	FFVHDPFTL	92	0.4000	4.65
26	MLTNLINSG	201	0.4000	4.65
27	LTNLINSGF	202	0.4000	4.65
28	FILEKGHHE	210	0.4000	4.65
29	VRIPITGSN	350	0.3000	3.49
30	YFGAEAEFY	128	0.2000	2.33
31	FRSPDSSGN	366	0.2000	2.33
32	LAFSAMLMA	377	0.2000	2.33
33	YLISTGIAD	117	0.1800	2.09
34	LLHHAPSLL	308	0.1000	1.16
35	IEPQAPVDK	394	-0.0200	0
36	VRFCDLPGI	22	-0.1000	0
37	IRGFQSIHE	57	-0.1200	0
38	FGDNGSGMH	267	-0.1200	0
39	YLTEGGVFT	435	-0.1200	0
40	LISTGIADT	118	-0.3000	0
41	MLMAGLDGI	382	-0.3000	0
42	LYELPPEEA	404	-0.3000	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	FRAAKTLNI	82	7.7200	66.55
2	FYIFDSVSF	135	6.9000	59.48
3	FFVHDPFTL	92	6.4000	55.17
4	YLAFSAMLM	376	5.0000	43.10
5	IHESDMLLL	63	4.9000	42.24
6	YLISTGIAD	117	4.6000	39.66
7	YVDVRFCDL	19	4.3000	37.07
8	VRFCDLPGI	22	4.3000	37.07
9	IRGFQSIHE	57	4.3000	37.07
10	WQNGKTVTF	253	4.2200	36.38
11	LLHHAPSLL	308	3.6000	31.03
12	YEFALYYDV	469	3.6000	31.03
13	LINSGFILE	205	3.4000	29.31
14	LVYSQRNRS	339	3.4000	29.31
15	YKYIIKNTA	244	3.3000	28.45
16	YFGAEAEFY	128	3.0000	25.86
17	INLVYSQRN	337	2.9000	25.00
18	LHHAPSLLA	309	2.8000	24.14
19	FDGSSIRGF	52	2.7000	23.28
20	LAFSAMLMA	377	2.7000	23.28
21	MLMAGLDGI	382	2.6000	22.41
22	IMQHFTIPA	30	2.5200	21.72
23	FKLAKDEKV	9	2.5000	21.55
24	LHAADDMQL	235	2.5000	21.55
25	FQSIHESDM	60	2.4000	20.69
26	IFDSVSFDS	137	2.4000	20.69
27	FYEVDAISG	151	2.4000	20.69
28	INYQFNSLL	227	2.3000	19.83
29	IPITGSNPK	352	2.3000	19.83
30	YQFNSLLHA	229	2.2000	18.97
31	FGAEAEFYI	129	2.1000	18.10
32	YFPVAPNDQ	185	2.0000	17.24
33	LRDKMLTNL	197	2.0000	17.24
34	LSDTARHYI	297	2.0000	17.24
35	FTNPTVNSY	318	1.9000	16.38
36	FSAMLMAGL	379	1.9000	16.38
37	FRSPDSSGN	366	1.7000	14.66
38	VEYVDVRFC	17	1.6000	13.79
39	LISTGIADT	118	1.6000	13.79

40	IKNTAWQNG	248	1.6000	13.79
41	MHCHQSLWK	274	1.6000	13.79
42	YEAPINLVY	333	1.6000	13.79
43	WWNTGAATE	160	1.5000	12.93
44	WKDGAPLMY	281	1.5000	12.93
45	IRPHPYEFA	464	1.5000	12.93
46	YVDLRDKML	194	1.4000	12.07
47	LLAFTNPTV	315	1.4000	12.07

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	FRAAKTLNI	82	7.7200	66.55
2	FYIFDSVSF	135	6.9000	59.48
3	FFVHDPFTL	92	6.4000	55.17
4	YLAFSAMLM	376	5.0000	43.10
5	IHESDMLLL	63	4.9000	42.24
6	YLISTGIAD	117	4.6000	39.66
7	YVDVRFCDL	19	4.3000	37.07
8	VRFCDLPGI	22	4.3000	37.07
9	IRGFQSIHE	57	4.3000	37.07
10	WQNGKTVTF	253	4.2200	36.38
11	LLHHAPSLL	308	3.6000	31.03
12	YEFALYYDV	469	3.6000	31.03
13	LINSGFILE	205	3.4000	29.31
14	LVYSQRNRS	339	3.4000	29.31
15	YKYIIKNTA	244	3.3000	28.45
16	YFGAEAEFY	128	3.0000	25.86
17	INLVYSQRN	337	2.9000	25.00
18	LHHAPSLLA	309	2.8000	24.14
19	FDGSSIRGF	52	2.7000	23.28
20	LAFSAMLMA	377	2.7000	23.28
21	MLMAGLDGI	382	2.6000	22.41
22	IMQHFTIPA	30	2.5200	21.72
23	FKLAKDEKV	9	2.5000	21.55
24	LHAADDMQL	235	2.5000	21.55
25	FQSIHESDM	60	2.4000	20.69

26	IFDSVSFDS	137	2.4000	20.69
27	FYEVDAISG	151	2.4000	20.69
28	INYQFNSLL	227	2.3000	19.83
29	IPITGSNPK	352	2.3000	19.83
30	YQFNSLLHA	229	2.2000	18.97
31	FGAEAEFYI	129	2.1000	18.10
32	YFPVAPNDQ	185	2.0000	17.24
33	LRDKMLTNL	197	2.0000	17.24
34	LSDTARHYI	297	2.0000	17.24
35	FTNPTVNSY	318	1.9000	16.38
36	FSAMLMAGL	379	1.9000	16.38
37	FRSPDSSGN	366	1.7000	14.66
38	VEYVDVRFC	17	1.6000	13.79
39	LISTGIADT	118	1.6000	13.79
40	IKNTAWQNG	248	1.6000	13.79
41	MHCHQSLWK	274	1.6000	13.79
42	YEAPINLVY	333	1.6000	13.79
43	WWNTGAATE	160	1.5000	12.93
44	WKDGAPLMY	281	1.5000	12.93
45	IRPHPYEFA	464	1.5000	12.93
46	YVDLRDKML	194	1.4000	12.07
47	LLAFTNPTV	315	1.4000	12.07

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	YIIKNTAWQ	246	7.0000	81.40
2	YKVRHKGGY	177	4.8000	55.81
3	FMPKPLFGD	261	4.0000	46.51
4	YKRLVPGYE	326	3.8000	44.19
5	VNIRPHPYE	462	3.6000	41.86
6	FRAAKTLNI	82	2.6000	30.23
7	FNSLLHAAD	231	2.6000	30.23
8	VRIPITGSN	350	2.6000	30.23
9	IRGFQSIHE	57	2.3000	26.74
10	YKYIIKNTA	244	2.2000	25.58
11	VNSYKRLVP	323	2.0000	23.26

12	YFPVAPNDQ	185	1.9000	22.09
13	YQFNSLLHA	229	1.9000	22.09
14	YLAFSAMLM	376	1.9000	22.09
15	YIFDSVSFD	136	1.8000	20.93
16	VDLRDKMLT	195	1.7000	19.77
17	LYKYIIKNT	243	1.7000	19.77
18	YSQRNRSAC	341	1.7000	19.77
19	WISFKRENE	450	1.7000	19.77
20	FYIFDSVSF	135	1.6000	18.60
21	FTIPASAFD	34	1.4000	16.28
22	LVYSQRNRS	339	1.3000	15.12
23	VTFMPKPLF	259	1.2000	13.95
24	MQHFTIPAS	31	1.1000	12.79
25	IEPVNIRPH	459	1.1000	12.79
26	YLISTGIAD	117	1.0000	11.63
27	VRHKGGYFP	179	1.0000	11.63
28	LEFRSPDSS	364	1.0000	11.63
29	VIDRLEADH	425	1.0000	11.63
30	VRFCDLPGI	22	0.9000	10.47
31	VEYVDVRFC	17	0.8000	9.30
32	FILEKGHHE	210	0.8000	9.30
33	WWNTGAATE	160	0.7000	8.14
34	FRSPDSSGN	366	0.6000	6.98
35	INLVYSQRN	337	0.4000	4.65
36	WQNGKTVTF	253	0.3000	3.49
37	VPGYEAPIN	330	0.3000	3.49
38	IKNKIEPQA	390	0.3000	3.49
39	MQLYKYIIK	241	0.2000	2.33
40	LMYDETGYA	287	0.2000	2.33
41	FSAMLMAGL	379	0.2000	2.33
42	FFVHDPFTL	92	-0.1000	0
43	FGDNGSGMH	267	-0.1000	0
44	LNINFFVHD	88	-0.2000	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	YIIKNTAWQ	246	6.2000	77.50
2	YKVRHKGGY	177	3.7000	46.25
3	FRAAKTLNI	82	2.4000	30.00
4	YKYIIKNTA	244	2.2000	27.50
5	YQFNSLLHA	229	1.9000	23.75
6	YSQRNRSAC	341	1.7000	21.25
7	VNSYKRLVP	323	1.6000	20.00
8	FMPKPLFGD	261	1.3000	16.25
9	LVYSQRNRS	339	1.3000	16.25
10	MQHFTIPAS	31	1.1000	13.75
11	YFPVAPNDQ	185	1.1000	13.75
12	LEFRSPDSS	364	1.0000	12.50
13	MQLYKYIIK	241	0.9000	11.25
14	VEYVDVRFC	17	0.8000	10.00
15	VDLRDKMLT	195	0.8000	10.00
16	LYKYIIKNT	243	0.8000	10.00
17	YKRLVPGYE	326	0.8000	10.00
18	YLAFSAMLM	376	0.8000	10.00
19	VRFCDLPGI	22	0.7000	8.75
20	FYIFDSVSF	135	0.7000	8.75
21	VRHKGGYFP	179	0.6000	7.50
22	VRIPITGSN	350	0.6000	7.50
23	VNIRPHPYE	462	0.6000	7.50
24	VTFMPKPLF	259	0.3000	3.75
25	IKNKIEPQA	390	0.3000	3.75
26	LMYDETGYA	287	0.2000	2.50
27	FNSLLHAAD	231	-0.1000	0
28	IEPVNIRPH	459	-0.1200	0
29	VIDRLEADH	425	-0.2200	0
30	YIGGLLHHA	304	-0.4000	0
31	LHHAPSLLA	309	-0.4000	0
32	ILEKGHHEV	211	-0.6000	0
33	WQNGKTVTF	253	-0.6000	0
34	IRGFQSIHE	57	-0.7000	0
35	LEPYSRDPR	100	-0.8000	0
36	FSAMLMAGL	379	-0.8000	0
37	VFKLAKDEK	8	-0.9000	0
38	IMQHFTIPA	30	-0.9000	0
39	YSRDPRNIA	103	-0.9000	0
40	YIFDSVSFD	136	-0.9000	0
41	FDSRANGSF	143	-0.9000	0

42	INSGFILEK	206	-0.9000	0
43	LRDKMLTNL	197	-1.0000	0
44	FFVHDPFTL	92	-1.1000	0
45	MLMAGLDGI	382	-1.1000	0
46	LISTGIADT	118	-1.2000	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	YIIKNTAWQ	246	5.2000	65.00
2	YKVRHKGGY	177	2.7000	33.75
3	VNSYKRLVP	323	2.6000	32.50
4	LVYSQRNRS	339	2.3000	28.75
5	MQHFTIPAS	31	2.1000	26.25
6	LEFRSPDSS	364	2.0000	25.00
7	MQLYKYIIK	241	1.9000	23.75
8	VEYVDVRFC	17	1.8000	22.50
9	VDLRDKMLT	195	1.8000	22.50
10	LYKYIIKNT	243	1.8000	22.50
11	VRFCDLPGI	22	1.7000	21.25
12	VRHKGGYFP	179	1.6000	20.00
13	VRIPITGSN	350	1.6000	20.00
14	VNIRPHPYE	462	1.6000	20.00
15	FRAAKTLNI	82	1.4000	17.50
16	VTFMPKPLF	259	1.3000	16.25
17	IKNKIEPQA	390	1.3000	16.25
18	YKYIIKNTA	244	1.2000	15.00
19	LMYDETGYA	287	1.2000	15.00
20	YQFNSLLHA	229	0.9000	11.25
21	IEPVNIRPH	459	0.8800	11.00
22	VIDRLEADH	425	0.7800	9.75
23	YSQRNRSAC	341	0.7000	8.75
24	LHHAPSLLA	309	0.6000	7.50
25	ILEKGHHEV	211	0.4000	5.00
26	IRGFQSIHE	57	0.3000	3.75
27	FMPKPLFGD	261	0.3000	3.75
28	LEPYSRDPR	100	0.2000	2.50

29	VFKLAKDEK	8	0.1000	1.25
30	IMQHFTIPA	30	0.1000	1.25
31	YFPVAPNDQ	185	0.1000	1.25
32	INSGFILEK	206	0.1000	1.25
33	MLMAGLDGI	382	-0.1000	0
34	LISTGIADT	118	-0.2000	0
35	YKRLVPGYE	326	-0.2000	0
36	YLAFSAMLM	376	-0.2000	0
37	ISFKRENEI	451	-0.2000	0
38	FYIFDSVSF	135	-0.3000	0
39	LVPGYEAPI	329	-0.3000	0
40	VSFDSRANG	141	-0.5000	0
41	MLTNLINSG	201	-0.6000	0
42	INLVYSQRN	337	-0.6000	0
43	IARKAENYL	110	-0.7000	0
44	VPGYEAPIN	330	-0.7000	0
45	LLLPDPETA	69	-0.9000	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	YIIKNTAWQ	246	6.0000	69.77
2	VNIRPHPYE	462	4.6000	53.49
3	YKVRHKGGY	177	3.8000	44.19
4	VRIPITGSN	350	3.6000	41.86
5	IRGFQSIHE	57	3.3000	38.37
6	FMPKPLFGD	261	3.0000	34.88
7	VNSYKRLVP	323	3.0000	34.88
8	YKRLVPGYE	326	2.8000	32.56
9	VDLRDKMLT	195	2.7000	31.40
10	LYKYIIKNT	243	2.7000	31.40
11	LVYSQRNRS	339	2.3000	26.74
12	VTFMPKPLF	259	2.2000	25.58
13	MQHFTIPAS	31	2.1000	24.42
14	IEPVNIRPH	459	2.1000	24.42
15	VRHKGGYFP	179	2.0000	23.26
16	LEFRSPDSS	364	2.0000	23.26

17	VIDRLEADH	425	2.0000	23.26
18	VRFCDLPGI	22	1.9000	22.09
19	VEYVDVRFC	17	1.8000	20.93
20	FRAAKTLNI	82	1.6000	18.60
21	FNSLLHAAD	231	1.6000	18.60
22	INLVYSQRN	337	1.4000	16.28
23	VPGYEAPIN	330	1.3000	15.12
24	IKNKIEPQA	390	1.3000	15.12
25	MQLYKYIIK	241	1.2000	13.95
26	YKYIIKNTA	244	1.2000	13.95
27	LMYDETGYA	287	1.2000	13.95
28	LRDKMLTNL	197	1.0000	11.63
29	YFPVAPNDQ	185	0.9000	10.47
30	YQFNSLLHA	229	0.9000	10.47
31	YLAFSAMLM	376	0.9000	10.47
32	LNINFFVHD	88	0.8000	9.30
33	YIFDSVSFD	136	0.8000	9.30
34	VSFDSRANG	141	0.8000	9.30
35	LISTGIADT	118	0.7000	8.14
36	MLTNLINSG	201	0.7000	8.14
37	ILEKGHHEV	211	0.7000	8.14
38	YSQRNRSAC	341	0.7000	8.14
39	WISFKRENE	450	0.7000	8.14
40	FYIFDSVSF	135	0.6000	6.98
41	LHHAPSLLA	309	0.6000	6.98
42	IIKNTAWQN	247	0.5000	5.81
43	FTIPASAFD	34	0.4000	4.65
44	IARKAENYL	110	0.3000	3.49
45	LEPYSRDPR	100	0.2000	2.33
46	IMQHFTIPA	30	0.1000	1.16
47	MLMAGLDGI	382	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	YIIKNTAWQ	246	6.2000	71.26
2	YKYIIKNTA	244	4.2000	48.28

3	YSQRNRSAC	341	3.5000	40.23
4	LVYSQRNRS	339	3.3000	37.93
5	YFPVAPNDQ	185	3.1000	35.63
6	FRAAKTLNI	82	3.0000	34.48
7	YKVRHKGGY	177	3.0000	34.48
8	YQFNSLLHA	229	2.5000	28.74
9	VNSYKRLVP	323	2.2000	25.29
10	LEFRSPDSS	364	2.2000	25.29
11	FMPKPLFGD	261	2.1500	24.71
12	VDLRDKMLT	195	1.8000	20.69
13	LRDKMLTNL	197	1.8000	20.69
14	YLAFSAMLM	376	1.8000	20.69
15	MQLYKYIIK	241	1.7800	20.46
16	FYIFDSVSF	135	1.7000	19.54
17	VRHKGGYFP	179	1.5000	17.24
18	MQHFTIPAS	31	1.3000	14.94
19	YSRDPRNIA	103	1.1000	12.64
20	VRFCDLPGI	22	0.9000	10.34
21	YIFDSVSFD	136	0.9000	10.34
22	ISFKRENEI	451	0.8000	9.20
23	VNIRPHPYE	462	0.8000	9.20
24	VEYVDVRFC	17	0.5000	5.75
25	VTFMPKPLF	259	0.5000	5.75
26	IKNKIEPQA	390	0.5000	5.75
27	FQSIHESDM	60	0.4000	4.60
28	LEPYSRDPR	100	0.4000	4.60
29	MLTNLINSG	201	0.4000	4.60
30	WQNGKTVTF	253	0.4000	4.60
31	FTNPTVNSY	318	0.4000	4.60
32	FRSPDSSGN	366	0.4000	4.60
33	WISFKRENE	450	0.4000	4.60
34	VFKLAKDEK	8	0.3000	3.45
35	IARKAENYL	110	0.3000	3.45
36	LYKYIIKNT	243	0.3000	3.45
37	WNTGAATEA	161	0.2000	2.30
38	LHHAPSLLA	309	0.2000	2.30
39	IRGFQSIHE	57	0.1800	2.07
40	YIGGLLHHA	304	0.1000	1.15
41	YKRLVPGYE	326	0.1000	1.15
42	MLMAGLDGI	382	0.1000	1.15
43	IMQHFTIPA	30	-0.0200	0

44	ILEKGHHEV	211	-0.1000	0
45	FNSLLHAAD	231	-0.1000	0
46	VRIPITGSN	350	-0.1000	0

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1

Rank	Sequence	At Position	Score	% of Highest Score
1	YIIKNTAWQ	246	7.0000	69.31
2	YKVRHKGGY	177	4.9000	48.51
3	VNIRPHPYE	462	4.7500	47.03
4	FMPKPLFGD	261	4.5000	44.55
5	FRAAKTLNI	82	4.4000	43.56
6	IRGFQSIHE	57	3.9000	38.61
7	YKRLVPGYE	326	3.9000	38.61
8	VNSYKRLVP	323	3.8000	37.62
9	YQFNSLLHA	229	3.7000	36.63
10	YLAFSAMLM	376	3.5000	34.65
11	VDLRDKMLT	195	3.3000	32.67
12	WISFKRENE	450	2.8000	27.72
13	VRIPITGSN	350	2.7000	26.73
14	YLISTGIAD	117	2.6000	25.74
15	FNSLLHAAD	231	2.6000	25.74
16	YKYIIKNTA	244	2.5000	24.75
17	VTFMPKPLF	259	2.3500	23.27
18	LYKYIIKNT	243	2.3000	22.77
19	MQHFTIPAS	31	2.2500	22.28
20	YFPVAPNDQ	185	2.2000	21.78
21	FYIFDSVSF	135	2.1000	20.79
22	VRFCDLPGI	22	2.0500	20.30
23	YIFDSVSFD	136	1.8000	17.82
24	MQLYKYIIK	241	1.8000	17.82
25	VRHKGGYFP	179	1.7000	16.83
26	YSQRNRSAC	341	1.7000	16.83
27	LVYSQRNRS	339	1.6000	15.84
28	FILEKGHHE	210	1.5000	14.85
29	VPGYEAPIN	330	1.4500	14.36
30	IKNKIEPQA	390	1.4500	14.36

31	FTIPASAFD	34	1.4000	13.86
32	LHHAPSLLA	309	1.4000	13.86
33	IEPVNIRPH	459	1.3000	12.87
34	FYEVDAISG	151	1.1000	10.89
35	LRDKMLTNL	197	1.1000	10.89
36	VEYVDVRFC	17	1.0000	9.90
37	VIDRLEADH	425	1.0000	9.90
38	WKDGAPLMY	281	0.9000	8.91
39	FCDLPGIMQ	24	0.8000	7.92
40	WQNGKTVTF	253	0.8000	7.92
41	IMQHFTIPA	30	0.7000	6.93
42	WWNTGAATE	160	0.7000	6.93
43	LEFRSPDSS	364	0.7000	6.93
44	FRSPDSSGN	366	0.6000	5.94
45	MAGLDGIKN	384	0.6000	5.94
46	INLVYSQRN	337	0.5000	4.95
47	VFTNDLIET	441	0.5000	4.95

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	FRAAKTLNI	82	4.2000	50.60
2	YQFNSLLHA	229	3.7000	44.58
3	YIIKNTAWQ	246	3.4000	40.96
4	YKYIIKNTA	244	3.1000	37.35
5	YLAFSAMLM	376	2.3000	27.71
6	MQHFTIPAS	31	2.1500	25.90
7	LVYSQRNRS	339	1.9000	22.89
8	VRFCDLPGI	22	1.8500	22.29
9	YFPVAPNDQ	185	1.5000	18.07
10	LHHAPSLLA	309	1.4000	16.87
11	YKRLVPGYE	326	1.3000	15.66
12	VEYVDVRFC	17	1.1000	13.25
13	IMQHFTIPA	30	1.1000	13.25
14	FYIFDSVSF	135	1.1000	13.25
15	VTFMPKPLF	259	1.0500	12.65
16	IRGFQSIHE	57	0.8000	9.64

17	YKVRHKGGY	177	0.8000	9.64
18	VNSYKRLVP	323	0.5000	6.02
19	FCDLPGIMQ	24	0.4000	4.82
20	FNSLLHAAD	231	0.3000	3.61
21	MHCHQSLWK	274	0.3000	3.61
22	YLISTGIAD	117	0.2000	2.41
23	INSGFILEK	206	0.2000	2.41
24	IEPVNIRPH	459	0.1800	2.17
25	FYEVDAISG	151	-0.1000	0
26	FFVHDPFTL	92	-0.2000	0
27	LAFSAMLMA	377	-0.3000	0
28	WISFKRENE	450	-0.3000	0
29	MQLYKYIIK	241	-0.4000	0
30	LMYDETGYA	287	-0.4000	0
31	YIGGLLHHA	304	-0.4000	0
32	VFTNDLIET	441	-0.4000	0
33	VDLRDKMLT	195	-0.6000	0
34	VFKLAKDEK	8	-0.8000	0
35	FQSIHESDM	60	-0.8000	0
36	LISTGIADT	118	-0.8000	0
37	WQNGKTVTF	253	-0.8000	0
38	IGGLLHHAP	305	-0.8000	0
39	WKDGAPLMY	281	-0.9000	0
40	LLAFTNPTV	315	-0.9500	0
41	FMPKPLFGD	261	-1.0000	0
42	MAGLDGIKN	384	-1.0000	0
43	LYELPPEEA	404	-1.0000	0
44	YVDVRFCDL	19	-1.2000	0
45	FSAMLMAGL	379	-1.2000	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	LVYSQRNRS	339	4.1000	48.81
2	YIIKNTAWQ	246	3.7000	44.05
3	MQHFTIPAS	31	3.1000	36.90
4	IMQHFTIPA	30	2.9000	34.52

5	VEYVDVRFC	17	2.4000	28.57
6	VRFCDLPGI	22	2.4000	28.57
7	MHCHQSLWK	274	2.3000	27.38
8	VYSQRNRSA	340	2.3000	27.38
9	FRAAKTLNI	82	2.1000	25.00
10	FFVHDPFTL	92	1.9000	22.62
11	YQFNSLLHA	229	1.7000	20.24
12	YKYIIKNTA	244	1.7000	20.24
13	IRPHPYEFA	464	1.6000	19.05
14	VNSYKRLVP	323	1.5000	17.86
15	IEPVNIRPH	459	1.4800	17.62
16	VTFMPKPLF	259	1.4000	16.67
17	LLHHAPSLL	308	1.3000	15.48
18	LHHAPSLLA	309	1.3000	15.48
19	IEPQAPVDK	394	1.1000	13.10
20	FYIFDSVSF	135	1.0000	11.90
21	VRHKGGYFP	179	1.0000	11.90
22	IRGFQSIHE	57	0.9000	10.71
23	MLTNLINSG	201	0.9000	10.71
24	LYKYIIKNT	243	0.8000	9.52
25	LEFRSPDSS	364	0.8000	9.52
26	MLMAGLDGI	382	0.8000	9.52
27	VFKLAKDEK	8	0.7000	8.33
28	IKNKIEPQA	390	0.5000	5.95
29	MQLYKYIIK	241	0.4000	4.76
30	YLAFSAMLM	376	0.4000	4.76
31	YFPVAPNDQ	185	0.3000	3.57
32	INSGFILEK	206	0.3000	3.57
33	FMPKPLFGD	261	0.3000	3.57
34	IETWISFKR	447	0.3000	3.57
35	IIKNTAWQN	247	0.2000	2.38
36	VNIRPHPYE	462	0.2000	2.38
37	IFDSVSFDS	137	0.1000	1.19
38	ILEKGHHEV	211	0.1000	1.19
39	VRIPITGSN	350	0.1000	1.19
40	INFFVHDPF	90	-0.2000	0
41	LMYDETGYA	287	-0.2000	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	FRAAKTLNI	82	3.2000	38.55
2	MQHFTIPAS	31	3.1500	37.95
3	LVYSQRNRS	339	2.9000	34.94
4	VRFCDLPGI	22	2.8500	34.34
5	YQFNSLLHA	229	2.7000	32.53
6	YIIKNTAWQ	246	2.4000	28.92
7	LHHAPSLLA	309	2.4000	28.92
8	VEYVDVRFC	17	2.1000	25.30
9	IMQHFTIPA	30	2.1000	25.30
10	YKYIIKNTA	244	2.1000	25.30
11	VTFMPKPLF	259	2.0500	24.70
12	IRGFQSIHE	57	1.8000	21.69
13	VNSYKRLVP	323	1.5000	18.07
14	MHCHQSLWK	274	1.3000	15.66
15	YLAFSAMLM	376	1.3000	15.66
16	INSGFILEK	206	1.2000	14.46
17	IEPVNIRPH	459	1.1800	14.22
18	VRIPITGSN	350	1.0000	12.05
19	LAFSAMLMA	377	0.7000	8.43
20	MQLYKYIIK	241	0.6000	7.23
21	LMYDETGYA	287	0.6000	7.23
22	VFTNDLIET	441	0.6000	7.23
23	YFPVAPNDQ	185	0.5000	6.02
24	VDLRDKMLT	195	0.4000	4.82
25	YKRLVPGYE	326	0.3000	3.61
26	VFKLAKDEK	8	0.2000	2.41
27	LISTGIADT	118	0.2000	2.41
28	IGGLLHHAP	305	0.2000	2.41
29	FYIFDSVSF	135	0.1000	1.20
30	LLAFTNPTV	315	0.0500	0.60
31	YKVRHKGGY	177	-0.2000	0
32	VNIRPHPYE	462	-0.2500	0
33	MLTNLINSG	201	-0.3000	0
34	VYSQRNRSA	340	-0.3000	0
35	IKNKIEPQA	390	-0.3500	0
36	INLVYSQRN	337	-0.4000	0
37	MLMAGLDGI	382	-0.4000	0

38	IEPQAPVDK	394	-0.4000	0
39	LLLPDPETA	69	-0.5000	0
40	VRHKGGYFP	179	-0.5000	0
41	LYKYIIKNT	243	-0.5000	0
42	ITGSNPKAK	354	-0.5000	0
43	MLLLPDPET	68	-0.5500	0
44	FCDLPGIMQ	24	-0.6000	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	FRAAKTLNI	82	3.2000	38.55
2	MQHFTIPAS	31	3.1500	37.95
3	LVYSQRNRS	339	2.9000	34.94
4	VRFCDLPGI	22	2.8500	34.34
5	YQFNSLLHA	229	2.7000	32.53
6	YIIKNTAWQ	246	2.4000	28.92
7	LHHAPSLLA	309	2.4000	28.92
8	VEYVDVRFC	17	2.1000	25.30
9	IMQHFTIPA	30	2.1000	25.30
10	YKYIIKNTA	244	2.1000	25.30
11	VTFMPKPLF	259	2.0500	24.70
12	IRGFQSIHE	57	1.8000	21.69
13	VNSYKRLVP	323	1.5000	18.07
14	MHCHQSLWK	274	1.3000	15.66
15	YLAFSAMLM	376	1.3000	15.66
16	INSGFILEK	206	1.2000	14.46
17	IEPVNIRPH	459	1.1800	14.22
18	VRIPITGSN	350	1.0000	12.05
19	LAFSAMLMA	377	0.7000	8.43
20	MQLYKYIIK	241	0.6000	7.23
21	LMYDETGYA	287	0.6000	7.23
22	VFTNDLIET	441	0.6000	7.23
23	YFPVAPNDQ	185	0.5000	6.02
24	VDLRDKMLT	195	0.4000	4.82
25	YKRLVPGYE	326	0.3000	3.61
26	VFKLAKDEK	8	0.2000	2.41

27	LISTGIADT	118	0.2000	2.41
28	IGGLLHHAP	305	0.2000	2.41
29	FYIFDSVSF	135	0.1000	1.20
30	LLAFTNPTV	315	0.0500	0.60
31	YKVRHKGGY	177	-0.2000	0
32	VNIRPHPYE	462	-0.2500	0
33	MLTNLINSG	201	-0.3000	0
34	VYSQRNRSA	340	-0.3000	0
35	IKNKIEPQA	390	-0.3500	0
36	INLVYSQRN	337	-0.4000	0
37	MLMAGLDGI	382	-0.4000	0
38	IEPQAPVDK	394	-0.4000	0
39	LLLPDPETA	69	-0.5000	0
40	VRHKGGYFP	179	-0.5000	0
41	LYKYIIKNT	243	-0.5000	0
42	ITGSNPKAK	354	-0.5000	0
43	MLLLPDPET	68	-0.5500	0
44	FCDLPGIMQ	24	-0.6000	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	LVYSQRNRS	339	5.2100	57.25
2	LMYDETGYA	287	5.1000	56.04
3	VRFCDLPGI	22	3.6000	39.56
4	LAKDEKVEY	11	2.8000	30.77
5	VSFDSRANG	141	2.8000	30.77
6	YIFDSVSFD	136	2.7700	30.44
7	YSRDPRNIA	103	2.6100	28.68
8	YKYIIKNTA	244	2.6100	28.68
9	MQHFTIPAS	31	2.5000	27.47
10	LWKDGAPLM	280	2.5000	27.47
11	IMQHFTIPA	30	2.3000	25.27
12	LFGDNGSGM	266	2.2700	24.95
13	VRIPITGSN	350	2.2000	24.18
14	INSGFILEK	206	2.1000	23.08
15	LAFDGSSIR	50	2.0700	22.75

16	FRAAKTLNI	82	1.9000	20.88
17	YIIKNTAWQ	246	1.9000	20.88
18	VTFMPKPLF	259	1.8000	19.78
19	MLMAGLDGI	382	1.7000	18.68
20	YEVDAISGW	152	1.6700	18.35
21	YQFNSLLHA	229	1.6000	17.58
22	LLLPDPETA	69	1.3000	14.29
23	IFDSVSFDS	137	1.3000	14.29
24	FTNDLIETW	442	1.3000	14.29
25	VFKLAKDEK	8	1.2000	13.19
26	VEYVDVRFC	17	1.2000	13.19
27	WQNGKTVTF	253	1.2000	13.19
28	LVPGYEAPI	329	1.2000	13.19
29	LLPDPETAR	70	1.1000	12.09
30	LHHAPSLLA	309	1.1000	12.09
31	YFPVAPNDQ	185	1.0100	11.10
32	IRPHPYEFA	464	0.9000	9.89
33	MLTNLINSG	201	0.8100	8.90
34	LAFSAMLMA	377	0.8000	8.79
35	IEPQAPVDK	394	0.8000	8.79
36	LLHHAPSLL	308	0.7700	8.46
37	VGSGGQAEI	219	0.6000	6.59
38	MHCHQSLWK	274	0.6000	6.59
39	LEFRSPDSS	364	0.5000	5.49
40	FVHDPFTLE	93	0.4000	4.40
41	VFTNDLIET	441	0.4000	4.40
42	VFDDGLAFD	45	0.3000	3.30
43	FFVHDPFTL	92	0.3000	3.30
44	IEPVNIRPH	459	0.2800	3.08
45	YLISTGIAD	117	0.2000	2.20
46	WNTGAATEA	161	0.2000	2.20
47	YIGGLLHHA	304	0.2000	2.20

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	YIIKNTAWQ	246	4.7000	55.95

2	FRAAKTLNI	82	3.1000	36.90
3	LVYSQRNRS	339	3.1000	36.90
4	FFVHDPFTL	92	2.9000	34.52
5	YQFNSLLHA	229	2.7000	32.14
6	YKYIIKNTA	244	2.7000	32.14
7	MQHFTIPAS	31	2.1000	25.00
8	FYIFDSVSF	135	2.0000	23.81
9	IMQHFTIPA	30	1.9000	22.62
10	VEYVDVRFC	17	1.4000	16.67
11	VRFCDLPGI	22	1.4000	16.67
12	YLAFSAMLM	376	1.4000	16.67
13	YFPVAPNDQ	185	1.3000	15.48
14	FMPKPLFGD	261	1.3000	15.48
15	MHCHQSLWK	274	1.3000	15.48
16	VYSQRNRSA	340	1.3000	15.48
17	YKVRHKGGY	177	0.6000	7.14
18	IRPHPYEFA	464	0.6000	7.14
19	VNSYKRLVP	323	0.5000	5.95
20	IEPVNIRPH	459	0.4800	5.71
21	VTFMPKPLF	259	0.4000	4.76
22	WISFKRENE	450	0.4000	4.76
23	YIGGLLHHA	304	0.3000	3.57
24	LLHHAPSLL	308	0.3000	3.57
25	LHHAPSLLA	309	0.3000	3.57
26	YSRDPRNIA	103	0.1000	1.19
27	IEPQAPVDK	394	0.1000	1.19
28	IRGFQSIHE	57	-0.1000	0
29	MLTNLINSG	201	-0.1000	0
30	WQNGKTVTF	253	-0.1000	0
31	LYKYIIKNT	243	-0.2000	0
32	LEFRSPDSS	364	-0.2000	0
33	MLMAGLDGI	382	-0.2000	0
34	VFKLAKDEK	8	-0.3000	0
35	FNSLLHAAD	231	-0.4000	0
36	YKRLVPGYE	326	-0.5000	0
37	IKNKIEPQA	390	-0.5000	0
38	MQLYKYIIK	241	-0.6000	0
39	INSGFILEK	206	-0.7000	0
40	FTNPTVNSY	318	-0.7000	0
41	IETWISFKR	447	-0.7000	0
42	FDGSSIRGF	52	-0.8000	0

43	IIKNTAWQN	247	-0.8000	0
44	VNIRPHPYE	462	-0.8000	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	FRAAKTLNI	82	4.0000	45.45
2	YIIKNTAWQ	246	4.0000	45.45
3	FYIFDSVSF	135	3.9000	44.32
4	FFVHDPFTL	92	3.8600	43.86
5	LVYSQRNRS	339	3.5000	39.77
6	YLAFSAMLM	376	2.9000	32.95
7	YQFNSLLHA	229	2.7000	30.68
8	YKYIIKNTA	244	2.7000	30.68
9	MQHFTIPAS	31	2.5000	28.41
10	FMPKPLFGD	261	2.4000	27.27
11	VRFCDLPGI	22	2.3000	26.14
12	VTFMPKPLF	259	2.3000	26.14
13	IMQHFTIPA	30	1.9000	21.59
14	YKVRHKGGY	177	1.9000	21.59
15	WQNGKTVTF	253	1.8000	20.45
16	WISFKRENE	450	1.8000	20.45
17	VNSYKRLVP	323	1.5000	17.05
18	VEYVDVRFC	17	1.4000	15.91
19	MHCHQSLWK	274	1.4000	15.91
20	IRGFQSIHE	57	1.3000	14.77
21	MLTNLINSG	201	1.3000	14.77
22	VYSQRNRSA	340	1.3000	14.77
23	LLHHAPSLL	308	1.2600	14.32
24	FDGSSIRGF	52	1.1000	12.50
25	VRHKGGYFP	179	1.0000	11.36
26	YKRLVPGYE	326	0.9000	10.23
27	IETWISFKR	447	0.8000	9.09
28	INFFVHDPF	90	0.7000	7.95
29	FNSLLHAAD	231	0.7000	7.95
30	MLMAGLDGI	382	0.7000	7.95
31	YFPVAPNDQ	185	0.6000	6.82

32	FTNPTVNSY	318	0.6000	6.82
33	VNIRPHPYE	462	0.6000	6.82
34	IRPHPYEFA	464	0.6000	6.82
35	LYKYIIKNT	243	0.5000	5.68
36	YFGAEAEFY	128	0.3000	3.41
37	FILEKGHHE	210	0.3000	3.41
38	YIGGLLHHA	304	0.3000	3.41
39	LHHAPSLLA	309	0.3000	3.41
40	YIFDSVSFD	136	0.2000	2.27
41	LEFRSPDSS	364	0.2000	2.27
42	IEPQAPVDK	394	0.2000	2.27
43	YSRDPRNIA	103	0.1000	1.14
44	YLISTGIAD	117	0.1000	1.14
45	ILEKGHHEV	211	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVYSQRNRS	339	4.1000	48.81
2	YIIKNTAWQ	246	3.7000	44.05
3	MQHFTIPAS	31	3.1000	36.90
4	IMQHFTIPA	30	2.9000	34.52
5	VEYVDVRFC	17	2.4000	28.57
6	VRFCDLPGI	22	2.4000	28.57
7	MHCHQSLWK	274	2.3000	27.38
8	VYSQRNRSA	340	2.3000	27.38
9	FRAAKTLNI	82	2.1000	25.00
10	FFVHDPFTL	92	1.9000	22.62
11	YQFNSLLHA	229	1.7000	20.24
12	YKYIIKNTA	244	1.7000	20.24
13	IRPHPYEFA	464	1.6000	19.05
14	VNSYKRLVP	323	1.5000	17.86
15	IEPVNIRPH	459	1.4800	17.62
16	VTFMPKPLF	259	1.4000	16.67
17	LLHHAPSLL	308	1.3000	15.48
18	LHHAPSLLA	309	1.3000	15.48
19	IEPQAPVDK	394	1.1000	13.10

20	FYIFDSVSF	135	1.0000	11.90
21	VRHKGGYFP	179	1.0000	11.90
22	IRGFQSIHE	57	0.9000	10.71
23	MLTNLINSG	201	0.9000	10.71
24	LYKYIIKNT	243	0.8000	9.52
25	LEFRSPDSS	364	0.8000	9.52
26	MLMAGLDGI	382	0.8000	9.52
27	VFKLAKDEK	8	0.7000	8.33
28	IKNKIEPQA	390	0.5000	5.95
29	MQLYKYIIK	241	0.4000	4.76
30	YLAFSAMLM	376	0.4000	4.76
31	YFPVAPNDQ	185	0.3000	3.57
32	INSGFILEK	206	0.3000	3.57
33	FMPKPLFGD	261	0.3000	3.57
34	IETWISFKR	447	0.3000	3.57
35	IIKNTAWQN	247	0.2000	2.38
36	VNIRPHPYE	462	0.2000	2.38
37	IFDSVSFDS	137	0.1000	1.19
38	ILEKGHHEV	211	0.1000	1.19
39	VRIPITGSN	350	0.1000	1.19
40	INFFVHDPF	90	-0.2000	0
41	LMYDETGYA	287	-0.2000	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	FRAAKTLNI	82	5.1000	58.62
2	YLAFSAMLM	376	3.8000	43.68
3	YQFNSLLHA	229	3.7000	42.53
4	YKYIIKNTA	244	3.1000	35.63
5	FYIFDSVSF	135	3.0000	34.48
6	VTFMPKPLF	259	2.9500	33.91
7	VRFCDLPGI	22	2.7500	31.61
8	YIIKNTAWQ	246	2.7000	31.03
9	YKRLVPGYE	326	2.7000	31.03
10	MQHFTIPAS	31	2.5500	29.31
11	LVYSQRNRS	339	2.3000	26.44

12	IRGFQSIHE	57	2.2000	25.29
13	YKVRHKGGY	177	2.1000	24.14
14	VNSYKRLVP	323	1.5000	17.24
15	FNSLLHAAD	231	1.4000	16.09
16	LHHAPSLLA	309	1.4000	16.09
17	YLISTGIAD	117	1.3000	14.94
18	FYEVDAISG	151	1.3000	14.94
19	VEYVDVRFC	17	1.1000	12.64
20	IMQHFTIPA	30	1.1000	12.64
21	WQNGKTVTF	253	1.1000	12.64
22	WISFKRENE	450	1.1000	12.64
23	YFPVAPNDQ	185	0.8000	9.20
24	VRIPITGSN	350	0.8000	9.20
25	FFVHDPFTL	92	0.7600	8.74
26	FQSIHESDM	60	0.7000	8.05
27	MHCHQSLWK	274	0.4000	4.60
28	WKDGAPLMY	281	0.4000	4.60
29	INSGFILEK	206	0.3000	3.45
30	VFTNDLIET	441	0.3000	3.45
31	IGGLLHHAP	305	0.2000	2.30
32	VNIRPHPYE	462	0.1500	1.72
33	VDLRDKMLT	195	0.1000	1.15
34	MLTNLINSG	201	0.1000	1.15
35	FMPKPLFGD	261	0.1000	1.15
36	LLAFTNPTV	315	0.0500	0.57
37	LISTGIADT	118	-0.1000	0
38	MAGLDGIKN	384	-0.2000	0
39	YVDVRFCDL	19	-0.2400	0
40	FSAMLMAGL	379	-0.2400	0
41	FCDLPGIMQ	24	-0.3000	0
42	MQLYKYIIK	241	-0.3000	0
43	LAFSAMLMA	377	-0.3000	0
44	LTNLINSGF	202	-0.4000	0
45	LMYDETGYA	287	-0.4000	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	LVYSQRNRS	339	4.5000	51.14
2	MQHFTIPAS	31	3.5000	39.77
3	VRFCDLPGI	22	3.3000	37.50
4	VTFMPKPLF	259	3.3000	37.50
5	FRAAKTLNI	82	3.0000	34.09
6	YIIKNTAWQ	246	3.0000	34.09
7	IMQHFTIPA	30	2.9000	32.95
8	FYIFDSVSF	135	2.9000	32.95
9	FFVHDPFTL	92	2.8600	32.50
10	VNSYKRLVP	323	2.5000	28.41
11	VEYVDVRFC	17	2.4000	27.27
12	MHCHQSLWK	274	2.4000	27.27
13	IRGFQSIHE	57	2.3000	26.14
14	MLTNLINSG	201	2.3000	26.14
15	VYSQRNRSA	340	2.3000	26.14
16	LLHHAPSLL	308	2.2600	25.68
17	VRHKGGYFP	179	2.0000	22.73
18	YLAFSAMLM	376	1.9000	21.59
19	IETWISFKR	447	1.8000	20.45
20	INFFVHDPF	90	1.7000	19.32
21	YQFNSLLHA	229	1.7000	19.32
22	YKYIIKNTA	244	1.7000	19.32
23	MLMAGLDGI	382	1.7000	19.32
24	VNIRPHPYE	462	1.6000	18.18
25	IRPHPYEFA	464	1.6000	18.18
26	LYKYIIKNT	243	1.5000	17.05
27	FMPKPLFGD	261	1.4000	15.91
28	LHHAPSLLA	309	1.3000	14.77
29	LEFRSPDSS	364	1.2000	13.64
30	IEPQAPVDK	394	1.2000	13.64
31	ILEKGHHEV	211	1.1000	12.50
32	IIKNTAWQN	247	1.0000	11.36
33	IGGLLHHAP	305	1.0000	11.36
34	LLAFTNPTV	315	1.0000	11.36
35	LRDKMLTNL	197	0.9600	10.91
36	YKVRHKGGY	177	0.9000	10.23
37	VRIPITGSN	350	0.9000	10.23
38	IEPVNIRPH	459	0.9000	10.23
39	VFKLAKDEK	8	0.8000	9.09
40	LEPYSRDPR	100	0.8000	9.09

41	WQNGKTVTF	253	0.8000	9.09
42	WISFKRENE	450	0.8000	9.09
43	VDLRDKMLT	195	0.7000	7.95
44	INYQFNSLL	227	0.6600	7.50
45	ISFKRENEI	451	0.6000	6.82
46	IFDSVSFDS	137	0.5000	5.68
47	VSFDSRANG	141	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FRAAKTLNI	82	4.0000	45.45
2	YIIKNTAWQ	246	4.0000	45.45
3	FYIFDSVSF	135	3.9000	44.32
4	FFVHDPFTL	92	3.8600	43.86
5	LVYSQRNRS	339	3.5000	39.77
6	YLAFSAMLM	376	2.9000	32.95
7	YQFNSLLHA	229	2.7000	30.68
8	YKYIIKNTA	244	2.7000	30.68
9	MQHFTIPAS	31	2.5000	28.41
10	FMPKPLFGD	261	2.4000	27.27
11	VRFCDLPGI	22	2.3000	26.14
12	VTFMPKPLF	259	2.3000	26.14
13	IMQHFTIPA	30	1.9000	21.59
14	YKVRHKGGY	177	1.9000	21.59
15	WQNGKTVTF	253	1.8000	20.45
16	WISFKRENE	450	1.8000	20.45
17	VNSYKRLVP	323	1.5000	17.05
18	VEYVDVRFC	17	1.4000	15.91
19	MHCHQSLWK	274	1.4000	15.91
20	IRGFQSIHE	57	1.3000	14.77
21	MLTNLINSG	201	1.3000	14.77
22	VYSQRNRSA	340	1.3000	14.77
23	LLHHAPSLL	308	1.2600	14.32
24	FDGSSIRGF	52	1.1000	12.50
25	VRHKGGYFP	179	1.0000	11.36
26	YKRLVPGYE	326	0.9000	10.23

27	IETWISFKR	447	0.8000	9.09
28	INFFVHDPF	90	0.7000	7.95
29	FNSLLHAAD	231	0.7000	7.95
30	MLMAGLDGI	382	0.7000	7.95
31	YFPVAPNDQ	185	0.6000	6.82
32	FTNPTVNSY	318	0.6000	6.82
33	VNIRPHPYE	462	0.6000	6.82
34	IRPHPYEFA	464	0.6000	6.82
35	LYKYIIKNT	243	0.5000	5.68
36	YFGAEAEFY	128	0.3000	3.41
37	FILEKGHHE	210	0.3000	3.41
38	YIGGLLHHA	304	0.3000	3.41
39	LHHAPSLLA	309	0.3000	3.41
40	YIFDSVSFD	136	0.2000	2.27
41	LEFRSPDSS	364	0.2000	2.27
42	IEPQAPVDK	394	0.2000	2.27
43	YSRDPRNIA	103	0.1000	1.14
44	YLISTGIAD	117	0.1000	1.14
45	ILEKGHHEV	211	0.1000	1.14

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	YIIKNTAWQ	246	4.5000	50.00
2	LVYSQRNRS	339	4.1000	45.56
3	IRGFQSIHE	57	3.9000	43.33
4	VNIRPHPYE	462	3.2000	35.56
5	MQHFTIPAS	31	3.1000	34.44
6	FMPKPLFGD	261	3.0000	33.33
7	IMQHFTIPA	30	2.9000	32.22
8	FFVHDPFTL	92	2.9000	32.22
9	IEPVNIRPH	459	2.7000	30.00
10	VRFCDLPGI	22	2.6000	28.89
11	VEYVDVRFC	17	2.4000	26.67
12	WISFKRENE	450	2.4000	26.67
13	FRAAKTLNI	82	2.3000	25.56
14	VTFMPKPLF	259	2.3000	25.56

15	LLHHAPSLL	308	2.3000	25.56
16	VYSQRNRSA	340	2.3000	25.56
17	MLTNLINSG	201	2.2000	24.44
18	IIKNTAWQN	247	2.2000	24.44
19	VRIPITGSN	350	2.1000	23.33
20	LNINFFVHD	88	1.9000	21.11
21	FYIFDSVSF	135	1.9000	21.11
22	VNSYKRLVP	323	1.9000	21.11
23	YQFNSLLHA	229	1.7000	18.89
24	LYKYIIKNT	243	1.7000	18.89
25	YKYIIKNTA	244	1.7000	18.89
26	MHCHQSLWK	274	1.6000	17.78
27	IRPHPYEFA	464	1.6000	17.78
28	YKRLVPGYE	326	1.5000	16.67
29	YLAFSAMLM	376	1.5000	16.67
30	VRHKGGYFP	179	1.4000	15.56
31	FNSLLHAAD	231	1.3000	14.44
32	LHHAPSLLA	309	1.3000	14.44
33	YFPVAPNDQ	185	1.1000	12.22
34	LRDKMLTNL	197	1.0000	11.11
35	INLVYSQRN	337	1.0000	11.11
36	MLMAGLDGI	382	1.0000	11.11
37	VAPNDQYVD	188	0.9000	10.00
38	VDLRDKMLT	195	0.9000	10.00
39	FILEKGHHE	210	0.9000	10.00
40	YIFDSVSFD	136	0.8000	8.89
41	LEFRSPDSS	364	0.8000	8.89
42	INFFVHDPF	90	0.7000	7.78
43	YLISTGIAD	117	0.7000	7.78
44	YKVRHKGGY	177	0.7000	7.78
45	INYQFNSLL	227	0.7000	7.78
46	LISTGIADT	118	0.6000	6.67
47	IKNKIEPQA	390	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	FRAAKTLNI	82	5.1000	58.62
2	YLAFSAMLM	376	3.8000	43.68
3	YQFNSLLHA	229	3.7000	42.53
4	YKYIIKNTA	244	3.1000	35.63
5	FYIFDSVSF	135	3.0000	34.48
6	VTFMPKPLF	259	2.9500	33.91
7	VRFCDLPGI	22	2.7500	31.61
8	YIIKNTAWQ	246	2.7000	31.03
9	YKRLVPGYE	326	2.7000	31.03
10	MQHFTIPAS	31	2.5500	29.31
11	LVYSQRNRS	339	2.3000	26.44
12	IRGFQSIHE	57	2.2000	25.29
13	YKVRHKGGY	177	2.1000	24.14
14	VNSYKRLVP	323	1.5000	17.24
15	FNSLLHAAD	231	1.4000	16.09
16	LHHAPSLLA	309	1.4000	16.09
17	YLISTGIAD	117	1.3000	14.94
18	FYEVDAISG	151	1.3000	14.94
19	VEYVDVRFC	17	1.1000	12.64
20	IMQHFTIPA	30	1.1000	12.64
21	WQNGKTVTF	253	1.1000	12.64
22	WISFKRENE	450	1.1000	12.64
23	YFPVAPNDQ	185	0.8000	9.20
24	VRIPITGSN	350	0.8000	9.20
25	FFVHDPFTL	92	0.7600	8.74
26	FQSIHESDM	60	0.7000	8.05
27	MHCHQSLWK	274	0.4000	4.60
28	WKDGAPLMY	281	0.4000	4.60
29	INSGFILEK	206	0.3000	3.45
30	VFTNDLIET	441	0.3000	3.45
31	IGGLLHHAP	305	0.2000	2.30
32	VNIRPHPYE	462	0.1500	1.72
33	VDLRDKMLT	195	0.1000	1.15
34	MLTNLINSG	201	0.1000	1.15
35	FMPKPLFGD	261	0.1000	1.15
36	LLAFTNPTV	315	0.0500	0.57
37	LISTGIADT	118	-0.1000	0
38	MAGLDGIKN	384	-0.2000	0
39	YVDVRFCDL	19	-0.2400	0
40	FSAMLMAGL	379	-0.2400	0
41	FCDLPGIMQ	24	-0.3000	0

42	MQLYKYIIK	241	-0.3000	0
43	LAFSAMLMA	377	-0.3000	0
44	LTNLINSGF	202	-0.4000	0
45	LMYDETGYA	287	-0.4000	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	YIIKNTAWQ	246	3.4000	50.00
2	YKYIIKNTA	244	2.8000	41.18
3	FRAAKTLNI	82	2.4000	35.29
4	YQFNSLLHA	229	1.9000	27.94
5	LVYSQRNRS	339	1.6000	23.53
6	YFPVAPNDQ	185	1.2000	17.65
7	YKRLVPGYE	326	1.2000	17.65
8	MQHFTIPAS	31	1.0000	14.71
9	VEYVDVRFC	17	0.9000	13.24
10	VRFCDLPGI	22	0.7000	10.29
11	YKVRHKGGY	177	0.7000	10.29
12	YLAFSAMLM	376	0.7000	10.29
13	FYIFDSVSF	135	0.6000	8.82
14	FNSLLHAAD	231	0.3000	4.41
15	IEPVNIRPH	459	-0.0200	0
16	VTFMPKPLF	259	-0.1000	0
17	VRIPITGSN	350	-0.1000	0
18	LHHAPSLLA	309	-0.4000	0
19	VFKLAKDEK	8	-0.5000	0
20	IMQHFTIPA	30	-0.5000	0
21	LMYDETGYA	287	-0.5000	0
22	FFVHDPFTL	92	-0.7000	0
23	IRGFQSIHE	57	-0.8000	0
24	FQSIHESDM	60	-0.8000	0
25	LISTGIADT	118	-0.8000	0
26	YIGGLLHHA	304	-1.1000	0
27	MLMAGLDGI	382	-1.1000	0
28	YVDVRFCDL	19	-1.2000	0
29	FCDLPGIMQ	24	-1.2000	0

30	FSAMLMAGL	379	-1.2000	0
31	WQNGKTVTF	253	-1.3000	0
32	VNSYKRLVP	323	-1.3000	0
33	YSQRNRSAC	341	-1.3000	0
34	FGDNGSGMH	267	-1.3200	0
35	YLISTGIAD	117	-1.4000	0
36	WISFKRENE	450	-1.4000	0
37	FMPKPLFGD	261	-1.5000	0
38	MHCHQSLWK	274	-1.5000	0
39	IGGLLHHAP	305	-1.5000	0
40	INLVYSQRN	337	-1.5000	0
41	VYSQRNRSA	340	-1.5000	0
42	YSRDPRNIA	103	-1.6000	0
43	YIFDSVSFD	136	-1.6000	0
44	MLTNLINSG	201	-1.6000	0
45	INSGFILEK	206	-1.6000	0
46	FYEVDAISG	151	-1.7000	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	FRAAKTLNI	82	3.2000	38.55
2	MQHFTIPAS	31	3.1500	37.95
3	LVYSQRNRS	339	2.9000	34.94
4	VRFCDLPGI	22	2.8500	34.34
5	YQFNSLLHA	229	2.7000	32.53
6	YIIKNTAWQ	246	2.4000	28.92
7	LHHAPSLLA	309	2.4000	28.92
8	VEYVDVRFC	17	2.1000	25.30
9	IMQHFTIPA	30	2.1000	25.30
10	YKYIIKNTA	244	2.1000	25.30
11	VTFMPKPLF	259	2.0500	24.70
12	IRGFQSIHE	57	1.8000	21.69
13	VNSYKRLVP	323	1.5000	18.07
14	MHCHQSLWK	274	1.3000	15.66
15	YLAFSAMLM	376	1.3000	15.66
16	INSGFILEK	206	1.2000	14.46

17	IEPVNIRPH	459	1.1800	14.22
18	VRIPITGSN	350	1.0000	12.05
19	LAFSAMLMA	377	0.7000	8.43
20	MQLYKYIIK	241	0.6000	7.23
21	LMYDETGYA	287	0.6000	7.23
22	VFTNDLIET	441	0.6000	7.23
23	YFPVAPNDQ	185	0.5000	6.02
24	VDLRDKMLT	195	0.4000	4.82
25	YKRLVPGYE	326	0.3000	3.61
26	VFKLAKDEK	8	0.2000	2.41
27	LISTGIADT	118	0.2000	2.41
28	IGGLLHHAP	305	0.2000	2.41
29	FYIFDSVSF	135	0.1000	1.20
30	LLAFTNPTV	315	0.0500	0.60
31	YKVRHKGGY	177	-0.2000	0
32	VNIRPHPYE	462	-0.2500	0
33	MLTNLINSG	201	-0.3000	0
34	VYSQRNRSA	340	-0.3000	0
35	IKNKIEPQA	390	-0.3500	0
36	INLVYSQRN	337	-0.4000	0
37	MLMAGLDGI	382	-0.4000	0
38	IEPQAPVDK	394	-0.4000	0
39	LLLPDPETA	69	-0.5000	0
40	VRHKGGYFP	179	-0.5000	0
41	LYKYIIKNT	243	-0.5000	0
42	ITGSNPKAK	354	-0.5000	0
43	MLLLPDPET	68	-0.5500	0
44	FCDLPGIMQ	24	-0.6000	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	FRAAKTLNI	82	4.4000	49.44
2	YKRLVPGYE	326	4.3000	48.31
3	YIIKNTAWQ	246	4.2000	47.19
4	IRGFQSIHE	57	3.8000	42.70
5	YQFNSLLHA	229	3.7000	41.57

6	YLAFSAMLM	376	3.4000	38.20
7	YKYIIKNTA	244	3.1000	34.83
8	FNSLLHAAD	231	3.0000	33.71
9	YLISTGIAD	117	2.9000	32.58
10	WISFKRENE	450	2.7000	30.34
11	YFPVAPNDQ	185	2.3000	25.84
12	MQHFTIPAS	31	2.1500	24.16
13	VRFCDLPGI	22	2.0500	23.03
14	FYIFDSVSF	135	2.0000	22.47
15	VRIPITGSN	350	2.0000	22.47
16	VTFMPKPLF	259	1.9500	21.91
17	YKVRHKGGY	177	1.9000	21.35
18	LVYSQRNRS	339	1.9000	21.35
19	VNIRPHPYE	462	1.7500	19.66
20	FMPKPLFGD	261	1.7000	19.10
21	LHHAPSLLA	309	1.4000	15.73
22	IEPVNIRPH	459	1.4000	15.73
23	FCDLPGIMQ	24	1.2000	13.48
24	FYEVDAISG	151	1.2000	13.48
25	VEYVDVRFC	17	1.1000	12.36
26	IMQHFTIPA	30	1.1000	12.36
27	YIFDSVSFD	136	1.1000	12.36
28	WWNTGAATE	160	1.1000	12.36
29	MAGLDGIKN	384	1.0000	11.24
30	VNSYKRLVP	323	0.9000	10.11
31	FFVHDPFTL	92	0.8000	8.99
32	FILEKGHHE	210	0.8000	8.99
33	FTIPASAFD	34	0.7000	7.87
34	LINSGFILE	205	0.6000	6.74
35	INLVYSQRN	337	0.6000	6.74
36	VFTNDLIET	441	0.5000	5.62
37	FQSIHESDM	60	0.3000	3.37
38	LNINFFVHD	88	0.3000	3.37
39	VDLRDKMLT	195	0.3000	3.37
40	IIKNTAWQN	247	0.3000	3.37
41	WKDGAPLMY	281	0.2000	2.25
42	LISTGIADT	118	0.1000	1.12
43	WQNGKTVTF	253	0.1000	1.12
44	FRSPDSSGN	366	-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	LVYSQRNRS	339	4.1000	48.81
2	YIIKNTAWQ	246	3.7000	44.05
3	MQHFTIPAS	31	3.1000	36.90
4	IMQHFTIPA	30	2.9000	34.52
5	VEYVDVRFC	17	2.4000	28.57
6	VRFCDLPGI	22	2.4000	28.57
7	MHCHQSLWK	274	2.3000	27.38
8	VYSQRNRSA	340	2.3000	27.38
9	FRAAKTLNI	82	2.1000	25.00
10	FFVHDPFTL	92	1.9000	22.62
11	YQFNSLLHA	229	1.7000	20.24
12	YKYIIKNTA	244	1.7000	20.24
13	IRPHPYEFA	464	1.6000	19.05
14	VNSYKRLVP	323	1.5000	17.86
15	IEPVNIRPH	459	1.4800	17.62
16	VTFMPKPLF	259	1.4000	16.67
17	LLHHAPSLL	308	1.3000	15.48
18	LHHAPSLLA	309	1.3000	15.48
19	IEPQAPVDK	394	1.1000	13.10
20	FYIFDSVSF	135	1.0000	11.90
21	VRHKGGYFP	179	1.0000	11.90
22	IRGFQSIHE	57	0.9000	10.71
23	MLTNLINSG	201	0.9000	10.71
24	LYKYIIKNT	243	0.8000	9.52
25	LEFRSPDSS	364	0.8000	9.52
26	MLMAGLDGI	382	0.8000	9.52
27	VFKLAKDEK	8	0.7000	8.33
28	IKNKIEPQA	390	0.5000	5.95
29	MQLYKYIIK	241	0.4000	4.76
30	YLAFSAMLM	376	0.4000	4.76
31	YFPVAPNDQ	185	0.3000	3.57
32	INSGFILEK	206	0.3000	3.57
33	FMPKPLFGD	261	0.3000	3.57
34	IETWISFKR	447	0.3000	3.57
35	IIKNTAWQN	247	0.2000	2.38
36	VNIRPHPYE	462	0.2000	2.38

37	IFDSVSFDS	137	0.1000	1.19
38	ILEKGHHEV	211	0.1000	1.19
39	VRIPITGSN	350	0.1000	1.19
40	INFFVHDPF	90	-0.2000	0
41	LMYDETGYA	287	-0.2000	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	YIIKNTAWQ	246	4.7000	55.95
2	FRAAKTLNI	82	3.1000	36.90
3	LVYSQRNRS	339	3.1000	36.90
4	FFVHDPFTL	92	2.9000	34.52
5	YQFNSLLHA	229	2.7000	32.14
6	YKYIIKNTA	244	2.7000	32.14
7	MQHFTIPAS	31	2.1000	25.00
8	FYIFDSVSF	135	2.0000	23.81
9	IMQHFTIPA	30	1.9000	22.62
10	VEYVDVRFC	17	1.4000	16.67
11	VRFCDLPGI	22	1.4000	16.67
12	YLAFSAMLM	376	1.4000	16.67
13	YFPVAPNDQ	185	1.3000	15.48
14	FMPKPLFGD	261	1.3000	15.48
15	MHCHQSLWK	274	1.3000	15.48
16	VYSQRNRSA	340	1.3000	15.48
17	YKVRHKGGY	177	0.6000	7.14
18	IRPHPYEFA	464	0.6000	7.14
19	VNSYKRLVP	323	0.5000	5.95
20	IEPVNIRPH	459	0.4800	5.71
21	VTFMPKPLF	259	0.4000	4.76
22	WISFKRENE	450	0.4000	4.76
23	YIGGLLHHA	304	0.3000	3.57
24	LLHHAPSLL	308	0.3000	3.57
25	LHHAPSLLA	309	0.3000	3.57
26	YSRDPRNIA	103	0.1000	1.19
27	IEPQAPVDK	394	0.1000	1.19
28	IRGFQSIHE	57	-0.1000	0

29	MLTNLINSG	201	-0.1000	0
30	WQNGKTVTF	253	-0.1000	0
31	LYKYIIKNT	243	-0.2000	0
32	LEFRSPDSS	364	-0.2000	0
33	MLMAGLDGI	382	-0.2000	0
34	VFKLAKDEK	8	-0.3000	0
35	FNSLLHAAD	231	-0.4000	0
36	YKRLVPGYE	326	-0.5000	0
37	IKNKIEPQA	390	-0.5000	0
38	MQLYKYIIK	241	-0.6000	0
39	INSGFILEK	206	-0.7000	0
40	FTNPTVNSY	318	-0.7000	0
41	IETWISFKR	447	-0.7000	0
42	FDGSSIRGF	52	-0.8000	0
43	IIKNTAWQN	247	-0.8000	0
44	VNIRPHPYE	462	-0.8000	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	LVYSQRNRS	339	4.5000	51.14
2	MQHFTIPAS	31	3.5000	39.77
3	VRFCDLPGI	22	3.3000	37.50
4	VTFMPKPLF	259	3.3000	37.50
5	FRAAKTLNI	82	3.0000	34.09
6	YIIKNTAWQ	246	3.0000	34.09
7	IMQHFTIPA	30	2.9000	32.95
8	FYIFDSVSF	135	2.9000	32.95
9	FFVHDPFTL	92	2.8600	32.50
10	VNSYKRLVP	323	2.5000	28.41
11	VEYVDVRFC	17	2.4000	27.27
12	MHCHQSLWK	274	2.4000	27.27
13	IRGFQSIHE	57	2.3000	26.14
14	MLTNLINSG	201	2.3000	26.14
15	VYSQRNRSA	340	2.3000	26.14
16	LLHHAPSLL	308	2.2600	25.68
17	VRHKGGYFP	179	2.0000	22.73

18	YLAFSAMLM	376	1.9000	21.59
19	IETWISFKR	447	1.8000	20.45
20	INFFVHDPF	90	1.7000	19.32
21	YQFNSLLHA	229	1.7000	19.32
22	YKYIIKNTA	244	1.7000	19.32
23	MLMAGLDGI	382	1.7000	19.32
24	VNIRPHPYE	462	1.6000	18.18
25	IRPHPYEFA	464	1.6000	18.18
26	LYKYIIKNT	243	1.5000	17.05
27	FMPKPLFGD	261	1.4000	15.91
28	LHHAPSLLA	309	1.3000	14.77
29	LEFRSPDSS	364	1.2000	13.64
30	IEPQAPVDK	394	1.2000	13.64
31	ILEKGHHEV	211	1.1000	12.50
32	IIKNTAWQN	247	1.0000	11.36
33	IGGLLHHAP	305	1.0000	11.36
34	LLAFTNPTV	315	1.0000	11.36
35	LRDKMLTNL	197	0.9600	10.91
36	YKVRHKGGY	177	0.9000	10.23
37	VRIPITGSN	350	0.9000	10.23
38	IEPVNIRPH	459	0.9000	10.23
39	VFKLAKDEK	8	0.8000	9.09
40	LEPYSRDPR	100	0.8000	9.09
41	WQNGKTVTF	253	0.8000	9.09
42	WISFKRENE	450	0.8000	9.09
43	VDLRDKMLT	195	0.7000	7.95
44	INYQFNSLL	227	0.6600	7.50
45	ISFKRENEI	451	0.6000	6.82
46	IFDSVSFDS	137	0.5000	5.68
47	VSFDSRANG	141	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVYSQRNRS	339	4.5000	51.14
2	MQHFTIPAS	31	3.5000	39.77
3	VRFCDLPGI	22	3.3000	37.50

4	VTFMPKPLF	259	3.3000	37.50
5	FRAAKTLNI	82	3.0000	34.09
6	YIIKNTAWQ	246	3.0000	34.09
7	IMQHFTIPA	30	2.9000	32.95
8	FYIFDSVSF	135	2.9000	32.95
9	FFVHDPFTL	92	2.8600	32.50
10	VNSYKRLVP	323	2.5000	28.41
11	VEYVDVRFC	17	2.4000	27.27
12	MHCHQSLWK	274	2.4000	27.27
13	IRGFQSIHE	57	2.3000	26.14
14	MLTNLINSG	201	2.3000	26.14
15	VYSQRNRSA	340	2.3000	26.14
16	LLHHAPSLL	308	2.2600	25.68
17	VRHKGGYFP	179	2.0000	22.73
18	YLAFSAMLM	376	1.9000	21.59
19	IETWISFKR	447	1.8000	20.45
20	INFFVHDPF	90	1.7000	19.32
21	YQFNSLLHA	229	1.7000	19.32
22	YKYIIKNTA	244	1.7000	19.32
23	MLMAGLDGI	382	1.7000	19.32
24	VNIRPHPYE	462	1.6000	18.18
25	IRPHPYEFA	464	1.6000	18.18
26	LYKYIIKNT	243	1.5000	17.05
27	FMPKPLFGD	261	1.4000	15.91
28	LHHAPSLLA	309	1.3000	14.77
29	LEFRSPDSS	364	1.2000	13.64
30	IEPQAPVDK	394	1.2000	13.64
31	ILEKGHHEV	211	1.1000	12.50
32	IIKNTAWQN	247	1.0000	11.36
33	IGGLLHHAP	305	1.0000	11.36
34	LLAFTNPTV	315	1.0000	11.36
35	LRDKMLTNL	197	0.9600	10.91
36	YKVRHKGGY	177	0.9000	10.23
37	VRIPITGSN	350	0.9000	10.23
38	IEPVNIRPH	459	0.9000	10.23
39	VFKLAKDEK	8	0.8000	9.09
40	LEPYSRDPR	100	0.8000	9.09
41	WQNGKTVTF	253	0.8000	9.09
42	WISFKRENE	450	0.8000	9.09
43	VDLRDKMLT	195	0.7000	7.95
44	INYQFNSLL	227	0.6600	7.50

45	ISFKRENEI	451	0.6000	6.82
46	IFDSVSFDS	137	0.5000	5.68
47	VSFDSRANG	141	0.5000	5.68

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	VNSYKRLVP	323	5.3000	54.08
2	IRGFQSIHE	57	5.0000	51.02
3	MQLYKYIIK	241	4.9000	50.00
4	LLAFTNPTV	315	4.7000	47.96
5	FYIFDSVSF	135	4.3000	43.88
6	VRFCDLPGI	22	4.2000	42.86
7	YLAFSAMLM	376	4.1800	42.65
8	LVYSQRNRS	339	4.0000	40.82
9	MQHFTIPAS	31	3.8500	39.29
10	FRAAKTLNI	82	3.7600	38.37
11	IMQHFTIPA	30	3.6600	37.35
12	LHHAPSLLA	309	3.5000	35.71
13	IRPHPYEFA	464	3.3000	33.67
14	FFVHDPFTL	92	3.1000	31.63
15	LYKYIIKNT	243	2.9500	30.10
16	YQFNSLLHA	229	2.9000	29.59
17	LLHHAPSLL	308	2.9000	29.59
18	MHCHQSLWK	274	2.7000	27.55
19	LHAADDMQL	235	2.6000	26.53
20	MLMAGLDGI	382	2.6000	26.53
21	LAFSAMLMA	377	2.5000	25.51
22	INFFVHDPF	90	2.4000	24.49
23	INYQFNSLL	227	2.3000	23.47
24	MLLLPDPET	68	2.2000	22.45
25	LEPYSRDPR	100	2.2000	22.45
26	VRIPITGSN	350	2.1600	22.04
27	LVPGYEAPI	329	2.1000	21.43
28	VFTNDLIET	441	2.1000	21.43
29	YKYIIKNTA	244	1.9000	19.39
30	IHESDMLLL	63	1.8000	18.37

31	VRHKGGYFP	179	1.8000	18.37
32	LTNLINSGF	202	1.6000	16.33
33	MAGLDGIKN	384	1.5000	15.31
34	IETWISFKR	447	1.5000	15.31
35	LFGDNGSGM	266	1.4800	15.10
36	LMYDETGYA	287	1.4600	14.90
37	VTFMPKPLF	259	1.4000	14.29
38	YLISTGIAD	117	1.3000	13.27
39	VPGYEAPIN	330	1.3000	13.27
40	YEFALYYDV	469	1.3000	13.27
41	INSGFILEK	206	1.2500	12.76
42	IDPFRAAKT	79	1.2000	12.24
43	ISGWWNTGA	157	1.2000	12.24
44	VDLRDKMLT	195	1.1000	11.22
45	LRDKMLTNL	197	1.1000	11.22
46	YIGGLLHHA	304	1.1000	11.22
47	INLVYSQRN	337	1.1000	11.22

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	FYIFDSVSF	135	5.3000	54.08
2	YLAFSAMLM	376	5.1800	52.86
3	FRAAKTLNI	82	4.7600	48.57
4	VNSYKRLVP	323	4.3000	43.88
5	FFVHDPFTL	92	4.1000	41.84
6	IRGFQSIHE	57	4.0000	40.82
7	YQFNSLLHA	229	3.9000	39.80
8	MQLYKYIIK	241	3.9000	39.80
9	LLAFTNPTV	315	3.7000	37.76
10	VRFCDLPGI	22	3.2000	32.65
11	LVYSQRNRS	339	3.0000	30.61
12	YKYIIKNTA	244	2.9000	29.59
13	MQHFTIPAS	31	2.8500	29.08
14	IMQHFTIPA	30	2.6600	27.14
15	LHHAPSLLA	309	2.5000	25.51
16	YLISTGIAD	117	2.3000	23.47

17	IRPHPYEFA	464	2.3000	23.47
18	YEFALYYDV	469	2.3000	23.47
19	YIGGLLHHA	304	2.1000	21.43
20	WISFKRENE	450	2.1000	21.43
21	LYKYIIKNT	243	1.9500	19.90
22	LLHHAPSLL	308	1.9000	19.39
23	FRSPDSSGN	366	1.8000	18.37
24	YSRDPRNIA	103	1.7000	17.35
25	MHCHQSLWK	274	1.7000	17.35
26	LHAADDMQL	235	1.6000	16.33
27	MLMAGLDGI	382	1.6000	16.33
28	WQNGKTVTF	253	1.5600	15.92
29	YEAPINLVY	333	1.5000	15.31
30	LAFSAMLMA	377	1.5000	15.31
31	INFFVHDPF	90	1.4000	14.29
32	FQSIHESDM	60	1.3800	14.08
33	FKLAKDEKV	9	1.3000	13.27
34	INYQFNSLL	227	1.3000	13.27
35	FSAMLMAGL	379	1.3000	13.27
36	YVDVRFCDL	19	1.2000	12.24
37	MLLLPDPET	68	1.2000	12.24
38	LEPYSRDPR	100	1.2000	12.24
39	YSQRNRSAC	341	1.2000	12.24
40	VRIPITGSN	350	1.1600	11.84
41	YVDLRDKML	194	1.1000	11.22
42	LVPGYEAPI	329	1.1000	11.22
43	VFTNDLIET	441	1.1000	11.22
44	FGAEAEFYI	129	1.0000	10.20
45	WNTGAATEA	161	1.0000	10.20
46	YLTEGGVFT	435	1.0000	10.20
47	IHESDMLLL	63	0.8000	8.16

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VNSYKRLVP	323	5.3000	54.08
2	IRGFQSIHE	57	5.0000	51.02

3	MQLYKYIIK	241	4.9000	50.00
4	LLAFTNPTV	315	4.7000	47.96
5	FYIFDSVSF	135	4.3000	43.88
6	VRFCDLPGI	22	4.2000	42.86
7	YLAFSAMLM	376	4.1800	42.65
8	LVYSQRNRS	339	4.0000	40.82
9	MQHFTIPAS	31	3.8500	39.29
10	FRAAKTLNI	82	3.7600	38.37
11	IMQHFTIPA	30	3.6600	37.35
12	LHHAPSLLA	309	3.5000	35.71
13	IRPHPYEFA	464	3.3000	33.67
14	FFVHDPFTL	92	3.1000	31.63
15	LYKYIIKNT	243	2.9500	30.10
16	YQFNSLLHA	229	2.9000	29.59
17	LLHHAPSLL	308	2.9000	29.59
18	MHCHQSLWK	274	2.7000	27.55
19	LHAADDMQL	235	2.6000	26.53
20	MLMAGLDGI	382	2.6000	26.53
21	LAFSAMLMA	377	2.5000	25.51
22	INFFVHDPF	90	2.4000	24.49
23	INYQFNSLL	227	2.3000	23.47
24	MLLLPDPET	68	2.2000	22.45
25	LEPYSRDPR	100	2.2000	22.45
26	VRIPITGSN	350	2.1600	22.04
27	LVPGYEAPI	329	2.1000	21.43
28	VFTNDLIET	441	2.1000	21.43
29	YKYIIKNTA	244	1.9000	19.39
30	IHESDMLLL	63	1.8000	18.37
31	VRHKGGYFP	179	1.8000	18.37
32	LTNLINSGF	202	1.6000	16.33
33	MAGLDGIKN	384	1.5000	15.31
34	IETWISFKR	447	1.5000	15.31
35	LFGDNGSGM	266	1.4800	15.10
36	LMYDETGYA	287	1.4600	14.90
37	VTFMPKPLF	259	1.4000	14.29
38	YLISTGIAD	117	1.3000	13.27
39	VPGYEAPIN	330	1.3000	13.27
40	YEFALYYDV	469	1.3000	13.27
41	INSGFILEK	206	1.2500	12.76
42	IDPFRAAKT	79	1.2000	12.24
43	ISGWWNTGA	157	1.2000	12.24

44	VDLRDKMLT	195	1.1000	11.22
45	LRDKMLTNL	197	1.1000	11.22
46	YIGGLLHHA	304	1.1000	11.22
47	INLVYSQRN	337	1.1000	11.22

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	YFPVAPNDQ	185	3.6000	36.73
2	MQLYKYIIK	241	3.5000	35.71
3	FRAAKTLNI	82	3.2000	32.65
4	IPITGSNPK	352	3.0000	30.61
5	FFVHDPFTL	92	2.9000	29.59
6	YKRLVPGYE	326	2.6000	26.53
7	ITGSNPKAK	354	2.5000	25.51
8	FYEVDAISG	151	2.4000	24.49
9	FYIFDSVSF	135	2.2000	22.45
10	YKYIIKNTA	244	2.2000	22.45
11	INLVYSQRN	337	2.1000	21.43
12	VRFCDLPGI	22	1.6000	16.33
13	YVDLRDKML	194	1.6000	16.33
14	YAGLSDTAR	294	1.6000	16.33
15	YVDVRFCDL	19	1.5000	15.31
16	YLISTGIAD	117	1.4000	14.29
17	YFGAEAEFY	128	1.4000	14.29
18	IEPVNIRPH	459	1.4000	14.29
19	LVYSQRNRS	339	1.3000	13.27
20	YLAFSAMLM	376	1.3000	13.27
21	IEPQAPVDK	394	1.3000	13.27
22	MHCHQSLWK	274	1.2000	12.24
23	FSAMLMAGL	379	1.2000	12.24
24	IETWISFKR	447	1.2000	12.24
25	FILEKGHHE	210	1.1000	11.22
26	VEYVDVRFC	17	1.0000	10.20
27	FQSIHESDM	60	1.0000	10.20
28	VRIPITGSN	350	1.0000	10.20
29	FCDLPGIMQ	24	0.9000	9.18

30	IRGFQSIHE	57	0.9000	9.18
31	YEFALYYDV	469	0.9000	9.18
32	YIIKNTAWQ	246	0.8000	8.16
33	MAGLDGIKN	384	0.7000	7.14
34	VTFMPKPLF	259	0.6000	6.12
35	LAFTNPTVN	316	0.6000	6.12
36	YKVRHKGGY	177	0.3000	3.06
37	INSGFILEK	206	0.3000	3.06
38	IKNTAWQNG	248	0.3000	3.06
39	WKDGAPLMY	281	0.3000	3.06
40	LIETWISFK	446	0.3000	3.06
41	WQNGKTVTF	253	0.2000	2.04
42	FRSPDSSGN	366	0.2000	2.04
43	VFKLAKDEK	8	0.1000	1.02
44	WWNTGAATE	160	0.1000	1.02
45	LLHHAPSLL	308	0.1000	1.02
46	LHHAPSLLA	309	0.1000	1.02
47	MLMAGLDGI	382	0.1000	1.02

ALLELE: DRB5_0105	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	YFPVAPNDQ	185	3.6000	36.73
2	MQLYKYIIK	241	3.5000	35.71
3	FRAAKTLNI	82	3.2000	32.65
4	IPITGSNPK	352	3.0000	30.61
5	FFVHDPFTL	92	2.9000	29.59
6	YKRLVPGYE	326	2.6000	26.53
7	ITGSNPKAK	354	2.5000	25.51
8	FYEVDAISG	151	2.4000	24.49
9	FYIFDSVSF	135	2.2000	22.45
10	YKYIIKNTA	244	2.2000	22.45
11	INLVYSQRN	337	2.1000	21.43
12	VRFCDLPGI	22	1.6000	16.33
13	YVDLRDKML	194	1.6000	16.33
14	YAGLSDTAR	294	1.6000	16.33
15	YVDVRFCDL	19	1.5000	15.31

16	YLISTGIAD	117	1.4000	14.29
17	YFGAEAEFY	128	1.4000	14.29
18	IEPVNIRPH	459	1.4000	14.29
19	LVYSQRNRS	339	1.3000	13.27
20	YLAFSAMLM	376	1.3000	13.27
21	IEPQAPVDK	394	1.3000	13.27
22	MHCHQSLWK	274	1.2000	12.24
23	FSAMLMAGL	379	1.2000	12.24
24	IETWISFKR	447	1.2000	12.24
25	FILEKGHHE	210	1.1000	11.22
26	VEYVDVRFC	17	1.0000	10.20
27	FQSIHESDM	60	1.0000	10.20
28	VRIPITGSN	350	1.0000	10.20
29	FCDLPGIMQ	24	0.9000	9.18
30	IRGFQSIHE	57	0.9000	9.18
31	YEFALYYDV	469	0.9000	9.18
32	YIIKNTAWQ	246	0.8000	8.16
33	MAGLDGIKN	384	0.7000	7.14
34	VTFMPKPLF	259	0.6000	6.12
35	LAFTNPTVN	316	0.6000	6.12
36	YKVRHKGGY	177	0.3000	3.06
37	INSGFILEK	206	0.3000	3.06
38	IKNTAWQNG	248	0.3000	3.06
39	WKDGAPLMY	281	0.3000	3.06
40	LIETWISFK	446	0.3000	3.06
41	WQNGKTVTF	253	0.2000	2.04
42	FRSPDSSGN	366	0.2000	2.04
43	VFKLAKDEK	8	0.1000	1.02
44	WWNTGAATE	160	0.1000	1.02
45	LLHHAPSLL	308	0.1000	1.02
46	LHHAPSLLA	309	0.1000	1.02
47	MLMAGLDGI	382	0.1000	1.02